Abstract
Novel species of fungi described in this study include those from various countries as follows: Australia, Chaetomella pseudocircinoseta and Coniella pseudodiospyri on Eucalyptus microcorys leaves, Cladosiphloea eucalypti, Terasphora dundii and Vermiculariospora dundii on Eucalyptus dundii leaves, Corymbia henryi from the gut of the beetle Molops piceus. Croatia, Mollisia endocrystallina from a fallen decorticated Picea abies tree trunk. Ecuador, Hygrocybe rodomaculata on soil. Hungary, Affoldia vorosii (incl. Affoldia gen. nov.) from Juniperus communis roots, Kuskansagia ubrzyszi (incl. Kuskansagia gen. nov.) from Fumana procumbens roots. India, Aureosidium tremulae as laboratory contaminant, Leucosporidium himalayensis and Naganishia indica from windblown dust on glaciers. Italy, Neodrevisia cycadica on Cycas sp. leaves, Pseudocercospora pseudomyrticola on Myrtus communis.

Key words
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Fungal Planet description sheets: 868–950
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Abstract (cont.)

leaves, Ramularia pistaciae on Pistacia lentiscus leaves, Neognomoniopsis quercina (incl. Neognomoniopsis gen. nov.) on Quercus ilex leaves. Japan, Diaportha fructicola on Passiflora edulis f. flavicarpa fruit, Entoloma nipponicum on leaf litter in a mixed Cryptomeria japonica and Acer spp. forest. Macedonia, Acreasaceae onon tintara leaves. Malaysia, Fuscidium eucalyptigenum on Eucalyptus sp. twigs, Neocordylorella eucalypti (incl. Neocordylorella gen. nov.) on Eucalyptus urophylla leaves. Mozambique, Meliola gorongosensis on dead Philepnera violacea leaflets. Nepal, Coniochaeta dendribiocola from Dendriobium longicornuc roots. New Zealand, Neodnevries sexualis and Thozetella neoeinea on Archontophoenix cunninghamiana leaves. Norway, Calopogon sandfordiendica from a piece of board on a rocky shore. Poland, Clavaria parvispora on soil. Donnelleya fin. from Palaeoloxodaceae from a piece of Phallus impudicus from sylvestris driftwood. Portugal, Sugiyama-tea trypani from soil. Portugal, Colletotrichum fijiicola from Acca sellowii. Russia, Crediptos lobularis on Populus tremula debris, Entoloma etakeriae, Entoloma erhardii and Suillus gastrovatus on soil, Nakazawaea ambrosiae from the galleries of Ips typographus under the bark of Picea abies. Slovenia, Pluteus ludwigi on twigs of broadleaved trees. South Africa, Anunnagomycesstellensobsociens (incl. Anunnagomyces gen. nov.) and Nieslia stellensobichiana on Eucalyptus sp. leaves, Bellirrianiella pseudoporphoience on Podocarpus falcatus leaf litter, Corynephora encephalartii on Encephalartos sp. leaves, Cytopsara paveliae on Pavetta revoluta leaves, Helminthosporum erythrinicola on Erythrina hurnea leaves, Helminthosporum szyszii on a Syzygium sp. bark canker, Libertamycosomes aloeic on Aloe sp. leaves, Penicillus luna from Musa sp. fruit, Phyllosticta lauridiae on Lauria tetragona leaves, Pseudotruncatella bolusanitchi (incl. Pseudotruncatellaaceae fam. nov.) and Dactylella bolusanitchi on Bolusanitchia speciosus leaves. Spain, Apenidiella foetida on submerged plant debris, Inocybe grammatoides on Quercus ilex subsp. ilex forest humus, Ovisciellus salomoni on soil, Phaeolium guarnig ori from soil. Thailand, Pantospora chromoleanese on Chromolea odorata leaves. Ukraine, Cadophora helenith from Helenithus annuus stems. USA, Boletus pseudoporphiifus on soil under slash pine, Botryochytrium foriae, Penicillum americanum and Penicillum minnesotense from air. Vietnam, Lycoperdon vietnamesense on soil. Morphological and culture characteristics are supported by DNA barcodes.

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Overview Mucoromycota, Ascomycota and Basidiomycota phylogeny – part 1

Consensus phylogram (50 % majority rule) of 40,878 trees resulting from a Bayesian analysis of the LSU sequence alignment (188 taxa including outgroup; 947 aligned positions; 656 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) >0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.0. The scale bar represents the expected changes per site. Families, orders, classes, subdivisions and phyla are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to Phytophthora capsici (GenBank HQ665266.1) 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 S24386).
Overview Dothideomycetes phylogeny – part 1
Consensus phylogram (50 % majority rule) of 22 278 trees resulting from a Bayesian analysis of the LSU sequence alignment (164 taxa including outgroup; 809 aligned positions; 394 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) >0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with bold face. The alignment and tree were deposited in TreeBASE (Submission ID S24386).
Overview Eurotiomycetes phylogeny

Consensus phylogram (50% majority rule) of 7,802 trees resulting from a Bayesian analysis of the LSU sequence alignment (46 taxa including outgroup; 816 aligned positions; 282 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) >0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to Candida broadrunensis (GenBank KY106372.1) 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 S24386).
Overview Diaporthales and Glomerellales (Sordariomycetes) phylogeny

Consensus phylogram (50 % majority rule) of 21 752 trees resulting from a Bayesian analysis of the LSU sequence alignment (54 taxa including outgroup; 781 aligned positions; 185 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) >0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to Candida broadrunensis (GenBank KY106372.1) 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 S24386).
Overview Hypocreales (Sordariomycetes) phylogeny

Consensus phylogram (50 % majority rule) of 13 052 trees resulting from a Bayesian analysis of the LSU sequence alignment (37 taxa including outgroup; 761 aligned positions; 181 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) >0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to Candida broadrunensis (GenBank KY106372.1) 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 S24386).
Overview other orders (Sordariomycetes) phylogeny

Consensus phylogram (50% majority rule) of 14 252 trees resulting from a Bayesian analysis of the LSU sequence alignment (35 taxa including outgroup; 724 aligned positions; 192 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) >0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to Ramularia endophylla (GenBank MH875006.1) 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 S24386).
Overview Xylariales (Sordariomycetes) phylogeny

Consensus phylogram (50 % majority rule) of 35 702 trees resulting from a Bayesian analysis of the LSU sequence alignment (65 taxa including outgroup; 736 aligned positions; 194 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) >0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to Ramularia endophylla (GenBank MH875006.1) 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 S24386).
Overview Orbiliomycetes, Lecanoromycetes and Leotiomycetes phylogeny

Consensus phylogram (50 % majority rule) of 58 402 trees resulting from a Bayesian analysis of the LSU sequence alignment (41 taxa including outgroup; 812 aligned positions; 350 unique site patterns) using MrBayes v. 3.2.6 (Ronquist et al. 2012). Bayesian posterior probabilities (PP) >0.84 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 Candida broadrunensis (GenBank KY106372.1) 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 S24386).
Niesslia stellenboschiana
Fungal Planet 868 – 19 July 2019

**Niesslia stellenboschiana** Crous, *sp. nov.*

**Etymology.** Name refers to Stellenbosch, South Africa, where this fungus was collected.

**Classification.** *Niessliaceae, Hypocreales, Sordariomycetes.*

Colonies flat, spreading, forming mucoid orange conidial masses on densely aggregated sporodochia. *Mycelium* of hyaline, smooth, branched, septate, 1.5–2.5 mm diam hyphae. *Conidiophores* aggregated in clusters, subcylindrical, hyaline, smooth, 1–3-septate, 7–35 × 2.5–3.5 mm, branched, with secondary and tertiary branches 6–10 × 2.5–3.5 mm, giving rise to 1–4 cymbiform phialides, 8–10 × 2–3 mm, with visible periclinal thickening, and short, non-flared collarettes, 0.5–1.5 mm long. *Conidia* aseptate, solitary, aggregating in mucoid mass, hyaline, smooth, guttulate, cylindrical, straight, apex obtuse, base tapered, truncate, 0.5 mm diam, (6–)6.5–7(–8) × (1.5–)2 mm.

*Culture characteristics.* Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA surface and reverse saffron. On PDA and OA surface and reverse amber with diffuse amber pigment.

**Typus. South Africa,** Western Cape Province, Stellenbosch Mountain, on leaves of *Eucalyptus* sp. (Myrtaceae), 2016, *P.W. Crous* (holotype CBS H-23933, culture ex-type CPC 34889 = CBS 145531, ITS and LSU sequences GenBank MK876400.1 and MK876441.1, MycoBank MB830822).

Notes — Species of *Niesslia* are commonly isolated from plant litter. As presently defined, *Niesslia* includes asexual morphs formerly known as *Monocillium* (Gams et al. 2019). *Niessliastellenboschiana* clustered between *N. tenuis* and ‘*Acremonium nigroscerotium*, and further phylogenetic studies will be required to resolve the taxonomy of this complex.

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Monocillium ligusticum* (GenBank MF681489.1; Identities = 530/568 (93 %), 10 gaps (1 %)), *Monocillium tenue* (GenBank MG826947.1; Identities = 538/577 (93 %), 16 gaps (2 %)) and *Niesslia subiculosa* (GenBank MG826970.1; Identities = 523/562 (93 %), 12 gaps (2 %)). Closest hits using the LSU sequence are *Acremonium nigroscerotium* (GenBank MH872160.1; Identities = 824/836 (99 %), 1 gap (0 %)), *Monocillium tenue* (GenBank MH870489.1; Identities = 822/836 (98 %), 1 gap (0 %)), *Niesslia exilis* (GenBank AY489720.1; Identities = 822/836 (98 %), 1 gap (0 %)) and *Acremonium pseudozeylanicum* (GenBank HQ232101.1; Identities = 811/826 (98 %), 2 gaps (0 %)).

Colour illustrations. *Eucalyptus* leaf *N. stellenboschiana* was isolated from. Colony on oatmeal agar; conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.
Pseudotruncellaceae Crous, fam. nov.

Etymology. Name refers to the genus Pseudotruncatella.

Classification — Pseudotruncellaceae, Amphisphaeriales, Sordariomycetes.

Conidiomata acervular to pycnidioid, gregarious, oval. Conidiophores arising from basal and lateral cells in cavity, cylindrical, septate, branched, at times reduced to conidiogenous cells, smooth, hyaline. Conidiogenous cells subcylindrical, hyaline, smooth, proliferating percurrently at apex. Conidia fusoid, straight, septate, with central tubular apical appendage, unbranched or bifurcate; basal cell, narrowly obconic with a truncate base, hyaline, smooth; two median cells dark brown, smooth, guttulate, thick-walled, fusoid. Sexual morph unknown.

Type genus: Pseudotruncatella R.H. Perera et al. MycoBank MB830823.

Pseudotruncatella bolusanthi Crous, sp. nov.

Etymology. Name refers to Bolusanthus, the host genus from which this fungus was isolated.

Conidiomata acervular to pycnidioid, gregarious, oval, 150–200 mm diam. Conidiophores arising from basal and lateral cells in cavity, cylindrical, 0–3-septate, branched, at times reduced to conidiogenous cells, smooth, hyaline, 10–30 × 3–4 mm. Conidiogenous cells subcylindrical, hyaline, smooth, proliferating percurrently at apex, 8–12 × 2–3 mm. Conidia (15–)17–20(–22) × (5–)6.5–7 mm, fusoid, straight, 2-septate, constricted at medium septum, with central tubular apical appendage, unbranched or bifurcate, 15–30 × 1.5–2 mm; basal cell 3–5 × 4–5 mm, narrowly obconic with a truncate base, hyaline, smooth; two median cells (13–)14–15(–17) × (5–)6.5–7 mm, dark brown, smooth, guttulate, thick-walled, fusoid.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface hazel, reverse isabelline. On PDA surface honey, reverse isabelline in centre, honey in outer region. On OA surface honey.

Type. SOUTH AFRICA, Mpumalanga Province, Kruger National Park, on leaves of Bolusanthus speciosus (Fabaceae), 19 Nov. 2010, P.W. Crous, HPC 2263 (holotype CBS H-23934, culture ex-type CPC 34700 = CBS 145532, ITS and LSU sequences GenBank MK876407.1 and MK876448.1, MycoBank MB830823).

Notes — The genera of appendaged coelomycetes in Sporocadaceae have recently been treated by Liu et al. (2019). The monotypic genus Pseudotruncatella was introduced by Perera et al. (2018) for a truncatella-like coelomycete occurring on dead branches of Cytisus and Helichrysum in Italy. Pseudotruncatella bolusanthi can be distinguished from P. arezzoensis (conidia 20–25 × 5.4–6.5 μm, 3-septate), based on its smaller, 2-septate conidia. Pseudotruncellaceae is allied to a sequence of Hyponectria buxi (Hyponectriaceae), although there are no cultures to confirm the placement of the latter family.

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to Pseudotruncatella arezzoensis (GenBank MG192321.1; Identities = 477/508 (94%), 9 gaps (1%)), Castanediella eucalypti (GenBank KR476723.1; Identities = 468/516 (90%), 14 gaps (2%)) and Castanediella communis (GenBank KY173393.1; Identities = 475/527 (90%), 14 gaps (3%)). Closest hits using the LSU sequence are Pseudotruncatella arezzoensis (GenBank MG192317.1; Identities = 784/786 (99%), 1 gap (0%)), Pseudophloeospora eucalyptorum (GenBank MH878224.1; Identities = 760/786 (97%), 1 gap (0%)) and Oxidothis garethjonesii (GenBank KY206762.1; Identities = 760/787 (97%), 3 gaps (0%)).
Dactylella bolusanthi
**Dactylella bolusanthi** Crous, sp. nov.

**Etymology.** Name refers to *Bolusanthus*, the host genus from which this fungus was isolated.

**Classification.** *Orbiliaceae, Orbiliales, Orbiliomycetes.*

Myelium consisting of branched, septate, hyaline, smooth, 2.5–3 mm diam hyphae, frequently forming hyphal coils. Conidiophores 0–1-septate, mostly reduced to conidiogenous cells, erect, straight, hyaline, smooth, with apical taper to truncate apex, 10–50 × 3–4 mm. Conidiogenous cells hyaline, smooth, subcylindrical with apical taper, phialidic, apex 2 mm diam, colarella mostly not visible, 10–30 × 3–4 mm. Conidia solitary, fusoid, straight to flexuous, widest in middle, apex subobtuse, base truncate, 2 mm diam, hyaline smooth, guttulate, 5–11-septate, (42–)50–65(–75) × 5(–6) mm.

Culture characteristics — Colonies flat, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface salmon, reverse saffron. On PDA surface and reverse dirty white. On OA surface pale luteous to saffron.

**Typus.** SOUTH AFRICA, Mpumalanga Province, Kruger National Park, on leaves of *Bolusanthus speciosus* (Fabaceae), 19 Nov. 2010, P.W. Crous, HPC 2263 (holotype CBS H-23935, culture ex-type CPC 34702 = CBS 145533, ITS and LSU sequences GenBank MK876387.1 and MK876428.1, MycoBank MB830825).

Notes — *Dactylella bolusanthi* is similar to other species of *Dactylella* (Seifert et al. 2011), as conidiophores are mostly reduced to solitary, erect, monopodial on superficial mycelium (periclinal thickening inconspicuous), and all structures remain hyaline with age. Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Dactylella zhongdianensis* (GenBank KT222436.1; Identities = 702/836 (84 %), 44 gaps (5 %)), *Dactylella rhopalota* (GenBank DQ494369.1; Identities = 493/559 (88 %), 25 gaps (4 %)) and *Orbilia cardui* (GenBank KT222403.1; Identities = 503/575 (87 %), 22 gaps (3 %)). Closest hits using the LSU sequence are *Dactylella zhongdianensis* (GenBank KT380101.1; Identities = 822/836 (98 %), 2 gaps (0 %)), *Orbilia cardui* (GenBank KT222403.1; Identities = 817/833 (98 %), no gaps) and *Dactylella rhopalota* (GenBank AY261177.1; Identities = 820/840 (98 %), 2 gaps (0 %)).
Vermiculariopsiella dunnii
**Vermiculariopsiella dunnii** Crous & Carnegie, sp. nov.

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

*Classification — Helminthosphaeriaceae, Sordariales, Sordariomycetes.*

Colonies sporulating profusely throughout on SNA. *Setae* erect, brown, cylindrical, straight to flexuous, 150–200 × 3–4 µm, thick-walled, smooth, 8–10-septate, tapering towards apex, developing a head of lateral coiled to whip-like branches (constricted at base where attached to setae), that are brown, septate, tapering, containing coiled, septate lateral branches that could again contain coiled, lateral, branched, mostly aseptate branches. *Conidiophores* arranged in a whorl around base of setae, pale brown, smooth, subcylindrical, branched or not, 0–6-septate, containing conidiogenous cells that are arranged laterally along its length or at times reduced to conidiogenous cells. *Conidiogenous cells* solitary, monophialidic, discrete, ampulliform to subulate, pale brown, 15–20 × 4–5 µm, apex 1–1.5 µm diam, with minute collarette (1–2 µm long), at times with percurrent proliferation at apex. *Conidia* asymmetrical, fusoid to subfusoid or oblong, attenuated, base bluntly rounded to somewhat inflated, aseptate, smooth, hyaline, finely granular, (6–)7.5–9(–10) × (2–)2.5(–3) µm.

*Culture characteristics —* Colonies flat, spreading, with sparse aerial mycelium and smooth, even margin, reaching 25 mm diam after 2 wk at 25 °C. On MEA surface and reverse ochreous. On PDA surface and reverse isabelline. On OA surface isabelline.

*Typus. AUSTRALIA, New South Wales, Yabbra State Forest, Boomi Creek plantation, on leaves of *Eucalyptus dunnii* (Myrtaceae), 19 Apr. 2016, A.J. Carnegie, HPC 2430 (holotype CBS H-23938, culture ex-type CPC 35649 = CBS 145637.1; Identities = 525/538 (98 %), 6 gaps (1 %)), *Vermiculariopsiella eucalypti* (GenBank NR_154637.1; Identities = 494/519 (95 %), 12 gaps (2 %)) and *Vermiculariopsiella lauracearum* (GenBank MK047436.1; Identities = 516/548 (94 %), 9 gaps (1 %)). Closest hits using the LSU sequence are *Vermiculariopsiella eucalypti* (GenBank KX228303.1; Identities = 806/812 (99 %), no gaps), *Vermiculariopsiella pediculata* (GenBank MH877476.1; Identities = 831/839 (99 %), 1 gap (0 %)) and *Vermiculariopsiella lauracearum* (GenBank MK047487.1; Identities = 804/812 (99 %), no gaps).

Notes — *Vermiculariopsiella dunnii* is closely related to *V. eucalypti* (conidia (5–)7–9(–10) × (2–)2.5 µm; on leaves of *Eucalyptus regnans*, Australia, Victoria, Toolangi State Forest; Crous et al. 2016). In our overview phylogeny of *Vermiculariopsiella* it clusters apart with isolate KAS819, suggesting it to be a distinct species. A revision of the genus is presently in preparation, and will be published elsewhere.

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Vermiculariopsiella eucalypti* (GenBank NR_154637.1; Identities = 525/538 (98 %), 6 gaps (1 %)), *Vermiculariopsiella eucalypti* (GenBank NR_154637.1; Identities = 494/519 (95 %), 12 gaps (2 %)) and *Vermiculariopsiella lauracearum* (GenBank MK047436.1; Identities = 516/548 (94 %), 9 gaps (1 %)). Closest hits using the LSU sequence are *Vermiculariopsiella eucalypti* (GenBank KX228303.1; Identities = 806/812 (99 %), no gaps), *Vermiculariopsiella pediculata* (GenBank MH877476.1; Identities = 831/839 (99 %), 1 gap (0 %)) and *Vermiculariopsiella lauracearum* (GenBank MK047487.1; Identities = 804/812 (99 %), no gaps).

