Fungal Planet description sheets: 558–624

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Key words
- ITS nrDNA barcodes
- LSU
- novel fungal species
- systematics

Abstract
Novel species of fungi described in this study include those from various countries as follows: Australia: Banksiotheca australiensis (incl. Banksiotheca cervicisides), Didymiellomyces austeni (incl. Didymiellomyces gen. nov.) on Cypereacea, Didymocyrtis banksiae on Banksia sessilis var. cygnorum, Disculoidea calophyllae on Corymbia calophylla, Hawknessia banksiae on Banksia sessilis, Hawknessia banksiae-repens on Banksia repens, Hawknessia banksiigena on Banksia sessilis var. cygnorum, Hawknessia communis on Podocarpus sp., Hawknessia platyphyllae on Eucalyptus platyphylla, Mytracremoinium eucalypti (incl. Mytracremoinium gen. nov.) on Eucalyptus globulus, Myrtapenidiella baeleariae on Eucalyptus sp., Myrtapenidiella eucalyptigena on Eucalyptus sp., Myrtapenidiella pleurocarpae on Eucalyptus pleurocarpa, Paraconiothyrium hakeae on Hakea sp., Paraphaeosphaeria xanthorrhoeae on decayed wood, and Phytomyces podocarpi (incl. Phytomyces gen. nov.) on Podocarpus sp., Readereilla ellippoidea on Eucalyptus sp., Rosellinia caesiariesensis on Banksia grandis, Tiarosporella corti on Corymbia calophylla, Verruconiothecium eucalyptigenum on Eucalyptus sp., Zasmidium commune on Xanthorrhoea sp., and Zasmidium podocarpi on Podocarpus sp.

Brazil: Cyathus aurantogriseocarpus on decayed wood, Perenniporia brasiliensis on decayed wood, Perenniporia paraguayensis on decayed wood, and Pseudocerocpora leandreae-fraggis on Leandra fragilis. China: Phialocephala cladorhizophoroides on human toe nail. Costa Rica: Pithryhnella striatoplastula from soil. Czech Republic: Mycopsis crema (incl. Mycotisina gen. nov.) on bat droppings. Ecuador: Humidicidioctis dicotrophes from soil, Hygrocybe macrosporaria from soil, Hygrocybe sangayensis from soil, and Polycephalomyces onorei on stem of Etingera sp. France: Westerdykella centenaria from soil. Hungary: Tubercagriptum from soil. India: Ganoderma mizoramense on decayed wood, Holodocys indicus from soil, Keratinophyton turigum in soil, and Russula aruni on Pterigota alata. Italy: Rhodocybe matiesina from soil. Malaysia: Apoharknessia eucalyptorum, Hawknessia mahavansis, Hawknessia pellitae, and Peyronellaea eucalypti on Eucalyptus cajuputi, Lectera capsici on Capsicum annuum, and Wallrothiella gmelinae on Gmelina arborea. Morocco: Neocordana musigena on Musa sp.

New Zealand: Acidiella americana on decayed wood, and Candida rongomai-pounamu on cup fungus. Poland: herbicola from soil. Portugal: Cylindrocladiella vitis on Vitis vinifera, Foliocyrtis eucalyptorum on Eucalyptus sp., Ramularia vacciniocola on Vaccinium sp., and Rhotorutulina ngohengohe on bird feather surface. Russia: Paraphoma rhaphiolepis on Rhaphiolepis indicus. USA: Acidiiella americana from wall of a cooling tower, Neodactylaria obpyriformis from human toe nail, and Saksenaea loutrophoriformis from soil. Vietnam: Phytophthora mekongensis from Citrus grandis, and Phytophthora prodigiosa from Citrus grandis. Morphological and culture characteristics along with DNA barcodes are provided.

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The alignment and tree were deposited in TreeBASE (Submission ID S20946).

Saccharata proteae

Overview Pezizomycetes, Eurotiales and Sordariomycetes phylology

Consensus phylogram (50% majority rule) of 21,302 trees resulting from a Bayesian analysis of the LSU sequence alignment (78 taxa including outgroup; 825 aligned positions; 368 unique site patterns) using MrBayes v. 3.2.6 (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 or Fungal Planet numbers are indicated behind the species names. The tree was rooted to Saccharata proteae (GenBank EU552145.1) and the taxonomic novelties 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 S20946).
Consensus phylogram (50% majority rule) of 16 202 trees resulting from a Bayesian analysis of the LSU sequence alignment (166 taxa including outgroup; 769 aligned positions; 300 unique site patterns) using MrBayes v. 3.2.6 (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 the following abbreviations: Botryosphaeriaceae, Capnodiales, Dothideomycetes, Mycosphaerellaceae, Pseudocercosporaceae (Fungal Planet 579). The tree was rooted to Botryosphaeria dothidea (GenBank HM469430.1) and the taxonomic novelties 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 S20946).
Overview Mucoromycotina, Pucciniomycotina, Saccharomycotina and Agaricomycotina phylogeny

Consensus phylogram (50% majority rule) of 64,278 trees resulting from a Bayesian analysis of the LSU sequence alignment (90 taxa including outgroup; 838 aligned positions; 611 unique site patterns) using MrBayes v. 3.2.6 (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 or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Phytophthora moyootj* (GenBank KP004499.1) and the taxonomic novelties 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 S20946).
Overview Mucoromycotina, Pucciniomycotina, Saccharomycotina and Agaricomycotina phylogeny (cont.)
Westerdykella centenaria
**Westerdykella centenaria** Crous, van Diepeningen & A.-C. Normand, sp. nov.

**Etymology.** Name reflects the 100th anniversary of the appointment of Prof. dr Johanna Westerdijk, the first female professor in the Netherlands, appointed at Utrecht University on the 10th of February 1917; centenaria = 100 years (1917–2017).

**Classification —** Sporormiaceae, Pleosporales, Dothideomycetes.

Conidiomata erumpent, subglobose, 100–200 µm diam on SNA, solitary, or in clusters of 2–3, pale to medium brown, uni- to multilocular, with 1–2 dark brown ostioles, 10–15 µm diam, exuding a creamy conidial mass. On OA conidiomata arranged in concentric circles, aggregated in clusters, dark brown, mostly unilocular, outer wall smooth, lacking setae; wall of 5–8 layers of brown textura angularis. Conidiophores reduced to conidiogenous cells. Conidiogenous cells lining the inner cavity, hyaline, smooth, ampulliform to doliform, 4–6 × 3–5 µm; phialidic with inconspicuous periclinal thickening at apex, or at times with percurrent proliferation. Conidia solitary, hyaline, smooth, granular, with large central guttule, clavate to ellipsoid or somewhat irregular, apex obtuse, base truncate, 1.5–2 µm diam, (3–)4–(4.5) × (2.5–)3 µm.

**Culture characteristics —** Colonies flat, spreading, with sparse aerial mycelium, sporulating in brown concentric circles; surface and margins smooth, reaching 60 mm diam after 3 wk at 25 °C. On OA surface umber with patches of orange. On PDA surface isabelline with patches of orange. On culture similar.

**Typus.** FRANCE, Marseille, public hospital, laboratory bench in sterile preparation ‘clean room’, 2016, A.-C. Normand (holotype CBS H-23075, culture ex-type CPC 31368 = CBS 142400, ITS, LSU, and tub2 sequences GenBank KY979734, KY979790, and KY979908, MycoBank MB820928).

Additional specimen examined. KUWAIT, Gulf of Kuwait, from saline soil, Aug. 1973, A.F. Moustafa, specimen CBS H-16164, culture CBS 262.74, ITS sequence GenBank KY979735.

Notes — Stolk (1955) introduced the genus Westerdykella based on a fungal isolate collected from soil in Mozambique by H.J. Swart. Westerdykella was named in honour of the then director of the Centraalbureau voor Schimmelcultures in Baarn (now Westerdijk Fungal Biodiversity Institute in Utrecht), the Netherlands. Species of Westerdykella occur on a wide range of substrates, including soil, dung, plant debris, and algae (Ebead et al. 2012), have been shown to exhibit antibiotic activity (Poch & Gloer 1991), but also to cause infections in immunocompromised patients (Sue et al. 2014). Delimitation of species in the genus has traditionally been based on the presence of the sexual morph, although some species (as in the case of *W. centenaria*) are known to produce a phoma-like asexual morph. Ten species are recognised in the genus, and although the majority are sexual, *W. centenaria* is clearly distinct based on its DNA data (ITS: highest similarities are with unnamed isolates from soil in Oman, e.g. 500/508 (98 %) identity, 1 gap (0 %), with GenBank KU945963; closest named species is *Westerdykella reniformis* GenBank KM678366, 409/436 (94 %) identity, 6 gaps (1 %)). On LSU, the best match is *Westerdykella cylindrica* GenBank NG_027595, 862/880 (98 %) identity, 1 gap (0 %), and on tub2, the best match is *Westerdykella dispersa* GenBank KJ413346, 308/366 (84 %) identity, 5 gaps (1 %)).
Davidiellomyces Crous, gen. nov.

Etymology. Named for Dr John C. David, recognising his contribution to our knowledge of the genus Cladosporium and its sexual morph.

Classification — Cladosporiaceae, Capnodiales, Dothideomycetes.

Ascomata pseudothecial, on dead leaves, amphigenous, black, subepidermal, globose; apical ostiole; wall consisting of 2–3 layers of medium brown textura angularis. Asci apophysate, fasciculate, bitunicate, subsessile, obovoid to broadly ellipsoid, straight to slightly curved, 8-spored. Ascospores multisieriate, overlapping, hyaline, prominently guttulate with angular inclusions, thick-walled, straight, fusoid-ellipsoidal with obtuse ends, widest above septum, medianly 1-septate; enclosed in a mucoid sheath (also visible inside asci), and becoming brown and verruculose in older asci.

Type species. Davidiellomyces australiensis Crous.

MycoBank MB820929.

Davidiellomyces australiensis Crous, sp. nov.

Etymology. Name refers to Australia, the country where this fungus was collected.

Ascomata pseudothecial, on dead leaves, amphigenous, black, subepidermal, globose, 70–120 µm diam; apical ostiole 5–10 µm diam; wall consisting of 2–3 layers of medium brown textura angularis. Asci apophysate, fasciculate, bitunicate, subsessile, obovoid to broadly ellipsoid, straight to slightly curved, 8-spored, 30–40 × 7–12 µm. Ascospores multisieriate, overlapping, hyaline, prominently guttulate with angular inclusions, thick-walled, straight, fusoid-ellipsoidal with obtuse ends, widest above septum, medianly 1-septate, constricted at the septum, tapering towards both ends, but more prominently towards lower end, (12–)13–15(–16) × (3–)3.5 µm; enclosed in a mucoid sheath (also visible inside asci), and becoming brown and verruculose in older asci.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium; surface folded, margins smooth, lobate, reaching 20 mm diam after 2 wk at 25 °C. On MEA surface ochreous, reverse sienna. On OA surface saffron. On PDA surface luteous, reverse pale luteous. Germinating from both ends, and elsewhere (irregular); ascospores becoming brown, verruculose, constricted at septum, 5–6 µm diam, with prominent mucoid sheath.

Types. AUSTRALIA, Western Australia, S35°01.320’E117°16.598, on leaves of Cyperaceae, 19 Sept. 2015, P.W. Crous (holotype CBS H-23077, culture ex-type CPC 29168 = CBS 141265; ITS, LSU, and actA sequences GenBank KY979736, KY979791, and KY979863, MycoBank MB820930); CPC 29170 ITS and LSU sequences GenBank KY979737, KY979792.

Notes — The isolates (sexual morph, no asexual morph observed in culture) included in this study cluster close to Toxicocladosporium (Crous et al. 2007b; see phylogeny in Bezerra et al. 2017), but are not congeneric with the genus Toxicocladosporium s.str., being separated by clades representing Cladosporium and Neocladosporium. This suggests that the present collection represents yet another genus in the Cladosporiaceae (see Bensch et al. 2012 for generic overview). Interestingly, ascospores of Davidiellomyces have angular inclusions such as those observed in ascospores of Cladosporium s.str. (see Crous et al. 2007b, Bensch et al. 2010), which appears to be a conserved character in the Cladosporiaceae. However, based on a megablast search of the NCBIs GenBank nucleotide database using the ITS sequence, the closest Cladosporium sequences have less than 90 % similarity over almost 500 nucleotides.
Paraphaeosphaeria xanthorrhoeae
**Paraphaeosphaeria xanthorrhoeae** Crous, sp. nov.

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

**Classification.** Didymosphaeriaceae, Pleosporales, Dothideomycetes.

Conidiomata erumpent, globose, pycnidial, brown, 80–150 µm diam, with central ostiole; wall of 3–5 layers of brown textura angularis. Conidiophores reduced to conidiogenous cells. Conidiogenous cells lining the inner cavity, hyaline, smooth, ampulliform, phialidic with periclinal thickening or percurrent proliferation at apex, 5–8 x 4–6 µm. Conidia solitary, golden brown, ellipsoid with obtuse ends, thick-walled, roughened, (6–) 7–8(–9) x (3–)3.5 µm.

**Culture characteristics.** Colonies flat, spreading, covering dish in 2 wk at 25 °C, surface folded, with moderate aerial mycelium and smooth margins. On MEA surface dirty white, reverse luteous. On OA surface dirty white with patches of luteous. On PDA surface dirty white, reverse apricot.

**Typus.** Australia, Western Australia, Denmark, Lights Beach, on Xanthorrhoea sp. (Xanthorrhoeaceae), 19 Sept. 2015, P.W. Crous (holotype CBS H-23120, culture ex-type CPC 29244 = CBS 142164; ITS, LSU, rpb2, tef1, and tub2 sequences GenBank KY979738, KY979793, KY979845, KY979888, and KY979909, MycoBank MB820931).

Notes — The genus *Paraconiothyrium* (based on *P. estuari-num*) was established by Verkley et al. (2004) to accommodate several microsphaeropsis-like coelomycetes, some of which had proven abilities to act as biocontrol agents of other fungal pathogens. In a recent study, Verkley et al. (2014) revealed *Paraconiothyrium* to be paraphyletic, and separated the genus from *Alloconiothyrium*, *Dendrothyrium*, and *Paraphaeosphaeria*. *Paraphaeosphaeria xanthorrhoeae* resembles asexual morphs of *Paraphaeosphaeria*, having pycnidial conidiomata with percurrently proliferating conidiogenous cells and aseptate, brown, roughened conidia. Phylogenetically, it is distinct from all taxa presently known to occur in the genus, the closest species on ITS being *Paraphaeosphaeria sporulosa* (GenBank JX496114; Identities = 564/585 (96 %), 4 gaps (0 %)).

**Colour illustrations.** Dead Xanthorrhoea sp.; conidiomata sporulating on PNA and OA (scale bars = 150 µm); conidiogenous cells and conidia (scale bars = 10 µm).
**Banksiophoma** Crous, *gen. nov.*

*Etymology.* Banksia (host), and Phoma (morphology).

*Classification.* Phaeosphaeriaceae, Pleosporales, Dothideomycetes.

Conidiomata pycnidial, brown, globose, with central ostiole, somewhat aggregated with a brown stroma on PNA; wall of 3–6 layers of brown textura angularis. Conidiophores reduced to conidiogenous cells or with a supporting cell lining the inner cavity, hyaline, smooth, subcylindrical to ampulliform; proliferating percurrently at apex. *Conidia* solitary, hyaline, smooth, guttulate, aseptate, ellipsoid to globose or subglobose.

*Type species.* *Banksiophoma australiensis* Crous.

MycoBank MB820932.

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**Banksiophoma australiensis** Crous, *sp. nov.*

*Etymology.* Name refers to Australia where this fungus was collected.

Conidiomata pycnidial, brown, globose, 90–120 µm diam, with central ostiole, somewhat aggregated with a brown stroma on PNA; wall of 3–6 layers of brown textura angularis. Conidiophores reduced to conidiogenous cells or with a supporting cell lining the inner cavity, hyaline, smooth, subcylindrical to ampulliform, 5–12 × 3–5 µm; proliferating percurrently at apex. *Conidia* solitary, hyaline, smooth, guttulate, aseptate, ellipsoid to globose or subglobose, (3–)4(–5) × (2.5–)3(–3.5) µm.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium and smooth, lobate margins, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface greyish sepia, reverse fulvous to ochreous. On OA surface greyish sepia. On PDA surface and reverse umber.

*Typus.* AUSTRALIA, Western Australia, Gull Rock, Albany, on leaves of *Banksia coccinea* (Proteaceae), 20 Sept. 2015, P.W. Crous (holotype CBS H-23121, culture ex-type CPC 20192 = CBS 142163; ITS, LSU rpb2, tef1, and tub2 sequences GenBank KY979739, KY979794, KY979846, KY979889, and KY979910, MycoBank MB820933).

Notes — The Proteaceae appears to harbour an unusually large number of new fungal genera (Crous et al. 2011), as was recently shown with the description of a new order of Dothideomycetes, namely Superstratomycetales, and the phoma-like species *Superstratomyces flavomucosus* occurring on *Hakea* (Van Nieuwenhuijzen et al. 2016). The present collection represents yet another phoma-like genus on Proteaceae, this time occurring on Banksia. *Banksiophoma* appears to be distantly related to *Neosetophoma* (De Gruyter et al. 2010). Only distant hits (less than 93 % similarity) with phaeosphaeria-like sequences were obtained from a megablast search of the NCBI GenBank nucleotide database; the LSU sequence was 99 % identical to species in numerous different genera, e.g. *Loratospora aestuarii* (GenBank GU301838), *Neosetophoma italic* (GenBank KP711361), and *Diederichomyces cladoniicola* (GenBank LN907482).
Perthomyces podocarpi
**Perthomyces** Crous, *gen. nov.*

*Etymology.* Named for the city of Perth, Australia, where this fungus was collected.

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

*Conidiomata* solitary, erumpent, globose, dark brown with central ostiole, exuding a white conidial mass; wall of 3–8 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, ampulliform to doliform or subcylindrical, phialidic with periclinal thickening or tightly aggregated, percurrent proliferations. *Conidia* solitary, hyaline, smooth, guttulate, aseptate, subcylindrical with obtuse ends, straight.

*Type species.* *Perthomyces podocarpi* Crous. MycoBank MB820934.

**Perthomyces podocarpi** Crous, *sp. nov.*

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

*Conidiomata* solitary, erumpent, globose, 200–250 µm diam, dark brown with central ostiole, exuding a white conidial mass; wall of 3–8 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, ampulliform to doliform or subcylindrical, 4–10 × 2.5–5 µm, phialidic with periclinal thickening or tightly aggregated, percurrent proliferations. *Conidia* solitary, hyaline, smooth, guttulate, aseptate, subcylindrical with obtuse ends, straight, (5–)6(–7) × 2(–2.5) µm.

*Culture characteristics.*—Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margins. On MEA surface pale grey olivaceous with diffuse brown pigment, reverse pale olivaceous grey. On OA surface olivaceous grey. On PDA surface and reverse olivaceous grey.

*Typus.* **AUSTRALIA**, Western Australia, Perth, King’s Park Botanic Gardens, on leaves of *Podocarpus* sp. (*Podocarpaceae*), 27 Sept. 2015, P.W. Crous (holotype CBS H-23122, culture ex-type CPC 28972 = CBS 142162; ITS, LSU, and tub2 sequences GenBank KY979740, KY979795, and KY979911, MycoBank MB820936).

*Notes.* *Perthomyces* is a phoma-like genus in the Pleosporales (Chen et al. 2015), being phylogenetically related to *Camarographium koreanum* (GenBank JQ044451; Identities = 813/834 (96 %), 2 gaps (0 %)), *Corynespora olivacea* (GenBank JQ044448; Identities = 810/834 (97 %), 1 gap (0 %)), and *Massaria platani* (GenBank DQ678065; Identities = 811/836 (97 %), 2 gaps (0 %)) based on its LSU sequence. Highest similarities based on ITS are for species of *Darksidea*, e.g. *Darksidea alpha* (GenBank JN859354; Identities = 404/441 (92 %), 7 gaps (1 %)).

**Colour illustrations.** Symptomatic leaves of *Podocarpus* sp.; conidiomata sporulating on PDA (scale bar = 250 µm), conidiogenous cells and conidia (scale bars = 10 µm).

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Myrtacremonium eucalypti
Fungal Planet 563 – 20 June 2017

**Myrtacremonium** Crous, *gen. nov.*

*Etymology.* Name reflects the host family Myrtaceae, and the fact that the fungus has an acremonium-like morphology.

*Classification —* Niessliaceae, Hypocreales, Sordariomycetes.

*Mycelium* consisting of hyaline, smooth, septate, branched, hyphae. *Conidiophores* solitary, erect, straight to flexuous, hyaline, smooth, with basal septum. *Conidiogenous cells* terminal, integrated, hyaline, smooth, thick-walled at base, subcylindrical; apex phialidic, with minute flared collarette. **Conidia** solitary, but accumulating in slimy mass, hyaline, smooth, subcylindrical, straight with obtuse ends.

**Type species.** Myrtacremonium eucalypti Crous. MycoBank MB820937.

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**Myrtacremonium eucalypti** Crous, *sp. nov.*

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

*Mycelium* consisting of hyaline, smooth, septate, branched, 1.5–2 µm diam hyphae. *Conidiophores* solitary, erect, straight to flexuous, hyaline, smooth, with basal septum, 20–60 × 2–3 µm. *Conidiogenous cells* terminal, integrated, hyaline, smooth, thick-walled at base, subcylindrical, 15–55 × 2–2.5 µm; apex phialidic, 1–1.5 µm diam with minute flared collarette. **Conidia** solitary, but accumulating in slimy mass, hyaline, smooth, subcylindrical, straight with obtuse ends, (5–)6–7(–8) × 1.5 µm.

*Culture characteristics —* Colonies flat, spreading, reaching 10–20 mm diam after 2 wk at 25 °C, with sparse aerial mycelium, folded surface, and smooth, lobed margins. On MEA surface and reverse buff. On OA surface pale luteous to luteous. On PDA surface and reverse pale luteous.

**Typus.** *AUSTRALIA,* Western Australia, Perth, on leaves of Eucalyptus globulus (Myrtaceae), 21 Sept. 2015, P.W. Crous (holotype CBS H-23123, culture ex-type CPC 29272 = CBS 142161, ITS, LSU, and tub2 sequences GenBank KY979741, KY979796, and KY979912, MycoBank MB820938).

*Notes —* Myrtacremonium is a new genus in the Acremonium complex (Gräfenhan et al. 2011, Lombard et al. 2015). Phylogenetically, it is related to *Eucapsphaeria* (e.g. *E. rustici*, LSU GenBank KY173501; Identities = 767/785 (98 %), 2 gaps (0 %)), *Niesslia* (e.g. *N. exilis*, LSU GenBank AY489718; Identities = 762/798 (98 %), 2 gaps (0 %)), and *Rosasphaeria* (e.g. *R. moravica*, LSU GenBank JF440985; Identities = 782/798 (98 %), 2 gaps (0 %)), although it appears to cluster apart (only distant hits were also obtained when the ITS sequences were compared).

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*Colour illustrations. Eucalyptus globulus; colony on SNA, conidiophores and conidia. Scale bars = 10 µm.*
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**Rosellinia australiensis** Crous & Barber, *sp. nov.*

**Etymology.** Name refers to Australia, the country from which this fungus was collected.

**Classification — Xylariaceae, Xylariales, Sordariomycetes.**

_Mycelium_ consisting of superficial to immersed, branched, septate, hyaline to pale brown, smooth, 3–4 µm diam hyphae. _Conidiophores_ erect, straight to flexuous, branched, septate, indeterminate, with numerous lateral branches, brown, warty, 4–5 µm diam. _Conidiogenous cells_ integrated, terminal or intercalary, subcylindrical to clavate, pale brown, smooth, 5–12 × 4–5.5 µm, with several terminal, hyaline denticles, 0.5 µm diam, inconspicuous, not thickened nor darkened. _Conidia_ solitary, rhexolytic conidiogenesis, acrogenous, obovate to broadly ellipsoid, guttulate, thin-walled, aseptate, brown, smooth; hilum truncate, 1.5 µm diam, not thickened nor darkened, (8–)9(–10) × (6.5–)7(–8) µm.

**Culture characteristics —** Colonies covering dish after 7 d at 25 °C, with fluffy aerial mycelium. On MEA and OA surface olivaceous grey, reverse umber. On PDA surface and reverse dirty white.

**Typus.** AUSTRALIA, Western Australia, Perth, Chichester Park, on Banksia grandis litter, 15 June 2015, P.A. Barber (holotype CBS H-23124, culture ex-type CPC 27694 = CBS 142160, ITS and LSU sequence GenBank KY979742 and KY979797, MycoBank MB820940).

**Additional isolates examined.** AUSTRALIA, Western Australia, Perth, Bedfordale, Hakea sp. (Proteaceae), 29 Sept. 2015, P.W. Crous, culture CPC 29482 = CBS 142079, ITS and LSU sequence GenBank KY979744 and KY979799; Western Australia, Perth, King’s Park Botanic Gardens, on Eucalyptus lane-poolei (Myrtaceae), 27 Sept. 2015, M.J. Wingfield, culture CPC 29422 = CBS 142078, ITS and LSU sequence GenBank KY979743 and KY979798.

Notes — _Rosellinia australiensis_ is known only by its asexual morph, which is hansfordia- to nodulisporium-like in morphology. Phylogenetically, however, it clusters among several species of _Rosellinia_, consequently a name in this genus was chosen for it. There is considerable confusion regarding the sexual and asexual morphs in _Xylariales_, and sequence data are required for a greater number of taxa in order to produce a solid taxonomic backbone for the order. Based on a megablast search using the ITS sequence of the ex-type culture, the best matches were with _R. thelena_ (GenBank KF719202; Identities = 491/513 (96 %), 9 gaps (1 %)), _R. aquila_ (GenBank KY610392; Identities = 494/518 (95 %), 11 gaps (2 %)), and _R. corticium_ (GenBank KT149736; Identities = 416/444 (94 %), 10 gaps (2 %)).

**Colour illustrations.** Banksia leaf litter; conidiophores and conidia on PNA. Scale bars = 10 µm.
Disculoides calophyllae
Fungal Planet 565 – 20 June 2017

Disculoideae calophyllae Crous, sp. nov.

Etymology. Name refers to Corymbia calophylla, the host from which this fungus was collected.

Classification — Incertae sedis, Diaporthales, Sordariomycetes.

Associated with Corymbia leaf litter. Conidiomata black, amphiogenous, subepidermal, acervular, opening by irregular rupture, 200–400 µm diam; wall of 6–10 layers of brown textura angularis. Conidiophores reduced to conidiogenous cells or 1–2-septate, 10–20 × 4–6 µm. Conidiogenous cells terminal and intercalary, hyaline, smooth, subcylindrical to ampulliform, tapering to a long thin neck, 10–15 × 3.5–4 µm, proliferating percurrently at apex, with minute flaring collarette. Conidia hyaline, smooth, thick-walled, guttulate, ellipsoid to fusoid, straight to curved, (9–)11–13(–15) × (4–)4.5(–5) µm; apex subobtuse, 1–1.5 µm diam, with minute marginal frill.

Cultural characteristics — Colonies flat, spreading, covering dish in 2 wk at 25 °C, with sparse aerial mycelium and feathery margins. On MEA surface and reverse buff, on OA surface olivaceous grey. On PDA surface and reverse dirty white with patches of olivaceous grey.

Typus. Australia, Western Australia, near Kojonup, on leaves of Corymbia calophylla (Myrtaceae), 18 Sept. 2015, P.W. Crous (holotype CBS H-23125, culture ex-type CPC 29246 = CBS 142080, ITS, LSU, cmrA, and tub2 sequences GenBank KY979745, KY979800, KY979866, and KY979913, MycoBank MB820941).

Notes — Disculoideae represents a genus of foliar pathogens of Corymbia and Eucalyptus (Crous et al. 2012a), which is presently known to accommodate three species. Disculoideae calophyllae is morphologically most similar to D. corymbiae (conidia 10–15 × 3.5–4.5 µm; Crous et al. 2016), although it is only 95 % similar to D. corymbiae (ITS GenBank KY173403; Identities = 397/420 (95 %), 9 gaps (2 %)), and 97 % similar to D. eucalyptorum (ITS GenBank JQ685518; Identities = 354/365 (97 %), 4 gaps (1 %)) and D. eucalypti (ITS GenBank NR_120089; Identities = 353/365 (97 %), 4 gaps (1 %)).
Parateratosphaeria stirlingiae
Parateratosphaeria stirlingiae Crous, sp. nov.

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

Classification — Teratosphaeriaceae, Capnodiales, Dothideomycetes.

Leaf spots amphigenous, irregular to subcircular, grey-brown with a raised dark brown border, 3–10 mm long, 2–4 mm wide. Pseudothecia amphigenous, black subepidermal, erumpent, globose, 70–90 µm diam; apical ostiole 5–10 µm diam; wall consisting of 2–3 layers of brown textura angularis. Asci ap paraphysate, fasciculate, bitunicate, subsessile, obovoid, straight to slightly curved, 8-spored, 25–30 × 10–11 µm. Ascospores tri- to multiseriate, overlapping, hyaline, guttulate, thin-walled, straight, obovoid, with obtuse ends, widest near middle of apical cell, medially 1-septate, constricted at septum, tapering towards both ends, but with more prominent taper towards lower end, (8–)9–10 × (3–)3.5 µm. Germinating ascospores irregular, with ascospores becoming brown, verruculose, with prominent distortion, 6–8 µm diam.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium, and smooth margins, reaching 8 mm diam after 2 wk. On MEA surface and reverse oliveaceous grey. On PDA surface oliveaceous grey, reverse iron-grey. On OA surface oliveaceous grey. Cultures sterile.

Typus. Australia, Western Australia, Albany, Stirling Range National Park, Stirling Range Drive, S34°23’24.4” E118°6’31.7”, on leaves of Stirlingia sp. (Proteaceae), 23 Sept. 2015, P.W. Crous (holotype CBS H-23078, culture ex-type CPC 29252 = CBS 142623; ITS, LSU, tef1, and tub2 sequences GenBank KY979747, KY979802, KY979890, and KY979914, MycoBank MB820942.

Notes — Although the Teratosphaeriaceae includes several important foliar pathogens of Proteaceae (Crous et al. 2008, Quaedvlieg et al. 2014), no species of Teratosphaeriaceae have thus far been reported on Stirlingia. Furthermore, Pa. stirlingiae appears to be phylogenetically distinct from all species of Parateratosphaeria thus known from DNA sequence data. This species is consequently introduced as a novel taxon. Based on a megablast search using the ITS sequence, the best matches were to Pa. bellula (GenBank EU707860; Identities = 525/531 (99 %), 1 gap (0 %)), Pa. altensteinii (GenBank FJ372394; Identities = 498/507 (98 %), 2 gaps (0 %)), and Pa. persoonii (GenBank NR_145096; Identities = 512/523 (98 %), 1 gap (0 %)).

Colour illustrations. Stirlingia sp.; ascoma (scale bar = 180 µm); asci, ascospores and germinating ascospores (scale bars = 10 µm).
Neocordana musigena Crous, sp. nov.