*Colour illustrations.* *Eucalyptus dunnii* plantation. Colony on oatmeal agar; setae and conidiogenous cells; conidia. Scale bars = 10 µm.

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Teratosphaeria henryi
**Teratosphaeria henryi** Crous & Carnegie, *sp. nov.*

**Etymology.** Name refers to Corymbia henryi, the host species from which this fungus was isolated.

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

*Conidiomata* pycnidial, solitary, brown, 90–120 mm diam; wall of 6–8 layers of brown *textura angularis*. *Conidiogenous cells* reduced to conidiogenous cells lining cavity. *Conidigenous cells* brown, verruculose, subcylindrical with slight apical taper, proliferating percurrently at apex, 6–12 × 3–4 mm. *Conidia* solitary, brown, verruculose, aseptate, fusoid, apex subtruncate, 2 mm diam, with minute marginal frill, (7–)8–10–(11) × (2.5–)3–(4) mm.

Culture characteristics — Colonies erumpent, spreading, (7–)8–10(–11) × (4.5–)5.5–6(–6.5) µm (Taylor et al. 2012) and *T. sieberi* (conidiate aseptate, 4–6–7 × (2.5–)3 µm) (Crous et al. 2018c), but is distinct based on its conidial dimensions.

On a megablaster search of NCBI's GenBank nucleotide database, the closest hits using the *ITS* sequence had highest similarity to *Teratosphaeria pseudocryptica* (GenBank KF442508.1; Identities = 465/490 (95 %), 10 gaps (2 %)), *Teratosphaeria rubida* (GenBank MH863388.1; Identities = 482/508 (95 %), 9 gaps (1 %)) and *Teratosphaeria sieberi* (GenBank MH327816.1; Identities = 474/501 (95 %), 5 gaps (0 %)). Closest hits using the *LSU* sequence are *Teratosphaeria stellensaebciani* (GenBank MH874553.1; Identities = 790/806 (98 %), no gaps), *Teratosphaeria nubilosa* (GenBank NG_057854.1; Identities = 790/806 (98 %), no gaps) and *Teratosphaeria destructans* (GenBank GU214702.1; Identities = 790/806 (98 %), no gaps). Closest hits using the *actA* sequence had highest similarity to *Teratosphaeria corymbiae* (GenBank KF903560.1; Identities = 505/541 (93 %), 3 gaps (0 %)), *Teratosphaeria viscida* (GenBank KF903563.1; Identities = 505/541 (93 %), 6 gaps (1 %)) and *Teratosphaeria destructans* (GenBank KF903447.1; Identities = 504/541 (93 %), 6 gaps (1 %)). Closest hits using the *cmdA* sequence had highest similarity to *Teratosphaeria gauchensis* (GenBank KF902727.1; Identities = 412/464 (89 %), 15 gaps (3 %)), *Teratosphaeria molleriana* (GenBank KF902737.1; Identities = 413/467 (88 %), 15 gaps (3 %)) and *Teratosphaeria majorizuulensis* (GenBank KF902733.1; Identities = 410/465 (88 %), 16 gaps (3 %)). Closest hits using the *rpb2* sequence had highest similarity to *Teratosphaeria sieberi* (GenBank MH327872.1; Identities = 824/929 (89 %), no gaps), *Teratosphaeria molleriana* (GenBank KX348104.1; Identities = 764/882 (87 %), 4 gaps (0 %)) and *Teratosphaeria gracilis* (GenBank MK047548.1; Identities = 766/886 (86 %), 2 gaps (0 %)). Closest hits using the *tef1* sequence had highest similarity to *Teratosphaeria gracilis* (GenBank MK047568.1; Identities = 357/427 (84 %), 24 gaps (5 %)), *Teratosphaeria zuulensis* (GenBank KF903369.1; Identities = 316/371 (85 %), 20 gaps (5 %)) and *Teratosphaeria corymbiae* (GenBank KF903293.1; Identities = 308/362 (85 %), 10 gaps (2 %)). Closest hits using the *tub2* sequence had highest similarity to *Teratosphaeria gracilis* (GenBank MK047583.1; Identities = 543/613 (89 %), 17 gaps (2 %)), *Teratosphaeria nubilosa* (GenBank AY725599.1; Identities = 515/606 (85 %), 21 gaps (3 %)) and *Teratosphaeria destructans* (GenBank KT343568.1; Identities = 508/603 (84 %), 22 gaps (3 %)).

Notes — *Teratosphaeria henryi* is phylogenetically closely related to *T. pseudocryptica* (conidia 0–3–septate, 26–31–40–(58) × (1.7–)2–2.5–(3.5) µm (Andjic et al. 2010), *P. rubida* (conidia aseptate, 11–)12.5–13.5–(16) × (4.5–)5.5–6–(6.5) µm (Taylor et al. 2012) and *T. sieberi* (conidiate aseptate, 4–6–7 × (2.5–)3 µm) (Crous et al. 2018c), but is distinct based on its conidial dimensions.

Based on the holotype CBS H-23939, culture ex-type CPC 35715 (holotype CBS H-23939, culture ex-type CPC 35715 (culture ex-type CPC 35715). Colour illustrations on leaves of *Corymbia henryi* (Myrtaceae), 17 Apr. 2016, A. J. Carnegie, HPC 2417 (holotype CBS H-23939, culture ex-type CPC 35715 = CBS 145539, ITF, LSU, actA, cmdA, rpb2, tef1 and tub2 sequences GenBank MK876410.1, MK876450.1, MK876464.1, MK876470.1, MK876492.1, MK876501.1 and MK876505.1, MycoBank MB830827).

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Coniella pseudodiospyri
Coniella pseudodiospyri Crous & Carnegie, sp. nov.

**Etymology.** Name refers to a morphological similarity with Coniella dio-
syri.

Classification — Schizoparameceae, Diaporthales, Sordaria-
omycetes.

Conidiomata separate, immersed to superficial, hyaline, becom-
ing black, 200–300 mm diam, with central dark brown ostiole;
wall of 3–6 layers of brown textura angularis. Conidiophores
densely aggregated, subulate, frequently branched below, 1–2-
septate, 15–25 × 3–4 mm. Conidiogenous cells hyaline, smooth,
subcylindrical with apical taper, 8–12 × 2.5–3.5 mm, covered in
mucoid sheath, apex with periclinal thickening and long collar-
ette. Conidia solitary, aseptate, subhyaline, cylindrical, straight,
smooth-walled, apex subobtuse, base truncate, guttulate, germ
silt absent, (21–)23–26(–27) × 3(–3.5) mm.

Culture characteristics — Colonies flat, spreading, with
sparse to moderate aerial mycelium, covering dish in 2 wk at
25 °C, with concentric circles of pycnidia on surface. On MEA
and PDA surface and reverse umber. On OA surface pale lute-
ous with patches of umber.

**Typus.** AUSTRALIA, New South Wales, Bulladelah State Forest, on leaves
de Eucalyptus microcorys (Myrtaceae), 16 Apr. 2016, A.J. Carnegie, HPC
2420 (holotype CBS H-23940, culture ex-type CPC 35725 = CBS 145540,
ITS, LSU, rpb2 and tef1 sequences GenBank MK876381.1, MK876422.1,
MK876479.1 and MK876493.1, MycoBank MB830828).

Notes — The genus Coniella was recently revised by Al-
varez et al. (2016). Coniella pseudodiospyri (on Myrtaceae) is
closely related to C. diospyri ((19–)21–23(–25) × 3(–3.5) mm, on
Diospyros and Trichilia in South Africa; Crous et al. 2018a),
but can be distinguished from that species based on its conidial
dimensions, which are generally larger than those of C. diospyri.

Based on a megablast search of NCBI’s GenBank nucleotide
database, the closest hits using the ITS sequence of CPC
35725 had highest similarity to Coniella diospyri (GenBank
NR_161131.1; Identities = 609/609 (100 %), no gaps), Coni-
ella duckerae (GenBank NR_154851.1; Identities = 602/613
(98 %), 2 gaps (0 %)) and Coniella quercicola (GenBank
AY339345.1; Identities = 564/579 (97 %), 6 gaps (1 %)). The
ITS sequences of CPC 35725 and CPC 35609 are identical
over 609 nucleotides. Closest hits using the LSU sequence of
CPC 35725 are Coniella diospyri (GenBank MK047490.1; Identi-
cies = 830/830 (100 %), no gaps), Coniella limoniformis
(GenBank NG_058964.1; Identities = 813/817 (99 %), no gaps)
and Coniella tibouchinae (GenBank JQ281777.2: Identities =
823/830 (99 %), no gaps). The LSU sequences of CPC 35725
and CPC 35609 are identical over 818 nucleotides. Closest hits
using the rpb2 sequence of CPC 35725 had highest similarity to
Coniella diospyri (GenBank MK047543.1; Identities = 789/813
(97 %), no gaps), Coniella limoniformis (GenBank KX833492.1;
Identities = 702/767 (92 %), no gaps) and Coniella tibouchi-
nae (GenBank KX833507.1; Identities = 701/767 (91 %), no
gaps). The rpb2 sequences of CPC 35725 and CPC 35609 are
identical over 831 nucleotides. Closest hits using the tef1 se-
quence of CPC 35725 had highest similarity to Coniella
diospyri (GenBank MK047563.1; Identities = 444/472 (94 %),
3 gaps (0 %)), Coniella tibouchinae (GenBank JQ281779.1; Identi-
cies = 301/346 (87 %), 11 gaps (3 %)) and Coniella africana (Gen-
Bank KX833600.1; Identities = 300/357 (84 %), 21 gaps (5 %)).
The tef1 sequences of CPC 35725 and CPC 35609 are identical
over 473 nucleotides.

Colour illustrations. Eucalyptus microcorys forest. Conidiomata on oat-
meal agar; conidiogenous cells; conidia. Scale bars = 300 μm (conidiomata),
10 μm (all others).
Phialoseptomonium eucalypti
Phialoseptomonium Crous & Carnegie, *gen. nov.*

**Etymology.** Phialo = phialides, septo = conidial septa, and -monium – from Acremonium.

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

*Mycelium* consisting of hyaline, smooth, branched, septate hyphae. *Conidiophores* erect, straight to flexuous, arising directly from hyphae or from a basal stalk, subcylindrical, 0–2-septate, 10–30 × 3–4.5 mm, giving rise to a rosette (2–6) of conidiophores. *Conidiophores* erect, flexuous, subcylindrical with apical taper, hyaline but base at times appearing greenish olivaceous, 5–7-septate, 190–220 × 2.5–3 mm. *Conidiogenous cells* apical, integrated, subcylindrical, phialidic with minute non-flared collarette (1 mm long), apex 1.5–2 mm diam, 90–120 × 2.5–3 mm. *Conidia* solitary, aggregating in mucoid mass, hyaline, smooth, granular, fusoid, straight, medianly 1-septate, apex obtuse, base truncate, 1.5 mm diam, (16–)19–21(–23) × 3(–3.5) mm.

Culture characteristics — Colonies flat, spreading, with folded surface, moderate aerial mycelium and smooth, lobate margin, reaching 60 mm diam after 2 wk at 25 °C. On MEA surface and reverse luteous. On PDA surface and reverse pale luteous. On OA surface saffron.

**Typus.** Australia, New South Wales, Boorabee State Forest, McCorquodale plantation, on leaves of *Eucalyptus grandis × camaldulensis* clone (*Myrtaceae*), 20 Apr. 2016, A.J. Carnegie, HPC 2431 (holotype CBS H-23941, culture ex-type CPC 35732 = CBS 145542, ITS and LSU sequences GenBank MK876402.1 and MK876443.1, MycoBank MB830830).

Notes — *Phialoseptomonium eucalypti* clusters with two acremonium-like isolates (Giraldo & Crous 2019), namely ‘A. lichenicola’ CBS 303.70 and ‘A. rhabdosporum’ CBS 438.66, which may be congeneric. Both the latter species have cylindrical, septate conidia.

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Acremonium lichenicola* (GenBank MH859549.1; Identities = 542/596 (91%), 14 gaps (2%)), *Acremonium rhabdosporum* (GenBank MH858850.1; Identities = 535/593 (90%), 10 gaps (1%)) and *Trichonectria rectipila* (GenBank NR_160175.1; Identities = 465/523 (89 %), 13 gaps (2%)). The ITS sequence is also 2–6 nucleotides similar to unidentified sequences from an unpublished study on dark pigmented epifoliar fungi forming sooty patches on trees in a tropical rainforest forest (GenBank HE584928.1–HE584933.1). Closest hits using the LSU sequence are *Acremonium lichenicola* (GenBank MH871536.1; Identities = 798/816 (98%), no gaps), *Sarcopodium flavolanaatum* (GenBank MH876362.1; Identities = 794/816 (97%), no gaps) and *Sarcopodium macalpinei* (GenBank MH876364.1; Identities = 791/816 (97%), no gaps).

Phialoseptomonium eucalypti Crous & Carnegie, *sp. nov.*

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

Notes — *Phialoseptomonium eucalypti* clusters with two acremonium-like isolates (Giraldo & Crous 2019), namely ‘A. lichenicola’ CBS 303.70 and ‘A. rhabdosporum’ CBS 438.66, which may be congeneric. Both the latter species have cylindrical, septate conidia.

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Acremonium lichenicola* (GenBank MH859549.1; Identities = 542/596 (91%), 14 gaps (2%)), *Acremonium rhabdosporum* (GenBank MH858850.1; Identities = 535/593 (90%), 10 gaps (1%)) and *Trichonectria rectipila* (GenBank NR_160175.1; Identities = 465/523 (89 %), 13 gaps (2%)). The ITS sequence is also 2–6 nucleotides similar to unidentified sequences from an unpublished study on dark pigmented epifoliar fungi forming sooty patches on trees in a tropical rainforest forest (GenBank HE584928.1–HE584933.1). Closest hits using the LSU sequence are *Acremonium lichenicola* (GenBank MH871536.1; Identities = 798/816 (98%), no gaps), *Sarcopodium flavolanaatum* (GenBank MH876362.1; Identities = 794/816 (97%), no gaps) and *Sarcopodium macalpinei* (GenBank MH876364.1; Identities = 791/816 (97%), no gaps).

Fungal Planet 874 – 19 July 2019

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

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

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

*Mycelium* consisting of medium brown, smooth, branched, septate, 2–2.5 mm diam hyphae. *Conidiophores* erect, 0–1-septate, mostly reduced to conidiogenous cells, straight to geniculose-sinuous, subcylindrical, 5–20 × 2.5–3 mm, medium brown, smooth, proliferating sympodially, scars thickened, darkened, not refractive, 1–1.5 mm diam. *Conidia* occurring in branched chains; ramoconidia medium brown, subcylindrical, 0–1-septate, 12–20 × 2–3 mm; conidia subcylindrical, straight, hyaline to pale brown, guttulate, medianly 1-septate; hila thickened and darkened, 1–1.5 mm diam, (13–)16–18(–20) × (1.5–)2–2.5 mm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 20 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse umber.

**Typus.** *Malaysia*, on twigs of *Eucalyptus* sp. (Myrtaceae), 22 Mar. 2018, M.J. Wingfield, HPC 2394 (holotype CBS H-23942, culture ex-type CPC 35746 = CBS 145543, ITS and LSU sequences GenBank MK876390.1 and MK876431.1, MycoBank MB830831).

Notes — *Fusicladium* eucalyptigenum is closely related to *Fusicladium* amoenum (conidia (6–)10.5–12.8(–17.3) × (1.5–)2.4–3(–3.8) μm) and *F.* paraamoenum (conidia (13–)15–20 (–28) × (3–)3.5(–4) μm; Crous et al. 2016), but is distinct based on its conidial dimensions. The *Fusicladium* generic complex is presently being revised and will be published elsewhere. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Fusicladium* amoenum (GenBank MH862514.1; Identities = 529/554 (95 %), 1 gap (0 %)), *Fusicladium* paraamoenum (GenBank NR_155093.1; Identities = 527/557 (95 %), 4 gaps (0 %)) and *Fusicladium* intermedium (GenBank EU035432.1; Identities = 489/530 (92 %), 3 gaps (0 %)). Closest hits using the LSU sequence are *Fusicladium* paraamoenum (GenBank NG_058242.1; Identities = 721/728 (99 %), no gaps), *Fusicladium* amoenum (GenBank EU035425.1; Identities = 720/728 (99 %), no gaps) and *Fusicladium* intermedium (GenBank EU035432.1; Identities = 712/729 (98 %), 1 gap (0 %)).

**Colour illustrations.** *Eucalyptus* forest. Colony on oatmeal agar; conidiophores, conidiogenous cells and conidia. Scale bars = 10 μm.

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Pseudosydowia eucalyptorum
**Pseudosydowia eucalyptorum** Crous & Carnegie, *sp. nov.*

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

**Classification.** *Saccotheciaceae, Dothideales, Dothidiomycetes.*

*Mycelium* consisting of branched, septate, smooth, hyaline, 5–6 mm diam hyphae. *Conidiomata* appearing as sporodochia on agar surface, consisting of aggregated clusters of conidiogenous cells arising directly from hyphae, reduced to loci on hyphae or ampulliform, hyaline, proliferating percurrently at apex, (2–)10–20 × (2–)5–6 mm. *Conidia* solitary, fusoid-ellipsoidal, aseptate, apex obtuse, base truncate, hyaline, smooth-walled, becoming thick-walled and medium brown with age, straight to curved; hyaline conidia 5–10(–13) × (2.5–)3(–3.5) mm; pigmented conidia (11–)15–17(–21) × (3.5–)4.5 mm.

**Culture characteristics.** Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA surface and reverse saffron. On PDA surface umber, reverse greenish olivaceous. On OA surface umber.

**Typus.** AUSTRALIA, New South Wales, Nundle State Forest, Boundary Road, on leaves of *Eucalyptus* sp. (Myrtaceae), 23 May 2016, A.J. Carnegie, HPC 2455 (holotype CBS H-23943, culture ex-type CPC 35811 = CBS 145546, ITS and LSU sequences GenBank MK876406.1 and MK876447.1, MycoBank MB830832).

**Notes.** *Pseudosydowia eucalyptorum* is closely related to *P. eucalypti* (hyaline conidia, 8–13(–15) × 2–4(–5) µm; pigmented conidia 6–8(–10) × (2.3–)3–5.5 mm; Cheewangkoon et al. 2009), but has larger conidia. Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Sydowia* sp. (GenBank MF683457.1; Identities = 583/594 (98 %), 2 gaps (0 %)). *Pseudosydowia eucalypti* (as *Selenophoma eucalypti*, GenBank AY293059.1; Identities = 551/568 (97 %), 4 gaps (0 %)) and *Saccothecium rubi* (GenBank NR_148096.1; Identities = 525/561 (94 %), 11 gaps (1 %)). Closest hits using the LSU sequence are *Pseudosydowia eucalypti* (GenBank GQ303327.2; Identities = 824/828 (99 %), no gaps), *Selenophoma mahoniae* (GenBank EU754213.1; Identities = 833/853 (98 %), no gaps) and *Saccothecium rubi* (GenBank NG_059644.1; Identities = 811/833 (97 %), 2 gaps (0 %)).

**Colour illustrations.** *Eucalyptus* forest. Colony on oatmeal agar; conidiogenous cells and conidia. Scale bars = 10 µm.
Beltraniella pseudoportoricensis
Beltraniella pseudoportoricensis Crous, sp. nov.

Etymology. Name refers to a morphology similar to that of Beltraniella portoricensis.

Classification — Beltraniaceae, Xylariales, Sordariomycetes.

Setae simple, erect, straight, thick-walled, coarsely verruculose toward apex, brown, 1–3-septate, arising from globose to lobate basal cell, tapering to acute apex, 75–230 × 3–6 mm. Conidiophores simple or branched, pale olivaceous, 10–20 × 4–6 mm, 1-septate, denticulate. Conidiogenous cells subcylindrical, smooth, pale brown, 8–12 × 4–6 mm, with several denticles, 1 mm diam. Supporting cells hyaline, oval to fusoid or obclavate with a single denticle, 10–12 × 3.5–4.5 mm. Conidia aseptate, smooth, lageniform to navicular, distal end truncate, proximal end rostrate, subhyaline with hyaline transverse band, (23–)25–27(–30) × 6–6.5(–7) mm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and even, smooth margins, covering dish after 2 wk at 25 °C. On MEA and PDA surface and reverse olivaceous grey. On OA surface smoke grey with patches of olivaceous grey.

Typus. SOUTH AFRICA, Western Cape Province, Cape Town, Kirstenbosch Botanical Garden, on leaf litter of Podocarpus falcatus (Podocarpaceae), 1 Mar. 2016, P.W. Crous (holotype CBS H-23944, culture ex-type CPC 34929 = CBS 145547, ITS and LSU sequences GenBank MK876377.1 and MK876416.1, MycoBank MB830833).

Notes — Beltraniella pseudoportoricensis forms part of the B. portoricensis species complex. The type (on Odina wodier from India) is not known from culture, but a recent reference isolate (on Mangifera indica, culture NFCCI 3993; conidia 20–25(–31) × 5.5–7 mm; Rajeshkumar et al. 2016) is phylogenetically distinct. We consequently describe the South African collection as new.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to Beltraniella sp. CGL-2017a (as Beltraniella ramosiphora, GenBank MG717500.1; Identities = 531/536 (99 %), no gaps), Beltraniella portoricensis (GenBank KU212349.1; Identities = 584/591 (99 %), 1 gap (0 %)) and Beltraniella fertilis (GenBank MF580247.1; Identities = 543/552 (98 %), 2 gaps (0 %)). Closest hits using the LSU sequence are Beltraniella pandanicola (GenBank MH260281.1; Identities = 828/834 (99 %), 1 gap (0 %)), Beltraniella portoricensis (GenBank MH871777.1; Identities = 828/834 (99 %), 1 gap (0 %)) and Beltraniella humicola (GenBank MH870044.1; Identities = 828/834 (99 %), 1 gap (0 %)).
Teratosphaeria dunnii
**Teratosphaeria dunnii** Crous & Carnegie, sp. nov.

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

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

*Conidiomata* pycnidial, solitary, brown, globose, 90–200 mm diam, with central ostiole; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* lining the inner cavity, subcylindrical, pale brown, 1–2-septate, branched or not, 7–20 × 2.5–4 mm, or reduced to conidiogenous cells. *Conidiogenous cells* subcylindrical to doliform, medium brown, verruculose, proliferating percurrently at apex, 5–8 × 3.5–4 mm. Conidia solitary, asceptate, thick-walled, guttulate, golden brown, verruculose, subcylindrical to fusoid-ellipsoid, apex subobtuse, base truncate, 1.5–2 mm diam with minute marginal frill, (6–)8–9–(11) × (2.5–)3–(3.5) mm.

**Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 25 mm diam after 2 wk at 25 °C.** On MEA surface pale olivaceous grey with scarlet aerial mycelium, reverse scarlet, with diffusate scarlet pigment. On PDA surface pale olivaceous grey with scarlet aerial mycelium and diffuse pigment, reverse olivaceous grey. On OA surface smoke grey.

**Typus. Australia**, New South Wales, Yabarra State Forest, Boomi Creek plantation, on leaves of *Eucalyptus dunnii* (Myrtaceae), 19 Apr. 2016, A.J. Carnegie, HPC 2430 (holotype CBS H-23945, culture ex-type CPC 35653 = CBS 145548, ITS, LSU, actA, cmdA, rpb2, tef1 and tub2 sequences GenBank KT343568.1; Identities = 514/597 (86 %), 13 gaps (2 %)).

**Notes —** *Teratosphaeria dunnii* is phylogenetically closely related (98 %, 8 bp difference in ITS) to *T. molleriana* (co-nidia (7–)9–12–(13) × (2.5–)3–3.5–(4) μm; Crous & Wingfield 1997), but can be distinguished based on its smaller conidia. Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Teratosphaeria molleriana* (GenBank MH862864.1; Identities = 515/523 (98 %), 1 gap (0 %)), *Teratosphaeria xenocryptica* (GenBank MH883258.1; Identities = 490/499 (98 %), 1 gap (0 %)) and *Teratosphaeria sieberi* (GenBank MH327816.1; Identities = 510/520 (98 %), 3 gaps (0 %)). Closest hits using the LSU sequence are *Teratosphaeria molleriana* (GenBank KF251777.1; Identities = 777/779 (99 %), no gaps), *Teratosphaeria profusa* (GenBank FJ493220.1; Identities = 773/779 (99 %), no gaps) and *Teratosphaeria dimorpha* (GenBank FJ493215.1; Identities = 773/779 (99 %), no gaps). Closest hits using the actA sequence had highest similarity to *Teratosphaeria molleriana* (GenBank KF903394.1; Identities = 525/540 (97 %), 2 gaps (0 %)), *Teratosphaeria viscosa* (GenBank KF903563.1; Identities = 504/542 (93 %), 7 gaps (1 %)) and *Teratosphaeria eucalypti* (GenBank KF903452.1; Identities = 504/543 (93 %), 8 gaps (1 %)). Closest hits using the cmdA sequence had highest similarity to *Teratosphaeria molleriana* (GenBank KF902737.1; Identities = 432/457 (95 %), no gaps), *Teratosphaeria blakelyi* (GenBank KF902704.1; Identities = 420/460 (91 %), 6 gaps (1 %)) and *Teratosphaeria toledana* (GenBank KF902774.1; Identities = 416/457 (91 %), 6 gaps (1 %)). Closest hits using the rpb2 sequence had highest similarity to *Teratosphaeria molleriana* (GenBank KX348104.1; Identities = 855/881 (97 %), no gaps), *Teratosphaeria eucalypti* (GenBank KX348102.1; Identities = 812/913 (89 %), 2 gaps (0 %)) and *Teratosphaeria gracilis* (GenBank MK047548.1; Identities = 790/886 (89 %), 2 gaps (0 %)). Closest hits using the tef1 sequence had highest similarity to *Teratosphaeria molleriana* (GenBank KF903326.1; Identities = 318/361 (88 %), 27 gaps (7 %)), *Teratosphaeria blakelyi* (GenBank KF903288.1; Identities = 316/365 (87 %), 10 gaps (2 %)) and *Teratosphaeria toledana* (GenBank KF903361.1; Identities = 314/367 (86 %), 17 gaps (4 %)). Closest hits using the tub2 sequence had highest similarity to *Teratosphaeria gracilis* (GenBank MK047539.1; Identities = 529/597 (89 %), 14 gaps (2 %)), *Teratosphaeria aff. nubilosa* (GenBank ATY726511.1; Identities = 514/597 (86 %), 13 gaps (2 %)).

**Colour illustrations.** *Eucalyptus dunnii* forest. **Conidiomata on malt extract agar; conidiogenous cells; conidia. Scale bars = 10 μm.**

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Chaetomella pseudocircinoseta
Chaetomella pseudocircinoseta Crous & Carnegie, sp. nov.

Etymology. Name refers to a morphology similar to that of Chaetomella circinoseta.

Classification — Chaetomellaceae, Chaetomellales, Leotiomycetes.

Conidiomata pycnidial, solitary, becoming aggregated, superficial, dark brown, globose, 300–400 mm diam with elongate raphe of paler pigment visible across top of conidiomata. Setae brown, smooth, unbranched, thick-walled, multi-septate, tapering towards obtuse to clavate apex, 150–750 x 10–20 mm. Conidiophores hyaline, smooth, filiform, subcylindrical, branched, 2–6-septate, 50–120 x 1.5–2 mm. Conidiogenous cells phialidic, subcylindrical, terminal and intercalary, smooth, hyaline, 10–50 x 1.5–2 mm. Conidia aseptate, hyaline, fusoid to falcate with pointed ends, slightly curved, (9–)11–12 x (2–)2.5 mm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and prominent circadian rings on surface, margin smooth, lobate, reaching 60 mm diam after 2 wk at 25 °C. On MEA surface chestnut, reverse umber. On PDA surface chestnut, reverse pale luteous with patches of umber. On OA surface chestnut.

Typus. Australia, New South Wales, Bulladelah State Forest, on leaves of Eucalyptus microcorys (Myrtaceae), 16 Apr. 2016, A.J. Carnegie, HPC 2420 (holotype CBS H-23946, culture ex-type CPC 35721 = CBS 145549, ITS and LSU sequences GenBank MK876379.1 and MK876418.1, MycoBank MB830835).

Notes — Chaetomella pseudocircinoseta is phylogenetically closely related to C. circinoseta (CBS 159.62, type), which is characterised by the fact that it has spiral setae (Rossman et al. 2004), which are, however, lacking in C. pseudocircinoseta. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to Chaetomella circinoseta (GenBank MH858129.1; Identities = 460/467 (99 %), no gaps), Chaetomella raphigera (GenBank MH864530.1; Identities = 435/473 (92 %), 14 gaps (2 %)) and Chaetomella cinnamomea (GenBank MH858845.1; Identities = 434/473 (92 %), 14 gaps (2 %)). Closest hits using the LSU sequence are Chaetomella circinoseta (GenBank MH869712.1; Identities = 813/818 (99 %), no gaps), Sphaerographium nyssicola (GenBank MH876287.1; Identities = 807/827 (98 %), no gaps) and Pilidium septatum (GenBank NG_060185.1; Identities = 763/783 (97 %), no gaps).

Colour illustrations. Eucalyptus microcorys forest. Conidiomata on malt extract agar; conidiomata with setae; conidiophore with conidiogenous cells; conidia. Scale bars = 400 μm (conidiomata), 10 μm (conidiophores and conidia).
Cladophialophora eucalypti
Fungal Planet 880 – 19 July 2019

**Cladophialophora eucalypti** Crous & Carnegie, *sp. nov.*

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

*Classification.* — *Trichomeriaceae, Chaetothyriales, Eurotiomycetes.*

*Mycelium* consisting of hyaline to olivaceous, smooth-walled, branched, septate, 1.5–2 mm diam hyphae. *Conidiophores* solitary, erect, subcylindrical, unbranched, straight to geniculate-sinuous, medium brown, smooth, 10–65 × 3–4 mm, 1–5-septate. *Conidiogenous cells* terminal, integrated, subcylindrical, medium brown, smooth, 10–15 × 3–4 mm; proliferating sympodially, scars terminal, thickened and darkened, 0.5–1 mm diam. *Conidia* in branched chains, olivaceous smooth-walled, granular, obclavate to subcylindrical, straight to flexuous; *ramoconidia* obclavate, 3–8-septate, 40–100 × 2–3 mm; conidia subcylindrical, 0(–1)-septate, (8–)13–15(–20) × 2.5(–3) mm.

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

**Typus.** *Australia*, New South Wales, Keybarbin State Forest, Tabulum, on leaves of *Eucalyptus dunni* (Myrtaceae), 17 Apr. 2016, A.J. Carnegie, HPC 2433 (holotype CBS H-23947, culture ex-type CPC 35667 = CBS 145551, ITS, LSU and actA sequences GenBank MK876380.1, MK876419.1 and MK876454.1, MycoBank MB830836).

Notes — *Cladophialophora eucalypti* is related to a *Cladophialophora* isolate (CBS 376.54) deposited under the name ‘*Pyricularia parasitica*’ and clusters in a clade typified by *Cladophialophora* and *Exophiala* spp.

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Exophiala encephalarti* (GenBank HQ599588.1; Identities = 446/534 (84 %), 32 gaps (5 %)), *Brycekendrickomyces acaciae* (GenBank KM246230.1; Identities = 505/620 (81 %), 57 gaps (9 %)) and *Knufia cryptophialidica* (GenBank NR_121501.1; Identities = 443/537 (82 %), 38 gaps (7 %)).

Closest hits using the LSU sequence are *Brycekendrickomyces acaciae* (GenBank MH874874.1; Identities = 795/826 (96 %), 4 gaps (0 %)), *Exophiala encephalarti* (GenBank HQ599589.1; Identities = 784/822 (95 %), 8 gaps (0 %)) and *Cladophialophora proteae* (GenBank EU035411.1; Identities = 785/829 (95 %), 6 gaps (0 %)). No significant hits were obtained when the actA sequence was used in blastn and megablast searches.

*Colour illustrations.* Eucalyptus forest. Hyphae; conidiophores with conidiogenous cells; conidial chains. Scale bars = 10 µm.
**Elsinoe salignae** Crous & Carnegie, *sp. nov.*

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

**Classification.** *Elsinoaceae, Myriangiales, Dothideomycetes.*

*Conidiomata* erumpent, sporodochial, 50–150 mm diam, based on a pale brown stroma giving rise to densely aggregated conidiophores. *Conidiophores* unbranched, hyaline to pale brown, smooth-walled, subcylindrical, 1–2-septate, 15–25 × 3–5 mm. *Conidiogenous cells* integrated, subcylindrical, hyaline, smooth-walled, mono- to polyphialidic, 8–12 × 3–4 mm. *Conidia* solitary, aggregating in mucoid mass, aseptate, hyaline, smooth-walled, guttulate, subcylindrical to ellipsoid, apex obtuse, base truncate, (4.5–)5–6(–6.5) × (2–)2.5 mm.

**Culture characteristics.** Colonies erumpent, surface folded, with sparse aerial mycelium and smooth, lobate margin, reaching 7 mm diam after 2 wk at 25 °C. On MEA surface sienna, reverse ochreous. On PDA surface ochreous to umber, reverse luteous with diffuse luteous pigment. On OA surface ochreous.

**Typus.** **AUSTRALIA,** New South Wales, Bulladelah State Forest, on leaves of *Eucalyptus saligna* (Myrtaceae), 16 Apr. 2016, A.J. Carnegie, HPC 2415 (holotype CBS H-23948, culture ex-type CPC 35713 = CBS 145552, ITS, LSU and rpb2 sequences GenBank MK876389.1, MK876430.1 and MK876485.1, MycoBank MB830837).

Notes — The genus *Elsinoe* was recently revised by Fan et al. (2017), who also provided a key to the species occurring on *Eucalyptus.* *Elsinoe salignae* is phylogenetically related to, but distinct from *E. leucopogonis* (on *Leucopogon* sp., Australia) (Crous et al. 2018c). Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Elsinoe leucopogonis* (GenBank NR_159836.1; Identities = 567/580 (98 %), 3 gaps (0 %)), *Elsinoe hederae* (GenBank NR_148146.1; Identities = 502/521 (96 %), 12 gaps (2 %)) and *Elsinoe lepagei* (GenBank MH856598.1; Identities = 519/549 (95 %), 14 gaps (2 %)). Closest hits using the LSU sequence are *Elsinoe hederae* (GenBank KX886994.1; Identities = 733/736 (99 %), no gaps), *Elsinoe lepagei* (GenBank KX887004.1; Identities = 732/736 (99 %), no gaps) and *Elsinoe fagarae* (GenBank KX886981.1; Identities = 732/736 (99 %), no gaps). Closest hits using the rpb2 sequence had highest similarity to *Elsinoe leucopogonis* (GenBank MH327874.1; Identities = 848/872 (97 %), no gaps), *Elsinoe hederae* (GenBank KX887113.1; Identities = 646/744 (85 %), no gaps) and *Elsinoe lepagei* (GenBank KX887122.1; Identities = 617/741 (83 %), 2 gaps (0 %)).
Neodevriesia cycadicola
Neodevriesia cycadicola Crous, sp. nov.

Etymology: Name refers to Cycas, the host genus from which this fungus was isolated.

Classification — Neodevriesiaceae, Capnodiales, Dothideomycetes.

Mycelium consisting of pale olivaceous, smooth, branched, septate, 2–3 mm diam hyphae. Conidiophores solitary, erect, pale olivaceous, smooth, subcylindrical, 1–2-septate, straight, 5–15 × 2–3 mm. Conidiogenous cells terminal, subcylindrical, pale olivaceous, smooth, 5–9 × 2–3 mm; scars thickened and darkened, 1.5 mm diam. Conidia occurring in branched chains, subcylindrical, pale olivaceous, smooth-walled, guttulate; ramoconidia 0–1-septate, 8–12 × 2.5–3 mm; conidia 0–1-septate, (7–)8–9 × 2–2.5 mm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 7 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus. ITALY, Sicily, on leaves of Cycas sp. (Cycadaceae), 10 Apr. 2018, P.W. Crous, HPC 2365 (holotype CBS H-23949, culture ex-type CPC 35833 = CBS 145553, ITS and LSU sequences GenBank MK876397.1 and MK876438.1, MycoBank MB830838).

Notes — Neodevriesia was established by Quaedvlieg et al. (2014) for a genus of hyphomycetes with medium brown, unbranched conidiophores, thick-walled, medium brown, rarely septate conidia, occurring in short and mostly unbranched conidial chains, and lacking chlamydospores. Neodevriesia cycadicola is closely related to N. lagerstroemiae (ramoconidia 9–15 × 3–5 μm, (0–)1(–2)-septate; conidia narrowly ellipsoid, 0–1-septate, (5–)8–12(–15) × 2–3(–4) μm (Crous et al. 2009, 2015a), but can be distinguished based on its conidial morphology.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to Neodevriesia metrosideri (GenBank NR_161141.1; Identities = 513/551 (93 %), 19 gaps (3 %)), Neodevriesia lagerstroemiae (GenBank GU214634.1; Identities = 515/554 (93 %), 23 gaps (4 %)) and Neodevriesia hilliana (GenBank NR_145098.1; Identities = 515/559 (92 %), 20 gaps (3 %)). Closest hits using the LSU sequence are Neodevriesia agapanthi (GenBank NG_042688.1; Identities = 806/820 (98 %), no gaps), Neodevriesia imbrexigena (as Devriesia imbrexigena, GenBank JX915749.1; Identities = 813/828 (98 %), no gaps) and Neodevriesia knoxdaviesii (GenBank MH874778.1; Identities = 802/817 (98 %), 2 gaps (0 %)).

Colour illustrations. Cycas sp. Symptomatic leaves; conidiophores, conidiogenous cells and conidia. Scale bars = 10 μm.
Pseudocercospora pseudomyrticola
Fungal Planet 883 – 19 July 2019

**Pseudocercospora pseudomyrticola** Crous, sp. nov.

**Etymology.** Name refers to a morphology similar to that of *Pseudocercospora myrticola*.

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

*Caespituli* hypophyllous, brown, erumpent, arising from a weakly developed brown stroma, 30–50 mm diam. *Conidiophores* tightly aggregated in fascicles, subcylindrical, medium brown, roughened, straight, mostly unbranched, 0–1-septate, 10–15 × 3–4 mm, proliferating percurrently at apex; conidiophores also reduced to loci on aerial mycelium, truncate, 2–7 × 2 mm. *Conidia* pale olivaceous brown, smooth-walled, guttulate, subcylindrical with apical taper, apex subobtuse, base truncate, 3–9-septate, straight to slightly flexuous, (30–)45–75(–90) × (2–)2.5 mm; hila not thickened nor darkened.