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

Classification — Pyriculariaceae, Magnaporthales, Sordariomycetes.

Leaf spots pale grey to brown, covering large areas of the leaf lamina. Mycelium consisting of pale brown to subhyaline, smooth, branched, septate, 2–3 µm diam hyphae. Conidiophores subcylindrical, flexuous, erect, medium brown, smooth, multi-septate, 50–100 × 4–6 µm. Conidiogenous cells polyblastic, terminal and intercalary, 15–50 × 4–6 µm, denticulate; denticles up to 1.5 µm long, 0.5–1 µm wide. Conidia oblong to obovoid, (15–)16–17(–18) × (7–)8(–9) µm, 1-septate, thick-walled, brown, with truncate base, 1 µm diam.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium, and feathery margins, reaching 30–40 mm diam after 2 wk. On MEA surface dirty white, reverse plate luteous. On PDA surface umber, reverse umber. On OA surface honey.

Typus. Morocco, leaves of Musa sp. (Musaceae), 2010, P.W. Crous (holotype CBS H-23079, culture ex-type 29777 = CBS 142624, ITS, LSU, actA, rpb1, and tub2 sequences GenBank KY979748, KY979803, KY979854, KY979885, and KY979915, MycoBank MB820943); CPC 29140, 29777, 29779, ITS, LSU, actA, rpb1, and tub2 sequences GenBank KY979749–KY979750, KY979804–KY979805, KY979855–KY979866, KY979886–KY979887, and KY979916–KY979917.

Notes — Hernández-Restrepo et al. (2015) introduced the genus Neocordana to accommodate four species of hyphomyces causing a foliar disease of Canna and Musa. Crous et al. (2016) added a fifth species, N. musarum, causing a foliar disease on bananas in La Réunion. Neocordana musigena (conidia 15–18 × 7–9 µm) is most similar to C. musicola (conidia 14.5–20 × 6.5–9.5 µm), but is phylogenetically distinct from it. Based on a megablast search using the ITS sequence of the ex-type culture, the best matches were to Neocordana musae (GenBank LN713281; Identities = 571/571 (100 %), no gaps), Neocordana musarum (GenBank KY173424; Identities = 565/571 (99 %), 1 gap (0 %)), and Neocordana musicola (GenBank LN713283; Identities = 544/550 (99 %), 1 gap (0 %)). Based on a megablast search using the rpb1 sequence of the ex-type culture, the strain is identical to Neocordana musarum (GenBank KY173577; Identities = 749/749 (100 %), no gaps), while the actA sequence is 99 % identical to Neocordana musarum (GenBank KY173568; Identities = 357/358 (99 %), no gaps).

Colour illustrations. Musa plants; symptomatic leaf; conidiophores and conidia. Scale bars = 10 µm.

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**Cylindrocladiella vitis** Crous & Thangavel, *sp. nov.*

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

**Classification.** *Nectriaceae, Hypocreales, Sordariomycetes.*

Conidiophores dimorphic, penicillate and subverticillate, mononematous and hyaline. **Penicillate conidiophores** comprising a stipe, a penicillate arrangement of fertile branches, a stipe extension and a terminal vesicle; stipe septate, hyaline, smooth, 40–60 × 5–7 μm; stipe extension asceptate, straight, 100–140 μm long, thick-walled with one basal septum, terminating in thin-walled, ellipsoidal to lanceolate vesicles, 4–6 μm wide. **Penicillate conidiogenous apparatus** with primary branches asceptate, 12–17 × 3–4 μm, secondary branches asceptate, 8–12 × 2–3 μm, each terminal branch producing 2–4 phialides; phialides doliform to reniform to cymbiform, hyaline, asceptate, 10–15 × 2–3 μm, apex with minute periclinal thickening and collarette. **Subverticillate conidiophores** sparse, comprising of a septate stipe, and primary branches terminating in 1–3 phialides; stipe straight, 0–1-septate, 30–40 × 2.5–3.5 μm; phialides cymbiform to cylindrical, hyaline, asceptate, 15–30 × 2.5–3 μm, apex with minute periclinal thickening and collarette. **Conidia** cylindrical, rounded at both ends, straight, 1-septate, (12–)13–16(–18) × (2–)2.5(–3) μm (av. = 14 × 2.5 μm), frequently slightly flattened at the base, held in asymmetrical clusters by colourless slime.

**Culture characteristics.** Colonies covering dish in 2 wk, with abundant aerial mycelium and smooth, lobate margins. On MEA and PDA surface dirty white, reverse sienna on MEA, luteous on PDA. On OA surface ochreous, with patches of pale luteous.

**Typus.** NEW ZEALAND, Ohau Wines, 2 Bishops Road, RD 20, Ohau 5570, Levin, on *Vitis vinifera* (Vitaceae), 2014, D. Davis (holotype CBS H-23080, culture ex-type CPC 28701 = CBS 142517 = ICMP 22045, ITS, LSU, tef1, and tub2 sequences GenBank KY979751, KY979806, KY979891, and KY979918, MycoBank MB820944).

**Notes.** The genus *Cylindrocladiella* accommodates a group of soil-borne fungi that are commonly associated with nursery diseases in subtropical and tropical regions worldwide (Crous 2002). In a recent revision of the genus, Lombard et al. (2012) delineated five species complexes based on morphology and phylogenetic inference. Van Coller et al. (2005) described *C. viticola* (vesicles ellipsoid to clavate, conidia 8–15 × 2–3 μm), a species associated with cutting rot of grapevines. *Cylindrocladiella vitis* is distinct in having ellipsoidal to lanceolate vesicles, and larger conidia (12–18 × 2–3 μm). Furthermore, it is also phylogenetically distinct from all other species known in the genus. Based on a megablast search using the ITS sequence, the best matches were to *Cylindrocladiella elegans* (GenBank JN100609; Identities = 505/512 (99 %), 2 gaps (0 %)) and *Cylindrocladiella novae-zelandiae* (GenBank NR_111055; Identities = 498/506 (98 %), 1 gap (0 %)). The best match based on tef1 was to *Cylindrocladiella cymbiformis* (GenBank JN098989; Identities = 475/499 (95 %), 7 gaps (1 %)) and based on tub2 it was closely related to *Cylindrocladiella elegans* (GenBank JN098755; Identities = 607/623 (97 %), no gaps).

**Colour illustrations.** Vineyard at Ohau Wines; conidiophores sporulating on PNA; conidiophores and conidia. Scale bars = 10 μm.
Apoharknessia eucalyptorum
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**Apoharknessia eucalyptorum** Crous & M.J. Wingf., *sp. nov.*

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

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

*Foliculicolous*, isolated from leaves incubated in moist chambers (presumed endophyte). *Conidiomata* pycnidiod, separate to gregarious, subepidermal, becoming erumpent, stromatic, amphiogenous, depressed globose, up to 250 μm diam; opening irregular, with yellowish, furfuraceous cells; wall of *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity. *Conidiogenous cells* 7–20 × 4–7 μm, ampulliform to lageniform, hyaline, smooth, invested in mucilage, percurrently proliferating once or twice near apex. *Conidia* (8–)9–10(–11) × (5–)6–6.5(–7) μm, obliquely gibbose, aseptate, brown, smooth, thick-walled, with prominent central guttule, lacking striations, with conical short apiculus. *Basal appendage* (1.5–)2–3(–3.5) × 2–2.5 μm, hyaline, tubular, smooth, thin-walled, devoid of cytoplasm, 0–2 μm long, 2 μm diam.

**Culture characteristics.** Colonies reaching 70 mm diam after 2 wk at 25 °C, flat, spreading, with sparse aerial mycelium and lobate, smooth margins. On MEA surface olivaceous black, margin dirty white, reverse olivaceous grey in centre, dirty white in outer region. On PDA surface and reverse dirty white. On OA surface black in centre, grey olivaceous in outer region. Colonies with slimy sporulation on superficial mycelium; sporulating within 1 wk, much faster than *Harknessia* spp., which usually only sporulate after 2–4 wk.

**Typus.** *Malaysia*, Sabah, on leaves of *Eucalyptus pellita* (Myrtaceae), May 2015. M.J. Wingfield (holotype CBS H-23082, culture ex-type CPC 27546 = CBS 142519, ITS, LSU, cmdA, and tub2 sequences GenBank KY979762, KY979807, KY979867, and KY979919, MycoBank MB820946).

Notes — *Apoharknessia eucalyptorum* is morphologically similar to *A. insueta* (conidia 10–11(–12.5) × 7.5–9 μm; Nag Raj 1993), other than the fact that it has smaller conidia (8–11 × 5–7 μm). The ITS sequence of *A. eucalyptorum* is only 93 % similar to that of *A. insueta* (GenBank JQ706083; Identities = 572/616 (93 %), 30 gaps (4 %)).
Wallrothiella gmelinae
Wallrothiella gmelinae Crous & M.J. Wingf., sp. nov.

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

Classification — Amplostromataceae, Hypocreales, Sordariomycetes.

Mycelium consisting of hyaline, branched, septate, 1.5–2.5 μm diam hyphae. Conidiophores solitary, erect, subcylindrical, pale brown, smooth, 0–1-septate, 20–60 × 2.5–3.5 μm. Conidiogenous cells pale brown, smooth, subcylindrical to subulate, with prominent taper in upper third, intercalary on conidiophores, or terminal, phialidic, with flared collarette, 2.5–3.5 μm diam, 18–40 × 2.5–3 μm. Conidia solitary, aggregating in slimy masses, subcylindrical with obtuse ends, straight, aseptate, minutely guttulate, pale brown, turning medium brown with age, (7–)8–9(–11) × (2.5–)3 μm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium, and smooth, lobate margins, reaching 12 mm diam after 2 wk at 25 °C. On MEA surface saffron, reverse pale luteous. On PDA surface pale luteous, reverse dirty white. On OA surface dirty white.

Typus. MALAYSIA, Sabah, on twigs of Gmelina arborea (Lamiaceae), May 2015, M.J. Wingfield (holotype CBS H-23083, culture ex-type CPC 27584 = CBS 142520; ITS and LSU sequences GenBank KY979753 and KY979808, MycoBank MB820947).

Notes — The genus Wallrothiella is commonly isolated from plant litter and soil, although its ecology remains largely unknown. Wallrothiella has a phialophora-like asexual morph, Pseudogliomastix (Gams & Boekhout 1985). Wallrothiella gmelinae is phylogenetically similar to W. subiculosa (= Pseudogliomastix protea; conidia 3.7–5.6 × 1.6–3 μm; Gams 1971). Based on a megablast search using the ITS sequence, the best match was to W. subiculosa (GenBank AB540576; Identities = 549/555 (99 %), no gaps), followed by Gliomastix murorum (GenBank JQ354922; Identities = 490/505 (97 %), 2 gaps (0 %)).

Colour illustrations. Gmelina arborea trees in Malaysia; conidiophores sporulating on PNA; conidiophores and conidia. Scale bars = 10 μm.
Paraconiothyrium hakeae
Paraconiothyrium hakeae Crous & Barber, sp. nov.

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

Classification — Didymosphaeriaceae, Pleosporales, Dothideomycetes.

Conidiomata solitary, globose, dark brown, up to 250 μm diam, with central papillate ostiole; surface with short brown setae; wall of 3–6 layers of brown textura angularis. Conidiophores lining the inner cavity, hyaline, smooth, subcylindrical to ampulliform, 0–1-septate, branched or not, 8–12 × 2–3.5 μm. Conidiogenous cells terminal and intercalary, subcylindrical with apical taper and a few inconspicuous percurrent proliferations at apex, 4–6 × 2–3 μm. Conidia solitary, brown, smooth, thick-walled, subcylindrical, apex obtuse, base truncate, (2.5–)3(–4) × 2 μm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and even, lobate margins, reaching 50 mm diam after 2 wk. On MEA surface dirty white, reverse ochreous. On PDA surface sienna in centre, pale luteous in outer region. On OA surface pale luteous, with patches of sienna.

Typus. AUSTRALIA, Western Australia, Perth, Periwinkle Park, on Hakea sp. (Proteaceae), 23 June 2015, P.A. Barber (holotype CBS H-23084, culture ex-type CPC 27651 = CBS 142521, ITS, LSU, rpb2, tef1, and tub2 sequences GenBank KY979754, KY979809, KY979847, KY979892, and KY979920, MycoBank MB820948).

Notes — Paraconiothyrium hakeae is phylogenetically similar to P. brasiliense (from fruit of Coffea arabica in Brazil; conidia 3–5 × 1.8–2.5 μm; Verkley et al. 2004; GenBank JX496099; Identities = 579/589 (98 %), 1 gap (0 %)), although its conidia are slightly smaller (2.5–4 × 2 μm). However, the tub2 sequences are only 93 % similar (GenBank JX496438; Identities = 419/450 (93 %), 1 gap (0 %)). The ecology of P. hakeae, which occurs on leaves of Hakea sp. in Australia, is unknown.

Colour illustrations. Periwinkle Park; conidiomata sporulating on PNA (scale bar = 250 μm), conidiomatal wall with setae, conidiogenous cells and conidia (scale bars = 10 μm).
Peyronellaea eucalypti
**Peyronellaea eucalypti** Crous & M.J. Wingf., sp. nov.

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

**Classification.** — *Didymellaceae, Pleosporales, Dothideomycetes.*

Ascomata pseudothecial, solitary, erect, pyriform, 120–200 µm diam; apex dark brown, basal two thirds pale brown, with central papillate ostiole; wall of 3–6 layers of brown *textura angularis.* Pseudoparaphyses absent. Asci bitunicate, stipitate, narrowly ellipsoid to subcylindrical with inconspicuous apical chamber, 45–70 × 8–12 µm. Ascospores bi- to triseriate, hyaline, smooth, constricted at median septum, prominently guttulate with mucoid sheath, widest just above septum, ends subobtusely rounded, (13–)14–15(–17) × (4–)5–6 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margins, reaching 60 mm diam after 2 wk at 25 °C. On MEA surface dirty white, reverse chestnut. On PDA surface and reverse isabelline. On OA surface olivaceous grey.

**Notes** — The genus *Peyronellaea* is characterised by species having setose pycnidia and dictyochlamydospores. Aveskamp et al. (2009, 2010) showed that these structures have evolved several times within the *Phoma* complex. *Peyronellaea eucalypti* is phylogenetically related to *Peyronellaea glomerata* (GenBank KM979831; Identities = 523/535 (98 %), 3 gaps (0 %)). It cannot be compared based on morphology because *P. eucalypti* only occurs as a sexual morph. This is interesting, because it links a didymella-like sexual morph to the genus. The protein-coding sequences did not reveal any highly similar sequences in the NCBI’s GenBank nucleotide database.

**Typus.** *Malaysia,* Sabah, on leaves of *Eucalyptus pellita* (Myrtaceae), May 2015, M.J. Wingfield (holotype CBS H-23085, culture ex-type CPC 27678 = CBS 142522, ITS, LSU, *rpb2*, *tef1*, and *tub2* sequences GenBank KY979755, KY979810, KY979848, KY979893, and KY979921, MycoBank MB820950; CPC 27682, ITS, LSU, *rpb2*, *tef1*, and *tub2* sequences GenBank KY979756, KY979811, KY979849, KY979894, and KY979922.

Colour illustrations. *Eucalyptus pellita* trees growing in Malaysia; ascomata sporulating on PNA (scale bar = 200 µm); asci and ascospores (scale bars = 10 µm).
Didymocyrtis banksiae
Didymocyrtis banksiae Crous & Barber, sp. nov.

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

Classification — Phaeosphaeriaceae, Pleosporales, Dothideomycetes.

Conidiomata pycnidial, dark brown, globose, multilocular, 200–300 μm diam, with 1–2 ostioles exuding a brown conidial mass; wall of 3–6 layers of brown textura angularis. Conidiophores lining the inner cavity, hyaline, smooth, subcylindrical, 0–3-septate, 8–20 × 4–6 μm. Paraphyses intermingled among conidiophores, hyaline, septate, at times branched, apices obtuse, 20–35 × 3–4 μm. Conidiogenous cells ampulliform to subcylindrical, hyaline, smooth, terminal and intercalary, 5–13 × 3–4 μm; proliferating percurrently at apex. Conidia solitary, subcylindrical to narrowly fusoid-ellipsoid, straight, widest in middle, apex obtuse, base truncate, 2–2.5 μm diam, (0–)11(–3)-septate, guttulate, medium brown, smooth, (8–)10–11(–14) × (3–)4 μm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium, and smooth, lobate margins, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface dirty white, with patches of red, reverse pale luteous, with patches of red. On PDA surface and reverse isabelline with patches of dirty white. On OA surface dirty white with patches of red.

**Typus.** Australia, Western Australia, Perth, St. Clair Park, on Banksia sesaliis var. cygnorum (Proteaceae), 24 June 2015, P.A. Barber (holotype CBS H-23086, culture ex-type CPC 28238 = CBS 142523, ITS, LSU, rpb2, tef1, and tub2 sequences GenBank KY979757, KY979812, KY979850, KY979895, and KY979923, MycoBank MB821081).

Notes — The genus Didymocyrtis was recently resurrected for lichenicolous species previously assigned to Diederichia, Diederichomyces, Leptosphaeria, and Phoma (Trakunyingcharoen et al. 2014, Ertz et al. 2015). Didymocyrtis banksiae appears to be a non-lichenicolous species, although it occurs on hard, leathery leaves of Banksia, which frequently have some lichen growth on the leaf surface. It is, therefore, quite possible that D. banksiae has some lichenicolous association not observed at the time of isolation. Based on a megablast search using the ITS sequence, the best match was to D. cladonidica (GenBank JQ238623; Identities = 563/585 (96 %), 3 gaps (0 %)), followed by D. foliaceiphila (GenBank JQ238638; Identities = 562/584 (96 %), 2 gaps (0 %)). The protein-coding sequences did not reveal any highly similar sequences in the NCBI GenBank nucleotide database.
**Paraphoma rhaphiolepidis** Crous & Toome, sp. nov.

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

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

*Conidiomata.* Pycnidial to stromatic, globose, 250–350 μm diam, in clusters of 2–5, with darker ostiolar region, 1–2 ostioles per pycnidium; outer surface covered with flexuous, brown, verruculose setae. *Conidiophores* lining the inner cavity, hyaline, smooth, densely aggregated, branched, 1–2-septate, subcylindrical, 10–17 × 3–5 μm. *Conidiogenous cells* hyaline, smooth, subcylindrical to ampulliform, terminal and intercalary, with prominent periclinal thickening at apex, 5–8 × 3–5 μm. *Conidia* solitary, hyaline, straight, smooth, guttulate, subcylindrical, apex obtuse, base truncate, (4.5–)5–6(–6.5) × 2(–2.5) μm.

*Culture characteristics.* — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margins, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface pale olivaceous grey, reverse olivaceous grey. On PDA surface and reverse olivaceous grey. On OA surface olivaceous grey.

*Typus.* Origin uncertain, intercepted during post entry quarantine in New Zealand, on *Rhaphiolepis indica* (Rosaceae). June 2015, M. Toome-Heller (holotype CBS H-23087, culture ex-type CPC 28707 = CBS 142524 = T15_03251A = ICMP 21068, ITS, LSU, rpb2, tof1, and tub2 sequences GenBank KY979758, KY979813, KY979851, KY979896, and KY979924, MycoBank MB820951).

Notes — Members of the genus *Paraphoma* have a wide geographic distribution, and include primary and secondary pathogens of agricultural crops (Moslemi et al. 2016). *Paraphoma rhaphiolepidis* is phylogenetically related, but distinct from *P. chrysanthemicola* (GenBank KF251165; Identities = 524/536 (98 %), 4 gaps (0 %)), a stem and root pathogen of *Chrysanthemum* (De Gruyter et al. 2010). The protein-coding sequences did not reveal any highly similar sequences in the NCBIs GenBank nucleotide database.
Readeriella ellipsoidea
**Readeriella ellipsoidea Crous, sp. nov.**

**Etymology.** Name refers to the characteristic narrowly ellipsoid conidia of this fungus.

**Classification.** Teratosphaeriaceae, Capnodiales, Dothideomycetes.

Conidiomata eustromatic, occurring in a stroma of dark brown textura angularis, up to 400 μm diam, 150–200 μm diam, with one to several ostioles, uni- to multilocular (resembling the genus Davisoniella). Conidiophores lining the inner cavity, subcylindrical, pale brown, branched, 0–2-septate, smooth, 10–20 × 3–4 μm. Conidigenous cells integrated, terminal and intercalary, pale brown, smooth, ampulliform to subcylindrical, with 1–2 inconspicuous percurrent proliferations at apex, 4–8 × 3–3.5 μm. Conidia solitary, narrowly ellipsoid, apex obtuse, tapering to a narrowly truncate base, 1 μm diam, yellow brown in mass, finely roughened, (4–)5(–6) × (2–)2.5 μm.

Culture characteristics: Colonies flat, spreading, with sparse aerial mycelium, and even lobate margins, reaching 20 mm diam after 2 wk. On MEA surface chestnut, reverse umber. On PDA surface greenish black, reverse olivaceous grey. On OA surface olivaceous grey.

*Typus. AUSTRALIA,* Western Australia, Albany, Stirling Range National Park, Bluff Knoll, S34°22'3.8"E118°14'31.3", on leaves of Eucalyptus sp. (Myrtaceae), 23 Sept. 2015, P.W. Crous (holotype CBS H-23088, culture ex-type CPC 29153 = CBS 142525, ITS, LSU, tef1, and tub2 sequences GenBank KY979759, KY979814, KY979897, and KY979925, MycoBank MB820952).

Notes — Crous et al. (2007a, c, 2009a, b) showed that *Readeriella* resides in the Teratosphaeriaceae, having Nothostrateria and Cibiessia synasexual morphs. *Readeriella ellipsoidea* is phylogenetically related to *R. dimorphospora* (Crous et al. 2007c), though only the *Readeriella* morph was observed in culture. Based on a megablast search using the ITS sequence, the best match was to *R. dimorphospora* (GenBank KF901544; Identities = 477/481 (99 %), 2 gaps (0 %)), followed by *R. nontingens* (GenBank EF394847; Identities = 540/545 (99 %), 1 gap (0 %)). Based on both tef1 and tub2, *R. ellipsoidea* was less than 85 % identical to *R. dimorphospora* (GenBank KF903252 and KF902956, respectively).

*Colour illustrations. Eucalyptus* sp. in Stirling Range National Park; conidiomata sporulating on OA (scale bar = 200 μm); conidiophores and conidia (scale bars = 10 μm).
**Myrtapenidiella eucalyptigena** Crous, sp. nov.

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

*Classification.* *Teratosphaeriaceae, Capnodiales, Dothideomycetes.*

*Conidiophores.* Erect, flexuous, mostly unbranched, fasciculate, subcylindrical, thick-walled, finely roughened, medium brown, multisepitate, 50–150 × 5–7 μm. *Conidiogenous cells* integrated, terminal, subcylindrical, medium brown, finely roughened, 10–20 × 4–6 μm; scars thickened, darkened, not refractive, 3–4 μm diam, proliferating sympodially. *Secondary ramoconidia* medium brown, verruculose, thick-walled, 1-septate, subcylindrical, 20–35 × 5–6 μm. *Conidia* occurring in branched chains of up to 10, medium brown, verruculose, thick-walled, 1(–2)-septate, (15–)17–20(–26) × (4–)5(–6) μm; hila thickened, darkened, 2–3 μm diam.

*Culture characteristics.* Colonies flat, spreading, with sparse aerial mycelium and feathery margins, reaching 15 mm diam after 2 wk at 25 °C. On MEA surface dark mouse grey, reverse mouse grey. On PDA surface violaceous black, reverse dark mouse grey. On OA surface olivaceous grey.

*Typus.* AUSTRALIA, Western Australia, Williams Nature Reserve, 10 km north west of the Williams town, on Eucalyptus leaf litter (Myrtaceae), 18 Sept. 2015, P.W. Crous (holotype CBS H-23089, culture ex-type CPC 29184 = CBS 142526, ITS, LSU, tef1, and tub2 sequences GenBank KY979780, KY979815, KY979898, and KY979926, MycoBank MB620955).

*Notes.* Quaedvlieg et al. (2014) introduced *Myrtapenidiella* to accommodate penidiella-like genera occurring on *Myrtaceae*. *Myrtapenidiella eucalyptigena* is phylogenetically closely related to *M. tenuiramis* (conidia (6–)8–10(–12) × 3–4 μm; Crous et al. 2009a) and *T. corymbiae* (conidia 7–9(–12.5) × 2.5–3(–3.5) μm; Cheewangkoon et al. 2009), but is distinct in having larger conidia. Based on a megablast search using the ITS sequence, the best match was *M. tenuiramis* (GenBank NR_145118; Identities = 476/482 (99 %), 4 gaps (0 %)), followed by *M. corymbia* (GenBank NR_145115; Identities = 470/482 (98 %), 4 gaps (0 %)). Based on both *tef1* and *tub2*, the closest matches in the NCBI’s GenBank nucleotide database are equal to or less than 90 % similar.

*Colour illustrations.* Leaf litter in Williams Nature Reserve; colony sporulating on PNA; conidiophores and conidia. Scale bars = 10 μm.
**Myrtapenidiella balenae** Crous, *sp. nov.*

**Etymology.** The name is derived from the Latin word Balena for whale, and refers to the fact that whales were present close to the shoreline at the time that this fungus was collected at Point Ann in Western Australia.

**Classification.** *Teratosphaeriaceae, Capnodiales, Dothideomycetes.*

**Conidiophores.** Erect, flexuous, unbranched, solitary (not fasciculate), subcylindrical, thick-walled, finely roughened, medium brown, multiseptate, 70–200 × 4–5 μm. **Conidiogenous cells.** Integrate, terminal, subcylindrical, medium brown, finely verruculose, 15–25 × 3–4 μm; scars thickened, darkened, 1.5–2 μm diam, proliferating sympodially. **Primary ramoconidia.** Medium brown, verruculose, 0–1-septate, guttulate, 20–40 × 4–5 μm, frequently with mucoid sheath; hila thickened, darkened, 2.5–3 μm diam. **Secondary ramoconidia.** Subcylindrical, 0–1-septate, medium brown, verruculose with mucoid sheath, proliferating sympodially, 17–20 × 4–5 μm. **Conidia.** In branched chains of up to 7, medium brown, verruculose with mucoid sheath, proliferating sympodially, (13–)15–17(–18) × (3–)4 μm; hila thickened and darkened, 1.5–2 μm diam.

**Culture characteristics.** Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margins, reaching 20 mm diam after 2 wk at 25 °C. On MEA surface and reverse olivaceous grey. On PDA surface olivaceous grey with patches of pale olivaceous grey, reverse olivaceous grey. On OA surface olivaceous grey.

**Typus. Australia,** Western Australia, Albany, Fitzgerald River National Park, Point Ann, on leaves of *Eucalyptus* sp. (Myrtaceae), at Phytophthora site, 22 Sept. 2015. P.W. Crous (holotype CBS H-23090, culture ex-type CPC 29235 = CBS 14257, ITS, LSU, *tef1* and *tub2* sequences GenBank KY979761, KY979816, KY979899, and KY979927, MycoBank MB 820954).

Notes — *Myrtapenidiella balenae* is phylogenetically closely related to *M. tenuiramis* (on *E. tenuiramis*, Tasmania; conidia (6–)8–10(–12) × 3–4 μm; Crous et al. 2009a), but morphologically distinct in having larger conidia, (13–)15–17(–18) × (3–)4 μm. Based on a megablast search using the ITS sequence, the best match was *M. tenuiramis* (GenBank NR_145118; Identities = 474/482 (98 %), 2 gaps (0 %)), followed by *M. corymbia* (GenBank NR_145115; Identities = 472/482 (98 %), 2 gaps (0 %)). Based on a megablast search using the *tub2* sequence, the best match was *M. corymbia* (GenBank KF442481; Identities = 328/349 (94 %), 2 gaps (0 %)).

**Colour illustrations.** Point Ann, Fitzgerald River National Park; conidiophores sporulating on PNA; conidiophores and conidia. Scale bars = 10 μm.
Zasmidium commune Crous, sp. nov.

Etymology. Name refers to the common occurrence of this species.

Classification — Mycosphaerellaceae, Capnodiales, Dothideomycetes.

Mycelium consisting of branched, septate, medium brown, verruculose, 1.5–2.5 μm diam hyphae. Conidiophores solitary, erect, arising from superficial mycelium, 25–100 × 3–5 μm, subcylindrical, somewhat flexuous, medium brown, thick-walled, smooth, 1–8-septate, unbranched. Conidiogenous cells integrated, terminal, subcylindrical, medium brown, smooth, 5–20 × 3–4 μm; scars thickened, darkened, sympodial, 1 μm diam, proliferating sympodially. Secondary ramoconidia medium brown, verruculose, narrowly obclavate to somewhat subcylindrical, 30–150 × 3 μm, multisepitate; hila thickened, darkened, 0.5 μm diam. Conidia in short (1–2) branched chains, medium brown, verruculose, narrowly obclavate to somewhat subcylindrical, apex obtuse, base truncate, hila thickened, darkened, (8–)15–35(–45) × (2.5–)3(–4) μm.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium, and feathery margins, reaching 15 mm diam after 2 wk at 25 °C. On MEA and PDA surface brown vinaceous, reverse isabelline. On OA surface olivaceous grey.

Typus. AUSTRALIA, Western Australia, Denmark, Mount Lindesay Walk Trail, on leaves of Xanthorrhoea sp. (Xanthorrhoeaceae), 19 Sept. 2015, P.W. Crous (holotype CBS H-23093, cultures CPC 29725 = CBS 142530, ITS, LSU, and actA sequences GenBank KY979765, KY979820, and KY979860, MycoBank MB820955); CPC 29547, CPC 29723, ITS, LSU, actA, and tub2 sequences GenBank KY979763–KY979764, KY979818–KY979819, KY979858–KY979859, and KY979929 (CPC 29547).

Notes — The genus Zasmidium (Mycosphaerellaceae) as it is presently defined is paraphyletic (Videira et al. in prep.). Most of the known species are associated with leaf spot diseases of various hosts. Some of these are agriculturally important, such as greasy leaf spot disease of Citrus (Huang et al. 2015). Zasmidium commune appears to be specific to leaves of a Xanthorrhoea sp. Phylogenetically, Z. commune is distinct from other Zasmidium spp. that are presently known based on their DNA sequences. Based on a megablast search using the ITS sequence, the best match was to Mycosphaerella pseudovespa (GenBank NR_137548; Identities = 501/507 (99 %), no gaps), followed by Periconiella velutina (GenBank EU041781; Identities = 526/547 (96 %), 1 gap (0 %)). Based on the actA sequence, Z. commune was only 95 % similar to Mycosphaerella pseudovespa (GenBank KF903535; Identities = 502/531 (95 %), 10 gaps (1 %)).
Zasmidium podocarpi
Zasmidium podocarpi Crous, sp. nov.

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

Classification. — Mycosphaerellaceae, Capnodiales, Dothideomycetes.