**Culture characteristics —** Colonies erumpent, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

**Typus.** ITALY, Rome, on leaves of *Myrtus communis* (Myrtaceae), 12 Apr. 2018, P.W. Crous, HPC 2357 (holotype CBS H-23950, culture ex-type CPC 35448 = CBS 145554, ITS, LSU, actA, rpb2 and tef1 sequences GenBank MK876405.1, MK876446.1, MK876461.1, MK876490.1 and MK876499.1, MycoBank MB830839).

Notes — *Pseudocercospora pseudomyrticola* differs from *P. myrticola* in that it sporulates primarily on superficial mycelium (mostly absent in *P. myrticola*), lacks well-developed fascicles (prominent in *P. myrticola*), and has shorter, narrower conidia (Crous 1999).

Based on a megablast search of NCBI’s GenBank nucleotide database, the ITS sequence is identical to sequences of several species, e.g., to *Pseudocercospora jahni* (GenBank KM393283.1; Identities = 537/537 (100 %), no gaps), *Pseudocercospora elaeodendri* (GenBank GU980950.1; Identities = 537/537 (100 %), no gaps) and *Pseudocercospora cerasiana* (GenBank MH63211.1; Identities = 535/535 (100 %), no gaps). The LSU sequence is identical to sequences of several species, e.g., to *Pseudocercospora pittospori* (GenBank MK210500.1; Identities = 836/836 (100 %), no gaps), *Pseudocercospora amelopis* (GenBank GU253846.1; Identities = 836/836 (100 %), no gaps) and *Pseudocercospora ravenalicola* (GenBank GU253828.1; Identities = 836/836 (100 %), no gaps). Closest hits using the actA sequence had highest similarity to *Pseudocercospora flavomarginata* (GenBank JX902134.1; Identities = 528/537 (98 %), no gaps), *Pseudocercospora schizolobii* (GenBank JX902151.1; Identities = 527/537 (98 %), no gaps) and *Pseudocercospora paraguayensis* (GenBankKF903444.1; Identities = 510/521 (98 %), no gaps). Closest hits using the rpb2 sequence had highest similarity to *Pseudocercospora punicea* (GenBank KX462655.1; Identities = 609/616 (99 %), no gaps), *Pseudocercospora ceridicola* (GenBank KX462618.1; Identities = 608/616 (99 %), no gaps) and *Pseudocercospora breonadiae* (GenBank MH108006.1; Identities = 636/671 (95 %), no gaps). Closest hits using the tef1 sequence had highest similarity to *Pseudocercospora sp.* (GenBank GU384466.1; Identities = 309/310 (99 %), no gaps) and *Pseudocercospora struthanthi* (GenBank KT290195.1; Identities = 498/498 (99 %), no gaps).

**Colour illustrations.** Leaf spots on *Myrtus* sp. Conidiogenous cells, conidiogenous loci and conidia. Scale bars = 10 µm.
Corynespora encephalarti
**Fungal Planet 884 – 19 July 2019**

**Corynespora encephalarti** Crous & M.J. Wingf., sp. nov.

*Etymology.* Name refers to *Encephalartos*, the host genus from which this fungus was isolated.

*Classification.* *Corynesporascaceae, Pleosporales, Dothideomycetes.*

*Conidiophores.* Erect, straight, unbranched, olivaceous brown, smooth-walled, subcylindrical, 150–400 x 6–8 mm, 5–11-septate. *Conidiogenous cells* monotretic, integrated, terminal, cylindrical to slightly swollen, 2–3 mm diam. *Conidia* solitary, obclavate, medium olivaceous brown, 1–12-distoseptate, apex subobtuse, base truncate, 4–5 mm diam, dark brown, (65–)100–150 (–200) x (10–)11–15(–18) mm.

*Culture characteristics.* Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface dirty white, reverse sienna. On PDA surface dirty white, reverse chestnut. On OA surface dirty white.

*Typus.* **SOUTH AFRICA**, Limpopo Province, Tzaneen, on leaves of *Encephalartos* sp. (Zamiaceae), 22 June 2016, *P.W. Crous*, HPC 2487 (holotype CBS H-23951, culture ex-type CPC 35867 = CBS 145555, ITS and LSU sequences GenBank MK876383.1 and MK876424.1, MycoBank MB830840).

**Notes.** *Corynespora* was recently treated by Voglmayr & Jaklitsch (2017). As far as we could establish, no species have ever been described from *Encephalartos*, and *C. encephalarti* is phylogenetically distinct from all species presently known from culture or DNA sequence. Based on a mega-blast search of NCBI’s GenBank nucleotide database, the closest hits using the *ITS* sequence had highest similarity to *Corynespora citricola* (GenBank FJ852593.1; Identities = 534/550 (97 %), 5 gaps (0 %)), *Corynespora smithii* (GenBank KY984300.1; Identities = 530/554 (96 %), 11 gaps (1 %)) and *Corynespora thailandica* (GenBank NR_161145.1; Identities = 522/553 (94 %), 12 gaps (2 %)). Closest hits using the *LSU* sequence are *Corynespora smithii* (GenBank GU323201.1; Identities = 894/896 (99 %), no gaps), *Corynespora cassicola* (GenBank MH869486.1; Identities = 889/894 (99 %), no gaps) and *Corynespora torulosa* (GenBank NG_058866.1; Identities = 863/871 (99 %), no gaps).

*Colour illustrations.* *Encephalartos* sp. Symptomatic leaves; conidiogenous cells and conidia. Scale bars = 10 µm.

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Libertasomyces aloeticus
**Libertasomyces aloeticus** Crous & M.J. Wingf., *sp. nov.*

*Etymology.* Name refers to *Aloe*, the host genus from which this fungus was isolated.

*Classification — Libertasomyctaceae, Pleosporales, Dothideomycetes.*

*Conidiomata* pycnidial, unilocular, separate, globose, immersed to erumpent, brown, globose, 150–250 mm diam, with central ostiole; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, ampulliform to doliiform with prominent periclinal thickening, 5–7 × 5–6 mm. *Conidia* solitary, golden-brown, becoming dark brown, ellipsoid to subglobose, muriformly septate, with (1–)3(–4) transverse septa and 1–4 oblique septa, thick-walled, roughened and with striations covering length of conidiomum body, apex obtuse, base bluntly rounded, (9–)11–13(–15) × (7–)8(–9) mm.

*Culture characteristics —* Colonies erumpent, spreading, surface folded with moderate aerial mycelium and smooth, lobate margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA surface dirty white, reverse sienna. On PDA surface and reverse dirty white. On OA surface dirty white to luteous.

*Typus. SOUTH AFRICA.* Limpopo Province, Tzaneen, on leaves of *Aloe* sp. (Asphodelaceae), 22 June 2016, P.W. Crous, HPC 2479 (holotype CBS H-23952, culture ex-type CPC 35863 = CBS 145558, ITS and LSU sequences GenBank MK876395.1 and MK876436.1, MycoBank MB830841).

*Notes — Libertasomyces aloeticus* is intermediate between *Neoplatysporoides* (based on *N. aloeicola*; conidia 0–1-septate, (8–)9–10(–12) × (4–)5(–6) μm, on leaves of *Aloe* sp. in Tanzania; Crous et al. 2015b) and *Libertasomyces*. *Neoplatysporoides aloeticus* has conidia that are similar in morphology to those of *L. quercus* (conidia (15–)17–19(–21) × (6–)7–8(–10) μm; Crous & Groenewald 2017), though larger in size. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Neoplatysporoides aloeicola* (GenBank MK398281.1; Identities = 535/583 (92 %), 13 gaps (2 %)), *Libertasomyces quercus* (GenBank NR_155337.1; Identities = 519/572 (91 %), 14 gaps (2 %)) and *Libertasomyces platani* (GenBank NR_155336.1; Identities = 515/572 (90 %), 13 gaps (2 %)). Closest hits using the LSU sequence are *Neoplatysporoides aloeicola* (GenBank NG_058160.1; Identities = 794/807 (98 %), 4 gaps (0 %)), *Libertasomyces myopori* (GenBank MH878216.1; Identities = 793/808 (98 %), 4 gaps (0 %)) and *Libertasomyces platani* (GenBank NG_059744.1; Identities = 791/806 (98 %), 4 gaps (0 %)).

*Colour illustrations.* Aloe sp. Conidioma on oatmeal agar; conidiogenous cells and conidia. Scale bars = 200 mm (conidioma), 10 μm (all others).
Phyllosticta lauridiae
**Phyllosticta lauridiae** Crous & M.J. Wingf., *sp. nov.*

**Etymology**
Name refers to *Lauridia*, the host genus from which this fungus was isolated.

**Classification** — Phylllostictaceae, Botryosphaeriales, Dothideomycetes.

Leaf spots amphigenous, 3–7 mm diam, round, medium brown, with a dark red-brown margin. *Conidiomata* pycnidial, aggregated, black, erumpent, globose, 200–250 mm diam, exuding a hyaline conidiomatal mass; wall of several layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* terminal, subcylindrical, hyaline, smooth, encased in mucoid layer, 7–12 × 3–4 mm, proliferating percurrently near apex. *Conidia* (9–)12–13–(14) × 6–(7) mm, solitary, hyaline, smooth-walled, guttulate, ellipsoid to ovoid, tapering towards truncate base, 3–4 mm diam, encased in mucoid sheath, 1–1.5 mm diam, bearing a single hyaline mucoid appendix, 15–20(–30) mm long, tapering to acutely rounded tip.

Culture characteristics — Colonies erumpent, spreading, with folded surface, sparse to moderate aerial mycelium and feathery margin, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface olivaceous grey, reverse iron-grey. On PDA and OA surface and reverse iron-grey.

**Typus.** **SOUTH AFRICA**, Eastern Cape Province, Haga Haga, Amathole, on leaves of *Lauridia tetragona* (*Celastraceae*), 15 Dec. 2016, M.J. Wingfield, HPC 2290 (holotype CBS H-23953, culture ex-type CPC 35305 = CBS 145559, ITS, LSU, actA, gapdh, rpb2 and tef1 sequences GenBank MK876404.1, MK876445.1, MK876460.1, MK876472.1, MK876489.1 and MK876498.1; MycoBank MB830842).

Notes — *Phyllosticta* was revised by Wikee et al. (2013). *Phyllosticta lauridiae* is closely related to *P. podocarpicola* (conidia 12–13–(16) × 8–9–(9.5) μm). On *Podocarpus maki* (Florida, USA), but morphologically distinct based on its shorter and narrower conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Phyllosticta podocarpicola* (GenBank NR_145233.1; Identities = 538/569 (95 %), 11 gaps (1 %)), *Phyllosticta foliorum* (GenBank NR_145231.1; Identities = 536/570 (94 %), 12 gaps (2 %)) and *Phyllosticta concentrica* (as *Guignardia philoinopa*, GenBank AF312014.1; Identities = 567/603 (94 %), 14 gaps (2 %)). Closest hits using the LSU sequence are *Phyllosticta gaultheriae* (as *Guignardia gaultheriae*, GenBank DQ678089.1; Identities = 804/813 (99 %), no gaps), *Phyllosticta hakeicola* (GenBank MH107963.1; Identities = 820/830 (99 %), 1 gap (0 %)) and *Phyllosticta philoinopa* (GenBank KF766341.1; Identities = 812/822 (99 %), 1 gap (0 %)). Closest hits using the actA sequence had highest similarity to *Phyllosticta hakeicola* (GenBank MH107984.1; Identities = 225/233 (97 %), 3 gaps (1 %)), *Phyllosticta abieticola* (GenBank KF289238.1; Identities = 220/228 (96 %), 3 gaps (1 %)) and *Phyllosticta liguisticola* (GenBank AB704212.1; Identities = 220/231 (95 %), 4 gaps (1 %)). Closest hits using the gapdh sequence had highest similarity to *Phyllosticta hakeicola* (GenBank MH107999.1; Identities = 478/520 (92 %), 7 gaps (1 %)), *Phyllosticta mumarum* (GenBank KM816632.1; Identities = 485/534 (91 %), 11 gaps (2 %)) and *Phyllosticta capitagensis* (GenBank KM816629.1; Identities = 485/534 (91 %), 11 gaps (2 %)). Closest hits using the rpb2 sequence had highest similarity to *Phyllosticta gautheriae* (as *Guignardia gaultheriae*, GenBank DQ677987.1; Identities = 528/579 (91 %), no gaps), *Phyllosticta aloeicola* (GenBank KY855816.1; Identities = 657/742 (89 %), 13 gaps (1 %)) and *Phyllosticta eugeniae* (GenBank KY855891.1; Identities = 632/726 (87 %), 7 gaps (0 %)). Closest hits using the tef1 sequence had highest similarity to *Phyllosticta hakeicola* (GenBank MH108025.1; Identities = 359/394 (93 %), 9 gaps (2 %)), *Phyllosticta illicii* (GenBank MF198236.1; Identities = 368/403 (91 %), 15 gaps (3 %)) and *Phyllosticta yuccae* (GenBank JX227948.1; Identities = 378/418 (90 %), 16 gaps (3 %)).

**Colour illustrations.** Ocean view at Haga Haga. Leaf spot on *Lauridia tetragona*; colony on potato dextrose agar; conidiogenous cells; conidia. Scale bars = 10 μm.

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**Phlogicylindrium pawpawense** Crous & Carnegie, sp. nov.

**Etymology**. Name refers to the location where this fungus was isolated, Paw Paw Skids Road, Australia.

**Classification** — Phlogicylindriaceae, Xylariales, Sordariomycetes.

Mycelium consisting of hyaline, branched, septate, 1.5–2 mm diam hyphae. Conidiomata sporodochial, 150–300 mm diam, erumpent, round, hyaline, consisting of tightly aggregated conidiophores or conidiophores erect, penicillate with tightly aggregated conidiogenous apparatus; conidiophores 80–150 mm tall, stipe 40–50 × 2.5–3 mm. Conidiophores with penicillate conidiogenous apparatus: branches (3–5) subcylindrical, hyaline, smooth, straight to curved, 5–7 × 2.5–3 mm. Conidiogenous cells terminal and intercalary, hyaline, smooth, subcylindrical, straight to slightly curved, 5–14 × 2–2.5 mm, proliferating sympodially. Conidia solitary, hyaline, smooth, guttulate to granular, subcylindrical, 1–3-septate, curved, rarely straight, tapering to subacutely rounded apex, base truncate, 1–1.5 mm diam, (12–)17–22(–25) × 2–2.5 mm.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 15 mm diam after 2 wk at 25 °C. On MEA surface luteous, reverse ochreous. On PDA surface and reverse pale luteous. On OA surface pale luteous.

**Typus. Australia**, New South Wales, Richmond Range SF, Paw Paw Skids Road, on juvenile leaves of *Eucalyptus tereticornis* (Myrtaceae), 19 Apr. 2016, A.J. Carnegie, HPC 2424 (holotype CBS H-23954, culture ex-type CPC 35536 = CBS 145580, ITS and LSU sequences GenBank MK876403.1 and MK876444.1, MycoBank MB830843).

Notes — ITS sequence data of *Phlogicylindrium pawpawense* is related to species of *Cylindrium* and *Polyscytalum*, which were treated by Crous et al. (2014, 2018b). Morphologically however, it is a better fit for *Phlogicylindrium*, being related to *P. dunnii* (conidia (32–)35–42(–47) × (2–)2.5(–3) µm; Crous et al. 2019), though distinct in having smaller conidia. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Polyscytalum chilense* (GenBank NR_158958.1; Identities = 523/565 (93 %), 11 gaps (1 %)), *Polyscytalum eucalyptigenum* (GenBank MH107909.1; Identities = 527/571 (92 %), 14 gaps (2 %)) and *Polyscytalum grevilleae* (GenBank NR_154719.1; Identities = 520/564 (92 %), 7 gaps (1 %)). Closest hits using the LSU sequence are *Phlogicylindrium dunnii* (GenBank MK442548.1; Identities = 727/736 (99 %), 1 gap (0 %)), *Phlogicylindrium tereticornis* (GenBank NG_058510.1; Identities = 726/736 (99 %), 1 gap (0 %)) and *Polyscytalum chilense* (GenBank MH107954.1; Identities = 724/735 (99 %), no gaps).

**Colour illustrations.** *Eucalyptus tereticornis* trees. Sporodochial conidioma; conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.
Neoacrodontiella eucalypti
Fungal Planet 888 – 19 July 2019

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

**Etymology.** Name refers to a morphological similarity with the genus *Acrodontiella*.

**Classification —** Acarosporaceae, Acarosporales, Lecanoromycetes.

*Mycelium* consisting of branched, septate, hyaline, smooth hyphae. *Conidiophores* aggregated in sporodochia, arising from a hyaline stroma, subcylindrical, smooth, branched, multi-septate. *Conidiogenous cells* terminal and intercalary, subcylindrical, irregularly curved, rarely straight, with apical taper and pimple-like loci, not to slightly thickened. *Conidia* solitary, hyaline, smooth-walled, guttulate, fusoid, straight, aseptate, apex subacute, not to slightly thickened.

**Type species.** *Neoacrodontiella eucalypti* Crous & M.J. Wingf. MycoBank MB830844.

**Neoacrodontiella eucalypti** Crous & M.J. Wingf., *sp. nov.*

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

*Mycelium* consisting of branched, septate, hyaline, smooth, 2–3 mm diam hyphae. *Conidiophores* aggregated in sporodochia, arising from a hyaline stroma, subcylindrical, smooth, branched, multisepatate, 30–50 × 3–4 mm. *Conidiogenous cells* terminal and intercalary, subcylindrical, irregularly curved, rarely straight, with apical taper, 20–30 × 2.5–3 mm, with pimple-like loci, not to slightly thickened. *Conidia* solitary, hyaline, smooth-walled, guttulate, fusoid, straight, aseptate, apex subacute, base truncate, not to slightly thickened, (11–)12–15 (–17) × (2.5–)3 (–3.5) mm.

**Culture characteristics —** Colonies erumpent, spreading, surface folded, with sparse aerial mycelium and smooth, lobate margin, reaching 15 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse luteous to orange.

**Typus.** *Malaysia*, on leaves of *Eucalyptus urophylla* (Myrtaceae), 31 Mar. 2018, M.J. Wingfield, HPC 2392 (holotype CBS H-23955, culture ex-type CPC 35693 = CBS 145561, ITS and LSU sequences GenBank MK876396.1 and MK876437.1, MycoBank MB830845).

**Notes —** *Neoacrodontiella* is somewhat reminiscent of *Acrodontiella* (Seifert et al. 2011), though distinct in that it forms sporodochia, and the conidiogenous loci are flattened and more prominent than in *Acrodontiella*, with conidia also having prominently truncate hila. No significant hits were obtained when the ITS sequence was used in a megablast search of NCBI GenBank nucleotide database; the closest hits were with *Corticifraga peltigerae* (GenBank KY462801.1; Identities = 377/451 (84 %), 42 gaps (9 %)), *Taitaia aurea* (GenBank NR_160480.1; Identities = 367/444 (83 %), 36 gaps (8 %)) and *Gomphillus americanus* (GenBank KY381580.1; Identities = 177/181 (98 %), no gaps). Closest hits using the LSU sequence are ‘*Spermospora avenae*’ (GenBank MH878416.1; Identities = 790/825 (96 %), 2 gaps (0 %)), *Cytopsorella chamaeropis* (GenBank MH871929.1; Identities = 759/810 (94 %), 4 gaps (0 %)) and *Acarospora thamnina* (GenBank KF024746.1; Identities = 475/508 (94 %), 4 gaps (0 %)). The LSU sequence of *Spermospora avenae* is most likely incorrect as it is not congeneric with other sequences of the genus in the database.

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Cytospora pavettae
**Fungal Planet 889 – 19 July 2019**

**Cytospora pavettae** Crous & M.J. Wingf., sp. nov.

**Etymology.** Name refers to *Pavetta*, the host genus from which this fungus was isolated.

**Classification.** Cytosporaceae, Diaporthales, Sordariomycetes.

Colonies nearly sterile, sporulating on PNA. *Conidiomata* pycnidial, erumpent, dark brown, globose, 200–300 mm diam. *Conidiophores* lining the inner cavity, hyaline, smooth-walled, branched, 1–3-septate, 10–25 × 2.5–3 mm. *Conidiogenous cells* terminal and intercalary, frequently in rosette, subcylindrical with apical taper, hyaline, smooth-walled, phialidic, with minute non-flared collarette, 1 mm long, 4–10 × 1.5–2 mm. *Conidia* aseptate, solitary, hyaline, smooth-walled, ellipsoid, curved, ends subobtuse, (3.5–)4(–5) × 1.5 mm.

**Culture characteristics.** Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, covering dish after 2 wk at 25°C. On MEA surface ochreous to sienna, reverse tawny. On PDA surface and reverse pale luteous. On OA surface ochre.

**Notes.** Several phylogenetic studies have recently been published on *Cytospora* (Jami et al. 2018, Lawrence et al. 2018). Based on available data, *C. pavettae* is most similar to *C. lumnitzericola*, which occurs on *Lumnitzera racemosa* in Thailand (conidia (3.7–)4.5 × 1–1.3(–1.5) µm; Norphanphoum et al. 2017). There are few morphological differences between the two species, which are best distinguished based on their DNA phylogeny.

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Cytospora nitschkei* (GenBank KY051843.1; Identities = 519/532 (98 %), 1 gap (0 %)), *Cytospora saccusulus* (GenBank KY051824.1; Identities = 517/534 (97 %), 3 gaps (0 %)), and *Cytospora brevispora* (GenBank KY051803.1; Identities = 517/534 (97 %), 3 gaps (0 %)). Closest hits using the LSU sequence are *Cytospora xilocarpi* (GenBank NG_064535.1; Identities = 790/797 (99 %), 2 gaps (0 %)), *Cytospora lumnitzericola* (GenBank NG_064534.1; Identities = 789/797 (99 %), 2 gaps (0 %)) and *Cytospora thailandica* (GenBank NG_064536.1; Identities = 789/797 (99 %), 2 gaps (0 %)). Closest hits using the actA sequence had highest similarity to *Cytospora lumnitzericola* (GenBank MH253457.1; Identities = 180/197 (91 %), 7 gaps (3 %)), *Cytospora xilocarpi* (GenBank MH253458.1; Identities = 166/183 (91 %), 2 gaps (1 %)) and *Cytospora para-kantschavelii* (GenBank MG972053.1; Identities = 163/181 (90 %), 8 gaps (4 %)). Closest hits using the rpb2 sequence had highest similarity to *Cytospora lumnitzericola* (GenBank MH253461.1; Identities = 686/741 (93 %), no gaps), *Cytospora xilocarpi* (GenBank MH253462.1; Identities = 684/741 (92 %), no gaps) and *Cytospora thailandica* (GenBank MH253464.1; Identities = 681/741 (92 %), no gaps). Closest hits using the tef1 sequence had highest similarity to *Cytospora saccusulus* (GenBank KP310860.1; Identities = 295/329 (90 %), 4 gaps (1 %)), *Cytospora punicae* (GenBank MG971654.1; Identities = 279/317 (88 %), 13 gaps (4 %)) and *Cytospora californica* (GenBank MG971662.1; Identities = 403/464 (87 %), 12 gaps (2 %)). Closest hits using the tub2 sequence had highest similarity to *Cytospora ceratosperma* (as *Valsa ceratosperma*, GenBank EU219136.1; Identities = 501/600 (84 %), 30 gaps (5 %)), *Cytospora saccuslus* (GenBank KRO456888.1; Identities = 501/601 (83 %), 33 gaps (5 %)) and *Cytospora cincta* (GenBank KRO456665.1; Identities = 443/524 (85 %), 20 gaps (4 %)).

**Colour illustrations.** *Pavetta revoluta*. Conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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Pantospora chromolaenae
Pantospora chromolaenae Crous & Cheew., sp. nov.

Etymology. Name refers to Chromolaena, the host genus from which this fungus was isolated.

Classification — Mycosphaerellaceae, Capnodiales, Dothideomycetes.

Mycelium consisting of pale brown, smooth-walled, septate, branched, 2.5–3 mm diam hyphae. Conidiophores solitary, erect, straight to flexuous, subcylindrical, 1–6-septate, 20–70 × 3–6 mm, medium brown, smooth to verruculose, mostly unbranched. Conidiogenous cells medium brown, subcylindrical, smooth to verruculose, 10–15 × 3–6 mm, terminal and intercalary, scars thickened, darkened, refractive, 2–3 mm diam. Conidia solitary, unbranched, obclavate, straight to flexuous, medium brown, verruculose, granular, apex obtuse, base truncate, 2–2.5 mm diam, thickened, darkened, refractive, 3–6–8–12 transversely septate, conidia becoming muriformly septate, starting with basal cells, (24–)50–65–80 × (4–)5–6–7 mm.

Culture characteristics — Colonies erumpent, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 25 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface olivaceous grey, reverse iron-grey.

Typus. THAILAND, Songkhla, Hat Yai, on leaves of Chromolaena odorata (Asteraceae), 2008, R. Cheewangkoon (holotype CBS H-23957, culture ex-type MC14 = CPC 34870 = CBS 145563, ITS, LSU, actA, his3 and rp2 sequences GenBank MK876401.1, MK876442.1, MK876459.1, MK876476.1 and MK876488.1, MycoBank MB830848).

Notes — Pantospora is characterised by conidiogenous cells with sympodial and percurrent proliferation, and pseudo-cercospore-like conidia that have transverse, and often also oblique to longitudinal septa (Minnis et al. 2011, Videira et al. 2017). Pantospora chromolaenae represents a new species on Chromolaena odorata in Thailand.

Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to Rhachisphaerella mozambica (GenBank MH866148.1; Identities = 506/514 (98 %), 3 gaps (0 %)) and Amycosphaerella africana (as Mycosphaerella aurantia, GenBank EU853468.1; Identities = 506/514 (98 %), 3 gaps (0 %)). Closest hits using the LSU sequence are Ragnhildiana diffusa (GenBank MH866148.1; Identities = 831/833 (99 %), 1 gap (0 %)), Ragnhildiana pseudothithoniana (GenBank NG_058049.1; Identities = 831/833 (99 %), 1 gap (0 %)) and Ragnhildiana perfoliati (GenBank GU214453.1; Identities = 815/817 (99 %), 1 gap (0 %)). Closest hits using the actA sequence had highest similarity to Amycosphaerella africana (GenBank KF903407.1; Identities = 496/520 (95 %), 5 gaps (0 %)), Rhachisphaerella mozambica (as Mycosphaerella mozambica, GenBank EU514319.1; Identities = 504/531 (95 %), 4 gaps (0 %)) and Camptomeriphila leucena (GenBank KY173563.1; Identities = 446/474 (94 %), 5 gaps (1 %)). No actA sequence of Pantospora was available for comparison. Closest hits using the his3 sequence had highest similarity to Rhachisphaerella mozambica (as Mycosphaerella mozambica, GenBank EU514317.1; Identities = 371/382 (97 %), 2 gaps (0 %)), Pseudocercosporella bakeri (GenBank KX288752.1; Identities = 353/371 (95 %), 3 gaps (0 %)) and Pseudocercosporella indonesiana (GenBank EU514393.1; Identities = 356/390 (91 %), 7 gaps (1 %)). No his3 sequence of Pantospora was available for comparison. Closest hits using the rp2 sequence had highest similarity to Amycosphaerella africana (GenBank MF951432.1; Identities = 765/871 (88 %), no gaps), Asperisporium caricae (GenBank MF951439.1; Identities = 794/908 (87 %), no gaps) and Asperisporium caricae (GenBank MF951438.1; Identities = 813/930 (87 %), no gaps). The rp2 sequence is 804/923 (87 %, including 4 gaps) similar to the rp2 sequence of Pantospora guazumae voucher BP1 880778 (JN190952.1).

Colour illustrations. Temple at Songkhla, Hat Yai. Leaf spots; conidiophores, conidiogenous cells, and muriformly septate conidia. Scale bars = 10 µm.
Ramularia pistaciae
**Ramularia pistaciae** Crous, *sp. nov.*

**Etymology**. Name refers to *Pistacia*, the host genus from which this fungus was isolated.

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

*Mycelium* consisting of branched, septate, hyaline, smooth-walled, 2–2.5 mm diam hyphae. *Conidiophores* reduced to conidiogenous cells on hyphae, or 1-septate, erect, straight to flexuous, hyaline, smooth-walled, 5–25 x 2.5–3 mm. *Conidiogenous cells* terminal, subcylindrical, hyaline, smooth, 5–12 x 2.5–3 mm, proliferating sympodially; scars thickened, darkened and refractive, 1 mm diam. *Conidia* subcylindrical to fusoid-ellipsoid, hyaline, smooth-walled; ramoconidia 0–1-septate, 10–18 x 2.5–3 mm; intermediary and terminal conidia in branched chains, aseptate, (5–)6–7(–8) x 2.5–3 mm; hila thickened, darkened, and refractive, 0.5–1 mm diam.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface and reverse saffron. On PDA surface dirty white, reverse olivaceous grey in middle, plate luteous in outer region. On OA surface saffron.

**Typus.** Italy, Rome, on leaves of *Pistacia lentiscus* (Anacardiaceae), 13 Apr. 2018, P.W. Crous, HPC 2340 (holotype CBS H-23958, culture ex-type CPC 35443 = CBS 145564, ITS, actA and gapdh sequences GenBank MK876408.1, MK876462.1 and MK876473.1, MycoBank MB830849).

Notes — *Ramularia* was recently revised by Videira et al. (2015, 2016). *Ramularia pistaciae* is the first species known to occur on *Pistacia*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Ramularia pratensis* var. *pratensis* (GenBank EU019284.2; Identities = 520/532 (98 %), 1 gap (0 %)), *Ramularia eucalypti* (GenBank EF394861.1; Identities = 520/532 (98 %), 1 gap (0 %)) and *Ramularia gei* (GenBank KX228412.1; Identities = 519/531 (98 %), 1 gap (0 %)). Closest hits using the actA sequence had highest similarity to *Ramularia gaultheriae* (GenBank KX228769.1; Identities = 540/585 (92 %), no gaps), *Ramularia unterseheri* (GenBank KP894376.1; Identities = 545/592 (92 %), 3 gaps (0 %)) and *Ramularia diervillae* (GenBank KX228769.1; Identities = 536/586 (91 %), 3 gaps (0 %)). Closest hits using the gapdh sequence had highest similarity to *Ramularia vizellae* (GenBank KP894637.1; Identities = 414/445 (91 %), 8 gaps (1 %)), *Ramularia actinidia* (GenBank KX2288152.1; Identities = 407/452 (90 %), 12 gaps (2 %)) and *Ramularia inaequalis* (GenBank KP894555.1; Identities = 405/451 (90 %), 12 gaps (2 %)).

**Colour illustrations.** Forest with diverse trees near Rome. Conidiophores sporulating on synthetic nutrient-poor agar; conidiophores and conidia. Scale bars = 10 µm.
Thozetella neonivea & Neodevriesia sexualis
**Thozetella neonivea** Crous & Thangavel, *sp. nov.*

**Etymology.** Name refers to a morphology similar to that of *Thozetella nivea*.

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

*Conidiomata* solitary, dispersed, sporodochial, erect, oval, 70–300 mm diam, superficial, cream to pale brown, arising from a hyaline hyphal network; supporting cells subcylindrical, pale brown to brown, giving rise to an apical layer of conidiogenous cells. *Conidiogenous cells* discrete, pale brown, smooth, doliiform to subcylindrical, 12–26 × 2.5–3.5 mm, apex 1.5–2 mm diam, phialidic, with periclinal thickening and minute colloarette. *Conidia* hyaline, smooth, asceptate, eguttulate, fusoid, straight or slightly curved, (12–)13–(14–)15 × (2.5–)3 mm with an unbranched appendage at each end, central at apex and excentric at base, 5–8 mm long. *Microawns* also produced enterothallastically from phialides, hyaline, tapering towards base, verruculose and curved towards obtuse apex, 40–55 × 3–4 mm.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium and feathery margin, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface olivaceous grey, reverse isabelline. On PDA surface and reverse olivaceous grey. On OA surface umber. On OA surface olivaceous grey, reverse isabelline. On PDA surface and reverse olivaceous grey. On OA surface umber.

**Typos.** *Neodevriesia sexualis* Crous & Thangavel, 2017, R. Thangavel, T17_03360H (holotype CBS H-23959, culture ex-type CPC 34886 = CBS 145534, ITS and LSU sequences GenBank MK876411.1 and MK876451.1, MycoBank MB830850).

**Note.** — *Thozetella neonivea* is characterised by sporodochia with asceptate, setululate conidia, (12–)13–14–(15–)16 × (2.5–)3 mm, and having microawns (verruculose, curved, 40–55 × 3–4 mm).

Based on ITS sequence data, it is phylogenetically closest to *Thozetella nivea* (conidia 17.5–24 × 3–3.8 µm, microawns curved, 50–70 × 1.3–3 µm; Pirozynski & Hodges 1973), but is distinct from that species based on its conidial dimensions and the morphology of its microawns. A key to species in the genus has been provided by Barbosa et al. (2011), with several species linked to *Chaetosphaeria* sexual morphs, although it is relevant to recognise that the latter genus is polyphyletic.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Thozetella nivea* (GenBank EU825201.1; Identities = 492/509 (97 %), 5 gaps (0 %)), *Thozetella tockiaensis* (GenBank MH857817.1; Identities = 457/474 (96 %), 6 gaps (1 %)) and *Thozetella pinicola* (as *Thozetella* sp. RJ-2008, GenBank EU825197.1; Identities = 490/510 (96 %), 5 gaps (0 %)).

**Neodevriesia sexualis** Crous & Thangavel, *sp. nov.*

**Etymology.** Name refers to the sexual morph that forms in culture.

**Classification.** — *Neodevriesiaeae*, Capnodiales, Dothideomycetidae.

Colonies nearly sterile, sporulating sparsely on PNA. *Ascomata* pseudothecial, solitary on aerial hyphae, globose, brown, 40–70 mm diam with central ostiole; wall of 2–3 layers of brown textura angularis. *Asci* bitunicate, obovoid, 8-spored, 20–30 × 7–11 mm, with apical chamber 2 mm diam. *Ascospores* multiseriate, hyaline, smooth-walled, guttulate, straight, thick-walled, widest in middle of apical cell, 12–13 × 3–4 µm; with non-persistent mucoid sheath.

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

**Typos.** *Neodevriesia sexualis* Crous & Thangavel, 2017, R. Thangavel, T17_03360H (holotype CBS H-23960, culture ex-type CPC 34887 = CBS 145568, ITS and LSU sequences GenBank MK876398.1 and MK876439.1, MycoBank MB830851).

**Note.** — *Neodevriesia sexualis* was established by Quaedvlieg et al. (2014) for a genus of hypomyces with teratosphaeria-like sexual morphs. *Neodevriesia sexualis* differs from the majority of species known in the genus, in that it produces only a sexual morph in culture.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Neodevriesia capensis* (as *Teratosphaeria capensis*, GenBank JN712501.1; Identities = 511/541 (94 %), 18 gaps (3 %)), *Neodevriesia agapanthi* (GenBank NR_111766.1; Identities = 451/482 (94 %), 11 gaps (2 %)) and *Neodevriesia imbrexigena* (as *Devriesia imbrexigena*, GenBank JX915748.1; Identities = 446/480 (93 %), 16 gaps (3 %)). Closest hits using the LSU sequence are *Neodevriesia imbrexigena* (as *Devriesia imbrexigena*, GenBank JX915749.1; Identities = 822/828 (99 %), 1 gap (0 %)), *Neodevriesia simplex* (GenBank KF310027.1; Identities = 758/764 (99 %), no gaps) and *Neodevriesia hilliana* (GenBank GU214414.1; Identities = 821/828 (99 %), 1 gap (0 %)).
Helminthosporium erythrinicola
Fungal Planet 894 – 19 July 2019

Helminthosporium erythrinicola Crous & M.J. Wingf., sp. nov.

Etymology. Name refers to Erythrina, the host genus from which this fungus was isolated.

Classification — Massarinaceae, Pleosporales, Dothideomycetes.

Colony on natural substrate black, hairy, effuse, 1–2 cm long. Mycelium mostly immersed, forming a brown stroma on the surface, 150–200 mm diam, giving rise to erect, flexuous conidiophores. Conidiophores 500–1200 × 6–10 mm, multiseptate, finely roughened, subcylindrical with slight apical taper, arising in fascicles, unbranched, brown, becoming pale brown at apex, rejuvenating percurrently. Conidiogenous cells terminal and intercalary with well-defined pores (4–5 × 2–3 mm), thickened and darkened, 25–40 × 6–8 mm. Conidia (70–)80–90(–110) × (9–)10–11(–12) mm, obclavate, straight to curved, apex subobtuse, medium brown, (6–)7–8(–12)-distoseptate, with angular lumina; wall 3–4 mm thick, hila thickened, darkened, 3–4 mm diam.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and feathery margin on PDA, smooth on OA and MEA, reaching 60 mm diam after 2wk at 25 °C. On MEA surface olivaceous grey, reverse iron-grey with patches of olivaceous grey. On PDA surface and reverse iron-grey. On OA surface iron-grey.

Typus. South Africa, Eastern Cape Province, Haga Haga, Hamathole, on leaves of Erythrina hueaina (Fabaceae), 26 Dec. 2016, M.J. Wingfield, HPC 2301 (holotype CBS H-23961, culture ex-type CPC 35291 = CBS 145569, ITS, LSU and rpb2 sequences GenBank MK876391.1, MK876432.1 and MK876486.1, MycoBank MB830852).

Notes — Helminthosporium was recently revised by Voglmayr & Jaklitsch (2017) and Hernández-Restrepo et al. (2018). Helminthosporium erythrinicola is related to H. genistae (CBS 142597), and represents the first species described from Erythrina hueaina. Helminthosporium erythrinicola (on Erythrina suberosa, India; conidia 4–8-septate, 39–62 × 8 mm; Thirumalachar 1950) differs in having smaller conidia with fewer septa. Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to Helminthosporium submersum (as Helminthosporium sp. ZLL-2017a, GenBank MG098780.1; Identities = 462/483 (96 %), 4 gaps (0 %)). Helminthosporium velutinum (GenBank JN198435.1; Identities = 473/499 (95 %), 4 gaps (0 %)) and Helminthosporium magnisporum (GenBank AB311452.1; Identities = 436/461 (95 %), 3 gaps (0 %)). Closest hits using the LSU sequence are Helminthosporium velutinum (GenBank KY984355.1; Identities = 814/823 (99 %), 1 gap (0 %)), Helminthosporium oligosporum (GenBank KY984333.1; Identities = 813/823 (99 %), 1 gap (0 %)) and Helminthosporium caespitosum (GenBank KY984305.1; Identities = 813/823 (99 %), 1 gap (0 %)). Closest hits using the rpb2 sequence had highest similarity to Helminthosporium genistae (GenBank KY984377.1; Identities = 832/884 (94 %), no gaps), Helminthosporium quercinum (GenBank KY984401.1; Identities = 828/884 (94 %), no gaps) and Helminthosporium velutinum (GenBank KY984416.1; Identities = 826/884 (93 %), no gaps).