Conidiophores solitary on underside of leaves (litter), erect, flexuous, dark brown, thick-walled, multisepitate, subcylindrical, verruculose to warty, branching in upper third of conidiophore, 200–300 × 9–12 µm; with 1–3 lateral branches, 1–3-septate, 40–70 µm long. Conidiogenous cells terminal and lateral, dark brown, verruculose, warty, thick-walled, obtusely rounded, 20–30 × 9–10 µm; scars numerous, darkened, thickened, prominently raised, up to 1 µm high, 3 µm diam. Conidia solitary, obclavate to subcylindrical, medium brown, verruculose to warty, apex subobtuse, (30–)35–40(–45) × (6–)8 µm; hilum truncate, 3–4 µm diam, somewhat thickened and darkened; a few conidia observed in culture were much longer, thinner and flexuous.

Culture characteristics. — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margins, reaching 25 mm diam after 2 wk at 25 °C. On MEA surface olivaceous grey, reverse iron grey. On PDA surface iron grey with patches of orange, reverse similar, but with diffuse orange pigment. On OA surface olivaceous grey, and sienna on SNA.

Typus. Australia, Western Australia, Denmark, Mount Lindesay Walk Trail, on leaf litter of Podocarpus sp. (Podocarpaceae), 19 Sept. 2015, P.W. Crous (holotype CBS H-23092, culture ex-type CPC 29284 = CBS 142529, ITS, LSU, actA, and tub2 sequences GenBank KY979766, KY979821, KY979861, and KY979930, MycoBank MB820956).

Notes — Zasmidium podocarpi represents a morphologically distinct species of Zasmidium that occurs on leaves of Podocarpus. At the time of collection, these leaves displayed prominent red leaf spots (devoid of fungal sporocarps). There was no evidence to link the disease to Z. podocarpi, as sporulation was observed only on the leaf litter. This suggests that Z. podocarpi is an endophyte, which is a common character trait for species of Zasmidium (see Huang et al. 2015). Further collections would be required to resolve the ecology of this fungus. Based on a megablast search using the ITS sequence, the best match was to Mycosphaerella pseudovespa (GenBank NR_137548; Identities = 497/509 (98 %), no gaps), followed by Periconiella velutina (GenBank EU041781; Identities = 525/548 (96 %), 3 gaps (0 %)). Based on both actA and tub2, the closest matches in the NCBI's GenBank nucleotide database were equal to or less than 93 % similar to species of Mycosphaerellaceae.

Colour illustrations. Mount Lindesay Walk Trail; colony on MEA; conidiophores with thickened darkened scars, and conidia. Scale bars = 10 µm.
Myrtapenidiella pleurocarpae
Fungal Planet 580 – 20 June 2017

**Myrtapenidiella pleurocarpae** Crous, sp. nov.

**Etymology.** Name refers to Eucalyptus pleurocarpa, the host species from which this fungus was collected.

**Classification.** *Teratosphaeriaceae, Capnodiales, Dothideomycetes.*

*Mycelium* consisting of branched, septate, pale brown, smooth, 3–4 μm diam hyphae. *Conidiophores* solitary to fasciculate, arising from superficial hyphae or a small stroma of a few cells, erect, subcylindrical, straight to geniculate-sinuous, 30–90 × 5–6 μm, thick-walled, medium brown, smooth, 1–4-septate. *Conidiogenous cells* terminal, integrated, subcylindrical, medium brown, smooth, 20–35 × 5–6 μm; scars flat, somewhat thickened and darkened, 2.5–3 μm diam; proliferating sympodially. *Secondary ramoconidia* medium brown, finely verruculose, 0–3-septate, 15–35 × 5–7 μm, subcylindrical to fusoid-ellipsoid; hila truncate, 2–2.5 μm diam, somewhat darkened and thickened. *Conidia* in branched chains (–7), medium brown, finely verruculose, thick-walled, fusoid-ellipsoid, (15–)19–22(–25) × (5–)6(–6.5) μm; hila thickened and darkened, 1–2 μm diam.

**Culture characteristics.** Colonies erumpent, slow growing, with sparse to moderate aerial mycelium and smooth, even margins, reaching 15 mm diam after 2 wk at 25 °C. On MEA and PDA surface and reverse olivaceous grey. On OA surface iron-grey.

**Typus.** **AUSTRALIA,** Western Australia, Albany, Fitzgerald River National Park, Cape Riche Lookout, on leaves of *Eucalyptus pleurocarpa* (Myrtaceae), 21 Sept. 2015, P.W. Crous (holotype CBS H-23094, culture ex-type CPC 29279 = CBS 142531, ITS, tef1, and tub2 sequences GenBank KY979767, KY979822, KY979900, and KY979931, MycoBank MBB20957); CPC 29234, ITS, LSU, tef1, and tub2 sequences GenBank KY979768, KY979823, KY979901, and KY979932.

**Notes.** *Myrtapenidiella pleurocarpae* is phylogenetically closely related to *M. tenuiramis* (on *E. tenuiramis*, Tasmania; conidia (6–)8–10(–12) × 3–4 μm; Crous et al. 2009a), but morphologically distinct in having larger conidia, (15–)19–22(–25) × (5–)6(–6.5) μm, which also distinguishes it from *M. balenae* (see FP577 in this paper. It differs 3 nucleotides on ITS and is 89 % similar on tef1 and 94 % similar on tub2). Based on a megablast search using the ITS sequence, the best match was to *M. tenuiramis* (GenBank NR_145118; Identities = 475/481 (98 %), 1 gap (0 %)), followed by *M. corymbia* (GenBank NR_145115; Identities = 473/481 (98 %), 1 gap (0 %)). Based on both tef1 and tub2, the closest matches in the NCBIs GenBank nucleotide database were equal to or less than 93 % similar to species of *Myrtapenidiella.*

** Colour illustrations.** Eucalyptus pleurocarpa in Fitzgerald River National Park; conidiophores and conidia. Scale bars = 10 μm.
Tiarosporella corymbiae
**Tiarosporella corymbiae** Crous & Barber, *sp. nov.*

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

*Classification — Botryosphaeriaceae, Botryosphaeriales, Dothideomycetes.*

*Conidiomata* brown, dark brown at apex, globose, 90–150 μm diam, with central ostiole, solitary on SNA, aggregated in clusters on OA, exuding crystalline conidial mass; wall of 2–4 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, subcylindrical to doliiform, hyaline, smooth, proliferating percurrently at apex, 5–10 × 3–5 μm. *Conidia* solitary, hyaline, smooth, guttulate, thick-walled, fusoid-ellipsoid to obclavate, base truncate, 3–4 μm diam with marginal frill; apex subobtuse with thickened tip, at times with flared mucoid cap, but rarely observed, (16–)17–18(–20) × (5–)6–7 μm.

*Culture characteristics — Colonies covering dish in 2 wk with moderate aerial mycelium at 25 °C. On MEA surface amber, reverse ochreous. On PDA surface iron-grey, reverse olivaceous grey. On OA surface olivaceous grey.*

*Typus. AUSTRALIA, Western Australia, Perth, Greenshank Park, on Corymbia calophylla (Myrtaceae), 26 June 2015, P.A. Barber* (holotype CBS H-23095, culture ex-type CPC 28201 = CBS 142532, ITS, LSU, *tef1*, and *tub2* sequences GenBank KY979769, KY979824, KY979902, and KY979933, MycoBank MB820958).

Notes — The poly- and paraphyletic nature of *Tiarosporella* was recently addressed by Crous et al. (2015a), who introduced several genera to accommodate tiarosporella-like genera occurring in other families. *Tiarosporella corymbiae* is phylogenetically related to the type species, *T. paludosa* (conidia 22–45 × 4–7 μm; GenBank NR_132907; Identities = 537/559 (96 %), 9 gaps (1 %)), although it is morphologically distinct, having much smaller conidia (16–20 × 5–7 μm).

*Colour illustrations.* Greenshank Park, Perth; conidiomata sporulating on OA (scale bar = 150 μm); conidiogenous cells and conidia (scale bars = 10 μm).
Lectera capsici
**Fungal Planet 582 – 20 June 2017**

**Lectera capsici** Crous & P.W.J. Taylor, *sp. nov.*

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

**Classification —** Plectosphaerellaceae, Glomerellales, Sordariomycetes.

Conidiomata initially closed, brown, globose on OA, but forming sporodochia on SNA, cushion-shaped, 100–200 μm diam, surrounded by grey-brown, verruculose setae, thick-walled, flexuous, 5–7-septate, tapering to acutely rounded apices, 60–80 x 3–4.5 μm. Conidiogenous cells cylindrical, proliferating percurrently at apex, 15–30 x 3–4 μm. Conidia (on SNA) hyaline, smooth (becoming olivaceous in mass, and appearing somewhat roughened), aseptate, fusoid-ellipsoid to navicular, straight, apex acutely rounded, base truncate, 0.5–1 μm diam, inequilateral, with inner plane flat, and outer plane convex, (6.5–)7–8(–9) x (2–)2.5(–3) μm on SNA.

**Culture characteristics —** Colonies flat, spreading with sparse aerial mycelium and even, lobate margins, reaching 60 mm diam on PDA and OA, 25 mm diam on MEA after 2 wk at 25 °C. On MEA surface folded, saffron, reverse saffron. On PDA surface apricot, reverse salmon. On OA surface saffron.

**Typus. MALAYSIA, leaf spots of Capsicum annuum (Solanaceae), 6 Aug. 2015, P.W.J. Taylor (holotype CBS H-23097, culture ex-type CPC 28723 = CBS 142534, ITS, LSU, tef1, and tub2 sequences GenBank KY979770, KY979825, KY979903, and KY979934, MycoBank MB820959).**

Notes — Cannon et al. (2012) introduced the genus *Lectera* to accommodate two soil-borne plant pathogens associated with diseases of Fabaceae. *Lectera capsicum* is phylogenetically related, but distinct from *L. colletotrichoides* (conidia on Medicago stem, 6.5–11.5 x 2.5–3 μm, av. 8.35 x 2.67 μm; on PCA and PDA, 6.5–9(–10.5) x 2–3 μm, av. 7.41 x 2.43 μm; Cannon et al. 2012). These two species cannot be distinguished based on their conidial dimensions, and are best separated based on their DNA sequence data. Based on a megablast search using the ITS sequence, the best match was to *L. colletotrichoides* (GenBank JQ647428; Identities = 500/505 (99 %), 2 gaps (0 %)), followed by *L. longa* (GenBank NR_111715; Identities = 494/510 (97 %), 12 gaps (2 %)). The tef1 and tub2 sequences were 84 % and 86 % similar to *L. colletotrichoides* (GenBank KM231987 and KM232121), respectively.

**Colour illustrations.** *Capsicum annuum* plants; conidiomata sporulating on OA; conidioma with setae (scale bar = 200 μm); setae and conidia (scale bars = 10 μm).
Verrucoconiothyrium eucalyptigenum
**Verrucoconiothyrium eucalyptigenum** Crous, sp. nov.

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

**Classification.** Didymosphaeriaceae, Pleosporales, Dothideomycetes.

Conidiomata separate, solitary, subglobose, papillate (having a prominent long neck in vivo), 200–250 μm diam, with central ostiole exuding a dark brown conidial mass; wall of 3–6 layers of brown textura angularis. Conidiophores reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, doliiform, 6–8 × 5–7 μm; proliferating percurrently at apex. Conidia solitary, golden brown, finely roughened, thick-walled, granular to finely guttulate, subcylindrical to narrowly ellipsoid, apex subobtuse, base truncate, 2–3 μm diam, (0–)1(–2)-septate, (8–)9–13(–15) × (4–)5(–6) μm (av. 12 × 5 μm).

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margins, covering dish in 2 wk. On PDA surface bay, reverse sienna. On OA surface sienna.

**Typus.** AUSTRALIA, Western Australia, Perth, King’s Park Botanic Gardens, on Eucalyptus leaf litter (Myrtaceae), 27 Sept. 2015, P.W. Crous (holotype CBS H-23098, culture ex-type CPC 29000 = CBS 142555, ITS, LSU, rpb2, tef1, and tub2 sequences GenBank KY979771, KY979826, KY979852, KY979904, and KY979935, MycoBank MB820960).

Notes — Verrucoconiothyrium was introduced by Crous et al. (2015b) to accommodate Coniothyrium nitidae, a foliar pathogen of Proteaceae. Coniothyrium prosopidis (associated with a bark disease of Prosopis; Crous et al. 2013) is allied to Verrucoconiothyrium, which is also true for the new species described here from Eucalyptus leaves collected in Australia. Based on a megablast search using the ITS sequence, the best match was to V. nitidae (GenBank KX306774; Identities = 534/542 (99 %), 1 gap (0 %)), followed by V. prosopidis (as C. prosopidis, GenBank NR_137604; Identities = 530/543 (98 %), no gaps).

**Verrucoconiothyrium prosopidis** (Crous & A.R. Wood) Crous, **comb. nov.** — MycoBank MB820961

Basionym. Coniothyrium prosopidis Crous & A.R. Wood, Persoonia 31: 207. 2013.
**Foliocryphia eucalyptorum** Crous & Thangavel, *sp. nov.*

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

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

*Conidiomata* eustromatic, separate, pulvinate, subglobose, up to 250 μm diam with central ostiole, pale to medium brown, singular to multilocular. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, subcylindrical to ampulliform with prominent apical taper towards narrowly cylindrical apical part, phialidic, with apical collarette and periclinal thickening, 5–12 × 3–5 μm. *Conidia* aseptate, hyaline, smooth, ellipsoid, straight to irregularly curved, apex obtuse, base truncate with protruding hilum, somewhat off-centre, smooth, thin-walled, (5–)6–8(–9) × (2–)2.5(–3) μm.

**Culture characteristics.** Colonies flat, spreading, covering dish in 2 wk with sparse aerial mycelium and smooth, even margins. On MEA surface dirty white to luteous, reverse luteous. On PDA surface and reverse pale luteous. On OA surface pale luteous.

**Typus.** **New Zealand.** Warkworth, Kaipara coast road, on *Eucalyptus* sp. (Myrtaceae), 2015, R. Thangavel (holotype CBS H-23099, culture ex-type CPC 29357 = CBS 142536 = T15_06344D = ICMP 21664, ITS, LSU, and *tub2* sequences GenBank KY979772, KY979827, and KY979936, MycoBank MB820962; CPC 29358, ITS, LSU, and *tub2* sequences GenBank KY979773, KY979828, and KY979937.

**Notes.** The genus *Foliocryphia* was established as monotypic genus by Cheewangkoon et al. (2009) to accommodate a foliicolous fungus occurring on *Eucalyptus*. *Foliocryphia eucalyptorum* can be distinguished from *F. eucalypti* (conidia 8.5–11.5 × 3.3–4.2 μm) by its smaller conidia. The two species are 99% similar on ITS (GenBank NR_135975; Identities = 571/579 (99%), no gaps) and 95% similar on *tub2* (GenBank JQ706128; Identities = 708/742 (95%), 12 gaps (1%)).

**Colour illustrations.** *Eucalyptus* trees along the Kaipara coastal road; conidioma sporulating on PNA (scale bar = 250 μm); conidiogenous cells and conidia (scale bars = 10 μm).
Ramularia vacciniicola
**Ramularia vacciniicola** Crous & Thangavel, sp. nov.

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

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

*Mycelium* consisting of hyaline, smooth, septate, branched, 1.5–2 μm diam hyphae. *Conidiophores* micronematous, reduced to conidiogenous cells. *Conidiogenous cells* erect on hyphae, subcylindrical, straight, hyaline, smooth, 3–10 × 1.5–2.5 μm; scars thickened, darkened, somewhat refractive, 0.5 μm diam. *Secondary ramoconidia* hyaline, smooth, subcylindrical to narrowly fusoid-ellipsoid, 0(–1)-septate, 10–20(–30) × 2–2.5 μm, with 1–3 apical hila, thickened, darkened, somewhat refractive, 0.5–1 μm diam. *Conidia* in branched chains (–8), hyaline, smooth, guttulate, aseptate, narrowly fusoid-ellipsoid, (5–)8–10(–11) × (2–)2.5(–3) μm; hila thickened, darkened, somewhat refractive, 0.5–1 μm diam.

**Culture characteristics.** Colonies flat, spreading, with sparse aerial mycelium and even, lobate margins, reaching 20 mm diam after 2 wk at 25 °C. On MEA surface dark violet, reverse sepia. On PDA surface and reverse dark violet. On OA surface dirty white with diffuse dark violet pigment in agar.

**Typus.** New Zealand, Rotorua, on Vaccinium sp. (Ericaceae), 2015, R. Thangavel (holotype CBS H-23100, culture ex-type CPC 29365 = T15_05165F = CBS 142537 = ICMP 22047, ITS, LSU, actA, his3, and tef1 sequences GenBank KY979877, KY979829, KY979862, KY979881, and KY979905, MycoBank MB820963; CPC 29368 = CBS 142537, CPC 29367–29368, ITS, LSU, actA, his3, and tef1 sequences GenBank KY979775–KY979777, KY979830–KY979832, KY979863–KY979865, KY979882–KY979884, and KY979906–KY979907.

Notes — The genus *Ramularia* is linked to *Mycosphaerella* sexual morphs (Videira et al. 2015a, b). However, the older name *Ramularia* was selected over that of *Mycosphaerella* (Kirk et al. 2013, Wijayawardene et al. 2014, Rossman et al. 2015) for these fungi. Braun (1998) treated two *Ramularia* spp. known from *Vaccinium*. *Ramularia vacciniicola* is easily distinguished from *R. vaccinii* based on its smaller conidial dimensions (USA, conidia ellipsoid-ovoid, subcylindrical-fusoid, 10–20 × 2–5 μm). Conidia of *R. multiplex* are also somewhat larger (USA, conidia ellipsoid-ovoid, subcylindrical-fusoid, 6–15 × 1.5–5 μm), and further distinct in that the latter species forms well-developed fascicles with conidiophores. Furthermore, *R. vacciniicola* is also phylogenetically distinct from all species presently known from culture (see Videira et al. 2016). Based on a megablast search using the ITS sequence of the ex-type strain, the best match was to *R. proteae* (GenBank NR_145097; Identities = 524/526 (99 %), no gaps), followed by *R. stellenboshensis* (GenBank NR_145101; Identities = 520/526 (99 %), no gaps). Based on a megablast search using the *actA* sequence of the ex-type strain, the best match is *R. stellenboshensis* (GenBank KX287798; Identities = 568/575 (99 %), no gaps), followed by *R. rumicicola* (GenBank KX287786; Identities = 543/576 (94 %), 2 gaps (0 %)). Based on a megablast search using the *his3* sequence of the ex-type strain, the best match was to *R. proteae* (GenBank KX288939; Identities = 374/376 (99 %), no gaps), followed by *R. stellenboshensis* (GenBank KX288966; Identities = 370/376 (98 %), no gaps).

**Colour illustrations.** Blueberry Cottage berry farm, New Zealand; conidiophores sporulating on PNA; conidiophores and conidial chains. Scale bars = 10 μm.
**Harknessia communis** Crous, sp. nov.

**Etymology.** Name refers to the wider host range of this species.

**Classification.** *Harknessiaceae, Diaporthales, Sordariales, Mycetes.*

Folicocolous. *Conidiomata* pycnidioide, separate to gregarious, subepidermal, becoming erumpent, stromatic, globose, up to 300 μm diam, with irregular opening and border of yellowish furfuraceous cells; wall of *textura angularis.* *Conidiophores* reduced to conidigenous cells lining the inner cavity. *Conidigenous cells* 5–12 × 3–6 μm, ampulliform to subcylindrical, hyaline, smooth, invested in mucilage, proliferating percurrently at apex. *Conidia* (13–)14–15(–16) × (9–)10(–11) μm (av. 14.5 × 10 μm) in vitro, broadly ellipsoidal, apex acutely rounded, aseptate, apiculate, pale yellow-brown, thick-walled, smooth, lacking striations, multi-guttulate. Basal appendage (3–)5–8(–11) × 2–2.5 μm in vitro, hyaline, tubular, smooth, thin-walled, devoid of cytoplasm. *Spermatia* not seen.

**Culture characteristics.** Colonies spreading, fluffy, with moderate to abundant aerial mycelium, covering dish in 2 wk at 25 °C. On MEA surface dirty white, reverse luteous. On PDA surface and reverse dirty white. On OA surface dirty white.

**Typus.** *Australia,* Western Australia, Denmark, Mount Lindsay Walk Trail, on leaf litter of *Podocarpus* sp. (*Podocarpaceae*), 19 Sept. 2015, P.W. Crous (holotype CBS H-23101, culture ex-type CPC 29028 = CBS 142538, ITS, LSU, and *cmdA* sequences GenBank KY979778, KY979833, and KY979868, MycoBank MB820964).

**Additional specimens examined.** *Australia,* Western Australia, Denmark, Lights Beach, on Leucopogon verticillatus (*Ericaceae*), 19 Sept. 2015, P.W. Crous, HPC 731, CPC 29468; Williams Nature Reserve, 10 km north west of the Williams town, on *Melaleuca* sp. (*Myrtaceae*), 18 Sept. 2015, P.W. Crous, HPC 732, CPC 29470, ITS, LSU, and *cmdA* sequences GenBank KY979779–KY979781, KY979834–KY979836, and KY979869–KY979871.

**Notes.** Species of *Harknessia* have a cosmopolitan distribution and are commonly associated with leaves and twigs of a wide range of plants, but they are especially common on *Myrtaceae* and *Proteaceae* (Crous et al. 2012b). Although they appear to be common endophytes, and several species are regarded as important foliar pathogens, the majority of species appear to be of little economic importance (Park et al. 2000). *Harknessia communis* is phylogenetically related to (see phylogenetic tree in *Fungal Planet* 591) *H. ravenstreetina* (conidia broadly ventricose, (14–)16–18(–20) × (7–)8(–9) μm (av. 17 × 9 μm); Crous et al. 2012b), although it is morphologically distinct in having shorter and wider, broadly ellipsoid conidia. *Harknessia podocari* (on *Podocarpus parlatorei* from Argentina) has conidia that are 17.5–26 × 11–15 μm (Nag Raj 1993), thus larger than those of *H. communis* reported here.

Based on a megablast search using the ITS sequence of the ex-type strain, the best matches were to numerous species of *Harknessia* with 99 % similarity, e.g. *H. ravenstreetina* (GenBank JQ706113; Identities = 429/431 (99 %), no gaps), followed by *H. spermatoidea* (GenBank JQ706120; Identities = 626/632 (99 %, 6 gaps (0 %)), and *H. uronycocoides* (GenBank AY720740; Identities = 597/603 (99 %), 5 gaps (0 %)). However, based on a megablast search using the *cmdA* sequence of the ex-type strain, the best matches were equal to or less than 96 % similar to species of *Harknessia* in the NCBI GenBank nucleotide database.

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Harknessia banksiae
Harknessia banksiae  

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

**Classification.** Harknessiaceae, Diaporthales, Sordariomycetes.

Folicolous. *Conidiomata* pycnidioïd, separate to gregarious, subepidermal, becoming erumpent, stromatic, globose, up to 250 μm diam., with irregular opening and border of yellowish furfuraceous cells; wall of *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity. *Conidiogenous cells* 6–10 × 3–4 μm, ampulliform to subcylindrical, hyaline, smooth, invested in mucilage, proliferating percurrently at apex. *Conidia* (20–)22–26(–28) × (11–)12–13(–14) μm (av. 23 × 12.5 μm) in vitro, broadly fusoid-ellipsoid, apex acutely rounded, aseptate, apiculate, pale yellow-brown, thick-walled, smooth, lacking striations, multi-guttulate. Basal appendage (3–)4–6(–10) × 2–2.5 μm in vitro, hyaline, tubular, smooth, thin-walled, devoid of cytoplasm. *Spermatia* not seen.

**Culture characteristics.** Colonies spreading, fluffy, with moderate to abundant aerial mycelium, covering dish in 2 wk at 25 °C. On MEA surface dirty white, reverse luteous. On PDA surface dirty white, reverse luteous. On OA surface salmon.

**Typus.** *Australia*, Western Australia, Albany, Stirling Range National Park, Stirling Range Drive, S34°22'19.4" E118°1'33.6", on leaves of *Banksia sessilis* (Proteaceae), 23 Sept. 2015, P.W. Crous (holotype CBS H-23102, culture ex-type CPC 29002 = CBS 142539, ITS, LSU, cmdA, and tub2 sequences GenBank KY979782, KY979837, KY979872, and KY979938, MycoBank MB820965).

**Additional specimen examined.** *Australia*, Western Australia, Murray Road (at Ranger Station), on leaves of *Banksia plumosa* (Proteaceae), 21 Sept. 2015, P.W. Crous, HPC 613, CPC 29443, ITS, LSU, cmdA, and tub2 sequences GenBank KY979783, KY979838, KY979873, and KY979939.

Notes — *Harknessia banksiae* is phylogenetically related to (see phylogenetic tree in Fungal Planet 591) *H. ravenstreetina* (conidia broadly venticose, (14–)16–18(–20) × (7–)8(–9) μm, av. 17 × 9 μm; Crous et al. 2012b), and *H. karwarrae* (conidia ellipsoid to ventricose, (12–)13–16(–19) × (10–)11(–12) μm, av. 15 × 11 μm; Lee et al. 2004), although it is distinct in having larger, broadly fusoid-ellipsoid conidia. Based on a megablast search using the ITS sequence of the ex-type strain, the best matches were to *H. ravenstreetina* (GenBank JQ706113; Identities = 429/431 (99 %), no gaps) and to *H. ellipsoidea* (GenBank JQ706087; Identities = 620/626 (99 %), 4 gaps (6 %)). However, based on a megablast search using the cmdA sequence of the ex-type strain, the best matches were to *H. eucalyptorum* (GenBank JQ706178; Identities = 467/483 (97 %), 2 gaps (0 %)) and to *H. ravenstreetina* (GenBank JQ706198; Identities = 463/484 (96 %), 4 gaps (0 %)). Based on a megablast search using the tub2 sequence of the ex-type strain, the best match was to *H. eucalyptorum* (GenBank JQ706136; Identities = 823/860 (96 %), 17 gaps (1 %)).
Harknessia banksiigena
Harknessia banksiigena Crous & Barber, sp. nov.

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

Classification — Harknessiaceae, Diaporthales, Sordariomycetes.

Foliicolous. Conidiomata pycnidoid, separate to gregarious, subepidermal, becoming erumpent, stromatic, globose, up to 250 μm diam., with irregular opening and border of yellowish furfuraceous cells; wall of textura angularis. Conidiophores reduced to conidiogenous cells lining the inner cavity. Conidiogenous cells 6–10 × 4–6 μm, ampulliform to subcylindrical, hyaline, smooth, invested in mucilage, proliferating percurrently at apex. Conidia (19–)21–24(–26) × (13–)14(–15) μm (av. 23 × 14 μm) in vitro, fusoid-ellipsoid, apex acutely rounded, aseptate, apiculate, pale yellow-brown, thick-walled, smooth, lacking striations, multi-guttulate. Basal appendage (1.5–)3–4(–7) × 2–2.5 μm in vitro, hyaline, tubular, smooth, thin-walled, devoid of cytoplasm. Spermatia not seen.

Culture characteristics — Colonies spreading, fluffy, with moderate to abundant aerial mycelium, covering dish in 2 wk at 25 °C. On MEA surface dirty white, reverse pale luteous. On PDA surface dirty white, reverse pale luteous. On OA surface dirty white.

Typus. AUSTRALIA, Western Australia, Perth, St. Claire Park, on leaves of Banksia sessilis var. cygnorum (Proteaceae), 24 June 2015, P.A. Barber (holotype CBS H-23103, culture ex-type CPC 28232 = CBS 142540, ITS, LSU, and cmdA sequences GenBank KY979784, KY979839, and KY979874, MycoBank MB820966).

Notes — Harknessia banksiigena is phylogenetically related to (see phylogenetic tree in Fungal Planet 591) H. renispora (conidia reniform, (13–)14–17 × 9–12.5 μm, av. 15.5 × 11 μm; Nag Raj 1993) and H. ellipsoidea (conidia broadly ellipsoid to subglobose, (9–)11–12(–13) × 7(–8) μm, av. 11.5 × 7 μm; Crous et al. 2012b), but can be distinguished morphologically by having larger, fusoid-ellipsoid conidia. Based on a megablast search using the ITS sequence, the best matches were to H. ravenstreetina (GenBank JQ706113; Identities = 430/431 (99%), no gaps) and to H. ellipsoidea (GenBank JQ706087; Identities = 618/624 (99%), 2 gaps (0%)). However, based on a megablast search using the cmdA sequence, the best matches were to H. eucalyptorum (GenBank JQ706178; Identities = 469/482 (97%), 1 gap (0%)) and to H. ravenstreetina (GenBank JQ706198; Identities = 465/483 (96%), 3 gaps (0%)).
Harknessia banksiae-repens
**Fungal Planet 589 – 20 June 2017**

**Harknessia banksiae-repens** Crous, sp. nov.

Etimology. Name refers to Banksia repens, the host from which this fungus was first collected.

Classification — Harknessiaceae, Diaporthales, Sordariomycetes.

Folicorous. *Conidiocoma* pycnidioïd, separate to gregarious, subepidermal, becoming erumpent, stromatic, globose, up to 250 μm diam, with irregular opening and border of yellowish furfuraceous cells; wall of *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity. *Conidiogenous cells* 5–10 × 4–6 μm, ampulliform to subcylindrical, hyaline, smooth, invested in mucilage, proliferating percurrently at apex. *Conidia* (19–)20–23(–26) × (10–)11–12(–13) μm (av. 22 × 12 μm) in vitro, fusoid, apex acutely rounded, aseptate, apiculate, pale yellow-brown, thick-walled, smooth, lacking striations, frequently with central zone of pale pigment along the length of conidium, multi-guttulate. Basal appendage (2–)3–8(–10) × 2–2.5 μm in vitro, hyaline, tubular, smooth, thin-walled, devoid of cytoplasm. *Spermatia* hyaline, smooth, narrowly fusoid-ellipsoid, (2–)3–8(–10) × 2–2.5 μm.

Culture characteristics — Colonies spreading, fluffy, with moderate to abundant aerial mycelium, covering dish in 2 wk at 25 °C. On MEA surface dirty white, reverse saffron. On PDA surface and reverse dirty white. On OA surface salmon.

**Typus. AUSTRALIA.** Western Australia, Murray Road (at Ranger Station), on leaves of *Banksia repens* (Proteaceae), 21 Sept. 2015, P.W. Crous (holotype CBS H-23104, culture ex-type CPC 29006 = CBS 142941, ITS, LSU, cmdA, and tub2 sequences GenBank KY979785, KY979840, KY979875, and KY979930, MycoBank MB820967).

Additional specimen examined. AUSTRALIA. Western Australia, Albany, Stirling Range National Park, Stirling Range Drive, on leaves of *Stirlingia* sp. (Proteaceae), 23 Sept. 2015, P.W. Crous, HPC 594, CPC 28874, ITS, LSU, and cmdA sequences GenBank KY979786, KY979841, and KY979876.

Notes — *Harknessia banksiae-repens* is phylogenetically related to (see phylogenetic tree in Fungal Planet 591) *H. ravenstreetina* (conidia broadly venticose, (14–)16–18(–20) × (7–)8–9 μm, av. 17 × 9 μm; Crous et al. 2012b) and *H. karwarrae* (conidia ellipsoid to ventricose, (12–)13–16(–19) × (10–)11(–12) μm, av. 15 × 11 μm; Lee et al. 2004), but is distinct in having larger, fusoid conidia. Based on a megablast search using the ITS sequence of the ex-type strain, the best matches were to *H. ravenstreetina* (GenBank JQ706113; Identities = 428/431 (99 %), no gaps) and to *H. ellipsosidaea* (GenBank JQ706087; Identities = 613/621 (99 %), 4 gaps (0 %)). However, based on a megablast search using the cmdA sequence of the ex-type strain, the best matches were to *H. eucalyptorum* (GenBank JQ706178; Identities = 467/482 (97 %), no gaps) and to *H. ravenstreetina* (GenBank JQ706198; Identities = 465/483 (96 %), 2 gaps (0 %)). Based on a megablast search using the tub2 sequence of the ex-type strain, the best matches were to *H. eucalyptorum* (GenBank JQ706136; Identities = 655/686 (95 %), 11 gaps (1 %)) and to *H. renispora* (GenBank AY720769; Identities = 653/687 (95 %), 9 gaps (1 %)).

Colour illustrations. Stirling Range National Park, Stirling Range Drive, with a diversity of plant species, including *Banksia victoria*; conidioma sporulating on PNA (scale bar = 250 μm); conidiogenous cells, conidia and spermatia (scale bars = 10 μm).

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Harknessia platyphyllae
**Harknessia platyphyllae** Crous, *sp. nov.*

**Etymology.** Name refers to *Eucalyptus platyphylla*, the host species from which this fungus was collected.

**Classification.** *Harknessiaceae, Diaporthales, Sordariomycetes.*

Folicolous. *Conidiomata* pycnidial, separate to gregarious, subepidermal, becoming erumpent, stromatic, globose, up to 250 μm diam, with irregular opening and border of yellowish furfuraceous cells; wall of *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity. *Conidiogenous cells* 10–20 × 3–4 μm, ampulliform to subcylindrical, hyaline, smooth, invested in mucilage, proliferating percurrently at apex. *Conidia* (16–)17–19(–21) × (11–)12–13(–15) μm (av. 18 × 12.5 μm) in vitro, broadly ellipsoid, apex acutely rounded, aseptate, apiculate, pale yellow-brown, thick-walled, smooth, striations along length of conidium, multi-guttulate. Basal appendage (4–)6–8(–20) × 2–2.5 μm in vitro, hyaline, tubular, smooth, thin-walled, devoid of cytoplasm. *Spermatia* hyaline, smooth, narrowly ellipsoid, 5–7 × 2–3 μm.

**Culture characteristics.** Colonies spreading, fluffy, with moderate to abundant aerial mycelium, covering dish in 2 wk at 25 °C. On MEA surface and reverse orange. On PDA surface and reverse pale luteous. On OA surface orange.

**Typus.** AUSTRALIA, Western Australia, Perth, King’s Park Botanic Gardens, on leaves of *Eucalyptus platyphylla* (Myrtaceae), 26 Sept. 2015, M.J. Wingfield (holotype CBS H-23105, culture ex-type CPC 28862 = CBS 142542, ITS, LSU, and cmdA sequences GenBank KY979787, KY979842, and KY979877, MycoBank MB820968).

**Notes.** *Harknessia platyphyllae* is phylogenetically related to (see phylogenetic tree in Fungal Planet 591) *H. ravenstreetina* and *H. karwarrae*. It is distinct from *H. karwarrae* (conidia ellipsoid to ventricose, (12–)13–16(–19) × (10–)11(–12) μm, av. 15 × 11 μm; Lee et al. 2004) and *H. ravenstreetina* (conidia broadly ventricose, (14–)16–18(–20) × (7–)8–(9) μm, av. 17 × 9 μm; Crous et al. 2012b), based on its broadly ellipsoid conidia. Based on a megablast search using the ITS sequence, the best matches were to *H. ravenstreetina* (GenBank JQ706113; Identities = 430/431 (99 %), no gaps) and to *H. karwarrae* (GenBank AY720748; Identities = 593/595 (99 %), no gaps). However, based on a megablast search using the cmdA sequence, the best matches were to *H. karwarrae* (GenBank AY720811; Identities = 468/473 (99 %), no gaps) and to *H. eucalyptorum* (GenBank JQ706177; Identities = 510/524 (97 %), no gaps).

**Colour illustrations.** *Eucalyptus platyphylla* in King’s Park Botanic Gardens; conidioma sporulating on PNA (scale bar = 250 μm), conidiogenous cells, conidia and spermatia (scale bars = 10 μm).
Harknessia pellitae
Fungal Planet 591 – 20 June 2017

**Harknessia pellitae** Crous & M.J. Wingf., *sp. nov.*

*Etymology.* Name refers to *Eucalyptus pellita,* the host species from which this fungus was collected.

*Classification.* — *Harknessiaceae,* Diaporthales, Sordariomycetes.

Folicolous. *Conidiomata* pycnidioïd, separate to gregarious, subepidermal, becoming erumpent, stromatic, globose, up to 200–350 \( \mu \)m diam, with irregular opening and border of yellowish furfuraceous cells; wall of *textura angularis.* *Conidiophores* reduced to conidiogenous cells lining the inner cavity. *Conidiogenous cells* 5–10 × 3–5 \( \mu \)m, ampulliform to subcylinindrical, hyaline, smooth, invested in mucilage, proliferating percurrently at apex. *Conidia* (12–)13–15(–16) × (8–)9(–10) \( \mu \)m (av. 14 × 9 \( \mu \)m) in vitro, ellipsoid, apex subobtusely rounded, aseptate, non-apiculate, pale yellow-brown, thick-walled, smooth, striations along length of the conidium, multi-guttulate. Basal appendage (3–)4–7(–10) × 2–2.5 \( \mu \)m in vitro, hyaline, tubular, smooth, thin-walled, devoid of cytoplasm. *Spermata* not seen.

Culture characteristics. — Colonies spreading, fluffy, with moderate to abundant aerial mycelium, covering dish in 2 wk at 25 °C. On MEA surface pale luteous, reverse luteous. On OA surface pale luteous.

**Typus.** MALAYSIA, Sabah, on leaves of *Eucalyptus pellita* (Myrtaceae), May 2015, M.J. Wingfield (holotype CBS H-23106, culture ex-type CPC 27606 = CBS 142543, ITS, LSU, and *cmdA* sequences GenBank KY979788, KY979843, and KY979878, MycoBank MB620869).

Notes — *Harknessia pellitae* is phylogenetically related to *H. ravenstreetina* (conidia broadly ventricose, (14–)16–18(–20) × (7–)8–9 \( \mu \)m; Crous et al. 2012b), but is distinct in having smaller, ellipsoid conidia. Based on a megablast search using the ITS sequence, the best matches were to *H. ravenstreetina* (GenBank JQ706113; Identities = 428/430 (99 %), no gaps) and to *H. renispora* (GenBank AY720737; Identities = 439/442 (99 %), 1 gap (0 %)). However, based on a megablast search using the *cmdA* sequence, the best matches were to *H. australiensis* (GenBank JQ706171; Identities = 467/482 (97 %), 1 gap (0 %)) and to *H. eucalyptorum* (GenBank JQ706177; Identities = 456/472 (97 %), no gaps).

**Colour illustrations.** *Eucalyptus pellita* trees growing in Malaysia; conidiomata sporulating on OA (scale bar = 300 \( \mu \)m); conidiogenous cells and conidia (scale bars = 10 \( \mu \)m).

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Harknessia malayensis
Harknessia malayensis Crous & M.J. Wingf., sp. nov.

Etymology. Name refers to Malaysia, the country from which this fungus was collected.

Classification — Harknessiaceae, Diaporthales, Sordariales. Foliicolous. Conidiomata pycnidoid, separate to gregarious, subepidermal, becoming erumpent, stromatic, globose, up to 250 μm diam, with irregular opening and border of yellowish furfuraceous cells; wall of textura angularis. Conidiophores reduced to conidiogenous cells lining the inner cavity. Conidiogenous cells 5–10 × 3–5 μm, ampulliform to subcylindrical, hyaline, smooth, invested in mucilage, proliferating percurrently at apex. Conidia (15)–16–18(–20) × (7–)8–9(–10) μm (av. 17 × 8.5 μm) in vitro, fusoid-ellipsoid, apex subobtusely rounded, aseptate, non-apiculate, pale yellow-brown, thick-walled, smooth, striations along length of the conidium, multi-guttulate. Basal appendage (1–)2–5(–8) × 2–2.5 μm in vitro, hyaline, tubular, smooth, thin-walled, devoid of cytoplasm. Spermata not seen.

Culture characteristics — Colonies spreading, fluffy, with moderate to abundant aerial mycelium, covering dish in 2 wk at 25 °C. On MEA surface and reverse luteous. On PDA surface and reverse pale luteous. On OA surface orange.

Typus. MALAYSIA, Sabah, on leaves of Eucalyptus pellita (Myrtaceae), May 2015, M.J. Wingfield (holotype CBS H-23107, culture ex-type CPC 28752 = CBS 142544, ITS, LSU, cmdA, and tub2 sequences GenBank KY979789, KY979844, KY979879, and KY979941, MycoBank MB820970).

Notes — Harknessia malayensis is phylogenetically related to (see phylogenetic tree in Fungal Planet 591) H. ravenstreetina (conidia broadly venticose, (14–)16–18(–20) × (7–)8–9 μm, av. 17 × 9 μm; Crous et al. 2012b) and H. renispora (conidia reniform, (13–)14–17 × 9–12.5 μm, av. 15.5 × 11 μm; Nag Raj 1993). Although it can be distinguished from H. renispora based on its conidial dimensions, it has similar conidial dimensions to that of H. ravenstreetina. However, conidia of the latter lack striations, whereas conidia of H. malayensis have striations along the length of the conidial body, which can be used to separate these two species if no DNA data were available. Based on a megablast search using the ITS sequence, the best matches were to H. ravenstreetina (GenBank JQ706113; Identities = 415/417 (99 %), no gaps) and to H. ellipsoidea (GenBank JQ706087; Identities = 608/622 (98 %), 11 gaps (1 %)). However, based on a megablast search using the cmdA sequence, the best matches were to H. ellipsoidea (GenBank JQ706174; Identities = 460/472 (97 %), 1 gap (0 %)) and to H. ravenstreetina (GenBank JQ706198; Identities = 459/473 (97 %), 2 gaps (0 %)). Based on a megablast search using the tub2 sequence, the best matches were to H. australiensis (GenBank JQ706130; Identities = 396/412 (96 %), 1 gap (0 %)) and to H. ravenstreetina (GenBank JQ706157; Identities = 395/413 (96 %), 2 gaps (0 %)).
Acidiella americana
Fungal Planet 593 – 20 June 2017

Acidiella americana M. Kolařík, Jurjević & Hubka, sp. nov.

Etymology. americana (Latin, fem. adj.) from America. Refers to the country of origin.

Classification — Teratosphaeriaceae, Capnodiales, Dothideomycetes.

Mycelium 2–3.5 µm diam, smooth, septate, pale to medium brown. Conidia produced by fragmentation of hyphae, oblong-elliptical to cylindrical, 7–21 × 2–3.5 µm.

Culture characteristics — (in the dark at 25 °C after 14 d): Colonies on 4 % malt extract agar (MEA, pH 7) attained 25 mm diam; compact, wrinkled, surface velvety, black. Growth optimum at pH 7 and minimum at pH 2. Growth on MEA at pH 3 was 3 mm diam. Growth at 37 °C (MEA, pH 7) was 12 mm diam. Growth in response to the acidity gradient was tested according to Hujslová et al. (2013).

Typus. USA, New Jersey, wall of a cooling tower, June 2014, isol. Ž. Jurjević as EMSL No. 2404 (holotype PRM 935805, culture ex-type CCF 5435 = CBS 141992, ITS, LSU, and SSU sequences GenBank LT627242, LT671442, and MycoBank MB819188).

Notes — Acidiella encompasses two species, A. bohemica and A. uranophila. They probably represent a single species, that has been isolated from highly acidic soil and mine water (Hujslová et al. 2013, Vázquez-Campos et al. 2014, Kolařík et al. 2015). Their colonies, arthroconidia and mycelium morphology is undistinguishable from A. americana. Acidiella bohemica and A. uranophila have a growth optimum at pH 5 and exhibit growth at pH 2 in contrast to A. americana. Based on ITS sequences, A. americana is 95 % similar to A. bohemica (490/516 bp, GenBank JN713913) and A. uranophila (489/515 bp, JQ904602). The LSU sequence shows highest level of similarity to A. bohemica (99 %, 740/746 bp, KF901984) and A. uranophila (99 %, 815/820 bp, KF857170). SSU sequence differs in a single position (1029/1030 bp) from A. uranophila (KF857169) and A. bohemica (JQ172750).

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Colour illustrations. Cooling tower in New Jersey; colonies on malt extract agar after 2 wk at 25 °C; mycelium disintegrating into conidia (scale bars = 10 µm).

A 50 % majority consensus rule maximum likelihood tree based on ITS and LSU rDNA sequences showing the relationships of taxa within the genus Acidiella. Partitioning scheme and substitution models for analyses were selected using PartitionFinder v. 1.1.1 (Lanfear et al. 2012): the HKY+I model was proposed for the ITS1 + ITS2 region, and a K80 model for the 5.8S + LSU region. The tree was constructed with IQ-TREE v. 1.4.0 (Nguyen et al. 2015). The dataset contained 13 taxa and a total of 813 characters of which 102 were variable and 23 parsimony-informative. Support values at branches were obtained from 500 bootstrap replicates. Only bootstrap support values ≥ 70 % are shown; ex-type strains are indicated by ‘T’. The tree is rooted with Eupenidiella venezuelensis CBS 106.75.
Coprinopsis pseudomarcescibilis
Coprinopsis pseudomarcescibilis Heykoop, G. Moreno & P. Alvarado, sp. nov.

Etymology. Name reflects its morphological similarity to Coprinopsis marcescibilis.

Classification — Psathyrellaceae, Agaricales, Agaricomycetes.

Cap 12–50 mm broad, 10–30 mm high, convex to conical convex, with prominent umbo, glabrous, sometimes somewhat wrinkled, orange brown when young, then dark beige brown or date colour, hygrophanous, after drying it becomes first pale greyish beige to ochreaceous beige, then greyish white. Margin in some specimens somewhat incurved, faintly striate when moist. Veil white, abundant in young specimens forming a firm collar, connecting margin of cap with stem and in addition a layer of radially arranged fibrils present in a 1–2 mm broad zone along margin; later, while detaching itself from stem, the collar forms an appendiculate belt soon splitting into more or less irregular foci; finally, in older specimens veil evanescent and progressively disappearing. Gilli close, ascending, adnate, first greyish, then blackish, with white fimbriate edge; lamellulae present. Stem (25–)65–130 × 2–7 mm, cylindrical, central, hollow, longitudinally striate (more pronounced in the upper part), white with pale ochreaceous tinges; apex pruinose, central, hollow, 1.86–2.08, ellipsoid, smooth, with apical germ pore, in NH₄OH (10 %) reddish brown to orange brown. Basidia 4-spored, 20–35 × 11–13 µm, clavate, hyaline; pseudoparaphyses often seen. Pleurocystidia not observed. Marginal cells: cheilocystidia 25–40 × 11–15 µm, very abundant and densely packed, narrow, utriform, sometimes subcapitate; sphaeropedunculate and clavate cells extremely rare and difficult to observe, e.g. 16 × 12 µm; all cells thin-walled, colourless. Hymenophoral trama in NH₄OH (10 %) consisting of hyaline thin-walled hyphae, without encrustations. Pileiellps a cutis consisting of a layer of thin elongate hyphae 8–18 µm diam, on top of a much thicker layer of more cellular structure consisting of broadly ellipsoid, subglobose or irregularly shaped cells, up to 40 µm diam. Clamp connections present. Stipitellips a cutis consisting of elongate septate hyphae 5–12 µm diam. Caulocystidia abundant, similar in size and shape to cheilocystidia. Veil fibrillose consisting of elongate and septate hyaline hyphae, 3–11 µm diam; many of these hyphae ending in terminal cystidia, 34–60 × 10–18 µm, utriform to subcapitate, or cylindrical, which probably are caulocystidia detached from stem together with veil.

Habitat & Distribution — Growing solitary to gregarious on calcareous loamy soil under Salsola vermiculata or different gramineae. So far known from Spain, Germany, Italy (Sicily), and Finland but probably often mistaken for Coprinopsis marcescibilis.

Typus. Span., Alcalá de Henares, Parque de los Cerros, under Salsola vermiculata on calcareous loamy soil, 4 Dec, 2014, M. Heykoop, G. Moreno & M. Lizárraga (holotype AH 33711, ITS and LSU sequences GenBank KY698008 and MF033345, MycoBank MB203344).

Colour illustrations. Spain, Alcalá de Henares, El Gurugú, calcareous loamy soil with Salsola vermiculata, where the holotype was collected; basidiomata; cheilocystidia; cheilocystidia basidium and spores; basidia; spores under LM; smooth spores with central germ pore under SEM (from the holotype); scale bars = 1 cm (basidiomata), 10 µm (cheilocystidia), 10 µm (cheilocystidia, basidium and spores), 10 µm (basidia), 10 µm (spores under LM), 2 µm (spores under SEM).

Consensus phylogram obtained in MrBayes v. 3.1 from an ITS alignment of genus Coprinopsis. Values next to nodes represent Bayesian PP and maximum likelihood BP (RAxML). Only nodes supported by > 0.95 PP or > 70 % BP are annotated. The main group of sequences has been collapsed for publication.

Additional specimens examined. Coprinopsis pseudomarcescibilis: Span., Alcalá de Henares, Parque de los Cerros, under Salsola vermiculata on calcareous loamy soil, 4 Dec, 2014, M. Heykoop, G. Moreno & M. Lizárraga, paratype AH 33710, ITS sequence GenBank KY698009; ibid., AH33712, ITS sequences GenBank KY698007; Alcalá de Henares, Campus Universidad de Alcalá, on calcareous soil among grasses, 1 Dec, 2016, J.A. Picado (paratype AH 33725, ITS sequence GenBank KY698006). Coprinopsis udidula: Span., Alcalá de Henares, El Gurugú, under Ulmus pumila and Dactylis glomerata in border of Pinus halepensis wood, 12 Dec, 2014. G. Moreno & M. Heykoop, AH 33714, ITS, LSU sequences GenBank KY698004, KY698005; ibid., AH 33715, ITS, LSU sequences GenBank KY698002, KY698003.

Notes — Coprinopsis pseudomarcescibilis is characterised by its moderately large basidiocarps with appendiculate veil splitting into more or less irregular foci, the absence of pleurocystidia, and the large and dark spores (11–16.5(–17) × 6–8 µm).

In our ITS phylogeny Coprinopsis pseudomarcescibilis is included in a clade together with C. marcescibilis and C. musae, the latter recently described by Örstadius et al. (2015). All three species are psathyrelloid members of Coprinopsis which share the presence of a pileipellis forming a cutis and the absence of pleurocystidia. Coprinopsis musae differs from C. pseudomarcescibilis in having smaller and paler spores and smaller basidiomata. Coprinopsis pseudomarcescibilis is genetically close to C. marcescibilis (2.21 % nucleotide differences in the ITS sequence, 11/497), but it differs from the latter by its slightly longer spores, 13.3–14.5 µm (mean values 4 coll.) vs 11.6–12.8 µm (mean values 18 coll.; Kits van Waveren 1985), and the veil splitting into more irregular foci on cap margin instead of triangular denticles. However, C. pseudomarcescibilis and C. marcescibilis seem to be sibling species (i.e., cryptic sister species; Bickford et al. 2008) which are difficult to separate only based on morphology.

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Cyathus aurantogriseocarpus
Cyathus aurantogriseocarpus R. Cruz, J.S. Góis, M.P. Martín, K. Hosaka & Baseia, sp. nov.

Etymology. Named in reference to the orange-grey colour of the exoperidium.

Classification — Nidulariaceae, Agaricales, Agaricomycetes. Basidiomata infundibuliform, 5–6 mm in height, 4–6 mm in width at the upper part, not expanded in the mouth or tapering abruptly at the base. Emplacement 1.5–2 mm in width, conspicuous, greyish brown (7F3 Komenerp & Wanscher 1978). Exoperidium hisutre, orange-grey (SB2), provided with 0.5–0.75 mm long tomentum, arranged in regular and flexible tufts. External wall conspicuously plicated, with 0.3–0.5 mm between the striae. Mouth finely frimbriated, in a continuous pattern, 0.2 mm in height, greyish brown (7F3). Endoperidium bright brown grey to greyish brown (7C2–7D3), conspicuously plicated, with 0.2–0.4 mm between the striae. Perceptible bright contrasting with the exoperidium. Stipe 1 mm long, greyish brown (7F3). Epiphragm not observed. Peridioles brown grey (7F2) to black, 1.5–1.75 × 1.2–1.5 mm, in number of 6 (average) in each basidiomata, circular to irregular in shape, smooth surface, tunic indistinct and provided with double layered cortex. Basidiospores smooth, hyaline, 32.5–47 × 22.5–28.5 µm (L = 38.9 µm; W = 25.9 µm; n = 30 spores), slightly ellipsoidal to elongated (Q = 1.25–1.79), elliptical in average (Qe = 1.51), apicule absent and spore wall 2.3–4.9 µm in thickness.

Type. BRAZIL, Rio Grande do Norte, Natal, Pitimbú, on decaying wood, 12 Feb. 2013, A.S. Medeiros (holotype UFRN-Fungos 2798, ITS and LSU sequences GenBank KX966026 and KX966027, MycoBank MB818580).

Notes — Following Brodie’s (1975) classification, C. aurantogriseocarpus can be grouped in group VI (poepigii) or in group VII (striatum), and in the classification of Zhao et al. (2007) this species belongs to the striatum group. Morphologically this species resembles C. bulleri, C. griseocarpus, and C. rudis. However, C. aurantogriseocarpus can be distinguished from those species by the strong plication in the external wall, larger spores (5 × 8.5 µm in C. bulleri), 7.5–9 × 5–6 µm in C. griseocarpus, and 9–12 × 5 µm in C. rudis), and the double-layered cortex, unlike the single-layered cortex of these three species (Brodie 1967, 1975, Brodie & Sharma 1980). Cyathus aurantogriseocarpus is also similar to C. poepigii since this species also has large spores (30–42 × 20–28 µm), but C. poepigii has small basidiomata (7–10 mm in height × 5–6 mm in width), with paler coloured peridium, and peridioles less than 2 mm diam (Tulasne & Tulasne 1844, Brodie 1975). From the species published after Brodie (1984), C. aurantogriseocarpus can be compared with C. magnomuralis due to its large spores (28–49.5 × 23–42 µm); however, C. magnomuralis differs from C. aurantogriseocarpus by having globose to elliptical spores (slightly elliptical to elongated in C. aurantogriseocarpus). Additionally, C. magnomuralis has thick spore walls up to 6.5 µm, endoperidium with strong bright colour contrasting with the external wall colour, and smaller emplacement (3–6 mm diam) (Cruz & Baseia 2014). In the ITS phylogeny, C. aurantogriseocarpus groups in the same clade with C. stercoreus and C. lignilantanae; all these species possess a double-layer cortex, and spores reaching more than 20 µm diam. However, C. stercoreus is distinguished by the absence of striae in the peridium, inconspicuous emplacement, woolly tomentum, endoperidium with platinum bright colour, spores not exceeding 31 µm in length, and spore walls less than 2.5 µm in thickness. Cyathus lignilantanae has basidiomata above 7 mm in height, internal wall with platinum bright colour, peridioles with 2.5–2 × 1.5–2 mm, spores smaller than 25.5 µm in length and 17 µm in width, and with thin walls not reaching 2 µm (Martín et al. 2015).

The 50 % majority rule Bayesian tree inferred from ITS sequences with the model T92 + G using MrBayes v. 3.2.6 (Ronquist et al. 2012). A maximum parsimony analysis was done (PAUP v. 4.0a147), and similar topology was obtained (not shown). Bayesian posterior probabilities (PP) from 10 M generations, and maximum parsimony bootstrap (MPbs) support values from 10 000 replications and random addition sequences repeated 10 times, are indicated on the branches. The star (*) represents the nodes with PP = 1.00 and MPbs = 100 %. Sequences from type species are marked with asterisks (*). The new species proposed is shown in bold. The scale bar indicates the estimated number of nucleotide substitutions per site. Sequence alignment is available in TreeBASE (submission ID: S20237).

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Eremiomyces innocentii
Eremiomyces innocentii Ant. Rodr. & Bordallo, sp. nov.

Etymology. Named after Mauro Innocenti, for his outstanding contribution to knowledge of hypogeous fungi of the Canary Islands.

Classification — Pezizaceae, Pezizales, Pezizomycetes.

Ascomata hypogeous, 2–4 cm diam, subglobose, pale brown colour with pink spots and yellowish cracks in fresh, pale brown colour in exsiccate. Peridium 150–400 µm thick, well-defined, concolorous with surface in cross section, prosenchymatous, composed of parallel arranged hyphae, 15–20 µm broad, walls 1–2 µm thick, some hyphal cells inflated to 50 µm diam, yellowish in KOH. Gleba composed of dark red pockets of fertile tissue marbled by yellowish, sterile veins of subparallel hyphae 3–5 µm diam. Odour faint, not distinctive. Asci amyloid, thin-walled, mostly cylindrical, sometimes clavate-cylindrical, sessile or short-stipitate, 150–180(–200) × 30–40 µm, with 6–8 uniseriate spores, randomly arranged in fertile pockets. Ascospores globose, (16–)17–20(–21) µm diam (av. = 18.5 µm) including ornamentation, (15–)16–18(–18.5) µm (av. = 17 µm) without ornamentation, by maturity yellow and ornamented with conical, blunt spines, 1–2 µm long, 1 µm diam at the base, sometimes truncated, often joined at the base to form ridges.

Habitat & Distribution — Arid zones of Tenerife (Canary Islands), in calcareous sandy soils, associated with Helianthemum canariense. The annual rainfall is about 50–300 mm in the lower levels (Inframediterranean), specifically around 200 mm in the study area. Rainfall can be high in a short period of time in the case of storms from the west or the south of the islands, reaching 200 mm or more in 3–4 d.

Typus. Span., Canary Islands, Tenerife, Fasnia, 1 Feb. 2006, M. Innocenti (holotype MUB Fung-j117, ITS sequence GenBank KJ678905, MycoBank MB820114).

Additional specimen examined. Span., Canary Islands, Tenerife, Fasnia, Feb. 2006, M. Innocenti, MUB Fung-j117.

Notes — The genus Eremiomyces was established by Ferdman et al. (2005) to accommodate E. echinulatus, a southern African desert truffle originally described as Choiromyces echinulatus from the Cape Province in South Africa by Marasas & Trappe (1973). The genus Eremiomyces has two accepted species, E. echinulatus also collected in the Kalahari Desert of Botswana and Namibia (Ferdman et al. 2005, Trappe et al. 2008, 2010) and E. magnisporus, collected in semi-arid hills around Alcalá de Henares, central Spain (Alvarado et al. 2011). Eremiomyces innocentii is the first Eremiomyces species described with amyloid asci. Eremiomyces magnisporus was described from a single ascoma where asci could not be found due to the advanced maturity of the sample (Alvarado et al. 2011). However, it differs from other Eremiomyces spp. by its amyloid asci with larger spores (16–18 µm) than E. echinulatus (10–14 µm) and E. magnisporus (14–17 µm), excluding the ornamentation.

The evolutionary history based on the ITS-rDNA alignment was inferred using the Neighbour-Joining method. The bootstrap consensus tree inferred from 500 replicates is taken to represent the evolutionary history of the taxa analysed. Branches corresponding to partitions reproduced in less than 50 % bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (500 replicates) are shown next to the branches. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Maximum Composite Likelihood method and are in the units of the number of base substitutions per site. All positions containing gaps and missing data were eliminated from the dataset (Complete deletion option). There was a total of 432 positions in the final dataset. Phylogenetic analyses were conducted in MEGA v. 4.

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Ganoderma mizoramense
**Fungal Planet 597 – 20 June 2017**

**Ganoderma mizoramense** Zothan Zama, Blanchette, Held, C.W. Barnes, *sp. nov.*

**Etymology.** Named after the state of Mizoram, where it was found growing on a tree near Mizoram University in Aizawl, Mizoram, northeast India.

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

Mature *basidiomata* annual, pileate, stipitate, aplaneous, soft and leathery when fresh and woody to corky when dried, more or less flabelliform, semi-circular, irregular surface; absence of any ‘growing zones’; dark brownish to dark reddish brown, homogenous context structure 2–20 mm. *Pileus* upper surface reddish brown when fresh, liver brown when dry, surface hard and glabrous, margin white, rounded, thickened, lower surface white when fresh, pale brown when dry. *Context* uniformly ochraceous or cinnamon, firm; tubes 1–12 mm long, dark brown, not stratified. *Stipe* sometimes absent, but more commonly present and often prominent; twisted and irregular; varnished and coloured like the cap; often bearing pores. *Pore surface* smooth, creamy to snuff brown when dry, 4–5 per mm, round to somewhat obliquely oval, 187–278 × 134–228 μm (av. 229 × 191 μm); SD 19, 20; n = 50), disseipments 33–88 μm (av. 56 μm; SD 14; n = 50). *Hyphal system* trimitic, generative hyphae hyaline, slightly thicker than skeletal hyphae with clamp connections at very few places, no branching observed; skeletal hyphae most prevalent in the basidiocarp, 1.5–7 μm (av. 4.29 μm; SD 1.14; n = 50); binding hyphae hyaline and highly branched, 2–5.5 μm (av. 3.83 μm; SD 0.92; n = 50). *Basidia* tetraeterigmatic basidium. *Basidiospores* brown, ellipsoid with a truncate base, bitunicate, verrucose, 10–12.5 × 6–9 μm (av. 11.10 × 7.6 μm; SD 0.62, 0.54; n = 30). *Chlamydospores* not observed.

**Culture characteristics —** No live culture obtained.

**Typos.** Hox, Mizoram State, on angiosperm trees in hill country near Aizawl, Mizoram, Apr. 2016, J.M.C. Vabeikhokei & Zohmangaiha (holotype MIN 948145, holotype ITS sequence GenBank KY643750 and LSU sequence GenBank KY747490, MycoBank MB818802).