Colour illustrations. Erythrina hueaina at Haga Haga. Sporulation on host tissue; conidiogenous loci and conidia. Scale bars = 10 μm.
Helminthosporium syzygii
**Helminthosporium syzygii** Crous & M.J. Wingf., *sp. nov.*

*Etymology.* Name refers to *Syzygium*, the host genus from which this fungus was isolated.

*Classification.* Massarinaceae, Pleosporales, Dothideomycetes.

Colony on natural substrate black, hairy, effuse, 1–2 mm long. Mycelium immersed, forming a brown stroma on the surface, 40–150 mm diam, giving rise to erect conidiophores. Conidiophores 150–400 × 10–15 mm, multiseptate, arising in fascicles, unbranched, dark brown, somewhat clavate at apex, rejuvenating percurrently. Conidiogenous cells terminal with well-defined pore, 3–4 mm diam, thickened and darkened, 20–40 × 13–15 mm. Conidia (70–)80–100(–150) × (19–)22–23(–25) mm, obclavate, curved, apex subobtuse, warty, inner surface striate, medium brown, (7–)9–12-distoseptate, with angular lumina; wall 5–7 mm thick; hila thickened and darkened, 4–5 mm diam.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 60 mm diam after 2 wk at 25 °C. On MEA surface mouse grey, reverse greyish sepia. On PDA surface mouse grey, reverse olivaceous grey. On OA surface pale luteous in centre, mouse grey in outer region.

*Typus.* South Africa, Eastern Cape Province, Haga Haga, Amathole, on bark canker of *Syzygium* sp. (Myrtaceae), 20 Dec. 2016, M.J. Wingfield, HPC 2295 (holotype CBS H-23962, culture ex-type CPC 35312 = CBS 145570, ITS, LSU and rpb2 sequences GenBank MK876392.1, MK876433.1 and MK876487.1, MycoBank MB830853).

**Notes.** — *Helminthosporium syzygii* is phylogenetically related to but morphologically distinct from *H. hispanicum* (Voglmayr & Jaklitsch 2017), and characterised by an association with bark cankers on *Syzygium* sp. in the Eastern Cape Province of South Africa. Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Helminthosporium hispanicum* (GenBank NR_155196.1; Identities = 551/588 (94 %), 7 gaps (1 %)), *Helminthosporium quercinum* (GenBank KY984337.1; Identities = 433/495 (87 %), 18 gaps (3 %)) and *Helminthosporium microsorum* (GenBank KY984329.1; Identities = 496/589 (84 %), 25 gaps (4 %)). Closest hits using the LSU sequence are *Helminthosporium magnisporum* (GenBank AB807522.1; Identities = 845/857 (99 %), 2 gaps (0 %)), *Helminthosporium quercinum* (GenBank KY984338.1; Identities = 844/857 (98 %), 2 gaps (0 %)) and *Helminthosporium microsorum* (GenBank KY984326.1; Identities = 844/857 (98 %), 2 gaps (0 %)). Closest hits using the rpb2 sequence had highest similarity to *Helminthosporium hispanicum* (GenBank KY984381.1; Identities = 912/949 (96 %), no gaps), *Helminthosporium quercinum* (GenBank KY984401.1; Identities = 892/949 (94 %), no gaps) and *Helminthosporium microsorum* (GenBank KY984386.1; Identities = 885/949 (93 %), no gaps).

*Colour illustrations.* Beach at Haga Haga. Conidiophores on host tissue; conidiogenous cells and conidia. Scale bars = 10 µm.
Calophoma sandfjordenica
Calophoma sandfjordenica Crous & Rämä, sp. nov.

Etimology. Name refers to Sandfjorden, Berlevåg, Norway, a landscape preservation area with a long sandy beach and dunes, where this fungus was collected.

Classification — Didymellaceae, Pleosporales, Dothideomycetes.

Conidiomata pycnidial, solitary, black, globose, immersed to erumpent, ostiolate, 200–300 mm diam; wall of 3–6 layers of brown textura angularis. Microsclerotia present. Conidiophores reduced to conidiogenous cells lining the inner cavity, ampulliform to doliiform, hyaline, smooth, phialidic with periclinal thickening, 5–10 × 5–7 mm. Conidia subcylindrical, straight to curved, ends obtuse, hyaline, smooth, 0(–1)-septate, guttulate, (8–)10–14(–18) × (2–)3 mm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, covering dish after 2 wk at 25 °C. On MEA surface dirty white, reverseumber with patches of sienna. On PDA surface and reverse hazel. On OA surface isabelline.

Typus. Norway, Finnmark, Berlevåg, Sandfjorden, isolated from a piece of board found in the breaker zone on a rocky shore, N70°47’36”, E29°16’43”, 7 Sept. 2010. T. Rämä, 077bU1.2 (holotype CBS H-23963, culture ex-type 050aE2.1 = CPC 36272 = CBS 145571, ITS, LSU, actA and rpb2 sequences GenBank MK676378.1, MK676417.1, MK876453.1 and MK876478.1, MycoBank MB830854).

Notes — Species of Phoma and related coelomycetous genera have long been known to be frequent in the marine environment, but little effort has been made to identify these fungi to species level. Due to their very indistinct morphological features, the only means to separate species is by phylogenetic inference based on DNA sequence data supplemented with culture characteristics (Kohlmeier & Volkman-Kohlmeier 1991, Jones et al. 2015). Calophoma sandfjordenica described here is the first marine member of this recently established genus (Chen et al. 2015). The species was isolated from driftwood at three locations along the Northern Norwegian coast. Two of the substrates were of Pinus and one on the wood of an unidentified tree. All locations are at the open ocean (Barents Sea). The ITS sequence showed greatest similarity with C. complanata. Some closely related species, such as Phoma herbarum and Phomatosides nebuloa are also known to thrive in the marine environment (Jones et al. 2015).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to Microsphaeropsis olivacea (GenBank MG020349.1; Identities = 521/536 (97 %), 7 gaps (1 %)), Calophoma aquilegii-cola (GenBank MH685149.1; Identities = 518/534 (97 %), 4 gaps (0 %)) and Epicoccum huancayense (GenBank MH661244.1; Identities = 520/537 (97 %), 7 gaps (1 %)). Closest hits using the LSU sequence are Calophoma complanata (GenBank EU754180.1; Identities = 875/875 (100 %), no gaps), Phomatoxes nebuloa (GenBank MH876211.1; Identities = 889/893 (99 %), no gaps) and Ascochyta farae (GenBank MH871928.1; Identities = 889/893 (99 %), no gaps). Closest hits using the actA sequence had highest similarity to Didymella rabiei (GenBank KM244530.1; Identities = 587/632 (93 %), 8 gaps (1 %)), Stagonosporopsis cucurbitae-carum (GenBank KX246908.1; Identities = 578/635 (91 %), 11 gaps (1 %)) and Stagonosporopsis citrulli (GenBank KX246907.1; Identities = 577/635 (91 %), 11 gaps (1 %)). Closest hits using the rpb2 sequence had highest similarity to Calophoma complanata (GenBank GU371778.1; Identities = 829/890 (93 %), no gaps), Ascochyta herbica (GenBank KP330421.1; Identities = 739/823 (90 %), 2 gaps (0 %)) and Nothopoma gossypicola (GenBank LT593082.1; Identities = 817/912 (90 %), 4 gaps (0 %)).
Didymella finnmarkica
**Didymella finnmarkica** Crous & Rämä, sp. nov.

**Etymology.** Name reflects the most north-eastern county of Norway, Finnmark, where the species was collected.

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

Conidiomata pycnidial, solitary to aggregated, globose, 200–300 mm diam, with 1–2 ostioles; conidiomata (on SNA) sub-hygaline with prominent dark ostiole, 20–30 mm diam, peripheral, with a dark brown rosette of cells and short setae, thick-walled, septate, cylindrical with obtuse apices, 15–50 × 3–4 mm. Conidiophores reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, ampulliform, phialidic with periclinal thickening, 5–8 × 4–5 mm. Conidia dimorphic, subcyindrical, straight to slightly curved, ends obtuse, hyaline, smooth, granular, guttulate, consisting of smaller asperate, and larger 1-septate conidia: asperate conidia (6–)7–9(–11) × (2–)2.5(–)3 mm; 1-septate conidia (12–)13–16(–18) × (3–)3.5(–)4 mm. Chlamydospores not observed.

**Culture characteristics —** Colonies flat, spreading, with sparse to moderate aerial mycelium and feathery margin, 4–5 mm. Conidia (–4) 2.5(–3) mm; 1-septate conidia (12–)13–16(–18) × (3–)3.5(–)4 mm. Chlamydospores not observed.

**Colour illustrations.** Type locality on seashore in Hamningberg, Norway. Conidiomata on oatmeal agar; ostiole; conidiogenous cells and conidia. Scale bars = 10 μm.

Notes — No new marine *Didymella* species has been described since 1985 (Jones et al. 2015). The four known species are *D. avicenniae* (found on *Avicennia* in mangroves), *D. fucicola* (on marine brown algae *Fucus* and *Pelvetia*), *D. glio­pettitis* (on red alga *Gloio­pettia furcata*) and *D. magnei* (on red alga *Palm­aria palmata*). These species are rarely collected and sequence data are available only for *D. fucicola*. *Didymella finnmarkica* described here is recognised as a new species based on ITS sequence data and ecology. None of the previously described *Didymella* species have been observed or isolated from driftwood (excluding mangroves). *Didymella finnmarkica* was isolated from a single piece of *Pinus sylvestris* driftwood in north-eastern Norway that was heavily colonised with marine dwelling invertebrates.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Didymella pinodella* (as *Phoma pinodella*, GenBank AY831556.1; Identities = 521/532 (98 %), 2 gaps (0 %)), *Didymella glomerata* (GenBank MH864401.1; Identities = 528/540 (98 %), 2 gaps (0 %)) and *Didymella macrostoma* (GenBank MH855806.1; Identities = 528/540 (98 %), 2 gaps (0 %)). Closest hits using the LSU sequence are *Didymella macrostoma* (GenBank MH871627.1; Identities = 835/838 (99 %), no gaps), *Didymella fabae* (GenBank FJ755246.1; Identities = 835/838 (99 %), no gaps) and *Ascochyta medicaginicola* var. *macrospora* (GenBank MH870279.1; Identities = 834/838 (99 %), no gaps). Closest hits using the actA sequence had highest similarity to *Peyronellaea combreti* (GenBank KJ869228.1; Identities = 586/634 (92 %), no gaps), *Stagonosporopsis caricae* (GenBank KX246909.1; Identities = 592/648 (91 %), 10 gaps (1 %)) and *Stagonosporopsis citrulli* (GenBank KX246907.1; Identities = 591/648 (91 %), 10 gaps (1 %)). Closest hits using the rpb2 sequence had highest similarity to *Didymella microchlamydospora* (GenBank MH133221.1; Identities = 635/695 (91 %), no gaps), *Macroventuria anomochaeta* (GenBank GU456346.1; Identities = 624/695 (90 %), no gaps) and *Didymella aliena* (GenBank MG571231.1; Identities = 621/697 (89 %), no gaps).

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**Neognomoniopsis** Crous, *gen. nov.*

*Etymology.* Name refers to the genus *Gnomoniopsis.*

*Classification.* *Gnomoniaceae, Diaporthales, Sordari- mycetes.*

*Ascomata* perithecial, solitary or in groups of up to three, dark brown, globose, with solitary, central neck, straight to curved, apex pale brown, obtuse. *Asci* hyaline, uniseriate, inoperculate, subcylindrical with a long, tapered stalk, with visible apical ring, containing eight multiseriate ascospores. *Ascospores* hyaline, smooth, guttulate, fusoid, widest at median septum, straight or slightly curved, ends subobtuse, lacking mucoid appendages, (17–)18–19(–24) × 2 µm.

*Culture characteristics.*—Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface sienna, reverse ochreous. On OA surface ochreous with patches of dirty white, reverse amber. On OA surface ochreous.

*Typus.* Italy, Rome, on leaves of *Quercus ilex* (Fagaceae), 13 Apr. 2018, P.W. Crous, HPC 2333 (holotype CBS H-23965, culture ex-type CPC 35562 = CBS 145575, ITS and LSU sequences GenBank MK878399.1 and MK876440.1, MycoBank MB830857).

Notes — Members of *Gnomoniaceae* are characterised by ascomata that are generally immersed, solitary, without a stroma, or aggregated in leaves or woody tissues of predominantly hardwood trees from temperate zones in the Northern Hemisphere. Monod (1983) included 22 genera in the family, some of which were excluded by Castlebury et al. (2002). Species of *Gnomonia* typically have solitary, thin-walled, immersed perithecia with long necks and lack any stroma, and generally have ascospores that are medianly septate. However, *Gnomonia* was shown to not be monophyletic (Sogonov et al. 2005, 2008). *Gnomoniopsis,* which is mostly associated with either *Fagaceae* or *Rosaceae,* was originally described for species having ascospores that develop additional septa (Sogonov et al. 2008). One species to consider is *Gnomonia quercus-iliensis,* which was described from *Quercus ilex* in Italy, was listed as ‘doubtful’ by Monod (1983), having not found any material in PAD. However, based on the original description provided by Saccardo (1895), perithecia are 100–110 mm diam, asci 45–50 × 12–16 mm, and ascospores 1-septate, 20–24 × 7–8 mm, thus quite different from the present collection, which we describe here as new.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Plagiostoma conradii* (GenBank KX929768.1; Identities = 437/491 (89 %), 11 gaps (2 %)), *Gnomoniopsis paraclavulata* (GenBank MH863162.1; Identities = 456/524 (87 %), 17 gaps (3 %)) and *Discula quercina* (GenBank GO452263.1; Identities = 456/524 (87 %), 17 gaps (3 %)). Closest hits using the LSU sequence are *Cryptodiaporthe aubertii* (GenBank KX929803.1; Identities = 831/845 (98 %), 2 gaps (0 %)), *Sirococcus castaneae* (GenBank KX929769.1; Identities = 831/845 (98 %), 2 gaps (0 %)) and *Ambarignomonia petiolorum* (as *Gnomonia petiolorum*; GenBank AY818963.1; Identities = 831/845 (98 %), 2 gaps (0 %)).

**Neognomoniopsis quercina** Crous, *sp. nov.*

*Etymology.* Name refers to Quercus, the host genus from which this fungus was isolated.

*Ascomata* perithecial, sparsely formed on SNA, immersed to superficial, solitary or in groups of up to three, dark brown, globose, with solitary, central neck, straight to curved, apex pale brown, obtuse. *Asci* hyaline, uniseriate, inoperculate, subcylindrical with a long, tapered stalk, 40–55 × 6–7 µm, with visible apical ring, containing eight multiseriate ascospores. *Ascospores* hyaline, smooth, guttulate, fusoid, widest at median septum, straight or slightly curved, ends subobtuse, lacking mucoid appendages, (17–)18–19(–24) × 2 µm.

*Culture characteristics.*—Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On OA surface sienna, reverse ochreous. On SNA surface sienna, immersed to superficial, solitary or in groups of up to three, dark brown, globose, with solitary, central neck, straight to curved, apex pale brown, obtuse.

Notes — Members of *Gnomoniaceae* are characterised by ascomata that are generally immersed, solitary, without a stroma, or aggregated in leaves or woody tissues of predominantly hardwood trees from temperate zones in the Northern Hemisphere. Monod (1983) included 22 genera in the family, some of which were excluded by Castlebury et al. (2002). Species of *Gnomonia* typically have solitary, thin-walled, immersed perithecia with long necks and lack any stroma, and generally have ascospores that are medianly septate. However, *Gnomonia* was shown to not be monophyletic (Sogonov et al. 2005, 2008). *Gnomoniopsis,* which is mostly associated with either *Fagaceae* or *Rosaceae,* was originally described for species having ascospores that develop additional septa (Sogonov et al. 2008). One species to consider is *Gnomonia quercus-iliensis,* which was described from *Quercus ilex* in Italy, was listed as ‘doubtful’ by Monod (1983), having not found any material in PAD. However, based on the original description provided by Saccardo (1895), perithecia are 100–110 mm diam, asci 45–50 × 12–16 mm, and ascospores 1-septate, 20–24 × 7–8 mm, thus quite different from the present collection, which we describe here as new.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Plagiostoma conradii* (GenBank KX929768.1; Identities = 437/491 (89 %), 11 gaps (2 %)), *Gnomoniopsis paraclavulata* (GenBank MH863162.1; Identities = 456/524 (87 %), 17 gaps (3 %)) and *Discula quercina* (GenBank GO452263.1; Identities = 456/524 (87 %), 17 gaps (3 %)). Closest hits using the LSU sequence are *Cryptodiaporthe aubertii* (GenBank KX929803.1; Identities = 831/845 (98 %), 2 gaps (0 %)), *Sirococcus castaneae* (GenBank KX929769.1; Identities = 831/845 (98 %), 2 gaps (0 %)) and *Ambarignomonia petiolorum* (as *Gnomonia petiolorum*; GenBank AY818963.1; Identities = 831/845 (98 %), 2 gaps (0 %)).

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Hypsotheca eucalyptorum
Hypsotheca eucalyptorum Crous & Carnegie, sp. nov.

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

Classification — Coryneliaceae, Coryneliales, Eurotiomycetes.

Conidiomata sparsely formed in culture, pycnidial, brown, globose, 180–200 µm diam, developing in aerial mycelium. Dominant morph hyphomycetous. Mycelium initially hyaline, smooth, becoming brown, verruculose to warty, septate, branched, 2–3 µm diam. Conidiophores erect on superficial hyphae, 0–1-septate, unbranched, subcylindrical, straight to flexuous, brown, verruculose, 5–20 × 1.5–2.5 µm. Conidiogenous cells terminal, pale brown, verruculose, subcylindrical, phialidic with flared collarette, 2–3 µm diam, 5–15 × 1.5–2.5 µm. Conidia aseptate, solitary, hyaline, smooth, guttulate, subcylindrical with obtuse ends, (3–)3.5–4(–4.5) × 1.5(–2) µm.

Conidiomata developing in aerial mycelium.

Notes — The genus Hypsotheca was recently resurrected as sister genus to Caliciopsis. Species of Hypsotheca are distinguished from Caliciopsis in having a phaeoacremonium-like synasexual morph in culture (Pascoe et al. 2018, Crous et al. 2019). Hypsotheca eucalyptorum is related to H. pleomorpha (conidia (3–)4–5(–6) × 1.5(–2) µm), but distinct in that the hyphomycetous morph is dominant in culture. Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence of CPC 35734 had highest similarity to Hypsotheca pleomorpha (GenBank MG641785.1; Identities = 500/552 (91 %), 23 gaps (4 %)), Caliciopsis eucalypti (GenBank NR_154836.1; Identities = 396/429 (92 %), 10 gaps (0 %)) and Corynelia uberata (GenBank KJ204606.1; Identities = 497/551 (90 %), 26 gaps (4 %)). The ITS sequences of CPC 35734 and CPC 35391 are 541/549 (99 %, including two gaps) similar. Closest hits using the LSU sequence are Hypsotheca pleomorpha (GenBank MK442528.1; Identities = 800/829 (97 %), 3 gaps (0 %)), Caliciopsis valentina (GenBank NG_060419.1; Identities = 776/824 (94 %), no gaps) and Caliciopsis pinea (GenBank DQ678097.1; Identities = 776/824 (94 %), no gaps). The LSU sequences of CPC 35734 and CPC 35391 are 831/835 (99 %, including one gap) similar.