**Notes —** The complete ITS sequence of the *G. mizoramense* holotype was used for the BLASTn search. The first 22 highest blast hits were to *G. steyaertanum*. The first three were downloaded for phylogenetic analysis (Glen et al. 2014). The next highest scoring other *Ganoderma* species was an isolated *G. lucidum* sequence. The *G. lucidum* sequence plus a few other isolated sequences interspersed among additional *G. steyaertanum* sequences were downloaded for phylogenetic analysis, with *G. destructans* used for the outgroup. The final alignment was edited by hand for alignment errors. Sequences were trimmed to the ITS1, after the CATTA motif (Schoch et al. 2014) and to the end of ITS2 to the CTCT/GACC motif described by Moncalvo & Buchanan (2008). *Ganoderma mizoramense* had 7 to 8 single bp differences, no gaps, from the three *G. steyaertanum* sequences included in the phylogenetic analysis.

The phylogenetic tree with *G. mizoramense* 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 destructans* (KR183857 and KR183858) is the outgroup. Bootstrap support values ≥ 50 % are given above branches. The phylogenetic position of *G. mizoramense* is indicated in bold. The *Ganoderma* species is followed by the sample ID and country code, in order of appearance: ZAF = South Africa; CHN = China; NPL = Nepal; IND = India; IDN = Indonesia.

**Colour illustrations.** Native trees and landscape in the Hill Country of Mizoram, India where the fungus was found on a dead tree, photo by Karlyn Eckman (background); young freshly collected basidiocarp; older basidiocarp; basidiospores by light microscopy; skeletal hyphae; Scale bars = 5 cm (basidiocarps), 10 μm (microscopic structures).

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Gyroporus pseudocyaneus
Gyroporus pseudocyanescens G. Moreno, Carлавilla, Heykoop, Manjón & Vizzini, sp. nov.

Eymology. Name reflects its morphological similarity to Gyroporus cyanescens.

Classification — Gyropraceae, Boletales, Agaricomycetes.

Pileus 4—10 cm diam, at first more or less hemispherical, then becoming convex to applanate convex, sometimes depressed at centre, the surface velutinous, dry, strawcoloured to yellow cream, often cracking at maturity becoming more or less brownish to brown yellowish; context in pileus whitish, staining strongly dark blue or blue indigo when bruised or cut, this colour being retained in drying and in some herbarium specimens; margin straight and regular, somewhat exceeding. Tubes short, 5—10 mm in length, free, sometimes emarginated towards the stipe, whitish; pore surface concolorous with the tubes when young, at maturity yellowish, very small, circular to angular at maturity, 1—2 per mm. Stipe 5—9 x 1.5—2.5 cm, cylindrical to clavate, brittle, developing cavities or becoming hollow at maturity, concolorous with the pileus, with a pseudo-annular zone in the upper part where it is paler and smooth, in pileus whitish, staining dark blue or blue indigo when handled or bruised, and by fruiting on acid soil under different deciduous Quercus species.

In our phylogeny (MycoBank supplementary data), Gyroporus pseudocyanescens belongs to a clade together with G. cyanescens, G. lacteus, G. pseudolacteus, G. ammophilus and G. castaneus. The closest species to G. pseudocyanescens is G. cyanescens, which should be considered a complex of cryptic species (Vizzini et al. 2015). These authors typified G. cyanescens by selecting Bulliard’s plate 369 (Bulliard 1788) as a lectotype (iconotype) and a collection from Italy under Pinus sylvestris as an epitype. Sequences of G. cyanescens have been deposited in GenBank. Gyroporus pseudocyanescens and G. cyanescens seem to be sibling species which are difficult to separate only based on morphology. Gyroporus lacteus differs from G. pseudocyanescens by its whitish pileus covered by large and irregular scales, and by fruiting in Mediterranean woods with Pinus pinea and Quercus ilex. Gyroporus pseudolacteus differs from G. cyanescens by its larger size, longer stipe in relation to the pileus diameter (up to 1.5—2 times longer) and by fruiting under Pinus pinaster. Gyroporus ammophilus, a species linked to Pinus species growing in littoral areas on sandy calcareous soils (Castro & Freire 1995), differs from G. pseudocyanescens by its slightly pinkish to salmon colored context staining light blue when handled or bruised (Muñoz 2005). According to our molecular studies it must be considered an autonomous species. Gyroporus castaneus differs from G. pseudocyanescens by its chestnut-brown pileus and white context not blueing when handled or bruised. Gyroporus sulfureus, known only from the type material (Kalamées 1899), is considered to be a synonym of G. cyanescens (Muñoz 2005). We have attempted to sequence this species (holotype) but have not succeeded, so no conclusion on the former can be drawn.
Hodophilus indicus
**Fungal Planet 599 – 20 June 2017**

**Hodophilus indicus** K.N.A. Raj, K.P.D. Latha & Manim., *sp. nov.*

**Etymology.** Name refers to India, the country where this species was first discovered.

**Classification — Clavariaceae, Agaricales, Agaricomycetes.**

*Basidiocarps* small, somewhat ophalminoid. *Pileus* 6–13 mm diam, hemispherical to convex with a very shallow central depression; surface greyish brown (6D3/OAC773) at the centre and on the striations, and brownish orange (6C5/OAC653) elsewhere, strongly hygrophanous and becoming paler soon after collection, finely pellucid-striate, somewhat tawky when wet, smooth or occasionally finely appressed-squamulose at the centre, somewhat plicate towards the margin; margin incurved when young, becoming decurved or slightly reflexed with age, crenate or somewhat wavy. *Lamella* 16–18, arcuate-subcurrent, rather waxy, moderately close, pale orange (6A4, 6A5/OAC655), up to 4 mm wide, with lamellulae in 1–3 tiers; edge entire to the naked eye, finely torn under a lens, concolorous with the sides. *Stipe* 12–26 × 1.5–3.5 mm, central, terete, rather, equal, flexuous, solid; surface greyish orange (6B3/OAC633) all over, glabrous to the naked eye, weakly pruinose all over under a lens, somewhat tawky when wet; base with scanty basal mycelium. *Odour* and *taste* not distinctive. *Basidiospores* 4–5 × 3–5 (4.57 ± 0.37 × 4.17 ± 0.45) µm, Q = 1.0–1.66, Qm = 1.11, subglobose to globose, smooth, thin-walled, hyaline, inamylloid, hilar appendage up to 1 µm. *Basidia* 32–46 × 4–7 µm, narrowly clavate, often tapered and flexuous towards the base, pale yellow, thin-walled, 4-spored; sterigmata up to 4 µm long. *Basidioles* 29–45 × 3–6 µm, cylindrical to narrowly clavate, often flexuous, thin-walled, pale yellow. *Pleurocystidia* absent. *Lamella-edge* sterile with crowded marginal elements. *Marginal cells* 14–48 × 3–8 µm, cylindrical or flexuous, occasionally septate, hyaline, thin-walled. *Lamellar trama* subregular to somewhat irregular; *hyphae* 2–16 µm wide, thin-walled, hyaline or pale yellow, inamylloid. *Subhymenium* poorly developed. *Pilea trama* parallel interwoven; *hyphae* 3–12 µm wide, thin-walled, hyaline, inamylloid. *Pileipellis* a hymeniderm with diverticulate elements; *hyphae* 3–10 µm wide, thin-walled, hyaline; terminal elements 12–32 × 10–16 µm, diverticulate, broadly clavate or inflated-clavate, thin- to slightly thick-walled, hyaline. *Stipitipellis* a cutis disrupted by patches of ascending or erect, somewhat diverticulate caulocystidia; *hyphae* 3–7 µm wide, thin- to slightly thick-walled, hyaline or with a pale-yellow wall pigment. *Caulocystidia* multiseptate, terminal elements 14–88 × 4–8 µm, cylindrical-flexuous, clavate, obtuse or at times with apical constrictions, thin- to slightly thick-walled, inamylloid. *Clamp connections* not observed on any hyphae.

**Habit, Habitat & Distribution —** In small groups, on humus-rich soil. Known only from the type locality in Kerala State, India.

**Typus.** **INDIA.** Kerala State, Wayanad District, Tirunelli, Brahmagiri Hill, from a shola forest of rolling shola grasslands of Western Ghats, 17 Nov. 2010, K.N. Anil Raj (holotype CAL 1526, ITS and LSU sequences GenBank KY807130 and GenBank KY815097, MycoBank MB820656).

**Notes —** The combination of characters such as the hymeniderm-type pileipellis composed of clavate or inflated-clavate terminal elements and the absence of clamp connections indicates that this species belongs to the genus *Hodophilus* (Adamčík et al. 2016, Birkebak et al. 2016). *Hodophilus hymenocephalus*, a species originally described from USA by Smith & Hesler (1942, as *Hygrophorus hymenocephalus*), shows similarity with *H. indicus* in having a similar-looking pileus with somewhat similar surface features, almost similar number and attachment of lamellae, similar-sized basidiospores (4–5 µm), an irregular lamellar trama and a similar pileipellis. *Hodophilus hymenocephalus*, however, is distinguished by its pale pinkish cinnamon to brown pileus, hair-brown lamellae, longer stipe (3–4 cm), a hymenium devoid of marginal cells and the geographical location. Additionally, a pairwise comparison of the ITS sequences (GenBank KY807130/DQ484066) of these two species showed only 87 % sequence similarity (with a hig h-e value). *Hodophilus micacea* shares a few features with *H. indicus* such as a hygrophanous pileus with somewhat similar surface features, rather similarly-attached lamellae, somewhat similar-sized basidiospores (3.5–4–5(–5.5) × (3–)3.5–4.5 µm), a hymenium devoid of pleurocystidia, an irregular lamellar trama, similar pileipellis and stipitipellis structure and clamped hyphae. *Hodophilus micacea*, however, differs from *H. indicus* in having slightly larger basidiomata with a dark grey-brown pileus, very distant, dark grey-brown, slightly purple-tinted lamellae with a pale brown edge, a beige-brown stipe with pruinosity confined to the apex, a weak aromatic odour, infrequent presence of ellipsoid or broadly ellipsoid basidiospores, occasional absence of cystidia on the lamella-edge, hyphae of lamellar trama with an encrusting pigment, a pileipellis with larger terminal elements (23–70 × 11–42 µm) and a stipitipellis with smaller (18–50 × 5–14 µm) and inflated-clavate terminal elements (Arnolds 1990).

A BLASTn search using the ITS (593 bp) sequence of *H. indicus* showed *H. micacea* (GenBank KU882873; 91 % identity) as the closest hit. While using the LSU (706 bp) sequence, *Hodophilus micacea* (GenBank KP257222; 93 % identity), a collection from Slovakia resulted as the closest hit. ML and BI analyses of the combined ITS and LSU dataset recovered two large clades designated as *Hodophilus micacea* and *Hodophilus foetens* superfamilies following Adamčík et al. (2016). *Hodophilus indicus* was found nested inside the *Hodophilus micacea* superclade with strong posterior probability (0.98 PP) and weak bootstrap support (58 % BS). Within this *Hodophilus micacea* superclade, *H. indicus* resolved as an independent lineage well-differentiated from other species of the clade with significant support values (0.93 PP/72 % BS) (MycoBank supplementary data).

**Colour illustrations.** Kerala State, Wayanad District, Tirunelli, Brahmagiri Hill, shola forest type locality; basidiocarps, basidiocarps, basidium, lamella-edge showing marginal cells, pileipellis, terminal elements of pileipellis. Scale bars = 10 mm (basidiocarps), 10 µm (microscopic structures).

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Humidicutis dictiocephala
**Humidicutis dictiocephala** A. Barili, C.W. Barnes & Ordoñez, sp. nov.

*Etymology.* Name reflects the morphology of the pileus.

*Classification.* — *Hygrophoraceae, Agaricales, Agaricomycetes.*

*Basidiomata.* stipitate, pileus conical, umbonate, 20 mm high, 22 mm diam, orange, velvety-rough surface, radially fibrillose, margin rimose. No distinct odour or taste. *Lamellae* emarginate, thick, waxy, pale orange to whitish, anastomosed, subdistant, with lamellae present, smooth margin. *Stipe* central, 80 × 5 mm, yellowish at the apex, pale orange at the base, hollow, smooth, dry. *Pileipellis* as cutis with cylindrical parallel hyphae, clamp connections absent. *Lamellar trama* irregular to subregular.

*Basidia* 36.5–54 × 6–10.5 μm, elongate, clavate, tetrasporic, toruloid clamp connections at the base, sterigmata 5.5–9 μm long. *Basidiospores* 6.5–9 × 4.5–6 μm, ellipsoid, subcylindrical, smooth with subtle wall, hyaline, non-amyloid, non-dextrinoid, not metachromatic, without germ pore, apiculate.

*Habit.* — Solitary, on the ground, high montane forest. *Typus.* Ecuador, Zamora Chinchipe province, Yacuri National Park, alt. 3234 m, May 2015, C. Vivanco (holotype QCAM6000, ITS and LSU sequences GenBank KY689661 and KY780120, MycoBank MB820098, TreeBASE Submission ID 20678).

Notes — According to the description of Young (1999), *Humidicutis dictiocephala* belongs to the subgenus *Humidicutis*. However, the combination of observed characters does not lead to a species identification. Horak’s (1990) key for *Humidicutis* indicates *H. conspicua* as the closest species, but it differs from *H. dictiocephala* by having a fibrillose, dry pileal surface, margin whole, lamellae not bright orange but whitish in colour, and larger basidia and basidiospores. The description of Lodge et al. (2014) places *H. dictiocephala* within the genus *Humidicutis*, differing from the closely related *Porpolomopsis* by the short hyphae of the lamellar trama and by the adnate lamellae. The complete ITS sequence of 571 bp of the *H. dictiocephala* holotype was used for the BLASTn search. Phylogenetic analysis was done using representative sequences from the top BLASTn hit species. The results gave the two highest scores as *Humidicutis* sp. from Belize (GenBank KF291110), and from Puerto Rico (GenBank KF291150) reported by Lodge et al. (2014). Following the *Humidicutis* sp. in the BLASTn search results were 11 sequences of *Hygrocybe auratocephalus*, but only two representative sequences were used for the sequence alignment. Finally, we included sequences from two uncultured fungal clones, both ectomycorrhizal, and two sequences of *Humidicutis marginata* for the outgroup.

The phylogenetic tree 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). *Humidicutis marginata* (GenBank KF291144 and DQ490625) was chosen as outgroup. Bootstrap support values ≥ 50% are given above branches. The phylogenetic position of *H. dictiocephala* is indicated in **bold**. The species name is followed by the GenBank ID, and where known, the country of origin indicated as: USA = United States; ECU = Ecuador; PRI = Puerto Rico; BLZ = Belize; MDG = Madagascar; AUS = Australia.

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Hygrocybe sangayensis
**Hygrocybe sangayensis** A. Barili, C.W. Barnes, J.A. Flores & Ordoñez, sp. nov.

**Etymology.** Name reflects the locality from where the fungus was collected, Sangay National Park.

**Classification —** Hygrophoraceae, Agaricales, Agaricomycetes.

*Basidiomata* stipitate, pileus flat, 50 mm diam, slightly depressed in the centre, margin smooth, slightly lobate, rimose, dry surface, covered by small dark brown scales, more concentrated towards the centre and dissociating towards the margin, fibrillose. Orange yellowish, slight to fleshy texture, fragile, flesh whitish yellow, with no colour changes upon mechanical injury. No distinct *odour or taste*. *Lamellae* adnate to unicate, thick, ventricose, smooth margin, whitish yellow to orange towards the margin, pruinose, with 3–7 lamellae in between. *Stipe* central, 70 × 8–9 mm, yellow at the apex, orange towards the centre and yellow to whitish at the base, hollow, fragile. *Pileipellis* filamentous as a cutis to subcutis, elongated hyphae 57 × 14 µm with septa and bifurcations, *gill trama* present, non-differentiated pileocystidia. *Clamp connections* present, non-differentiated pileocystidia. *Gill trama* parallel to subregular. *Macrobasidia* 14 × 14 µm with septa and bifurcations, multiguttulate, *sterigmata* 5.5–10 µm. *Microbasidia* 49 × 12 µm, 2- and 4-spored, clavate, elongate, multiguttulate, sterigmatia 5.5–10 µm. *Microbasidia* 45 × 7.5 µm 2-, 3- and 4-spored, clavate, elongate, similar to macrobasidia but much narrower, guttulate, sterigma ~ 8.5 µm. *Macrospores* 12 × 7.5 µm, cylindrical to ellipsoid, sometimes depressed in the centre, smooth, hyaline, non-amyloid, apiculate. *Microspores* 6.5 × 4.5 µm, cylindrical to ellipsoid, sometimes depressed in the centre, smooth, hyaline, non-amyloid, apiculate. *Cheilocystidia* 45.5 × 10 µm, pleurocystidia mucronate to lageniform 39.5 × 6.5 µm.

**Habitat —** Solitary, on the ground among leaf litter, foothill forest.

**Typus.** ECUADOR, Morona Santiago province, Sangay National Park, alt. 1510 m, Jan. 2015, C. Vivanco (holotype QCAM4254, ITS-LSU sequence GenBank KY582489, MycoBank MB819814).

Notes — According to the description of Pegler & Fiard (1978), *H. sangayensis* belongs to the section *Firmae*, with *H. occidentalis* as the closest species based on morphological characters. However, it differs by having a scaly pilial surface, non-glabrous, non-translucent, non-striated, with the lamellae margin non-heterogeneous. The complete ITS sequence of the *H. sangayensis* holotype was used for the BLASTn search. The results gave the highest score to a *Hygrocybe* sp. (GBM-2014, GenBank KP012900) from Australia, but with only 44 % coverage and 87 % identity. The top seven BLASTn hit species with full ITS sequences were downloaded for the phylogenetic analysis. There were significant indels among the aligned sequences. Noting gaps greater than five bases, ITS1 showed gaps of 7, 13, 6 and 10 bases, and ITS2 had gaps of 16, 6 and 9 bases.

The phylogenetic tree with *H. sangayensis* 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 Akaiake Information Criterion (AICc). *Hygrocybe appalachianensis* (GenBank FJ596914 and FJ596915) is the outgroup. Bootstrap support values ≥ 50 % are given above branches. The phylogenetic position of *H. sangayensis* is indicated in **bold**. The *Hygrocybe* species is followed by the GenBank ID, and where known, the country of origin, in order of appearance: USA = United States; ECU = Ecuador; PRI = Puerto Rico; AUS = Australia; RUS = Russia; ITA = Italy.
Hygrocybe macrosiparia
**Hygrocybe macrosiparia** A. Barili, C.W. Barnes, J.A. Flores & Ordoñez, sp. nov.

**Etymology.** Name reflects the morphological similarity to *Hygrocybe siparia*, but with reference to its larger size.

**Classification.** Hygrophoraceae, Agaricales, Agaricomycetes.

**Basidiomata** stipitate, pileus flat, 25 mm diam, margin smooth, involute, surface dry, covered by dark brown scales, more concentrated towards the centre and dissociating towards the margin, orange yellowish, slight fleshy texture, with no colour changes upon mechanical injury. No distinct odour or taste. Lamellae adnate, distant, with one lamella in between, thick, ventricose, smooth margin, yellow, lighter in colour towards the margin.

**Stipe** central, 70 × 5 mm, yellow at the apex and base, orange at the centre, the orange pigment is distributed in striae parallel to the stipe, cylindrical, hollow, fragile. Pileipellis as a cutis subtrichoderm, hyphae 70 × 22.5 µm. Gill trama parallel.

**Macrobasidia** 51.5 × 13.5 µm, 2- and 4-spored, clavate, elongate, guttulate, sterigmata 6.5 µm. **Microbasidia** 41.5 × 7 µm, 4-spored, clavate, elongate similar to macrobasidia but much more narrow, non-guttulate but if present sparse, sterigmata 6 µm. **Macrospores** 10.5 × 6.5 µm, cylindrical to ellipsoid, some times depressed in the centre, smooth, hyaline, non-amyloid, apiculate. **Microspores** 7 × 4.5 µm, cylindrical to ellipsoid, sometimes depressed in the centre, smooth, hyaline, non-amyloid, apiculate. Cheilocystidia and pleurocystidia absent. Clamp connections present.

**Habitat.** Solitary, on the ground among leaf litter, foothill forest.

**Typus.** Ecuador, Morona Santiago province, Sangay National Park, alt. 1524 m, Jan. 2015, A. Salazar (holotype QCAM 4359, ITS-LSU sequence GenBank KY582490, MycoBank MB819896).

Notes — According to the description of Pegler & Fiard (1978), *H. macrosiparia* belongs to the section Firmae. The closest species based on morphological characters is *H. siparia*. However, it differs by having a flat and non-umbilicate pileus which exceeds in 5 mm the maximum size reported, and an orange yellowish colour instead of crimson. The complete 578 bases of ITS sequence of the *H. macrosiparia* holotype was used for the BLASTn search. The results gave the highest score to a *H. occidentalis* (PR-6493, GenBank EU435151) from Puerto Rico, but with only 63 % coverage and 87 % identity. The top seven BLASTn hit species were downloaded for phylogenetic analysis. There were significant indels among the aligned sequences. Noting gaps greater than five bases, ITS1 showed gaps of 10, 6, 7 and 6 bases, and ITS2 had gaps of 10, 10, 6 and 6 bases.

The phylogenetic tree with *H. macrosiparia* 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). *Hygrocybe appalachianensis* (GenBank FJ596914 and FJ596915) is the outgroup. Bootstrap support values ≥ 50 % are given above branches. The phylogenetic position of *H. macrosiparia* is indicated in bold. The *Hygrocybe* species are followed by the GenBank ID, and where known, the country of origin, in order of appearance: USA = United States; ECU = Ecuador, PRI = Puerto Rico; ITA = Italy; RUS = Russia; CAN = Canada.
Inocybe parvicystis
Inocybe parvicystis

F.J. Rodr.-Campo & Esteve-Rav., sp. nov.

Etymology. From Latin parvus and cystidium, referring to the small size of cystidia.

Classification — Inocybaceae, Agaricales, Agaricomycetes.

Basidiomata agaricoid and stipitate. Pileus 15–40 mm, convex to plano-convex, not or hardly umbonate, not or very slightly hygrophanous; margin deflexed to straight, often wavy with age, in young basidiomata often showing appendiculate rests of the velipellis; colour initially very pale, cream whish (Mu 7.5Y 9/2), then yellow ochraceous (Mu 10YR 6/6) or pale yellowish brown (Mu 7.5Y 8/4), in old or washed specimens often becoming copper yellow to orange yellow (Mu 7.5YR 3/6), often paler at the centre or in areas where velipellis is present; surface smooth, becoming rather fibrillose at margin but never rimose, often agglutinating soil remains, when young covered by white to greyish velipellis, often persisting in old specimens, especially towards the centre. Lamellae rather crowded (L = 36–44), adnexed to emarginate, ventricose, with lamellulae (l = 1–2), initially pale grey to beige, then yellowish brown with a faint olivaceous reflection at maturity, edge whish to concearious, crenulate. Stipe 35–55 x 5–8 mm, straight to curved towards base, cylindrical with a bulbous to abruptly bulbous base, less often subbulbous or clearly marginate bulbous, bulb 8–10.2 mm wide; colour whish (Mu 7.5Y 9/2), ochraceous (Mu 10YR 6/6) or even yellowish brown (Mu 7.5Y 8/4) in old basidiomata, often conceaneous to pleus in aged specimens, especially towards base; surface sparsely fibrillose, fibrillo-pruinose towards the apex (descending to 1/6–1/4, rarely –1/3), sometimes covered by abundant fibrillose veil towards the lower half in young basidiomata. Texture fibrous, whitish, unchanging. Smell slightly pungent, taste slightly raphanoid. Spores (7.5–)8–9–10–11.5) x (4.5–)5–5.5–6–(6.5) µm, Qm: 1.25–1.6–2 (n = 165), smooth, yellowish, ellipsoid to mostly amygdaliform to rhomboid with subovagal apex, most often showing a typical ‘callus’ or sometimes a small and distinct germ pore at the apex, walls –0.5 µm thick. Basidia (25.5–)27–31.5–36.5(–46.5) x (6.5–)7–8–9–10(–12) µm (n = 32), (2–)4–spored, clavate. Lamella edge practically sterile, composed by numerous cheilocystidia and more or less common clavate to pyriform paracystidia, hyaline to yellowish in some specimens. Cheilocystidia very numerous, not protruding, narrow, (30.5–)34–43–46–(54.5) x (8–)8.5–9.5–11.5–(12.5) µm (n = 41), cylindrical, subsutiform or subclavate, often attenuate pedicellate towards base and with sinuose outline, heavily crystallophorous at the apex, walls (1.5–)2–3 µm thick, moderately to pale to distinctly yellow in 5 % NH₄OH. Pleurocystidia numerous, similar to cheilocystidia, (35–)37.5–45.5–52–(56) x (7–)8.5–10–12(–13.5) µm (n = 51). Hymenophoral trama regular, formed by cylindrical to ellipsoidal cells, 4–20 µm wide. Stipitellips a cutis bearing sparse caulocystidia at the apex (so 1½–1/4, rarely –1/3), similar to hymenial cystidia and often broader, (34.5–)35.5–42–(43.5) x (9–)9.5–13–(15.5) µm, mostly crystalliferous, accompanied by cylindrical, sublageniform, clavate or pyriform paracystidia.

Notes — Colour codes are taken from Munsel (1988) and Kuyper (1986). The presence of a well-developed velipellis, pale yellow-ochraceous colour, bulbous stipe, cauliocystidia reduced to the upper 1/4 of the stipe, hymenial cystidia short, narrow, pedicellate and very crystallophorous, and spores provided with a ‘pseudopore’ in most cases, are distinct features of I. parvicystis. It grows in acidic soils in evergreen oak forests (Quercus ilex, Q. suber), often mixed with maquis (Cistus spp.) vegetation in the western Mediterranean areas. Among other leiosporeous species showing short cystidia and a bulbous stipe, I. mystica is devoid of velipellis, its colours are warmer orange-ochraceous, the spores are devoid of a germ pore and smaller (7.5–)8.5–9.4(–9.7) x (4.7–)5.2–5.7(–5.8) µm, Qm: 1.45–1.6–1.8 (n = 30), holotype measurements; it develops in frondose temperate forests in Europe (Stangi & Glowinski 1980). Kuyper (1986) considered the American species I. cryptocystis conspecific with I. mystica, but the results of our ITS analyses from both prove that, though phylogenetically closely related, they are distinct species. Inocybe cryptocystis (Stuntz 1954) is also devoid of a distinct velipellis and shows very short, mostly subtriform to oblong-ellipsoid cystidia, with obtuse to truncate, non-pedicellate base. The interpretation of I. confusa in Heim (1931), could well be referred to I. parvicystis; Heim’s description fits the general characters of the new species, and the habitat is said to be ‘Mediterranean, under evergreen oaks’; unfortunately, no voucher material has been preserved of Heim’s collections.

ITS sequences of I. parvicystis do not seem related to those generated from I. cryptocystis or I. mystica type collections. The most closely related ITS sequences come from ectomycorrhizae studies in Californian oaks (KC791069, Taniguchi et al. 2013) and Pakistani Himalayan pine forests (KF679813, Hanif & Khalid, unpubl.). Both collections gathered under Abies pinsapo (AH 18898, 18899) differ from I. parvicystis, because of their paler colour. They probably represent an independent phylogenetic lineage different from I. parvicystis, as the ITS sequence produced from one of them had up to 19/562 bp different from the other I. parvicystis samples (including 4-bp and 7-bp insertions, and a 3-bp deletion not observed in any other sequence of the latter species). Collections studied by the authors are indicated in bold in the phylogenetic tree for ITS sequences (see figure in MycoBank).
Keratinophyton turgidum

Rahul Sharma, & Shouche, sp. nov.

Etymology. Refers to the swollen nature of conidiogenous cells (Latin turgidus means swollen).

Classification — Onygenaceae, Onygenales, Eurotiomycetes.

Hyphae hyaline, septate, smooth-walled, 1.5–6.5 μm wide, straight, profusely branched. Conidiophores made up of swollen hyphae which are otherwise undifferentiated from vegetative hyphae, hyaline, unbranched, 2–18 × 1.5–2 μm. Conidiogenous cells non-specialised, swollen, 2.5–4 μm wide and 6.5–8.5 μm long. Conidia pyriform to oval, smooth-walled, terminal or lateral aleuropiconidia, 5–7 × 3.5–5 μm, borne singly on mostly elongate and swollen fertile hyphae. Conidia have a broad basidial scar, 1.5–2.5 μm diam, left after rhizoidal dehiscence from conidiophores. Intercalary conidia present, elongated barrel-shaped, 11.5 × 4.5 μm. Chlamydotheca absent. Racquet hyphae present. Keratinolytic. Sexual morph not observed.

Culture characteristics — Colony on Sabouraud dextrose agar (SDA) at 28 °C white, circular, cottyton with central area having dense sporulation (5–5.5 cm diam after 16 d), reverse pale brown with dark brown central spot. Growth at 37 °C on SDA 3.5 cm diam after 7 d of incubation.

Typus. INDIA, Buldana, barber shop soil, 2016, R. Sharma (holotype MCC H-1006, cultures ex-type MS 335 = CBS 142596, ITS and LSU sequences GenBank KY290503 and KY962732, MycoBank MB819848).

Notes — An NCBI BLASTn search of ITS sequences showed closest similarity to be 95 % with Chrysosporium indicum (CBS 117.63, NR_145203); 94 % with Keratinophyton terreus (CBS 504.63, AJ439443); 93 % with Keratinophyton punsolae (IMI 334818, AJ439440); 91 % with Keratinophyton hispanicus (IMI 335379, AJ439438); 88 % with Keratinophyton durum (FMR 5651, AJ439434). The description of the new species is based on the morphology of its chrysosporium-like aleuropiconidia, and the ITS sequence similarity which positions it in the Keratinophyton clade. The genus Keratinophyton currently has six recognised species which are all sexual and produce ascomata (Sutton et al. 2013). These species can be distinguished on the basis of morphologically different ascospores and genetically by differences in the ITS region (Cano et al. 2002, Guarro et al. 2012). Due to the one-fungus one-name concept asexual species are now placed in genera conventionally comprising only sexual forms. A recent example is the dermatophyte genus Nannizziella which previously comprised of species which were all sexual but now contain two asexual species, N. duboisii and N. praecox (De Hoog et al. 2016). Currently, species within a genus are recognized as entities which are phylogenetically distinct from their neighbours irrespective of whether they are sexual or asexual. Likewise, the monophyletic Keratinophyton clade also contains several asexual species which have a Chrysosporium morph, and require renaming in Keratinophyton. In the present case the name Keratinophyton is chosen to represent this new species instead of Chrysosporium since it is phylogenetically more distant from the type species of Chrysosporium (C. merdarium). The two species that produce smooth-walled conidia and form a monophyletic cluster with K. turgidum are K. hispanicum and K. punsolae. Conidia of K. turgidum are pyriform and smaller (5–7 × 3.5–5 μm) than those of K. punsolae (8.5–13 × 5.5–9 μm) but slightly larger than those of K. hispanicum (3.5–8 × 2–3 μm).

Colour illustrations. A village barber’s shop in Maharashtra, India. Macron morphology: Colony after 15 d on SDA (5 cm diam). Micromorphology: conidia attached to swollen conidiophores, intercalary conidia, conidia formed on conidiophores on extensively branched hyphae, smaller conidia on swollen conidiophores formed when grown at 37 °C on SDA. Scale bars = 10 μm.

Neighbour-Joining phylogram of ITS sequence data using MEGA v. 5.05, showing the phylogenetic position of CBS 142596 in the Keratinophyton clade. Branches with bootstrap support values ≥ 50 % are shown (based on 1 000 replicates).
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**Myotisia** Kubátová, M. Kolařík & Hubka, *gen. nov.*

*Etymology.* Refers to the bat (*Myotis myotis*) on who’s excrement the fungus was found.

*Classification — Onygenaceae, Onygenales, Eurotiomycetes.*

*Ascomata* gymnothecial, solitary or in clusters, whitish, spherical. *Peridium* consisting of a network of branched hyaline septate hyphae; surface peridial hyphae undulated or dichotomously branched, asperulate, 2.5–3 µm thick. *Asci* 8-spored, globose, 6–7 µm diam; *ascospores* 1-celled, globose, hyaline, whitish in mass, smooth walled (delicately reticulate by SEM), 2–3 µm diam. *Conidial* morph malbranchea-like, *arthroconidia* verruculose, terminal arthroconidia obvoid to ellipsoidal, intercalary arthroconidia alternate, barrel-shaped to ellipsoidal, 3.5–6.5 × 2.5–3 µm.

*Culture characteristics —* (in the dark at 25 °C after 28 d): Colonies on cornmeal agar (CMA) attained 39–48 mm diam, mycelium sparse, granular appearance due to production of ascomata, reverse uncoloured. Colonies on potato dextrose agar (PDA) and yeast extract malt extract agar (YM) similar to CMA, however with apricot-coloured reverse. Colonies at 20, 15 and 10 °C on all three media were similarly coloured. Well-developed ascomata occurred on CMA and PDA at 20 and 25 °C after 2–3 wk. Growth rates at different temperatures on CMA/PDA/YM (in mm): 10 °C 12–14/14–18/10–17; 15 °C 31–34/29–35/23–29; 20 °C 45–48/40–45/25–36; 25 °C 39–48/40–46/35–55; 30 °C 10–16/10–16/8–18; 37 °C no growth.

**Notes —** CCF 5407 has an identical ITS sequence to that of CCF 5406. Based on ITS sequences, *M. cremea* is 99 % (486/492) similar to strain UAMH 3124 (GenBank KF477240) isolated from a reptile during the study of Sigler et al. (2013); the similarity of the other sequences deposited in GenBank did not exceed 87 %. The LSU rDNA sequence exhibited the highest similarity (95 %) to various species of *Arthroderma, Microsporum* and *Onygyena*. Sigler et al. (2013) investigated taxonomic position of the strain UAMH 3124 and classified it as an undetermined fungus at generic as well as species level, which belonged to the phylogenetic lineage of *Arachnotheca glomerata*. We used the LSU sequence dataset of onygenalean fungi published by Hirooka et al. (2016) to assess the phylogenetic position of *M. cremea* (data not shown). The fungus was resolved as a member of the family *Onygenaceae* and clustered with members of the ‘*Onygenaceae* 3’ clade together with *Arachnotheca glomerata* UAMH 3551 (NR_111884) with 94 % sequence similarity (553/591). Morphologically, *Myotisia* can be easily distinguished from *Arachnotheca* by smooth-walled ascospores.

**Myotisia cremea** Kubátová, M. Kolařík & Hubka, *sp. nov.*

*Etymology.* Refers to the cream colour of ascomata and mycelium.

*Ascomata* gymnothecial, solitary or in clusters, whitish, spherical, 320–480 µm diam. *Peridium* consisting of a network of branched hyaline septate hyphae; surface peridial hyphae undulated or dichotomously branched, asperulate, 2.9–4.5 µm thick. *Asci* 1-celled, globose, hyaline, whitish in mass, smooth-walled (delicately reticulate by SEM), 2–3 µm diam. *Conidial* morph malbranchea-like, *arthroconidia* undulated or dichotomously branched, asperulate, 2.5–3 µm.

*Culture characteristics —* (in the dark at 25 °C after 2–3 wk): Well-developed ascomata occurred on CMA and PDA at 20, 15 and 10 °C on all three media were similarly coloured. Growth rates at different temperatures on CMA/PDA/YM (in mm): 10 °C 12–14/14–18/10–17; 15 °C 31–34/29–35/23–29; 20 °C 45–48/40–45/25–36; 25 °C 39–48/40–46/35–55; 30 °C 10–16/10–16/8–18; 37 °C no growth.

**Notes —** CCF 5407 has an identical ITS sequence to that of CCF 5406. Based on ITS sequences, *M. cremea* is 99 % (486/492) similar to strain UAMH 3124 (GenBank KF477240) isolated from a reptile during the study of Sigler et al. (2013); the similarity of the other sequences deposited in GenBank did not exceed 87 %. The LSU rDNA sequence exhibited the highest similarity (95 %) to various species of *Arthroderma, Microsporum* and *Onygyena*. Sigler et al. (2013) investigated taxonomic position of the strain UAMH 3124 and classified it as an undetermined fungus at generic as well as species level, which belonged to the phylogenetic lineage of *Arachnotheca glomerata*. We used the LSU sequence dataset of onygenalean fungi published by Hirooka et al. (2016) to assess the phylogenetic position of *M. cremea* (data not shown). The fungus was resolved as a member of the family *Onygenaceae* and clustered with members of the ‘*Onygenaceae* 3’ clade together with *Arachnotheca glomerata* UAMH 3551 (NR_111884) with 94 % sequence similarity (553/591). Morphologically, *Myotisia* can be easily distinguished from *Arachnotheca* by smooth-walled ascospores.

**Additional material examined.** CZECH REPUBLIC, Bohemian Karst, Malá Amerika mine, specimen PRC 3708, ITS sequence GenBank LT627243, LT627240, and LT671443, MycoBank MB819230.

**Colour illustrations.** Underground tunnel of Malá Amerika mine (Czech Republic) with cluster of Myotis myotis individuals; colonies on cornmeal agar after 2 mo at 25 °C; malbranchea-like asexual morph; arthroconidia; gymnothecial ascoma, peridial hyphae; ascospores. Scale bars = 20 µm, scale bar of ascospores = 2 µm.

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Neodactylaria obpyriformis
**Neodactylaria** Guevara-Suarez, Deanna A. Sutton, Wiederhold & Gené, *gen. nov.*

**Etymology.** Neo- meaning new; -dactylaria referring to the asexual genus *Dactylaria*. Name reflects its morphological similarity with the genus *Dactylaria*.

**Classification — Incertae sedis, Dothideomycetes.**

*Mycelium* consisting of branched, septate, smooth-walled, hyaline to subhyaline hyphae. *Conidiophores* macronematous, mononematous, erect, straight or flexuous, septate, unbranched, brown. *Conidiogenous cells* integrated, terminal or intercalary, polyblastic, sympodial, with several denticle-like loci. *Conidia* solitary, 1-celled or sepatate, obpyriform or rostrate, often constricted at the septum, smooth-walled or echinulate, brownish, subhyaline towards the apex, often with a protuberant hilum. **Sexual morph** unknown.

**Type species.** *Neodactylaria obpyriformis* Guevara-Suarez, Deanna A. Sutton, Wiederhold & Gené. MycoBank MB820857.

**Neodactylaria obpyriformis** Guevara-Suarez, Deanna A. Sutton, Wiederhold & Gené, *sp. nov.*

**Etymology.** Name refers to the conidial shape.

*Mycelium* superficial or immersed, composed of branched, septate, thin-walled, smooth-walled, hyaline to subhyaline, 1–2 μm wide hyphae. *Conidiophores* solitary, straight or flexuous, septate, unbranched, smooth-walled, pale to mid-brown, 25–40 (–70) × 3–4 μm. *Conidiogenous cells* terminal or intercalary, polyblastic, sympodial, with short-cylindrical denticles. *Conidia* solitary, (0–)1-septate, constricted at the septum, obpyriform to slightly rostrate, 10–14 × 3–5 μm, with an obtuse apex and a hilum up to 1 μm long, finely echinulate, pale brown, subhyaline towards the apex. **Sexual morph** not observed.

Culture characteristics — (in darkness, at 25 °C after 7 d). Colonies attaining 14–19 mm diam on PDA, OA and PCA. On PCA and OA colonies flat, fleecose at the centre, cottyne towards the periphery, olive grey (3F2), margin smooth and entire; reverse grey (3E1); sporulation abundant. On PDA flat, white to cream-coloured, margin entire; sporulation sparse. The fungus does not grow at 37 °C.

**Typus.** USA, Arizona, Phoenix, from human bronchoalveolar lavage, D.A. Sutton, 2015 (holotype CBS H-23131, cultures ex-type UTHSCSA DI 15-121 = FMR 14604; ITS and LSU sequences GenBank LT839090 and LT839091, MycoBank MB820858).

Notes — *Neodactylaria obpyriformis* is morphologically similar to *Dactylaria kumamotoensis* and to *D. madresensis*, two *Dactylaria* species described by Matsushima (1981, 1983) from soil and plant debris in Japan and India, respectively. Although these fungi could be congeneric with *N. obpyriformis*, they are only known from the type collection and no living cultures are available for molecular comparison. Morphologically, both species mainly differ from the novel fungus in having larger conidia which can have more than one septum; i.e., in *D. kumamotoensis* they are 12–40 × 4–8 μm, 1–3-septate, and in *D. madresensis* 9–19 × 4.5–6 μm, 1–2 septa. *Neodactylaria obpyriformis* also resembles some *Pyricularia* species, such as *P. higginsii*, now accommodated in *Pseudopyricularia* (Klaubauf et al. 2014), or *P. valdalurensis*. However, the former has smooth, 2-septate conidia, 17.5–36.5 × 5.3–6.5 μm (Luttrell 1954, Klaubauf et al. 2014), and the latter has larger conidiophores (up to 240 μm long), and hyaline, smaller conidia (9–10 × 3–4 μm) (Subramanian & Vittal 1974). It is noteworthy that *Dactylaria* sensu De Hoog (1985) is a heterogeneous genus with species of different phylogenetic affinities (Crous et al. 2016), although its type species, *D. purpurella*, as well as those of the genera *Pyricularia* and *Pseudopyricularia* belong to the *Magnaporthales* (Sordariomycetes) (Bussaban et al. 2005, Klaubauf et al. 2014). Our phylogenetic analysis shows that *Neodactylaria* is related to *Dothideomycetes*, but with uncertain taxonomic position at the ordinal level.

Maximum likelihood (ML) tree obtained from the analysis of LSU sequence data. Bootstrap support values above 70 % are shown at the nodes. The alignment included 552 bp and was performed with ClustalW. The General Time Reversible model (GTR) with Gamma distribution and invariant sites (G+I) was used as the best nucleotide substitution model. Both the alignment and tree were constructed with MEGA v. 6.06 (Tamura et al. 2013).

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Candida rongomai-pounamu
Candida rongomai-pounamu Padamsee, B.S. Weir, Petterson & P.K. Buchanan, sp. nov.

Etymology. The specific epithet ‘rongomai-pounamu’ (Māori), referring to the ‘treasure of Rongomai’. The students who discovered this new species and chose the name are in a Science, Technology, Engineering and Maths (STEM) education immersion class at Rongomai School, Otara, Auckland, New Zealand. Pounamu is the Māori word for the treasured greenstone (or jade), representing the students as the school’s precious treasure and also the future.

Classification — Debaryomyces, Saccharomyces, Saccharomyces, Saccharomyces, Saccharomyces, Saccharomyces, Saccharomyces, Saccharomyces.

On Yeast extract Malt agar (YM), after 9 d at 22 °C, colony is white, somewhat glistening, apically-hirsute, with a raised undulating, membranous margin. After 6 d growth at 22 °C in YM broth, cells are ellipsoidal and cylindrical, 7–9(–11) × 3–5(–5.5) µm (av. 8.5 × 4 µm), occurring singly, in clusters, as pseudohyphae, and proliferating by budding. Dalmatian plate culture after 10 d was white with pseudohyphae and the margin was also fringed with pseudohyphae. Fermentation and assimilation of carbon compounds — see MycoBank MB819344.

Typus. NEW ZEALAND, Auckland, The Gardens, Totara Park, on agaric mushroom surface, 8 Mar. 2016 (holotype PDD 105303, culture ex-type ICMP 22125, ITS and LSU sequences GenBank KY285000 and KY285009, MycoBank MB819344).

Notes — This study began as a project to raise awareness of fungal diversity and function among New Zealand school students and teachers. Mycologists at Landcare Research assisted 20 students (9–11 yr) at Rongomai Primary School, Otara, Auckland to collect and identify fungi in a native forest at Totara Park, 5 km from the school. The students’ challenge was to discover and describe a fungal species new to science. Students prepared cultures from swabs of the surface of collected specimens; colonies arising were subcultured and sequenced. Students then observed the process to differentiate and publish a new species, and collectively chose the name for the species epithet. The students involved in this project are as follows: Fotu Holikiahua, Serenity Iako, Gina Kavemnu, Michaela Langdon, Julius Marino, Te Rangihau Matthews, Carlos McCabe Davis, Janine Mulipola, James Nansen, Matarii Nicholias, Daychelle Paniani-Tietie, Daize Puaha, Sam Ratahi, Ulia Sefo, Micheal Simona, Harlyn Teau-Rewa, Florence Tafaoga, Sherbyn Tiatia, Vanisha Vaeteru, Watson Wilson.

Phylogenetic analyses using an alignment of concatenated sequences of the nuclear large subunit and the internal transcribed spacer regions show that the three conspecific strains, ICMP 22125, 22126, and 22128, represent a novel yeast species and are sister to the Candida tanzawaensis clade, which is mainly composed of yeasts isolated from the digestive tract of basidocarp-feeding beetles (Suh et al. 2004). Physiological profiles further support the separation of the new species as distinct from C. tanzawaensis and C. panamericana. The new species can be distinguished from C. tanzawaensis by its ability to grow in 50 % glucose. The new species can be distinguished from C. panamericana by its ability to assimilate arbutin and its inability to ferment either D-xylene or galactose. The new species can be distinguished both from C. tanzawaensis and C. panamericana by its inability to grow at 30 °C. All supplementary data including assimilation tests and sequence alignments are available at doi:10.7931/J2XW4GQT, specimen and strain data is available at https://scd.landcareresearch.co.nz.

Bayesian inference phylogenetic tree of concatenated ITS and LSU sequences using MrBayes v. 3.2.6, showing the relationship of Candida rongomai-pounamu to closely related species. The novel species is printed in bold. All strains are ex-type.

Colour illustrations. Rongomai School students and teacher collecting fungi in Totara Park, Auckland, New Zealand; light micrographs of Candida rongomai-pounamu budding cells in YM broth. Scale bar = 10 µm.

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Candida rongomai-pounamu Padamsee, B.S. Weir, Petterson & P.K. Buchanan, sp. nov.
Candida vespimorsuum
**Candida vespimorsuum** Padamsee, B.S. Weir, Petterson, P.K. Buchanan, *sp. nov.*

**Etymology.** The specific epithet ‘vespimorsuum’, referring to ‘wasp stings’.

Five students from the class of 32 at Karamu High School, Hastings, New Zealand who discovered this new species and chose the name were stung by invasive wasps during the fungal collecting trip. Hence ‘the Candida of the wasp-stings’.

**Classification — Incertae sedis, Saccharomycetales, Saccharomycetes, Saccharomycothina.**

On Yeast extract Malt agar (YM), after 9 d at 22 °C, colony is white, moist and glistening, with a somewhat raised, lobed, membranous margin. After 5 d growth at 22 °C in YM broth, cells are subglobose to globose, ellipsoidal and cylindrical, (3−)4.5−7.5−8 × (2.5−)3.5−6−7.5 µm (av. 5.6 × 4.8 µm), occurring singly, in clusters or chains, as pseudohyphae, and proliferating by budding. Dalmau plate culture after 10 d was white with an undulating to entire margin. Fermentation and assimilation of carbon compounds – see MycoBank MB819395.

**Typus. New Zealand.** Hawke’s Bay Region, White Pine Bush Scenic Reserve, on cup fungus surface, 2 Mar. 2016 (holotype PDD 105304, culture ex-type = ICMP 22109, ITS and LSU sequences GenBank KY285004 and KY285007, MycoBank MB819395).

Notes — This study began as a project to raise awareness of fungal diversity and function among New Zealand school students and teachers. Mycologists at Landcare Research assisted 32 students (15–17 yr) at Karamu High School, Hastings, Hawke’s Bay to collect and identify fungi in a native forest at White Pine Bush Scenic Reserve, 45 km north of the school. The students’ challenge was to discover and describe a fungal species new to science. Students prepared cultures from swabs of the surface of collected specimens; colonies arising were subcultured and sequenced. Students then observed the process to differentiate and publish a new species, and collectively chose the name for the species epithet. The students involved in this project are as follows: Keegan Beets, Gurkamal Bhangel, Tom Black, Zara Blake, Emma Bone, Georgia Boyes, Mia Braddock, Jesca-Lee Bron, Caleb Brothers, Shayne Brown, Isla Christensen, Niels Clayton, Holly Davison, Holly Foulkes, Yvaan Hapuku-Lambert, Dominique Harmer-Higgins, Hannah Hemi-Robinson, Kate Jacobs, Kate Jones, Kevin Kambach, Ana Marks, Kirsten Rutten, Cerys Sanders-Jones, Bailey Seymour, Reece Sullivan, Mason Templeton, Felix Thornton, Camryn Toki, Liam Urquhart, Sophie Wells, Jaymie Wright, Cameron Young.

Phylogenetic analyses using an alignment of concatenated sequences of the nuclear large subunit and the internal transcribed spacer regions show that the two conspecific strains, ICMP 22119 and 22115, represent a novel yeast species and are sister to *Candida sake*. Physiological profiles further support the separation of the new species as distinct from *C. sake* and *C. parapsilosis*.

The new species can be distinguished from *C. sake* by its inability to assimilate L-sorbose or to ferment sucrose. The new species can be distinguished both from *C. sake* and *C. parapsilosis* by its ability to assimilate D-glucosamine and D-arabinose and inability to assimilate D-melezitose. All supplementary data including assimilation tests and sequence alignments are available at doi:10.7931/J2XW4GQT, specimen and strain data is available at https://scd.landcareresearch.co.nz.

Bayesian inference phylogenetic tree of concatenated ITS and LSU sequences using MrBayes v. 3.2.6, showing the relationship of *Candida vespimorsuum* to closely related species. The novel species is indicated in **bold**. All strains are ex-type.

_Colour illustrations._ White Pine Bush Scenic Reserve, Hawke’s Bay, New Zealand; Karamu High School students examining a mushroom; light micrographs of *Candida vespimorsuum* budding cells and pseudohyphae in YM broth. Scale bar = 10 µm.
Rhodotorula ngohengohe
**Rhodotorula ngohengohe** Padamsee, B.S. Weir, Petterson & P.K. Buchanan, sp. nov.

**Etymology.** The specific epithet ‘ngohengohe’ (Māori), referring to ‘be humble, agreeable’. Students who discovered this new species are from Te Kura Kaupapa Māori o Kaikohe, and chose ngohengohe for this species from their school motto E rere, Kia koi, Kia ngohengohe = Fly, Be on to it, Be humble in your successes (pronounced ngohe-ngohe).

**Classification.** Sporidiobolaceae, Sporidiobolales, Microbotryomycetes, Pucciniomycotina.

On Yeast extract Malt agar (YM), after 9 d at 22 °C, colony is flat, pink, moist and glistening, with a curved margin. After 5 d growth at 22 °C in YM broth, cells are mostly ellipsoidal and occasionally oval, (4.5–)6.5–8(–9) × 3–4.5(–5.5) µm (av. 7 × 3.8 µm), occurring singly, in clusters, and proliferating by budding. Dalmau plate culture after 10 d was pink with an entire margin. Fermentation and assimilation of carbon compounds – see MycoBank MB819394.

**Typus.** New Zealand, Northland, Kaikohe water catchment, on bird feather surface, 12 Feb. 2016 (holotype PDD 105305, culture ex-type ICMP 22106, ITS and LSU sequences GenBank KY285005 and KY285006, MycoBank MB819394).

Notes — This study began as a project to raise awareness of fungal diversity and function among New Zealand school students and teachers. Mycologists at Landcare Research assisted 18 students (13–14 yr) at Te Kura Kaupapa Māori o Kaikohe, Kaikohe, Northland to collect and identify fungi in a native forest of the nearby water catchment. The students’ challenge was to discover and describe a fungal species new to science. Students prepared cultures from swabs of the surface of collected specimens; colonies arising were subcultured and sequenced. Students then observed the process to differentiate and publish a new species, and collectively chose the name for the species epithet. The students involved in this project are as follows: Jayson Gotz-Edmonds, Kahurangi Hauraki, Awhina Herewini Honu, Temepara Hita, Sean Kaka, Sione Kata, Te Ao Kohatu Kaukau-Troughton, Niki Lawrence, Shaden Marsh, Kahurangi Maxwell, Te Painga Osborne, Reiata Phillips Heihei, Tawauwau Rakete, Tasha Richards, Romeo Tau-Ashby, Vincent Tau-Roberts, Mikaira Te Haara, Monique Terei.

Phylogenetic analyses using an alignment of concatenated sequences of the nuclear large subunit and the internal transcribed spacer regions show that ICMP 22106 represents a novel yeast species and is sister to *Rhodotorula evergladiensis*. Physiological profiles further support the separation of the new species as distinct from *R. evergladiensis* and *R. kratochvilovae*. The new species can be distinguished from *R. evergladiensis* by its ability to assimilate D-arabinose, L-arabinose, and D-ribose as well as its ability to use nitrate as a nitrogen source. The new species can be distinguished from *R. kratochvilovae* by its inability to assimilate D-raffinose, its ability to assimilate xylitol, and its weak growth in 10 % NaCl. All supplementary data including assimilation tests and sequence alignments are available at doi:10.7931/J2XW4GQT, specimen and strain data are available at https://scd.landcareresearch.co.nz.

Bayesian inference phylogenetic tree of concatenated ITS and LSU sequences using MrBayes v. 3.2.6, showing the relationship of *Rhodotorula ngohengohe* to closely related species. The novel species is indicated in **bold**. All strains are ex-type.
Penicillium parvofructum
**Penicillium parvofructum** Guevara-Suarez, Cano-Canals, Cano & Stchigel, sp. nov.

**Etymology.** From Latin parvum-, small, and -fructum, fruit, in reference to the small size of the conidiophores.

**Classification.** Aspergillaceae, Eurotiales, Eurotiumycetidae, Eurotiumycetes.

*Mycelium* sparse, uncoloured, septate, branched. *Conidiophores* typically monoverticillate; stipes 13–18 × 2.5–3 μm, smooth-walled, hyaline. *Conidigenous cells* phialidic, solitary to in verticils of up to 3, ampulliform, 8–10 × 1.5–2 μm, smooth-walled, hyaline. *Conidia* in chains, broadly ovoid to bacilliform, 3–3.5 × 2–2.5 μm, smooth-walled, hyaline to subhyaline.

**Culture characteristics.** — (after 7 d at 25 °C in darkness).

On MEA colonies attaining 13–15 mm diam, flat, with a raised centre and a concave edge, radially sulcate, margins entire, whitish (M.ZA1); sporulation absent; exude and soluble pigment absent. On CYA colonies attaining 17–19 mm diam, similar to those on MEA, but light yellow (M.2A5) centrally and at the margins; sporulation poor; exude and soluble pigment absent. On YES colonies attaining 15–17 mm diam, cerebriform, of raised centre with a concave edge, margins entire, greenish grey (M.1B2) at the margins and centrally greyish yellow (M.1B5); sporulation moderately abundant; exude and soluble pigment absent. Optimum temperature of growth 30–37 °C (CYA at 30 °C, 21–25 mm diam; CYA at 37 °C, 23–24 mm diam; MEA at 30 °C, 19–20 mm diam; MEA at 37 °C, 18–19 mm diam; YES at 30 °C, 21–25 mm diam; YES at 37 °C, 25–28 °C). Does not grow at above 40 °C.

**Typus.** Spain, Tarragona province, Prades, from a forest soil sample, 13 June 2015, J. Cano-Canals (holotype CBS H-22733, cultures ex-type FMR 15047 = CBS 141690; ITS, LSU, BenA, and CaM sequences GenBank LT559091, LT559092, LT627645, and LT627646; MycoBank MB819947).

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Notes — According to a sequence comparison with available data (ITS, BenA and CaM), *P. parvofructum* is most closely related with *P. dimorphosporum* in the *P. parvum* clade, section Exilicaulis (Visage et al. 2016).

**ITS.** Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence are *Penicillium dimorphosporum* (GenBank NR 121271; Identities = 534/553 (97 %), Gaps = 4/553 (0 %)), *Penicillium erubescens* (GenBank NR 121245; Identities = 532/551 (97 %), Gaps = 6/551 (1 %)), and *Penicillium rubidurum* (GenBank NR 121243; Identities = 531/551 (96 %), Gaps = 5/551 (0 %)).

**BenA.** Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the BenA sequence are *Penicillium rubidurum* (GenBank HQ646574; Identities = 408/466 (88 %), Gaps = 4/466 (0 %)), *Penicillium dimorphosporum* (GenBank KF900165; Identities = 383/429 (89 %), Gaps = 5/429 (1 %)), and *Penicillium pimiteouiense* (GenBank KC449594; Identities = 406/467 (87 %), Gaps = 7/467 (1 %)).

**CaM.** Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the CaM sequence are *Penicillium dimorphosporum* (GenBank KF900176; Identities = 472/544 (87 %), Gaps = 13/544 (2 %)), *Penicillium vinaceum* (GenBank AV678543; Identities = 452/544 (83 %), Gaps = 18/544 (3 %)), and *Penicillium pimiteouiense* (GenBank HQ646580; Identities = 454/548 (83 %), Gaps = 25/548 (4 %)).

*Penicillium parvofructum* differs from *P. dimorphosporum* (the species phylogenetically more closely related) in the size of the stipes of the conidiophores (13–18 μm long in *P. parvofructum* vs 15–30 μm long in *P. dimorphosporum*), in the morphology of the conidia (*P. parvofructum* produces hyaline to subhyaline, smooth-walled, broadly ovoid to bacilliform conidia, which turn brown, ornamented and globose with age in *P. dimorphosporum*), and in the optimum temperature of growth (*P. parvofructum* displays the best growth at 37 °C, while the optimum temperature for *P. dimorphosporum* is 25 °C).

Phylogenetic tree built by using BenA (401 bp) nucleotide sequences of *Penicillium* section *Exilicaulis* belonging to the *P. parvum* clade, using Maximum-likelihood and Bayesian inference. The tree was built by using MEGA v. 6. Posterior probabilities and/or bootstrap support values higher than 0.95 and 70 %, respectively, are indicated at the nodes. *Penicillium corylophilum* and *Penicillium cravenianum* were chosen as outgroup. Ex-type strains of the different species are indicated with *. The new species is indicated in **bold**. The alignment and tree is available in TreeBASE (ID 19427).

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Colour illustrations. Prades, Tarragona, Spain; colonies after 7 d at 25 °C on YES, MEA and CYA, respectively; texture of colonies on YES at 37 °C; conidiophores with conidia. Scale bars = 10 μm.

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**Perenniporia brasiliensis** Lira, A.M.S. Soares, Ryvarden & Gibertoni, sp. nov.

**Etymology.** Referring to the country where this fungus was collected, Brazil.

**Classification — Polyporaceae, Polyporales, Agaricomycetes.**

**Basidiomata** annual, resupinate, smooth and even, hard to brittle, 10 × 1.5 cm in the holotype and 0.5 mm thick; pore surface cream greyish to tan (31 vinaceous buff to 10 cinnamon); pores slightly thick-walled, round to angular, mostly 6–7 per mm; dissepiments entire, thick; tubes concolorous with the pore surface, up to 0.5 mm deep; context about 100 mm thick, cottony and concolorous with the pore surface; margin smooth, narrow and concolorous with the pore surface. **Hyphal system** dimitic, generative hyphae thin-walled, smooth and with clamp connections, 2–4 μm wide, skeletal hyphae weakly dextrinoid, 2–3 μm. **Cystidia** or other sterile elements absent. **Basidia** 14–20 × 4–6 μm, clavate with four sterigmata. **Basidiospores** 3–4 × 2–4 μm, globose to subglobose, hyaline, thick-walled and dextrinoid.

**Type.** *Brazil*, Amapá, Porto Grande, Floresta Nacional do Amapá, on wood decay, Sept. 2013, A. Soares, AS 914 (holotype URM 89947, isotype in O, ITS and LSU sequences GenBank KX619595, MycoBank MB816407).

Additional material examined. **Perenniporia centrali-africana**: *Brazil*, Ceará, Missão Velha, Cachoeira de Missão Velha, Jan. 2011, C.R.S. Lira, PPBio 128, URM 83175; Crato, Floresta Nacional do Araripe, May 2012, C.R.S. Lira, PPBio 883, URM 85599; Pernambuco, Cabrobó, Fazenda Mosquito, Jan. 2010, C.R.S. Lira, CL 007, URM 82624; ibid., May 2010, C.R.S. Lira, CL 007, URM 82640; Jaqueira, Reserva do Patrimônio Natural Frei Caneca, Mar. 2012, G.S. Nogueira-Melo, NM 103, URM 84685; Triunfo Triunfo, Sítio Carro Quebrado, Jan. 2010, C.R.S. Lira, CL 003, URM 82568; ibid., Mar. 2010, C.R.S. Lira, CL 011, URM 82578; ibid., Apr. 2010, C.R.S. Lira, CL 23, URM 82584; ibid., July 2012, C.R.S. Lira, CL 160, URM 88910; ibid., Sept. 2010, CL 26, URM 82957; ibid., July 2012, C.R.S. Lira, CL 160, URM 88810; ibid., CL 699, URM 85597; ibid., Jan. 2014, C.R.S. Lira, CL 772, URM 87999; ibid., CL 768, URM 88016 (previously known only from Cameroon).

Notes — Based on a BLASTn search of NCBIs GenBank database, the closest hits using the ITS sequence are Perenniporia sp. (GenBank KT156689; Identities = 588/598 (98 %), Gaps = 1/598 (0 %)), Dichromitus squalens (GenBank KM411455; Identities = 631/666 (95 %), Gaps = 4/666 (0 %)), and *P. tenuis* (GenBank JQ001859; Identities = 631/667 (95 %), Gaps = 4/667 (0 %)). Using the LSU sequence, the highest similarity was to *P. aridula* (GenBank JQ001847; Identities = 801/817 (98 %), Gaps = 7/817 (0 %)), *P. aridula* (GenBank JQ001846; Identities = 801/817 (98 %), Gaps = 7/817 (0 %)), and *P. tibetica* (Gen-Bank JF706332; Identities = 801/817 (98 %), Gaps = 7/817 (0 %)). Although genetically close to *P. aridula*, *P. tenuis* and *P. tibetica*, *P. brasiliensis* is morphologically different (Table 1 - see FP 612). *Perenniporia brasiliensis* is similar to *P. albo-incarnata*, *P. centrali-africana*, and *P. guyanensis*, sharing the same whitish colour. However, they are micro-morphologically different (Table 1 - see FP 612).