Typus. AUSTRALIA, New South Wales, Boorabee State Forest, McCorquodale plantation, on leaves of Eucalyptus grandis × camaldulensis clone (Myrtaceae), 20 Apr. 2016, A.J. Carnegie, HPC 2431 (holotype CBS 145576, ITS and LSU sequences GenBank MK876393.1 and MK876434.1, MycoBank MB830858).

Additional material examined. AUSTRALIA, New South Wales, Orara State Forest, on leaves of Eucalyptus grandis, 7 Mar. 2016, D. Sargeant, HPC 2304, CPC 35391 = CBS 145577, ITS and LSU sequences GenBank MK876394.1 and MK876435.1.

Colour illustrations. Eucalyptus grandis × camaldulensis plantation.

Hyphae with solitary conidiophores and conidiogenous cells; conidia. Scale bars = 10 µm.
Cylindrium grande
**Cylindrium grande** Crous & Carnegie, sp. nov.

**Etymology.** Name refers to *Eucalyptus grandis*, the host species from which this fungus was first isolated.

**Classification.** *Cylindriaceae*, Hypocreales, Sordariomycetes.

**Mycelium** consisting of branched, septate, hyaline, 1.5–2.5 μm diam hyphae that form large, black, globose to lobed fertile structures up to 500 μm diam on SNA, MEA, PDA and OA. *Conidiomata* sporodochial, sporulating on SNA, brown, 80–200 μm diam. *Conidiophores* arising from a pale brown stroma, smooth, pale brown, subcylinodrical, branched below, 1–3-septate, 20–30 × 4–6 μm. *Conidiogenous cells* integrated, pale brown, smooth, subcylinodrical to somewhat ampulliform, proliferating sympodially, terminal and intercalary, 15–20 × 2–4 μm; scars inconspicuous. *Conidia* solitary, subcylinodrical, straight, aseptate, hyaline, smooth, apex obtuse, base bluntly rounded to truncate, (13–)18–20–(22) × (2–)2.5–3 μm.

**Culture characteristics.** Colonies flat, spreading, with sparse to moderate aerial mycelium and smooth, lobate margin, covering dish after 2 wk at 25 °C. On MEA surface ochreous with patches of dirty white, reverse umber to sienna. On PDA covering dish after 2 wk at 25 °C. On MEA surface ochreous sparse to moderate aerial mycelium and smooth, subcylindrical to somewhat ampulliform, 1–3-septate, 20–30 μm diam; scars inconspicuous. *Conidiomata* sporodochial, sporulating on SNA, brown, 4–6 μm.

**Notes.** - *Cylindrium* was treated by Crous et al. (2018b). *Cylindrium grande* is phylogenetically related to *C. elongatum* (on *Quercus* leaf litter; conidia 15–18 × 2 mm; Ellis & Ellis 1997), but the latter has smaller conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS of CPC 35403 sequence had highest similarity to *Cylindrium elongatum* (GenBank KM231852.1; Identities = 528/544 (97 %), 3 gaps (0 %)), *Cylindrium syzygi* (GenBank NR_157430.1; Identities = 519/545 (95 %), 16 gaps (2 %)) and *Cylindrium algarvense* (GenBank NR_132857.1; Identities = 495/528 (94 %), 14 gaps (2 %)). The ITS sequences of CPC 35403 and CPC 35622 are 537/541 (99 %, including one gap) similar. Closest hits using the LSU sequence of CPC 35403 are *Tristratiperidium microsporum* (GenBank KT696539.1; Identities = 732/736 (99 %), no gaps), *Cylindrium syzygi* (as *Pseudordiella syzygi*). GenBank J0044441.1; Identities = 833/839 (99 %), 1 gap) and *Cylindrium purgamentum* (GenBank KY173525.1; Identities = 813/820 (99 %), 1 gap). The LSU sequences of CPC 35403 and CPC 35622 are 827/833 (99 %, including one gap) similar. Closest hits using the actA sequence of CPC 35403 had highest similarity to *Cylindrium elongatum* (GenBank KM231264.1; Identities = 616/672 (92 %), 16 gaps (2 %)) and *Cylindrium aeruginosum* (GenBank KM231265.1; Identities = 515/560 (92 %), 16 gaps (2 %)). The actA sequences of CPC 35403 and CPC 35622 are 631/667 (95 %, including three gaps) similar. Closest hits using the cmdA sequence of CPC 35403 had highest similarity to *Cylindrium elongatum* (GenBank KM231448.1; Identities = 557/692 (80 %), 42 gaps (6 %)) and *Cylindrium aeruginosum* (GenBank KM231450.1; Identities = 492/604 (81 %), 35 gaps (6 %)). The cmdA sequences of CPC 35403 and CPC 35622 are 645/727 (89 %, including 16 gaps) similar. Closest hits using the rpb2 sequence of CPC 35403 had highest similarity to *Cylindrium elongatum* (GenBank KM232428.1; Identities = 707/801 (88 %), 6 gaps (0 %)) and *Cylindrium aeruginosum* (GenBank KM232430.1; Identities = 748/859 (87 %), 3 gaps (0 %)). The rpb2 sequences of CPC 35403 and CPC 35622 are 798/864 (92 %, no gaps) similar. Closest hits using the tef1 sequence of CPC 35403 had highest similarity to *Cylindrium elongatum* (GenBank KM231988.1; Identities = 358/408 (88 %), 20 gaps (4 %)). The tef1 sequences of CPC 35403 and CPC 35622 are 414/469 (88 %, including 10 gaps) similar. Closest hits using the tub2 sequence of CPC 35403 had highest similarity to *Cylindrium elongatum* (GenBank KM232123.1; Identities = 521/640 (81 %), 29 gaps (4 %)).

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Anungitiomyces stellenboschiensis
Fungal Planet 901 – 19 July 2019

Anungitiomyces Crous, gen. nov.

Etymology. Name relates to the host genus Anungitea on which this fungus was collected.

Classification — Incertae sedis, Xylariales, Sordariomycetes.

Mycelium consisting of hyaline, branched, septate hyphae. Conidiophores arising directly from hyphae, erect, flexuous to geniculate-flexuous, subcylindrical, brown, smooth, unbranched or branched below, septate. Conidiogenous cells integrated, terminal, medium brown, smooth, subcylindrical, with slight apical taper to truncate apex, proliferating sympodially; loci flattened, not thickened nor darkened. Conidia solitary, hyaline, guttulate, smooth, (0–)1-septate, obclavate, straight to slightly curved, base truncate, apex obtuse, thick-walled.

Type species: Anungitiomyces stellenboschiensis Crous. MycoBank MB830860.

Anungitiomyces stellenboschiensis Crous, sp. nov.

Etymology. Name refers to Stellenbosch, South Africa, where this fungus was collected.

Mycelium consisting of hyaline, branched, septate, 2–2.5 mm diam hyphae. Conidiophores arising directly from hyphae, erect, flexuous to geniculate-flexuous, subcylindrical, brown, smooth, unbranched or branched below, 3–8-septate, 50–100(–150) × 3–5 mm. Conidiogenous cells integrated, terminal, medium brown, smooth, subcylindrical, with slight apical taper to truncate apex, proliferating sympodially, 20–50 × 3–4 mm; loci flattened, 1.5–2 mm diam, not thickened nor darkened. Conidia solitary, hyaline, guttulate, smooth, (0–)1-septate, obclavate, straight to slightly curved, base truncate, apex obtuse, thick-walled. (22–)29–35(–42) × (3–)3.5(–4) mm.

Culture characteristics — Colonies flat, spreading, hardly growing, lacking aerial mycelium on MEA, PDA and SNA. On OA umber, with sparse to no aerial mycelium, reaching 3–4 mm diam after 2 wk at 25 °C.

Typus. SOUTH AFRICA, Western Cape Province, Stellenbosch Mountain, on leaves of Eucalyptus sp. (Myrtaceae), 2010, P.W. Crous (holotype CBS H-23968, culture ex-type CPC 34726, ITS and LSU sequences GenBank MK876376.1 and MK876415.1, MycoBank MB830861).

Notes — The present collection is reminiscent of Anungitea/Anungitopsis (Seifert et al. 2011), except that the conidiogenous loci are terminal, and the conidia are solitary, not in chains, and obclavate, (0–)1-septate. A new genus is therefore introduced to accommodate it. Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to Robillarda sessilis (GenBank FJ825373.1; Identities = 496/622 (80 %), 47 gaps (7 %)), Robillarda terrae (GenBank NR_132902.1; Identities = 493/620 (80 %), 45 gaps (7 %)) and Seimatosporium pistaciae (GenBank KP004464.1; Identities = 493/622 (79 %), 46 gaps (7 %)). Closest hits using the LSU sequence are Oxydothis metroxylonis (GenBank KY206764.1; Identities = 792/830 (95 %), 4 gaps (0 %)), Entosordaria quer cina (GenBank MF488994.1; Identities = 793/832 (95 %), 5 gaps (0 %)) and Oxydothis garethjonesii (GenBank KY206762.1; Identities = 803/843 (95 %), 5 gaps (0 %)).

Colour illustrations. Leaf of Eucalyptus sp. Colony on oatmeal agar; conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.
Alfoldia vorosii
**Fungal Planet 902 – 19 July 2019**

**Alfoldia** D.G. Knapp, Imrefi & Kovács, *gen. nov.*

*Etymology.* Referring to the sampling site, the Great Hungarian Plain, which is called ‘Alfold’ in Hungarian.

*Classification.* — Amorosiacaeae, Pleosporales, Dothideomycetes.

**Alfoldia vorosii** D.G. Knapp, Imrefi & Kovács, *sp. nov.*

*Etymology.* We name the species in honour of the 90th anniversary of the birth of the outstanding Hungarian mycologist József Vörös (1929–1991), who contributed significantly to the discipline.

*Alfoldia vorosii* differs from its closest phylogenetic neighbour, *Angustissaros saros* (MFLUCC 13-0034), by unique fixed alleles in the ITS, LSU, SSU and *tef1* loci based on alignments of the separate loci deposited in TreeBASE as study S24077; ITS positions: 96 (T), 102 (insertion), 122 (C), 202 (T), 206 (T), 227 (T), 235 (T), 236 (C), 237 (T), 250 (A), 254 (A), 423 (T), 428 (T), 436 (G), 462 (T), 466 (insertion), 474 (A), 492 (T), 544 (G), 546 (C), 553 (A), 554 (A), 555 (A), 572 (T), 573 (A), 575 (G), 576 (C), 577 (A), 578 (C), 581 (C), 585 (T), 592 (T); LSU positions: 92 (C), 93 (T), 416 (C), 418 (T), 423 (A), 429 (T), 435 (T), 439 (G), 451 (A), 452 (T), 505 (T), 507 (T), 532 (T), 534 (C), 550 (T); SSU positions: 32 (A), 38 (insertion), 117 (A), 246 (insertion), 341 (T), 349 (G); *tef1* positions: 224 (G), 245 (C), 248 (A), 275 (T), 311 (G), 319 (C), 329 (G), 360 (T), 366 (G), 368 (T), 369 (T), 443 (C), 467 (C), 510 (G), 512 (T), 533 (C), 554 (C), 599 (C), 607 (T), 609–611 (deletion), 629 (C).

*Culture characteristics.* — Colonies covering the Petri dish in 3 wk. Colony on PDA fluffy, smoke, olivaceous grey to white, spreading with abundant aerial mycelium, exudates often observed in concentric rings. Colony on MEA smoke grey to white with an entire edge and sparse aerial mycelium, exudates generally observed. Cultures sterile.

*Typus.* HUNGARY, Fülöpháza, from roots of *Juniperus communis* (Cupressaceae), 2008, D.G. Knapp & G.M. Kovács (holotype BP110341, culture ex-type REF116 = CBS 145501, ITS, LSU, SSU and *tef1* sequences GenBank JN859336, MK589354, MK589346 and MK599320, MycoBank MB830106).

*Additional materials examined.* HUNGARY, Fülöpháza, from roots of *J. communis*, 2008, D.G. Knapp & G.M. Kovács, REF117, ITS, LSU, SSU and *tef1* sequences GenBank JN859337, MK589355, MK589347 and MK599321; ibid., from roots of *Allanthus altissima* (Smaracubaceae), 2008, D.G. Knapp & G.M. Kovács, REF114, ITS sequence GenBank JN859334; Tatarszentgyörgy, from roots of *J. communis*, 2008, D.G. Knapp & G.M. Kovács, REF113, ITS, LSU, SSU and *tef1* sequences GenBank JN859333, MK589353, MK589345 and MK599319; ibid., REF115, ITS sequence GenBank JN859335.

**Notes** — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits of *Alfoldia vorosii* (CBS 145501) using the ITS sequence are *Lophiotoma corticola* (GenBank KU712227.1; Identities = 507/538 (94 %), 15 gaps (2 %)), *Angustissaros saros* (GenBank MF409170.1; Identities = 491/521 (94 %), 14 gaps (2 %)) and *Angustissaros sarosaros* (GenBank MG828869.1; Identities = 483/514 (94 %), 15 gaps (2 %)). The closest hits using the LSU sequence are *Angustissaros saros* (GenBank MF409166.1; Identities = 892/907 (98 %), no gaps), *Angustissaros sarosaros* (GenBank MF167432.1; Identities = 876/891 (98 %), 1 gap (0 %)) and *Exosporium stylobatum* (GenBank JQ044447.1; Identities = 875/890 (98 %), no gaps). The closest hits using the SSU sequence are *Ulospora biligrannii* (GenBank DQ384071.1; Identities = 522/526 (99 %), no gaps), *Phoma herbarum* (GenBank KY293777.1; Identities = 522/526 (99 %), no gaps) and *Lepidosphaeria nicotiae* (GenBank NG_061050.1; Identities = 521/526 (99 %), no gaps). The closest hits using the *tef1* sequence are *Angustissaros sarosaros* (GenBank MF167433.1; Identities = 892/907 (98 %), 15 gaps (0 %)), *Cycascola goaenesis* (GenBank MG829198.1; Identities = 876/935 (94 %), no gaps), and *Ptenidiospora javanica* (GenBank KJ739606.1; Identities = 885/921 (93 %), no gaps). *Alfoldia vorosii* represents ‘Group 9’ *sensu* Knapp et al. (2012). No sporulation was observed in any of the media PDA, MEA, MNN and WA supplemented with autoclaved plant tissues *sensu* Knapp et al. (2015).

**Supplementary material**

**FP902** Maximum Likelihood (RAxML) tree of concatenated ITS, LSU, SSU and *tef1* sequences of isolates of *Alfoldia vorosii* and representative taxa of related lineages. RAxML analysis was performed by raxmlGUI 1.3 (Silvestro & Michalak 2012), bootstrap support values (≥ 70 %) are shown above branches and before slashes; Bayesian analysis was performed with MrBayes v. 3.1.2 (Ronquist & Huelsenbeck 2003) and Bayesian posterior probabilities (≥ 0.90) are shown below branches and after slashes. *Melanomma pulvis-pyrii* (CBS 124080) served as an outgroup. The scale bar indicates expected changes per site per branch.

After ref. 116, the species described in the *Alfoldia* genus can be collected from surface-sterilised roots and can be cultured and maintained on general media. Isolates of the genus *Alfoldia* are root endophytes associated with woody plant species of semiarid grasslands of the Great Hungarian Plain.

*Type species.* *Alfoldia vorosii* D.G. Knapp, Imrefi & Kovács. MycoBank MB830105.
Kiskunsagia ubrizsyi
**Fungal Planet description sheets**

**Kiskunsagia** D.G. Knapp, Imrefi & Kovács, *gen. nov.*

**Etymology.** Referring to the sandy collection site within the Kiskunság National Park.

**Classification — Lophiostomataceae, Pleosporales, Dothideomycetes.**

Kiskunsagia isolates can be collected from surface-sterilised roots and can be cultured and maintained on general media. Isolates of the genus *Kiskunsagia* are root endophytes associated with woody plant species of semi-arid grasslands near Fülőpháza, Hungary.

**Type species.** *Kiskunsagia ubrizsyi* D.G. Knapp, Imrefi & Kovács. MycoBank MB830107.

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**Kiskunsagia ubrizsyi** D.G. Knapp, Imrefi & Kovács, *sp. nov.*

**Etymology.** We name the species in honour of the 100th anniversary of the birth of the outstanding Hungarian mycologist Gábor Ubrizsy (1919–1973), who contributed significantly to our knowledge on fungi. *Kiskunsagia ubrizsyi* differs from its closest phylogenetic neighbour, *Guttulispora crataegi* (MFLUCC 13_0442), by unique fixed alleles in ITS, LSU, SSU and tef1 loci based on alignment of the separate loci deposited in TreeBASE as study S24077: ITS positions: 14 (A), 16–21 (insertion), 23 (C), 25 (G), 26 (G), 27 (G), 28 (C), 30 (T), 31 (T), 32 (A), 33 (A), 38–40 (deletion), 41 (C), 42 (T), 46 (C), 47 (G), 50 (G), 52–56 (insertion), 59 (C), 65 (T), 74 (G), 75 (C), 77 (T), 78 (A), 80 (deletion), 82 (G), 83 (T), 86 (C), 102 (C), 170 (G), 191 (C), 192 (A), 205 (T), 217 (C), 230 (C), 231 (C), 233 (T), 234 (T), 398 (insertion), 441 (A), 444 (G), 504 (T), 506 (T), 529 (T), 532 (T), 536 (A), 537 (A), 539 (C), 541 (T), 547 (T), 550 (G), 552 (A), 575 (A), 576 (A), 580 (T), 581 (C), 585 (G), 585 (G), 586 (G); LSU positions: 113 (C), 134 (T), 165 (G), 186 (T), 196 (C), 201 (C), 202 (T), 223 (C), 226 (C), 404 (T), 405 (A), 419 (G), 424 (C), 444 (T), 445 (A), 446 (C), 487 (A), 505 (T), 524 (T), 527 (G), 665 (C), 692 (C), 697 (G); SSU position: 21 (deletion); tef1 positions: 108 (T), 108 (C), 159 (G), 195 (G), 200 (A), 202 (A), 204 (C), 207 (A), 243 (T), 246 (A), 264 (C), 267 (C), 309 (A), 310 (C), 311 (C), 358 (A), 359 (C), 365 (T), 366 (T), 384 (A), 396 (C), 406 (C), 408 (C), 411 (G), 432 (T), 468 (C), 483 (C), 486 (T), 517 (G), 526 (G), 531 (T), 543 (C), 558 (T), 648 (T), 651 (G), 691 (C), 693 (G), 696 (T), 702 (C), 726 (C), 738 (C), 756 (G), 768 (A), 777 (T), 837 (T), 840 (C), 918 (T), 927 (A), 957 (T).

**Culture characteristics — Colonies covering the Petri dish in 2 wk. Colony on PDA flat, spreading, with moderate aerial mycelium and smooth, lobate margin, no exudates observed. Colony on MEA creamy, yellow to white with an entire edge and sparse aerial mycelium, no exudates observed. Strains generally stain the media to pale orange. Cultures sterile.**

**Typus.** HUNGARY, Fülőpháza, from roots of *Fumana procumbens* (Cistaceae), 2008, D.G. Knapp & G.M. Kovács (holotype BP110342, culture ex-type REF121 = CBS 145502, ITS, LSU, SSU and tef1 sequences GenBank JN859341, MK589359, MK589351 and MK599325, MycoBank MB830107).