Colour illustrations. Porto Grande, Floresta Nacional do Amapá; basidiomata (scale bar = 1 cm); basidiospores (scale bar = 5 μm).

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Perenniporia paraguayensis
**Fungal Planet 612 – 20 June 2017**

**Perenniporia paraguyanensis** Lira & Gibertoni, *sp. nov.*

_Etymology._ Referring to morphological similarity to _P. guyanensis._

**Classification._** Referring to morphological similarity to _P. guyanensis._

**Basidiomata.** Perennial, resupinate, 5–12 cm long × 1.5–5.5 cm wide, 1–4 mm thick at the margin, with the base strongly adnate to the substrate and hard when dry; _pore surface_ cream (D 4); _pores_ round to angular 6–8/mm; _dissepiments_ thin and entire; _context_ reduced to a thin layer above the substrate, less than 1 mm thick, homogeneous and concolorous with the pore surface; _tubes_ thin, stratified and concolorous with the pore surface. _Hyphal system_ dimitic; _generative hyphae_ hyaline, clamped, but difficult to observe think-walled, 1–2 µm wide and branched. _Skeletal hyphae_ hyaline to pale yellow, with 1–2 (–3) branches, thick-walled, narrow, 1–2.3 µm diam, non- to strongly dextrinoid, often variable in the same basidiomata; pyramidal crystals present in the trama and hymenium. _Cystidia_ or other sterile elements absent; _basidia_ with 4 sterigmata, clavate with a narrow base, 17–25 × 6–10 µm; _basidiospores_ subglobose to broad round, slightly truncate at the apex, 3.4–5.2 × 3.4–4.7 µm.

_Typus._ _Brazilia_, Pernambuco, Jaqueira, Reserva do Patrimônio Natural Frei Caneca, on dead wood, Mar. 2012, G.S. Nogueira-Melo, NM 103 (holotype URM 84685, isotype in O, ITS and LSU sequences GenBank KX584461 and KX619588, MycoBank MB816440).

**Additional specimens examined.** _Brazilia_, Amapá, Porto Grande, Floresta Estadual do Amapá, Sept. 2013, A. Soares, AS 1054; _Brazilia_, Estadual do Amapá, Sept. 2013, A.S. 1054, URM 87053.

**Table 1.** Morphology of resupinate, similar _Perenniporia_ species.

| Species                  | Pores/mm | Basidiomata | Basidiospores (µm) | References                  |
|--------------------------|----------|-------------|--------------------|-----------------------------|
| _P. albo-incamata_       | (4–)5–6(–7) | Resupinate | (5.5–)6.0–7.0(–7.5) × (4.5–)5.0–6.0(–6.3) | Decock & Ryvarden (2011)    |
| _P. aridula_             | 6–7      | Resupinate | 6.0–7.0 × 5.1–6.0  | Cui & Zhao (2012)           |
| _P. brasiliensis_        | 6–7      | Resupinate | 3.0–4.0 × 2.0–3.0  | Present study               |
| _P. centralli-africana_  | (6–)7–8  | Resupinate – Effused-reflexed | 4.5–6.0(–6.5) × 3.5–5.5 | Decock & Mossebo (2001)    |
| _P. cinereofusca_        | 4–6      | Resupinate | 6.5–7.7 × 5.3–6.3  | Zhao et al. (2014)          |
| _P. guyanensis_          | (7–)8–9  | Resupinate | 5.0–5.5(–6.0) × (3.5–)4.0–4.5 | Decock & Ryvarden (2011)    |
| _P. hainaniana_          | 5–6      | Resupinate | 4.0–4.5 × 3.0–4.0  | Zhao & Cui (2013)           |
| _P. japonica_            | 5–7      | Resupinate | 4.0–5.0 × 2.5–3.5  | Ryvarden & Gilbertson (1994) |
| _P. medulla-panis_       | 5–7      | Resupinate | 4.0–7.0 × 3.5–6.0  | Ryvarden & Johansen (1980)  |
| _P. paraguyanensis_      | 6–8      | Resupinate | 4.5–5.2 × 3.4–4.7  | Present study               |
| _P. parvispora_          | (6–)7–8  | Resupinate | (3.5–)3.7–4.1(–4.5) × 3.0–3.7(–4.0) | Decock & Ryvarden (2000)    |
| _P. subacida_            | (4–)5–6  | Effused-reflexed | 4.5–6.0 × 3.5–4.5  | Ryvarden & Johansen (1980)  |
| _P. substramina_         | 9–12     | Resupinate | 3.0–3.9 × (2.1–)2.4–3.0 | Zhao et al. (2013)          |
| _P. subtephephora_       | 6–8      | Resupinate | 4.0–5.0 × (3.0–)3.5–4.5 | Zhao & Cui (2013)           |
| _P. tenuis_              | 3–5      | Effused-reflexed | 4.5–6.0 × 3.5–4.5  | Ryvarden & Gilbertson (1994) |
| _P. tibetica_            | 6–10     | Pileate    | (6–)6.7–8.7(–9) × (5–)5.3–6.8(–7) | Cui & Zhao (2012)          |

Notes — Based on the BLASTn search of GenBank database, according to the LSU sequence, the closest hits are _Perenniporia subacida_ (GenBank AY333796: Identities = 900/935 (96 %), Gaps = 7/935 (0 %)), _P. japonica_ (GenBank JX141469, Identities = 897/931 (96 %), Gaps = 7/931 (0 %)), and _P. japonica_ (GenBank JX141468, Identities = 897/931 (96 %), Gaps = 7/931 (0 %)). Furthermore, using the ITS sequence, the sequence had similarity to _Polyporales_ ‘sp. 4’ (GenBank JQ312166, Identities 531/604 (88 %), Gaps = 26/604 (0 %)), and _P. tenuis_ (GenBank JQ001859, Identities = 539/623 (87 %), Gaps = 28/623 (4 %)). Despite the genetic proximity with those three species, _P. japonica_ has no crystals in the hymenium, _P. subacida_ has larger pores, unbranched skeletal hyphae and no truncate basidiospores and _P. tenuis_ has a bright lemon yellow pore surface. Morphologically, _Perenniporia paraguyanensis_ is also very similar to _P. guyanensis_, but the latter has thinner basidiomata (1–1.2 mm), strongly adhering to the substrate and smaller pores (Decock & Ryvarden 2011) (Table 1).

Colour illustrations. Pernambuco, Jaqueira, Reserva do Patrimônio Natural Frei Caneca; basidiomata (scale bar = 1 cm); basidiospores (scale bar = 10 µm); crystals (scale bar = 5 µm).

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Phialocephala cladophilophoroides
Fungal Planet 613 – 20 June 2017

**Phialocephala cladophialaphoroides** Madrid, C. Tapia, V. Silva & M. Lafourcade, sp. nov.

**Etymology.** The name refers to the morphological similarity between this fungus and members of the genus *Cladophialaphora*.

**Classification —** *Vibrisseaceae, Helotiales, Leotiomycetes.*

On water agar with sterilised pine needles (PNA): *Mycelium* consisting of septate, branched, subhyaline to dark olivaceous brown, smooth to verruculose, thin- to thick-walled, 1–6 µm wide hyphae, with moniliform segments showing swollen cells up to 8 µm wide. *Conidiophores* micronematous, often reduced to conidiogenous cells, pale to dark olivaceous brown, smooth to verruculose. *Conidiogenous cells* mostly subcylindrical, 12–25 × 4–6 µm. *Conidia* in acropetal, simple, strongly coherent chains, mostly subglobose to subcylindrical, aseptate, pale olivaceous brown to dark brown, smooth-walled to verruculose, 5–17(–22) × (4–)5–6(–7) µm. *Chlamydospores* and sexual morph not observed.

**Culture characteristics —** Colonies after 21 d at 25 °C attaining 25 mm on PNA and 29 mm on MEA, fuscicolus, with a fimbriate margin, olivaceous black on the former medium, dark grey on the latter; reverse concolorous with obverse on each medium.

**Typus.** Chile, Santiago, isolated from human toe nail, Nov. 2016, C. Tapia (holotype SGO 167859, ex-type culture CCCT 17.04, ITS and LSU sequences GenBank KY798313 and KY798314, MycoBank MB820847).

Notes — This fungus was isolated from toe nail lesions of an immunocompromised patient. The clinical case is currently under study and will be reported elsewhere. The isolate remained sterile or sporulated poorly on routine mycological media, such as malt extract agar or Sabouraud dextrose agar. Therefore, it was grown on PNA in order to stimulate sporulation. On this medium, undifferentiated fertile hyphae produced cladosporoidal, coherent chains of aseptate, subglobose to elongate dematiaceous conidia without dark scars. These morphological features closely resembled those of *Cladophialaphora* (*Chaetothyriales*), a genus which includes important clinically-relevant species with a broad clinical spectrum, including chromoblastomycosis, phaeohyphomycosis, mycetoma and onychomycosis (Badali et al. 2008, Brasch et al. 2011). BLAST searches with the ITS sequence of isolate CCCT 17.04, however, revealed affinities with species of *Phialocephala* (*Helotiales*), and the closest match was the type species, *P. dimorphospora* (ex-type strain, CBS 300.62, ITS sequence GenBank AF486121, and other strains, 97–98 % identical). Considering that the ITS region provides little resolution for closely related taxa in *Phialocephala* (Tanney et al. 2016), isolate CCCT 17.04 was considered to represent a species different from *P. dimorphospora*.

The genus *Phialocephala* traditionally has been characterised by micronematous conidiophores bearing penicillately arranged, phialidic conidiogenous cells with deep collarettes and aseptate conidia in slimy masses (Kendrick 1961, Seifert et al. 2011). These structures are produced by *P. dimorphospora* in cultures on MEA at 25 °C (Mouton et al. 1993), but were not observed in isolate CCCT 17.04. Several studies have revealed a high degree of morphological plasticity in the asexual morphs of *Phialocephala*, including the occasional presence of an accompanying anavirga-like or diplococcium-like morph in some species, or the production of a synnematous conidial apparatus with blastic, non-philidic, conidiogenous cells in *P. oblonga* (Descals & Sutton 1976, Tanney et al. 2016). In spite of this morphological variability, no cladophialaphor-like morph has been reported previously in *Phialocephala*, supporting the proposal of the novel species described herein.

 Colour illustrations. Urban landscape in Santiago de Chile; colony after 21 d at 25 °C on water agar with sterilised pine needles; moniliform hypha; developing and detached conidial chains. Scale bars = 10 µm.
Pholiota longistipitata
**Pholiotina longistipitata** E.F. Malysheva & Kiyashko, sp. nov.

**Etymology.** The epithet emphasises the important character of the new species – basidiocarps with long stipes.

**Classification.** Boblitaceae, Agaricales, Agaricomycetes.

**Pileus.** 5–17 mm, broadly campanulate or obtuse conical, without distinct umbo, with even margin; hygrophanous, up to centre striate; pale brownish orange (7C3–4), sometimes without distinct umbo, with even margin; hygrophanous, up to 27–55 µm wide), often pigmented and thick-walled.

**Lamellae.** Entirely pure white or slightly yellowish; longitudinally fibrillose, minutely pruinose or almost smooth; veil absent. **Basidia** 5–9.5 × 4.3–5.4 µm, Q = (1.23–1.35–2.00, Q* = 1.72, narrowly to broadly ellipsoid, elongate-ellipsoid, yellow-brown in KOH, slightly thick-walled, with distinct germ pore. **Basidiospores** 8–17 × 5–6.11 µm, narrowly to broadly lageniform, fusiform with inflated base and obtuse, occasionally bifurcated, apex, some proportion utriform, thin- or slightly thick-walled. **Pileocystidia** rowly to broadly ellipsoid, elongate-ellipsoid, yellow-brown in KOH, slightly thick-walled, with distinct germ pore. **Cheilocystidia** large, and more often irregular-shaped, 45–110 × 8–17 µm. **Clamp connections** present.

Habitat & Distribution — In a small group, on litter in mixed forest. Up to now known only from the type locality.

**Typus.** RUSSIA, Krasnoyarsk Territory, Sayano-Shushenskiy State Biospheric Nature Reserve, floodplain of Malaya Golaya River, mixed forest (Abies sibirica, Pinus sibirica, Betula pendula), among moss, 17 Aug. 2015, A. Kiyashko & E. Malysheva (holotype LE312984, ITS and LSU sequences GenBank KY627842 and KY627843, MycoBank MB819993).

Notes — *Pholiotina longistipitata* is characterised by the following features: rather slender basidiocarps with conical pilei strongly striated up to the centre, long whitish stipes, relatively small elongate-ellipsoid basidiospores, and numerous pileocystidia in the pileus.

Due to absence of a veil and lageniform cheilocystidia, *Pholiotina longistipitata* can be placed in sect. *Piliferae*. This new species is quite similar to *Ph. striipes* on the basis of a complex of microscopic features, but the latter noticeably differs in habit, forming rather stout basidiocarps that commonly grow in fascicles, having a lower ratio of stipe length to pileus diameter as well as differently shaped and weakly striated pileus (Hausknecht 2009). An additional difference is based on an ITS sequence analysis which demonstrated strong dissimilarity with more than 30 % distance between sequences (in comparison with WU269997 specimen of *Ph. striipes* originated from Austria). *Pholiotina pygmaeoaffinis* differs in having significantly larger basidiospores, smaller caulocystidia and geographical distribution restricted by Europe (Hausknecht 2009).

**Colour illustrations.** Russia, South Siberia, Sayano-Shushenskiy State Biospheric Nature Reserve, site in taiga where fungus was found; basidiocarps, basidiospores, chelocystidia, caulocystidia (all from holotype). Scale bars = 1 cm (basidiocarps), 10 µm (microscopic structures).
*Phytophthora mekongensis*
Phytophthora mekongensis Cacciola & N.V. Hoa, sp. nov.

**Etymology.** Name refers to the area from where the species was isolated, Mekong River Delta in Vietnam.

**Classification.** Peronosporaceae, Peronosporales, Peronosporomycetes.

Sporangia produced on V8-agar (V8A) flooded with both distilled water and non-sterile soil extract (Jung et al. 2017), formed in dense symidia and were limoniform, ovoid-obpyriform, ellipsoid to fusiform, papillate, frequently bi-papillate and bi- or tri-lobed, often caducous (pedicel length 5–15 μm) with a conspicuous basal plug at the point where the pedicel attaches to the sporangium; average size of sporangia was 35 × 24 μm (overall range 25–50 × 20–36 μm) with a mean length/breadth ratio of 1.5. Gametangia were not produced in single culture or in dual cultures with A1 and A2 mating type tester strains of *P. nicotianae* and *P. citrophthora* (Puglisi et al. 2017). Minimum, optimum and maximum temperatures for growth were 12 °C, 28 °C and 36 °C, respectively. Radial growth rate on V8A in the dark at 28 °C was 6.7 ± 0.1 mm/d.

**Culture characteristics.** Colonies are stellate to roaceous on V8A and stellate on PDA.

**Typus.** Southern Vietnam, Vĩnh Long province, Mekong Delta region, from *Citrus grandis* (syn.: *C. maxima*) fruit, 2012, A. De Patrizio & G. Magnano di San Lio (holotype PF6a2, culture ex-type PF6a2 = CBS 135136, ITS and COI sequences GenBank KC875838 and KT366920, MycoBank MB820796).

**Additional specimens examined.** Southern Vietnam, Vĩnh Long province, Mekong Delta region, from *Citrus grandis* fruits, 2012, A. De Patrizio & G. Magnano di San Lio, 68 isolates; Ben Tre, Mekong Delta region, from *Citrus grandis* roots, five isolates.

Notes — Phylogenetically (phylogenetic tree reported in Puglisi et al. 2017; supplementary figure in MycoBank), *Phytophthora mekongensis* resides in the *Phytophthora* major Clade 2, subclade 2a, and is closely related to *P. meadii* and *P. colocasiae* (Puglisi et al. 2017). In nature, *P. mekongensis* was found associated with root rot and fruit brown rot of pomelo (*C. grandis*). In artificial inoculations it induced brown rot on various *Citrus* species, including pomelo, grapefruit, sweet orange and bergamot as well as gum exudation from the bark of pomelo ‘Chandler’ and sweet orange ‘Lane late’ (Puglisi et al. 2017).
Phytophthora prodigiosa Cacciola & M.V. Tri, sp. nov.

**Etymology.** Name refers to the bizarre (*prodigiosum* in Latin) and unusual shape of the hyphal swellings.

**Classification.** *Peronosporaceae, Peronosporales, Peronosporomycetes.*

Sporangia produced on V8-agar (V8A) flooded with both distilled water and non-sterile soil extract (Jung et al. 2017), were non-caducous, ovoid to obpyriform, and non-papillate; average size of sporangia was 45 × 32 μm (overall range 30–50 × 19–34 μm) with a mean length/breadth ratio of 1.4. Sporangia proliferated internally in both nested and extended way. Chlamydospores of variable size (20–48 μm), globose to obpyriform, sometimes laterally attached. Catenulate, elongated to globose *hyphal swellings*, often with a bizarre shape, were abundantly formed on V8A. *Gametangia* not produced in single culture or in dual cultures with A1 and A2 mating type tester strains of *P. nicotianae* and *P. citrophthora* (Puglisi et al. 2017). Minimum, optimum and maximum temperatures for growth were 12 °C, 32 °C and 36 °C, respectively. Radial growth rate on V8A in the dark at 32 °C was 6.5 ± 1.4 mm/d.

**Culture characteristics.** A rosaceous colony growth pattern was produced on V8A and PDA.

**Typus.** SOUTHERN VIETNAM, Vĩnh Long province, Mekong Delta region, from *Citrus grandis* (syn.: *C. maxima*) fruit, 2012, A. De Patrizio & G. Magnano di San Lio (holotype PF6e, culture ex-type PF6e = CBS 135138, ITS and COI sequences GenBank KC875840 and KT366918, MycoBank MB820797).

*Additional specimens examined.* SOUTHERN VIETNAM, Vĩnh Long province, Mekong Delta region, from *Citrus grandis* fruits, 2012, A. De Patrizio & G. Magnano di San Lio, nine isolates; Đồng Tháp, Mekong Delta region, from Mandarin / Volkamer lemon roots, five isolates.

Notes — Phylogenetically (phylogenetic tree reported in Puglisi et al. 2017; supplementary figure in MycoBank), *Phytophthora prodigiosa* resides in *Phytophthora* major Clade 9 and shows many morphological characteristics corresponding to the original description of *P. insolita* (Ann & Ko 1980). The major difference between the two species is the sterile breeding system of *P. prodigiosa*, whereas *P. insolita* is homothallic. In nature, *P. prodigiosa* was found associated with brown rot of pomelo (*C. grandis*) fruit fallen to the ground or floating on water as well as on rotten rootlets of citrus trees (Puglisi et al. 2017).

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**Colour illustrations.** Typical habitat for the recovery of *P. prodigiosa*; persistent, non-papillate ovoid sporangium; obpyriform, persistent sporangium; sporangium with internal nested proliferation; sporangium with internal nested and extended proliferation; globose, small, sessile chlamydospores; irregularly shaped hyphal swellings. Scale bars = 10 μm.
Polycephalomyces onorei
**Polycephalomyces onorei** Kautman & Kautmanova, *sp. nov.*

**Etymology.** Named after Giovanni Onore, a great Italian naturalist living in Ecuador and founder of the Otonga foundation.

**Classification —** Ophiocordycipitaceae, Hypocreales, Hypocreomycetidae, Sordariomycetes.

**Stromata** numerous, irregularly growing in various directions from the whole body of hairy, red-headed caterpillar of undetermined moth species, probably of subfamily Arctinae (Lepidoptera, Erebididae); stromata solitary, simple or 2–3 times branched, 10–25–(45) × 0.5–1.5 mm, ampulliform, thickened at the base, cinnamon brown, darker when wet, fading with age and drying to greyish brown. Fertile parts with perithecia — 4 mm diam, subcap- 
al, forming lateral pads around stipe, pale brown to ochraceous orange. Sterile apical parts whitish, often twisted, simple or 2–3 times branched, in old specimens sometimes missing, probably broken with age. Perithecia 854–950 × 330–395 μm, narrowly pyriform, with dark brown protruding apices, close to each other and immersed when young, emerged and apart when mature. Asci 450–510 μm long, ascospores filiform, cylindrical, breaking to small truncate, bacilliform part-spores (3.5–4)–(5.5) × 0.5–1 μm, sometimes part-spores not divided, then up to 6 μm long.

**Habitat & Ecology —** Western slopes of Los Andes (Ecuador), mostly secondary pre-montane forest with residues of primary forest. Parasitised caterpillars were found on bare soil, sometimes half buried, or among leaves and debris, in shaded places, one specimen was found on a stem of *Ettlingera* sp. plant c. 1 m above ground.

**Typus.** **ECUADOR.** Prov. Cotopaxi, Union de Toachi village, 50°19.256′ W78°57.101′, alt. 840 m, on caterpillar of *Lepidoptera* (cf. *Arctinae*), on stem of *Ettlingera* sp., in secondary pre-montane rainforest close to Otongachi fieldstation, at the right bank of Toachi River, 27 Mar. 2011, V. Kautman (holotype BRA CR23902, ITS sequence GenBank KU898841, MycoBank MB819988).

Additional specimens examined. **ECUADOR.** Prov. Cotopaxi, Union de Toachi village, 50°19.256′ W78°57.101′, alt. 830 m, on caterpillar of *Lepidoptera* (cf. *Arctinae*), on bare soil among shrubs, 1 Apr. 2011, V. Kautman, BRA CR23903, ITS sequence GenBank KU898842; ibid., alt. 840 m, on caterpillar of *Lepidoptera* (cf. *Arctinae*), in soil among herbs and fallen leaves, 2 Mar. 2014, V. Kautman, BRA CR23904, ITS sequence GenBank KU898843; ibid., alt. 845 m, on caterpillar of *Leioptera* (cf. *Arctinae*), buried in soil, 2 Mar. 2014, V. Kautman, BRA CR23905, ITS sequence GenBank KU898844; ibid., on caterpillar of *Lepidoptera* (cf. Arctinae), on ground, 26 Mar. 2016, V. Kautman, BRACR25968.

Notes — *Polycephalomyces onorei* belongs to a group of sexual species of *Polycephalomyces* s.l., which until now was unknown to have asexual morphs, as defined by Kepler et al. (2013). It is well distinguished from all other *Polycephalomyces* species by the following combination of characters: lepidopteran host, large stromata up to 3.5 cm tall, perithecia big, pyriform and in maturity protruding, part-spores small.

**Colour illustrations.** Type locality — interior of the secondary pre-montane rainforest at the vicinity of the Otongachi Field Station, Union de Toachi, Cotopaxi Province, Ecuador, holotype; mature stroma; detail of the fertile part with perithecia; immature stroma; perithecia; ascus; part-spores (from holotype). Scale bars: lower row = 1 cm, part-spores = 10 μm, ascus and perithecia = 100 μm.

Macroscopically, *P. onorei* is the most similar to *P. lianzhouensis* which also parasitises lepidopteran caterpillars. However, *P. lianzhouensis* is much smaller (2–12 mm long), with a semi- 
ncap formite part with very few, immersed, narrow- ovoid perithecia, which are also much smaller (355–473 × 156–197 μm). Part-spores are larger, up to 7.5 μm long. Bare stroma tips characteristic for *P. onorei* were also not observed in *P. lianzhouensis*. In the ML tree of the ITS region (Myco- Bank supplementary figure) *P. lianzhouensis* is positioned on a distant branch together with the *Cicadidae* nymphs parasite *P. ramosopulvinus*, with which it shares also similarity in some macro- and micro-characters (Wang et al. 2014).

The closest species to *P. onorei* in the ITS tree is *P. agaricus*, an asexual hyperparasite growing in the form of very small synnemata (0.3–1.2 mm) on *Ophiocordyceps* sp. parasitising melolonthid larvae (Wang et al. 2015).

*Polycephalomyces onorei* is the first published record of a sexual *Polycephalomyces* species from the American continent. Until recently all published records were from Asia, mostly China and Japan.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Tamura-Nei model (Tamura & Nei 1993). The tree with the highest log likelihood (-1013.9678) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbour-Joining and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 36 nucleotide sequences. All positions containing gaps and missing data were eliminated. There was a total of 322 positions in the final dataset. The evolutionary analyses were conducted in MEGA v. 7 (Kumar et al. 2016).
Psathyrella striatoannulata
Psathyrella striatoannulata Heykoop, G. Moreno & M. Mata, sp. nov.

Etymology. Name refers to the presence of a striate ring on the stipe of this fungus.

Classification — Psathyrellaceae, Agaricales, Agaricomycetes.

Cap 12–36 mm broad, convex to apexannulate, convex, with umbo, glabrous, pale brown (121 C, mikado brown) to greyish brown (219 B, army brown), becoming paler brown when drying (223 D tawny olive). Margin deflexed, hygrophanous, striate. Context of pileus 1 mm thick, concolorous to whitish. Veil white, forming an annulus on stem and fagiaceous, small, scattered fibrils at margin of cap and lower part of stem. Gills 1–4 mm broad, adnate to subdecurrent, close, coffee brown greyish (Mu 9.0 YR 5.5/2.5) to brown (219 B army brown), with entire edge; lamellulae present. Stem 42–110 × 1–5 mm, cylindrical, central, hollow, fibrillose, white, with some brownish tinges, especially below the ring, equipped with an apical conspicuous well-developed upper-right membranous annulus, white to brownish at margin (221 A warm sepa), its margin longitudinally striate. Odour and taste not distinctive. Spores 7.5–9.5(–10) × 4–5.5 µm, av. 8–8.3 × 4.4–4.6 (2 collections), Q–1, 1.74–1.86, ellipsoid, smooth, with apical germ pore, in NH₄OH (10 %) reddish brown. Basidia 4-spored, 18–27 × 7–9 µm, clavate, hyaline. Pleurocystidia 45–52 × 14–21 µm, numeros, utriform to cylindrical or clavate, thin-walled, sometimes at the upper part slightly thick-walled and wall refractive, then ochraceous brown to reddish brown, hyaline or frequently with reddish brown granular content in their apical part, at and around apex sometimes covered with mucoid droplets or granular deposits, variable in number and size, staining reddish brown in NH₄OH (10 %) when (still fairly) fresh. Marginal cells: sphaeropedunculate and clavate cells 18–32 × 11–16 µm, abundant and almost exclusively forming the cellular lining of gill edge; pleurocystidoid cheilocystidia 25–35 × 11–13 µm, scarce, utriform; all cells thin-walled, colourless. Hymenophoral trama in NH₄OH (10 %) consisting of hyaline thin-walled hyphae, without encrustations. Clamp connections present (especially in thin hyphae of hymenium) but difficult to observe.

Habitat & Distribution — Growing gregarious on woody debris or terrestrial. So far only known from Costa Rica.

Psathyrella striatoannulata Heykoop, G. Moreno & M. Mata

Typos. COSTA RICA, Puntarenas, La Amistad Pacífico, unprotected area, Finca Santa Marta, at the base of the Cerro Quijada del Diablo, 1 600–1 700 m; 8:53:51.7890N-82:45:30.1370W, on soil, 12 June 2008, E. Navarro (holotype INB0004162132, ITS sequence GenBank KY350220, MycoBank MB819509; isotype AH 46129).

Additional specimens examined. Psathyrella striatoannulata: COSTA RICA, Puntarenas, La Amistad Pacífico, unprotected area, Mellizas, near the catholic church, 1400–1500 m, 8:53:09.5830N-82:46:16.0650W, on woody debris, 29 Aug. 2005, E. Navarro, paratype INB0003978642, E. Navarro 9454, ITS sequence GenBank KY350221.

Psathyrella phegophila: SPAN, Navarra, Elizaburu, in dead leaves of Fagus sylvatica, 28 Oct. 1978, L.M. García Bona, AH 45940, ITS sequence GenBank KY350219.

Psathyrella fatua: SPAN, Madrid, Alcalá de Henares, El Gurugú, under Kochia prostrata close to Pinus halepensis wood, 12 Nov. 2014, G. Moreno & M. Heykoop, AH 33718, ITS sequence GenBank KY350222.

Psathyrella ammophila: SPAN, Asturias, Oviedo, in sand on beach, 4 May 1974, G. López & G. Moreno, AH 947, ITS sequence GenBank KY350223; Madrid, Alcalá de Henares, El Gurugú, in humus of Kochia prostrata, 9 Oct. 1998, M. Heykoop, J. Rejos & G. Moreno, AH 24456, ITS sequence GenBank KY350224.

Notes — For the description of the colours the Naturalist’s colour guide of Smithe (1975) as well as the Munsell soil colour charts (Munsell 1975) were used. Psathyrella striatoannulata is characterised by its conspicuous well-developed and persistent membranous ring, abundant utriform pleurocystidia, which sometimes are slightly thick-walled and covered with reddish brown mucoid droplets or granular deposits (similar to those of P. lutensis), and by growing with gregarious habit on soil or woody debris.

In our ITS phylogeny (MycoBank supplementary data), P. striatoannulata belongs to the spadiceogriseae clade in which it is related to P. phegophila. The presence of this monophyletic assemblage, corresponding to subsection Spadiceogriseae of Kits van Waveren (1985) has already been noted by Vasutová et al. (2008), larsson & Örstadius (2008), Nagy et al. (2013) and Örstadius et al. (2015). As pointed out by Nagy et al. (2013), in the spadiceogriseae clade the basidiomes are fairly large (more than 3 cm), non-deliquescent with medium-sized, ellipsoid-subphaseoliform spores (7–9 µm), and fibrillose, scatty veil that is visible only on young specimens. The gill edge is lined mainly with poorly developed globose-sphaeropedunculate cells (paracystidia), whereas true, utriform cheilocystidia are very scarce.

Because of the gill-edge lined with large numbers of predominantly sphaeropedunculate and clavate cells and few scattered utriform cheilocystidia, P. striatoannulata keys out in Kits van Waveren’s monograph (1985) close to P. phegophila. Psathyrella striatoannulata, however, differs from P. phegophila by the presence of a persistent well-developed annulus, the pleurocystidia often covered with reddish brown mucoid droplets or granular deposits and by their slightly thick-walled apices which frequently show reddish brown granular contents, and by its different habitat not restricted to Fagus sylvatica woods. The presence of cystidia covered with mucoid droplets or granular deposits is not a constant character since in old specimens they very gradually disappear. If thoroughly searched for, however, some reddish brown deposits may still be found. Other species of Psathyrella s.l. with cystidia covered with mucoid droplets or granular deposits are, e.g., P. lutensis with bluish green mucoid deposits; Cystoagaricus sylvestris (= P. populina) with bluish green deposits; C. hirtosquamulosum (= P. hirtosquamulosum) with greenish deposits; P. supernula (= P. narcolica) with greenish deposits; P. jacobsonii with greenish deposits; and P. nivobadia with yellowish brown deposits. However, P. striatoannulata differs from all these species by a very different set of macro- and microscopical characters.
Pseudocercospora leandrae-fragilis
**Pseudocercospora leandrae-fragilis** O.L. Pereira & M. Silva, sp. nov.

**Etymology.** Name derived from the plant host, *Leandra fragilis*.

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

Leaf spots amphigenous, irregular, initially chlorotic, becoming brown with age, 3–8 mm diam. *Internal mycelium* indistinct. *External mycelium* absent. Stromata well-developed, subglobose to irregular, brown, cells of brown *textura subglobose*. Conidiophores hypophyllous, aggregated in sporodochia, arising from the upper cells of the stroma, subcylindrical, 16.5–34 × 3–4.5 µm, 0–2-septate, straight or geniculate, unbranched, brown, smooth, mostly restricted to conidiogenous cells. *Conidiogenous cells* terminal, subcylindrical, brown, smooth. Conidia solitary, guttulate, pale brown, smooth, subcylindrical, straight to curved, 80–164.5 × 4–5 µm, apex obtuse, base truncate, septate, hila unthickened, neither darkened nor refractive.

Culture characteristics — Colonies on PDA 18 mm diam after 2 wk at 25 °C in the dark; slow-growing raised, margins irregular, with aerial mycelium sparse, grey, reverse iron-grey, sterile.

**Typus.** BRAZIL, Minas Gerais, Araponga, Parque Estadual da Serra do Brigadeiro, on leaves of *Leandra fragilis* (Melastomataceae), 28 Mar. 2015, O.L. Pereira & M. Silva (holotype VIC 44202, culture ex-type COAD 1977; ITS and LSU sequences GenBank KYS74288 and KYS74287, MycoBank MB819904).

Notes — Nineteen *Pseudocercospora* species have been described from hosts in the *Melastomataceae*: *P. aciotidis*, *P. curta*, *P. dissotidis*, *P. erythrogena*, *P. leandrae*, *P. melastomobia*, *P. miconiae*, *P. miconiicola*, *P. miconigena*, *P. mirandensis*, *P. monochaetica*, *P. osbeckiae*, *P. oxyxypora*, *P. sub-synnematosa*, *P. tamoneae*, *P. tibouchina-herbaceae*, *P. tibouchiniae*, *P. tibouchinicola* and *P. tibouchingena* (Pareira et al. 2014, Silva et al. 2016, Farr & Rossman 2017). However, only one species of *Pseudocercospora* is known to occur on a member of *Leandra* (Crous & Braun 2003, Farr & Rossman 2017), namely *P. leandrae* on *Leandra subseriata* from Colombia and Ecuador (Crous & Braun 2003). *Pseudocercospora leandrae* clearly differs from *P. leandrae-fragilis* by having longer conidiophores (20–80 µm) and smaller conidia (40–140 µm) (Braun 1999). Among these species in *Melastomataceae*, *Pseudocercospora melastomobia* is morphologically similar but distinguishable from *P. leandrae-fragilis* by having longer and wider conidiophores (10–50 × 3.5–5.5 µm) and smaller conidia (50–150 µm). Additionally, *P. leandrae-fragilis* does not correspond to any sequences available in GenBank at present. Hence, it is described here as a new species.

**ITS.** Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Pseudocercospora basitruncata* (GenBank KF901632; Identities = 441/446 (99 %), Gaps = 3/446 (0 %)), *Pseudocercospora* sp. (GenBank DQ303084; Identities = 440/445 (99 %), Gaps = 2/445 (0 %)), and *Pseudocercospora paranaensis* (GenBank KT037523; Identities = 438/445 (98 %), Gaps = 2/445 (0 %)).

**LSU.** Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Pseudocercospora rhabdothamni* (GenBank JQ324964; Identities = 849/849 (100 %), no gaps), *Pseudocercospora cyathicola* (GenBank JF951159; Identities = 849/849 (100 %), no gaps), and *Pseudocercospora humuli* (GenBank GU214676; Identities = 849/849 (100 %), no gaps).

Colour illustrations. Inflorescence of *Leandra fragilis* growing in the Atlantic rainforest at Parque Estadual da Serra do Brigadeiro, state of Minas Gerais, Brazil; leaf spot symptoms; conidiophores aggregated in sporodochia and conidia. Scale bar = 20 µm.

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Rhodocybe matesina
**Rhodocybe matesina** Picillo & Vizzini, *sp. nov.*

**Etymology.** The epithet refers to the locality, Monti del Matese, where this species was found.

**Classification — Entolomataceae, Agaricales, Agaricomycetes.**

**Pileus** 25–60 mm diam, at first convex, then plane and often shallowly depressed at centre with age; surface hygrophanous, beige-salmon-pink to beige-hazel nut when wet, cream with darker zonations towards the pileus margin when dry, pruinose when young, then smooth, dry; margin slightly involuted when young, soon plane, strongly undulate, lobate when old, cracking longitudinally at times, not striate. **Lamellae** broadly adnate to shortly decurrent, close, up to 3 mm high, intermixed with 1–4(–5) lamellae of variable length (lamellulae), at first whitish, then beige, finally pinkish when very old, easily detachable from the pileus context (as in *Lepista* species); edge entire or slightly eroded, concolorous. **Stipe** 30–60 × 4–9 mm, central, cylindrical to slightly clavate, straight to somewhat flexuose towards the base, solid; at first whitish, then concolorous with the pileus or slightly paler, white pruinose at apex, fibrillose-flocculent 1–4(–5) lamellae of variable length (lamellulae), at first whitish, to shortly decurrent, close, up to 3 mm high, intermixed with 1–4(–5) lamellae of variable length (lamellulae), at first whitish, then beige, finally pinkish when very old, easily detachable from the pileus context (as in *Lepista* species); edge entire or slightly eroded, concolorous. 

**Notes** — **Rhodocybe matesina** belongs to sect. *Rufobrunnea*, typified by *R. roseiavellanea*, which encompasses the **Rhodocybe** species characterised by a reddish beige, salmon pink, pinkish brown, ochre or reddish brown pileus, adnate to decurrent lamellae, and the absence of clamp-connections (Baroni 1981). Within this section, the new species is circumscribed by medium-sized basidiomes (up to 60 mm broad), an aromatic odour, bitter taste, a thin-fleshed depressed pileus, broadly ellipsoid to ellipsoid basidiomes, pileipellis hyphae with weakly incrusting pigment, and absence of pileo- and caulocystidia. Phylogenetically (MycoBank supplementary data), the ITS sequence analysis shows it sister (BPP = 1, MLB = 100 %) to a recently described species from Turkey, *R. asanii* which differs by shorter basidiomes, (4.5–)5.5–6.5(–7) × (3–)3.5–4.5(–5) μm (av. 5.8 × 4.1 μm), indistinct odour and taste, and adnexed to sinuate lamellae (Sesli & Vizzini 2017). The LSU sequence analysis (data not shown) also indicates *R. asanii* as its closest species. Morphologically, the most similar species are *R. alutacea*, *R. asyae*, *R. incarnata*, *R. pseudopiperita*, and *R. roseiavellanea*. *Rhodocybe alutacea* from North America has a smaller pileus (up to 35 mm diam), a pileus margin remaining involuted to incurved, a farinaceous odour and taste (mild), septate cheilocystidia with often capitulate terminal elements, and presence of cylindrical to clavate caulocystidia (Singer 1946, Baroni 1981, Baroni & Horak 1994). *Rhodocybe asyae* from Turkey differs in having smaller basidiomes (pileus up to 30 mm diam and stipe up to 5 mm diam), a mild taste, mainly 2-spored basidia, versiform cheilocystidia (Singer 1946, Baroni 1981, Baroni & Horak 1994). *Rhodocybe incarnata* from Venezuela differs by a pileus at first fire red, flame red, flame scarlet than becoming paler, a mild taste, but with latent sharpness in back of throat, shorter basidiomes (5.7 μm long on average), pileipellis as a trichoderm and presence of caulocystidia (Baroni & Halling 1992). *Rhodocybe pseudopiperita* from Tasmania is distinguished by a weakly umbonate pileus with shallow depression around umbo, indistinct odour or like mown grass and mild taste, the presence of scattered cystidial elements in the pileipellis, and dimorphic basidiome morphology with most of the them being distinctly undulate-pustulate and smaller (5.5–6.5 × 4–5 μm) while c. 30–45 % of the basidiomes are almost smooth and distinctly larger (7–9 × 5–5.5 μm) (Baroni & Gates 2006, Noorde loos & Gates 2012). Finally, the North American *R. roseiavellanea* is distinguished by a robust habitus (pileus 35–70 mm broad and stipe 30–60 × 10–25 mm), a mild taste, and large ellipsoid to subamygdaliform spores, (6.5–)7–9(–10) × (4–5)–5.5–7(–5) μm (Baroni 1981).
Russula arunii S. Paloi, A.K. Dutta & K. Acharya, sp. nov.

Etymology. Named after Arun Kumar Sharma, the founder of the Botanic Garden at the University of Calcutta, from where the specimen was collected.

Classification — Russulaceae, Russulales, Agaricomycetes.

Pileus 39–68 mm diam, convex when young becoming broadly convex to applanate with slightly depressed towards centre at maturity, surface viscid and smooth at early stages that often becomes slightly velvety when mature, semi moist to moist, translucent, cracked that often extends to the centre, disc greyish brown (5D3) to yellowish brown (5D4) when young, becoming light orange (5A4) to greyish orange (5B4) when old, margin pale orange (5A3), no colour change on bruising turns yellow (2B7) with KOH, reddish white (8A2) with guaiacol, negative in phenol, NH₄OH and SV, context c. 2 mm thick at the centre, gradually thinner towards margin (≤ 1 mm), yellowish white (1A2), turning pale yellow (4A3) when exposed, yellow (2A7) with KOH, reddish brown (8DS) with guaiacol, no colour change with NH₄OH, FeSO₄, SV and phenol. Lamellae c. 2 mm broad, adnexed, entire, regular, white (1A1), even, concolorous, turns reddish brown (8DS) with guaiacol, negative in phenol and NH₄OH, lamellae of one series. Stipe 20–29 × 5–7 mm, central, cylindrical, more or less equal, white (1A1), smooth, moist, fleshy, no colour change on bruising, turns greyish yellow (4B3) with KOH, light brown with SV and red (9B8) with guaiacol, context solid when young, becoming multi-chambered at maturity, white (1A1), turns light yellow with KOH and red (9B8) with guaiacol. Taste acid. Odour fishy-like. Spore print white. Basidiospores (5.5‒)7.5–8.7(‒9.5) × (4.5‒)5.5–6.5(‒7.5) μm, Q = 1.07‒1.16, globose to subglobose, ornamentation amyloid, composed of short (0.2‒0.5 μm) and long (0.7‒1.0 μm) warts with obtuse to acute apex, connected with a line between three or more warts, often free from each other, forming incomplete reticulum, suprahilar spot amyloid. Basidia (32‒)36–40.1–44(‒49) × (8.5‒)9.5–9.9(‒10.5) μm, clavate to subclavate, hyaline, thin-walled, oil droplets present when viewed with KOH, 4-spored, sterigmata 4.5–7 × 1–2.5 μm, cylindrical. Hymenial cystidia c. (50‒)53‒56(‒61) × 7–8(‒9) μm on gill sides, near gill edge c. 39.5–43(‒48) × 6.5–7.5 μm, clavate to subclavate with capitate or moniliform apex, hyaline, thin-walled, oil granule present when viewed with KOH. Pileipellis orthocomichromic in cresyl blue, context composed of densely arranged sphaerocytes, c. 53.5–61 μm deep; subpellellis non-gelatinous, c. 247–286 μm deep, composed of loosely arranged hyphae (measuring 1.5–3 μm wide), branched, oil granule present when viewed with KOH; suprapellis 79–122 μm deep, composed of erect to suberect hyphae with acute to obtuse apex, oliferous hyphae measuring 2.5–4 μm wide, more abundant towards pileus centre. Pileocystidia (17.5‒)19‒20(‒25.5) × 3‒4 μm, abundant towards pileus centre, scattered to absent towards margin, 1-celled, mostly with capitate apex, hyaline, thin-walled, base attached with nodular like cells. Lamellar trama composed of loosely arranged sphaerocytes, measuring 9‒25.5 × 7.5–23 μm, thin-walled. Subhymenium pseudo-parenchymatous. Stipitipellis 41–63 μm thick, composed of 3.5‒5.5 μm broad, branched, septate, hyaline hyphae, hyphal end subulate, oil granule present when viewed with KOH, caulocystidia abundant, clavate with capitate apex, 2‒3-celled, hyaline, dense with cytoplasmic contents. Stipe trama composed of almost subglobose sphaerocytes, measuring 14.5‒34 × 10.5‒26 μm.

Typus. Inoc, West Bengal, Kolkata, Botanical Garden of the Ballygunge Science College campus, N22°31’37.30″ E88°21’43.50″, alt. 10.6 m, on the base of Pterigota alata (Stercaliaceae), 28 July 2014, S. Paloi (holotype CUH AM261, ITS and LSU sequences GenBank KR872619 and KY946732, MycoBank MB819728).

Additional specimen examined. Inoc, West Bengal, Kolkata, Ballygunge Science College campus, N22°31’37.30″ E88°21’43.50″, alt. 10.6 m, on the base of Pterigota alata, 2 Aug. 2015, S. Paloi & A.K. Dutta, CUH AM270, ITS and LSU sequences GenBank KY450661 and KY946733.

Notes — The combination of features such as a greyish brown or yellowish brown to greyish orange pileus with translucent margin, adnexed attachment of lamellae, white spore print, fishy-like odour, acrid test, and presence of oliferous hyphae and pileocystidia in the pileipellis undoubtedly place Russula arunii in subg. Ingratula (Sarnari 1998).

Being a good representative member of subg. Ingratula, the newly described species appears morphologically close to R. pulverulenta, R. ventricosipes, and R. pectinatoideas. However, R. ventricosipes has a pale brownish to pink reddish brown or dark reddish orange pileus, negative reaction of the pileus surface with KOH, much longer basidiospores (7‒13.6 μm) coloured pale orange yellow with ornamentation that are never partial reticulate (Shaffer 1972). Russula pulverulenta differs from R. arunii by its yellowish white to dark orange yellow or moderate brown lamellae, pileus surface that turns deep reddish orange to strong reddish brown with KOH, and dark yellowish green colouration of the pileus and stipe context with guaiacol (Shaffer 1972). Russula pectinatoideas, commonly encountered throughout Europe and North America, has a much longer stipe (up to 50 mm), broader lamellae (4‒7 mm) that are forked and interveined, nauseating odour of the pileus context, bitter taste, somewhat differently sized basidiospores (6.7‒8.7 × 5.2‒7.5 μm), and much longer hymenial cystidia (65‒110 × 7‒11.5 μm; Romagnesi 1967). The previously described Indian species Russula dubidia differs by the stipe context that turns dark green with guaiacol, cream spore print, and absence of caulocystidia (Das et al. 2013) (MycoBank supplementary data).

Colour illustrations. India, West Bengal, vegetation cover of the collection site (background); left column: field photograph of the basidiocarp, fresh basidiocarp showing lamellae, SEM microphotograph of the basidispor; right column: basidia, hymenial cystidia, caulocystidia (all from holotype). Scale bars = 5 mm (basidiocarp), 10 μm (microscopic structures), 1 μm (basidiospore).

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Saksenaea loutrophoriformis
**Saksenaea loutrophoriformis** D.A. Sutton, Stchigel, Chander, Guarro & Cano, *sp. nov.*

**Etymology.** From the ancient Greek λούτροφορός, and from the Latin -formis, because of the vessel-shape of the sporangiosphere.

**Classification.** Saksenaeaceae, Mucorales, Mucormycotina.

_Hyphae_ sparsely septate, branched, hyaline, smooth-walled, 3–15 μm wide. _Sporangiphores_ erect, generally arising singly, at first hyaline, soon becoming brown, unbranched, 50–75 μm long, 5–10 μm wide, slightly verrucose. _Sporangia_ terminal, multi-spored, flask-shaped, asperate, 70–125 μm long, with a long (60–100 μm) neck; apex of the neck closed with a mucilaginous plug. _Sporangiospores_ mostly bacilliform, bilaterally compressed and rounded at both ends, more or less trapezoidal in lateral view, smooth-walled, 3.5–6(–7) × 2–3.5 μm, pale olive brown. _Rhizoids_ present, well-developed, terminal or lateral respect to the main axis of the sporangiosphere. _Zygospores_ not observed.

_Culture characteristics._ _Colonies_ on CZA at 37 °C practically filling the Petri dish (90 mm diam) after 4 d of incubation, whitish, with scarce aerial mycelium; reverse concordant. _Colonies_ on MEA, PDA and SAB showing similar features as on CZA, but they were more floccose and white, sporulation absent. The optimum temperature of growth was between 35 and 42 °C (reaching 75–85 mm diam). Minimum growth was observed at 15 °C (colonies of 31–35 mm diam), and the diameter reached at 25 °C was 57–63 mm. The fungus did not grow at 45 °C.

_Typus._ USA, Utah, from eye, 11 June 2009, D.A. Sutton (holotype CBS H-23041; cultures ex-type UTHSC 08-379 = FMR 10674; ITS, LSU, and EF1-α sequences GenBank FR687330, HM776682, and HM776693, MycoBank MB820008).

_Additional specimens examined._ India, Chandigarh, from palate necrotic tissue, 8 Aug. 2015, J. Chander, living cultures M-1012/15 = FMR 14516; ITS, LSU, and EF1-α sequences GenBank LT796164, LT796165, and LT796166.

_Notes._ — The ex-type strain and a second isolate of _S. loutrophoriformis_ have been isolated from human clinical specimens but in two very distant countries, USA and India, respectively. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hit with the ex-type strain using the ITS sequence is _Saksenaea vasiformis_ PWQ2338 (GenBank KP132601; Identities = 694/739 (94 %), Gaps 27/739 (3 %)); using the LSU sequence it is _Saksenaea erythrospora_ strain UTHSC 06-576 (GenBank HM776683; Identities = 714/735 (97 %), Gaps 3/735 (0 %)); and using the EF1-α sequence it is _Saksenaea vasiformis_ strain FMR 10131 (HM776689; Identities = 465/477 (97 %), no gaps). Our phylogenetic tree, built from the ITS, LSU, and EF1-α nucleotide sequences, corroborated that our isolates represent a new species, the closest species being _S. vasiformis_, with 93.6 % similarity with respect to the ex-type strain (NRRL 2443). The sporangiospores of _S. loutrophoriformis_ are similar in size to the _S. vasiformis_ species complex (5–7 × 2–3 μm), a bit larger than in _S. erythrospora_ (5–5.5 × 2–3 μm), but narrower than in _S. oblongispora_ (5–6.5 × 3–4.5 μm) and in _S. trapezispora_ (av. = 7 × 3.5 μm) (Alvarez et al. 2010, Crous et al. 2016). However, the sporangiospores of _S. loutrophoriformis_ appear pale olive brown under the microscope, whereas these are hyaline to subhyaline in _S. vasiformis_; also, the sporangiospores of _S. loutrophoriformis_ are bilaterally more compressed at the middle than in _S. vasiformis_. The minimum growth temperature for the _S. vasiformis_ species complex has been reported at 15 °C. However, the strains of _S. loutrophoriformis_ grew well at that temperature. Also, the optimum growth temperature for _S. vasiformis_ has been reported between 25 °C and 37 °C, being higher (35 °C to 42 °C) for both _S. loutrophoriformis_ strains.

Maximum likelihood tree obtained from the combined DNA sequences dataset from three loci (ITS, LSU, EF1-α) of our isolates and sequences retrieved from GenBank. The tree was built by using MEGA v. 6. Bootstrap support values ≥ 70 % are presented at the nodes. _Apophosomyces elegans_ CBS 476.78 was used as outgroup. The new species proposed in this study is indicated in bold. * represents the ex-type strains. The scale bar indicates the expected number of changes per site.
Tolypocladium fumosum
*Toilocladium fumosum* Ruszkiewicz-Michalska, Pawłowska & Wrzosek, *sp. nov.*

**Etymology**—Named after the fameous grey colour of the stroma.

**Classification** — Ophiocordycipitaceae, Hypocreales, Sordariomycetes.

Stromata connected with a yellowish rhizomorph-like structure to a buried caterpillar case of lepidopteran host belonging to the Psychidae family (bagworm moths), unidentified to species level; stroma single, unbranched, with well-defined, rounded apex, pale chalcedony yellow at the base (plate XVII in Ridgway 2005) to dark gull grey at the apex (plate LIII in Ridgway 2005). The stalk slightly twisted, 10 × 1 mm, built with branched, septate hyaline hyphae, cells inflated at the basal septum (up to 3.5 µm). Fertile part of stroma almost 1/5–1/4 of the total length, ellipsoidal when young and capitated when mature, enlarged up to 3.8 mm diam, with stellate appearance due to aggregated perithecia erumpent from stroma (up to one half of the length). **Perithecial apex** partly covered by dense matt of the stroma outer layer (up to 46.5 µm thick), grey in colour, easily peelable. Interior distinctly paler, visible around some ostioles. **Perithecia** ovoid to pear-shaped, 740–760 × 444–558 µm, perithecial wall of brown pigmented textura angularis (outer layer, cells thin-walled, 6–10 µm diam) and of paler textura epidermoidea (inner layer, hyphae 4–5 µm diam, with wall thick up to 1.2 µm). Ostiolum papillate up to 79 µm long, and 25 µm diam at the apex. Ascii numerous, cylindrical, narrow, up to 200 × 5–6 µm, non-amyloid, the walls fragile at spore maturity, the apex with conspicuously thickened cup (up to 3 µm), with a narrow, central pore. **Ascospores** eight per ascus, hyaline, filiform, smooth, disarticulating into part-spores within ascus. Part-spores short cylindrical to cubic, with flattened ends and wall equally thick, 2–4.5(–6) × 1.5(–2) µm, apical part-spores long obovoid, 4–5 × 1 µm. Asexual morph present at the base of the stromal stalk. **Conidiomata absent. Conidiophores** 1(–2)-celled, discrete, micronematic, arranged irregularly, perpendicular to conidiophore, hyaline, monopolar, flask-shaped with enlarged base and tapering into narrow neck, sometimes bent from the axis, smooth-walled, 8–10(–12) × 1.5–2 µm. **Conidia** produced abundantly, aggregated, in slimy heads, obovate to cylindrical, smooth, hyaline, asceptate, without oil drops, 2–3.5 × 1.5–2 µm. **Chlamydospores** absent.

**Culture characteristics** — Both part-ascospores and conidia germinate *in vitro* on artificial media (MEA, PDA, OA). Growth of mycelium on mentioned media is sparse, slow, maximum 1 cm / 3 d, white, with abundant aerial mycelium, no soluble pigments present. Numerous anastomoses are formed on the colony edge.

**Notes** — The genus *Toilocladium* (= *Elaphocordyceps*) was established in 1971 for three species of soil-isolated fungi and currently is defined mainly on a molecular basis (Sung et al. 2007). Quandt et al. (2014) accepted 27 species in the genus and Gazis et al. (2014) described three species isolated from *Hevea* (rubber tree). Diverse ecologies of *Toilocladium* taxa (parasites of insects, insects and rotifers, soil saprobes, plant endophytes) are explained by the ‘host habitat hypothesis’ (Nikoh & Fukatsu 2000, Gazis et al. 2014). Only *T. inflatum* has a known sexual morph. The asexual morph has been also reported for *T. japonicum* (cultural studies by Ke & Ju 2015).

**Morphological characters** of both morphs of *T. fumosum* agree with the generic concept of the genus (Quandt et al. 2014). It differs from other species in the gross morphology of stromata: they are smoky grey, bereft of brownish, greenish or olivaceous tints that are characteristic for the majority of *Toilocladium* species. Only two other *Elaphomyces*-associated species have grey stromata: *T. minazukienese* and *T. miomoteanum* (Kobayashi & Shimizu 1982). However, both species form much bigger stromata (50–120 × 5–12 mm and 65 × 6 mm, respectively vs 10 × 3.8 mm) as well as perithecia and part-spores (16–18 × 3 µm and 8–11 × 1.5–2 µm vs 2.45 × 1.2–1.5 µm).

In terms of stromal shape and size of perithecia and part-spores the species seems to be the most similar to *T. inflatum*. However, the asexual morph differs by size and shape of phialides (base inflated, 3–5 × 2–3 µm vs base slightly swollen, 8–10 × 1.5–1.8 µm) and shape of conidia that are ± equal in size (ellipsoidal, 2–2.5 × 1.4–2 µm vs obovate to cylindrical, 2–3.5 × 1.8–2 µm). Both in *T. fumosum* and *T. inflatum* the first phialides produced are acreronium-like (Hodge et al. 1996). The distinctive character of *T. fumosum* is the presence of asexual morph at the base of stromal stipe, a character that it shares with *T. ophioglossoides* (according to Saccardo 1883), conidia from the initial mycelium of stroma are mentioned in the species description) and *T. inflatum* (asexual morph observed on host body and wood surrounding it; Hodge et al. 1996). Nevertheless, the asexual morphs in the genus seem to be highly variable and the new species is best separated based on its DNA phylogeny. According to the ITS phylogeny (Mycobank supplementary data), *T. fumosum* is different from all other *Toilocladium* species (96 % similarity to *T. clyndrosorum*, *T. ophioglossoides*, *T. inflatum* and *T. tundrense*).

**Colour illustrations.** The habitat of the fungus – the alder tree base covered with moss; ascus with disarticulating ascospores; perithecium; part-ascospores; stroma emerging from the mosses; phialides and conidia; the edge of the colony with anastomosing hyphae. Scale bars = 10 µm.
Tuber magentipunctatum
Tuber magentipunctatum Z. Merényi, I. Nagy, Stielow & Bratek, sp. nov.

**Etymology.** The name magentipunctatum is derived from 'magenti' (from Latin 'magenta') and 'punctatum' (from Latin patched, punctate, spotted).

**Classification.** Tuberaceae, Pezizales, Pezizomycetes.

Ascomata hypogeous globose to subglobose or moderately lobed 5–16 (26) mm diam; smooth; or rarely with some minutely warts in patches but never pubescent, always stained with the following colours: bay (19), purplish chestnut (21), dark brick (20), brown vinaceous (25) and fuscos black (36) in dried state (Royal Botanical Garden, Edinburgh (RBGE) 1969). Peridium 289 ± 171 µm (127–683 µm) thick in total, with an external layer of 122 ± 45 µm (53–227 µm), composed of cells arranged as a hyaline or pale yellow pseudoparenchyma, while the inner layer 148 ± 98 µm (46–400 µm) thick, intricately interwoven with the hyaline hyphae. The uppermost cells (layer: 106 ± 100 µm) are highly pigmented. The size of the largest isodiametric peridial cells are 19.5 ± 3.4 µm (14.5–24 µm).

Gleba is whitish at first, becoming hazel (27), milky coffee (28), marbled with medium spaced white veins. Colour of meshes is 2.66 ± 0.21 µm (2.38–3.05 µm). In dried state (RBGE) 1969).

Ascospores ellipsoid and contain randomly arranged spores. The distribution of spore numbers per ascis is 1: 2 ± 1%, 2: 4 ± 2%, 3: 8 ± 4%, 4: 11 ± 3%, 5: 16 ± 4%, 6: 20 ± 7%, 7: 22 ± 5%, and 8: 18 ± 8% (these are mean and standard deviation value pairs). Thus, the 6- and the 7-spored ascis are the most common. Ascospores globose to ellipsoid, Q = 1.03–1.53, yellow to pale brown, 18.3 ± 14.9 µm (16.5–21.4 ± 12.6–17.4 µm) in 4-spored ascis and 18.1 ± 14.1 µm (15.8–20.1 ± 12.6–16.3 µm), in 8-spored ascis excluding ornamentation. Spore volume is 2 178 ± 444 µm³ (1 524–2 903 µm³) in 4-spored ascis, while 1 895 ± 257 µm³ (1 561–2 344 µm³) in 8-spored ascis. Spores are ornamented with spines connected by low ridges to form a more or less regularly alveolate reticulum where the spicle height is 1.51 ± 0.39 µm (0.99–2.35 µm) and the average size of meshes is 2.66 ± 0.21 µm (2.38–3.05 µm).

**Distribution & Habitat.** The fruiting period is almost exclusively in summer (June–July, occasionally August–October). Ascomata can be found under a variety of potential host trees (e.g., Carpinus betulus, Quercus robur, Q. cerris, Corylus avellana, Corylus columa, Ostrya carpinifolia, Tilia tomentosa, Populus × canescens, Fagus sylvatica, and Picea abies). The soils of their habitats are slightly basophilic pH (pH_H₂O = 7.57 ± 0.10), heavy soil (‘sticky point according to Arany’ ≥ Ks = 65 ± 7.6). They have been found only in four European countries, from Italy to Romania. Occurs in plains and hilly regions between 80–900 m a.s.l.

**Notes.** Tuber magentipunctatum is distinguishable with not only molecular differences, but also with the high rate of 6–8-spored ascis, containing small spores with remarkable fine meshes. Tuber magentipunctatum is morphologically similar to Tuber regianum but differs in the volume of spores, which is larger in T. magentipunctatum: 1 895 ± 257 µm³ (in the range of 1 561–2 344 µm³) vs 1 225 ± 146 µm³ (1 075–1 491 µm³) in 8-spored ascis; additionally, the ratios of 8-spored ascis (R8) in T. magentipunctatum never exceed 35% (18% ± 8% (8–31 %)) while in T. regianum it varies between 38–45%. Tuber magentipunctatum is distinguishable from T. bernardinii with the smooth surface of its ascomata (which is often pubescent in T. bernardinii) and the excessively small meshes on spores (2.66 ± 0.21 µm vs 6.67 ± 0.3 µm, respectively). There are some other Tuber species which were characterised by 6–8-spored ascis. Tuber melenconii has warts, and its spores are larger (22–26 ± 16–18 µm; Montecchi & Sarasini 2000) than T. magentipunctatum. The ascomata of T. pseudoexcavatum always have a basal cavity, its surface is verrucose, warty, and it has larger spores (24–28 × 18–19 µm), and occurs in Asia (Wang et al. 1998).

**ITS.** Based on a megablast search against the INSDC (GenBank) nucleotide database, the closest hits using the ITS sequence of type material are several sequences originating from Tuber excavatum groups: GQ217540: Identities 294/344 (85 %), Gaps 8/344 (2 %); FM205567: 306/361 (85 %), Gaps 13/361 (3 %), with less than 70 % query cover.

**LSU.** The closest hits using the LSU sequence of type material are Tuber species from different species groups: KT067698: Identities 512/566 (90 %), Gaps 6/566 (1 %); KT067703: 511/566 (90 %), Gaps 6/566 (1 %).

Maximum likelihood phylogeny inferred from concatenated internal transcribed spacer (ITS) and 28S rRNA (LSU) regions, rooted to Choiromyces spp. Analysis was performed using RAxML through the CIPRES website (http://www.phylo.org) using the GTR+I−invar model. Bootstrap branch support > 70 % is shown. The scale bar represents 0.06 expected nucleotide changes per site.

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