**Notes.** Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits of *Kiskunsagia ubrizsyi* (CBS 145502) using the ITS sequence are *Guttulispora crataegi* (GenBank NR_154070.1; Identities = 437/469 (93 %), 6 gaps (1 %), *Platystomum roseum* (GenBank KY264742.1; Identities = 443/480 (92 %), 11 gaps (2 %)) and *Neopaucispora rosea* (GenBank MG828294.1; Identities = 438/474 (92 %), 7 gaps (1 %)). The closest hits using the LSU sequence are *Tre­matosphaeria terricola* (GenBank JX985750.1; Identities = 884/905 (98 %), no gaps), *Lophiotrema compressum* (GenBank KP888643.1; Identities = 885/907 (98 %), no gaps) and *Lophiotrema quadri­nucleatum* (GenBank GU385184.1; Identities = 877/896 (98 %), no gaps). The closest hits using the SSU sequence are *Massariosphaeria grandidora* (GenBank EF165038.1; Identities = 512/514 (99 %), 2 gaps (0 %), *Trematosphaeria biappendiculata* (GenBank GU205254.1; Identities = 511/513 (99 %), 1 gap (0 %)) and *Ulospora bilia* (GenBank DQ384071.1; Identities = 520/527 (99 %), 1 gap (0 %)). The closest hits using the tef1 sequence are *Platystomum scabridisporum* (GenBank GU479856.1; Identities = 886/921 (96 %), no gaps), *Coelodictyosporium rosaneum* (GenBank MG829195.1; Identities = 885/937 (94 %), no gaps) and *Lophiotrema compressum* (GenBank KR075165.1; Identities = 874/921 (95 %), no gaps).

*Kiskunsagia ubrizsyi* represents ‘Group 10’ sensu Knapp et al. (2012). No sporulation of the strains was observed in any of the media PDA, MEA, MMN and WA supplemented with autoclaved plant tissues sensu (Knapp et al. 2015).

**Supplementary material**

**FP903** Maximum Likelihood (RAxML) tree of concatenated ITS, LSU, SSU and tef1 sequences of isolates of *Kiskunsagia ubrizsyi* and representative taxa of related lineages. RAxML analysis was performed by raxmlGUI 1.3 (Silvestro & Michalak 2012), bootstrap support values (≥ 70 %) are shown above branches and before slashes; Bayesian analysis was performed with MrBayes v. 3.1.2 (Ronquist & Huelsenbeck 2003) and Bayesian posterior probabilities (≥ 0.90) are shown below branches and after slashes. Melanomma pulvis-pyrius (CBS 124030) served as an outgroup. The scale bar indicates expected changes per site per branch.

**Colour illustrations.** Semi-arid sandy grassland in the Kiskunság National Park with flowering needle sunrises. The host (*Fumana procumbens*) of *Kiskunsagia ubrizsyi*; colony on PDA; pigmented hyphae of the strain REF121. Scale bar = 10 μm.
Apenidiella foetida
**Fungal Planet 904 – 19 July 2019**

**Apenidiella foetida** Iturrieta-González, Gené, Dania García, *sp. nov.*

*Etymology.* Name refers to the unpleasant odour produced in older cultures.

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

*Mycelium* consisting of branched, septate, subhyaline to pale olivaceous, smooth-walled, 1–2 µm diam hyphae. **Conidiophores** mononematous, macronematous, unbranched, erect, subcylindrical, up to 6-septate, pale olivaceous, smooth-walled, up to 130 µm long, 3–5 µm wide. **Conidiogenous cells** terminal, integrated, mono- or polyblastic, with up to 5 conidiogenous loci thickened and darkened, commonly giving rise to a set of ramoconidia at the same level, ramoconidia at different levels also present, pale olivaceous, smooth-walled, 12–21 × 4–5 µm, forming conidia in acropetal chains. **Conidia** aseptate, fusiform, limoniform or lanceolate, pale olivaceous, smooth-walled, some slightly verruculose, 7–21 × 3–5 µm. **Sexual morph** not observed.

*Culture characteristics.* Colonies on PDA reaching 28–33 mm diam after 30 d at 25 °C, olive brown (4F3) (Komerup & Wanscher 1978), velvety, radially folded, aerial mycelium scarce, reverse yellowish reaching 20–23 mm diam after 30 d at 25 °C, olive (3F3), slightly granular, flat, aerial mycelium scarce, regular margin; on PCA reaching 27 mm after 30 d at 25 °C, olive (3F3/3E3), scarce, regular margin; reverse dark green (30F8) to black.

Cardinal temperature for growth — Optimum 25 °C, maximum 28 °C, minimum 5 °C.

Notes. *Apenidiella* is a monotypic genus recently introduced in the family **Teratosphaeriaceae** to accommodate *A. strumelloidea* (previously *Cladosporium strumelloideum*), a fungus isolated from a leaf of *Carex* sp. collected in stagnant water from the Sutka River in Russia (Crous et al. 2007, Quaedvlieg et al. 2014). Interestingly, the novel species was recovered from a similar habitat than the type species of the genus. *Apenidiella strumelloidea* differs from *A. foetida* in having shorter conidiophores (up to 80 µm long) and conidiogenous cells (8–12 µm) and its conidia frequently show one side flat and the other convex, even slightly curved conidia are also present (Crous et al. 2007). In addition, in *A. strumelloidea* macro- and microconidiophores were described, while in our species only macroconidiophores were observed.

Based on a megablast search of NCBI GenBank nucleotide database, the **LSU** sequence of *A. foetida* showed a similarity of 98.82 % (839/849) with that of *A. strumelloidea* (CBS 114484, GenBank KF937229), while the similarity between ITS sequences (GenBank LR536044 vs GenBank EU019277) was 93.67 % (459/490).

Maximum likelihood tree obtained from the analysis of LSU sequences of *Apenidiella* and related genera of the family **Teratosphaeriaceae**. Bootstrap support values above 70 % are indicated on the nodes. The alignment included 751 bp and was performed with ClustalW. Kimura 2 parameters with Gamma distribution (K2+G) was used as the best nucleotide substitution model. Both the alignment and tree were constructed with MEGA v. 6 software (Tamura et al. 2013). The new species proposed in this study is indicated in **bold.** A superscript † denotes ex-type cultures.

**Colour illustrations.** Arboli, Catalonia, Spain. Colony sporulating on PCA after 30 d at 25 °C, and conidiophores and conidia after 14 d at 28 °C. Scale bars = 10 µm.

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Aspergillus bezerrae J.P. Andrade, C.N. Figueiredo, H.G. de Souza, J.T. De Souza & P.A.S Marbach, sp. nov.

Etymology. bezerrae, in honour of Dr José Luiz Bezerra, a Brazilian mycologist who has significantly contributed to our knowledge of Brazilian fungal biodiversity and the training of young mycologists in general.

Classification — Aspergillaceae, Eurotiales, Eurotymycetes. Conidial heads columnar. Stipes frequently sinuous or curved, smooth, frequently septate, (4–)13–718(–963) × 2–3(–4) μm, sometimes with subterminal branches, mycelial coils occur frequently and nodding heads occasionally present. Conidial heads uniseriate, vesicles pyriform to subglobose, pigmented, 6–16 × 4–16 μm (av. 12 ± 2 × 9 ± 3), phialides ampulliform, covering half to upper half of vesicle. Conidia globose to subglobose, delicately rough, 2–3 × 2–3 μm (av. 2 ± 0.12 × 2 ± 0.17), light green in mass, average width/length = 1 ± 0.01, n = 81. Sexual morph was observed in compatible combinations of isolates. Heterothallic; ascocoma visible after 4 wk of incubation on OA at 25 and 30 and absent at 37 °C, mature ascospores present in 5 wk. Cleistotheca white to pale, globose or subglobose (80–)150–890 μm diam, covered by a dense felt of white hyphae; ascii 8-spored, globose to subglobose, 9–12.5 × 7.5–12.5 μm; ascospores lenticular, with equatorial crests, spore bodies 2–5 × 3–5 μm.

Colour characters — Colonies on Czapek Yeast Auto-lysat agar (CYA) 40–43 mm diam at 25 °C after 7 d, floccose, radially and concentrically wrinkled, mycelium white (ISC-NBS No. 263; Kelly 1964), sporulation light yellow (No. 86), pale yellow (No. 89), no exudate, soluble pigment brilliant yellow (No. 83), reverse pale greenish yellow (No. 104), pale yellow (No. 89). After 14 d, sporulation pale yellow green (No. 121), brilliant greenish yellow (No. 98), yellow exudate, soluble pigment light yellow (No. 86), reverse light yellow (No. 88) and moderate yellow (No. 87). Colonies at 37 °C 29–34 mm, lanose to floccose, radially and concentrically wrinkled, sporulation pale yellow (No. 89), reverse pale yellow (No. 89). Colonies on Blakeslee’s Malt extract agar (MEAbl) 35–41 mm, floccose, slightly radially and concentrically wrinkled; mycelium white (No. 263); sporulation pale greenish yellow (No. 104), pale yellow (No. 89), light yellow (No. 86), no exudate, soluble pigment brilliant yellow (No. 83) sometimes present; reverse yellowish white (No. 92), pale yellow (No. 89), moderate yellow (No. 87), light yellow (No. 86). After 14 d, slightly radially wrinkled, sporulation moderate yellow green (No. 120); reverse pale yellow (No. 89), moderate yellow (No. 87). Colonies on Yeast extract sucrose agar (YES) 36–44 mm, floccose, concentrically and irregularly wrinkled, mycelium white (No. 263), sporulation light greenish yellow (No. 101), yellowish white (No. 92), no exudate, no soluble pigment, reverse light greenish yellow (No. 101), brilliant yellow (No. 83). Colonies on Czapek’s agar (CZ) 36–41 mm, floccose, sometimes with areas submerged, plane, white mycelium (No. 263), very pale green (No. 148), sporulation absent, no exudate, no soluble pigment, reverse white (No. 263), very pale green (No. 148). Colonies on Creatine sucrose agar (CREA) 35–41 mm, moderate mycelial growth, no acid production. Isolates did not grow in MEAbl at 47 °C, only some isolates were able to grow restrictedly (up to 7) at 45 °C and all grew at 42 °C 7–24 mm.

Typus. BrAZil, Bahia, in soil from the Guaiabim sandbank, S13°18′W38°57′, 20 Nov. 2011. P.A.S. Marbach (holotype HUBR 23232 - dried culture on MEAbl, culture ex-type CCDDA 11511 = 9EM2, BenA and CaM sequences GenBank MK597913 and MK597915, MycoBank MB830186).

Additional materials examined. BrAZil, Bahia, in soil from the Guaiabim sandbank, CCDDA 11513 = 4MS, 5 Oct. 2011. P.A.S. Marbach, LSU, BenA and CaM sequences GenBank MK595451, MK597912 and MK597914; ibid., 10 Dec. 2011. P.A.S. Marbach, cultures 63EM7, 9EM7, 22EM3 and 33EM6. A dried pair cultures of isolates CCDDA 11511 (= 9EM2) × 63EM7 containing the sexual fruiting bodies was deposited as HURB 22371.

Notes — Phylogenetically and morphologically A. bezerrae resembles A. wyomingensis (Novákova et al. 2014, Samson et al. 2014) included in the section Fumigati. The characteristics distinguishing A. bezerrae from A. wyomingensis are: 1) A. bezerrae grows slower than A. wyomingensis on all media and temperature tested; 2) A. bezerrae may produce a brilliant yellow soluble pigment in CYA and no acid in CREA; 3) A. bezerrae has longer stipes, produces mycelial coils, ascocoma are absent at 37 °C, the cleistothecia are larger and the ascospores have equatorial crests. All macroscopic and microscopic measurements were done twice, independently, for isolates CCDDA 11511 and CCDDA 11513.

Maximum likelihood tree obtained by phylogenetic analysis of the combined BenA and CaM sequences from Aspergillus bezerrae and phylogenetically related species in section Fumigati performed in MEGA v. 6.06 software employing K2+G model with 1 000 bootstrap re-samplings. Bootstrap support values (BS > 80 %) are presented at the nodes. Aspergillus tsurutae CBMFA 0933 was used as outgroup. The new species is presented in bold (* = ex-type).
Astraeus macedonicus
**Astraeus macedonicus** Rusevska, Karadelev, Telleria & M.P. Martín, *sp. nov.*

**Etymology.** Named after the country where this species was collected, the Republic of Macedonia.

**Classification — Diplomyctaceae, Boletales, Agaricomycetes.** Basidiomata from closed specimens 17 × 22 mm, not fully opened 25 × 30 mm, and almost opened 27 × 37 mm; regularly glosbose to slightly subglobose, epigeous, sessile. *Outer peridium* splitting to star shaped when mature into (6)—8—10 rough rays, expanding to 14–33 mm in length, 10–11 mm in width (at the middle, at the longest part), hygroscopic. *Endoperidium* sessile, subglobose to globose, papery-thin sack, 18–23 mm diam, pale cream to very light grey coloured, the surface papery-fibrillose; opening as an irregular slit. *Gleba* pale brownish to dark brownish, without columella. *Capillitium* hyaline, thick-walled, branched and interwoven, 4.2–10 µm diam, with capitates ends up to 12 µm diam, with rare septa, some with a clamp connection-like structure. *Basidiospores* globose, 7.3–10.1 µm diam, with dense, rounded, narrow, tapered, separate tubercles (up to 1 µm) which coalesce in groups.

**Type.** **Macedonia.** Bistra, Lazaropole village, footpath to St. Gjorgija church, 1300 m asl, 8 Aug, 2005, K. Rusevska (holotype 05MCF5221, ITS and LSU sequences GenBank MK491320 and MK496886, MycoBank MB829660).

Additional materials examined. **Macedonia.** Bilina Planina, Zhidilovo vill., deciduous forest (Quercus sp., Fagus, Betula pendula), 19 May 2011, K. Rusevska, 11MCF12901, ITS sequence GenBank MK491321; Kozhot, r. Stara Reka (vicinity), riparian vegetation, 16 July 2005, K. Rusevska, 05MCF5136, ITS sequence GenBank MK491319; Osogovski Plainini, Stanci vill., deciduous forest (Carpinus, Fagus, Betula), 900–970 m asl, 13 May 2007, K. Rusevska, 07MCF6706, ITS and LSU sequences GenBank MK491317 and MK496884; ibid., Ponikva, Fagus forest, 1500–1600 m asl, 11 July 2007, K. Rusevska, 07MCF8434, ITS sequence GenBank MK491322; ibid., Sasa, Quercus frainetto forest, 685 m asl, 9 Apr. 2008, K. Rusevska, 08MCF1040, ITS and LSU sequence GenBank MK49318 and MK496885; Plachovcika, above Laki vill., Selska Reka, Fagus forest with Pinus nigra, 21 Oct. 2014, K. Rusevska, 14MCF11641, ITS sequence GenBank MK491323. — Srses, Vuchje (vicinity), edge of deciduous forest, 12 Sept. 2009, K. Rusevska, 09MCF11183, ITS and LSU sequences GenBank MK491316 and MK496886.

Additional materials examined of other Astraeus species from Macedonia. Herbarium number is indicated, as well as the ITS sequence GenBank between brackets: **Astraeus hygrometricus.** 05MCF5511 [MK491324]. — **Astraeus pteridis.** 06MCF5817 [MK491326]; 07MCF8009 [MK491327]; 09MCF10671 [MK491325]. — **Astraeus telleriae.** 83MCF7728 [MK491314]; 83MCF7729 [MK491297]; 83MCF7730 [MK491294]; 83MCF7731 [MK491927]; 87MCF9566 [MK491300 and MK491304]; 88MCF9574 [MK491295]; 98MCF6531 [MK491280]; 01MCF3439 [MK491303]; 03MCF2896 [MK491296]; 04MCF4362 [MK491292]; 04MCF6532 [MK491288]; 05MCF911 [MK491310]; 05MCF4906 [MK491293]; 05MCF5329 [MK491284]; 05MCF5422 [MK491283]; 05MCF7977 [MK491275]; 06MCF1244 [MK491305]; 06MCF8811 [MK491309]; 07MCF6640 [MK491287]; 07MCF6887 [MK491281]; 07MCF6896 [MK491306]; 07MCF8028 [MK491282]; 07MCF8228 [MK491279]; 07MCF8549 [MK491290]; 08MCF9078, [MK491277]; 08MCF1019 [MK491285]; 08MCF10272 [MK491286]; 08MCF10282 [MK491293]; 09MCF9816 [MK491298]; 09MCF11502 [MK491313]; 09MCF11527 [MK491315]; 09MCF13788 [MK491302]; 10MCF12021 [MK491289]; 10MCF12678 [MK491308]; 11MCF9817 [MK491291]; 11MCF12654 [MK491278] and [MK491279]; 12MCF14080 [MK491311]; 12MCF15352 [MK491312]; 13MCF14623 [MK491301].

Notes — **Astraeus macedonicus** is known from deciduous forests in four Macedonian localities (the mountains located in the west, north, south and east part of the country). Morphologically, this species is very similar to **A. hygrometricus, A. pteridis and A. telleriae**, not only in its habitat but also in its microscopic characters, such as capillitium and spores; therefore all records (collected up to 2007) were previously published as **A. hygrometricus** (Karadelev et al. 2008). However, the Bayesian analyses, based on 53 collections from Macedonia, and a number of published sequences mainly from Phosri et al. (2007, 2013, 2014), Fangfuk et al. (2010) and Ryoo et al. (2017), clearly grouped eight Macedonian collections as a sister clade of **Astraeus ryoocheoninii**, a species described from Japan and Korea, and separated **A. hygrometricus, A. pteridis and A. telleriae**.

Colour illustrations. Macedonia, Bistra mountain, beechn forest, 1300 m asl, where the holotype species was collected (05MCF5221); basidiomata; basidiospores and capitillium under LM; basidiospores under SEM. Scale bars = 1 cm (basidiomata), 10 µm (basidiospores and capitillium) and 5 µm (basidiospores).

The 50 % majority rule Bayesian tree inferred from ITS nDNA sequences with the GTR+I+G model and using MrBayes v. 3.1.2 (Ronquist & Huelsenbeck 2003) for 2 M generations. Posterior probabilities values > 0.90 are marked as thick branches. In every collapsed clade, the number of sequences is indicated in or close to the triangle. **Astraeus macedonicus** holotype in bold. Pisolithus arnhicus (GenBank AJ629887) and Siclerodermum verrucosum (GenBank AJ629886) were included as outgroup.

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Aureobasidium tremulum

Inamdar, Roh. Sharma & Adhapure, sp. nov.

Etymology. Named after the shaking and trembling behaviour of the yeast when observed under a light microscope (Latin tremulum- shaking, trembling).

Classification — Aureobasidiaceae, Dothideales, Dothideomycetes.

Initial growth as creamy white colonies on potato dextrose agar, later turning brown to dark brown. Colonies appear to be rough and dry. Each colony is round with a convex elevation from a cross-sectional viewpoint and the edges appear to be undulated. Growth is optimal on Saboraud dextrose agar (SDA). Colonies on nutrient agar did not become dark brown. Cells are generally oblong-shaped with very few cells assuming an irregular shape. Budding occurs frequently. The average size of mature, non-budding cells is 2.8 × 6.4 µm. Sexual reproduction was not observed. Pseuophyphal formation not observed. Optimal growth occurred at 20–25 °C, with some growth at 5–15 °C. The following carbon compounds are assimilated: D-glucose, L-arabinose, D-xyllose, D-maltose, D-saccharose, D-Trehalose, D-melezitose, D-raf, D-sorbitol, and D-glycerol, calcium-2-keto-gluconate, L-lactose while weak assimilation was observed for adonitol, xyitol, D-galactose, methyl-alpha-D-glucopyranoside and D-cellobiose.

Habitat — Aureobasidium tremulum was isolated as a culture contaminant in the laboratory of Department of Biotechnology and Microbiology of Vivekanand Arts, Sardar DalipSingh Commerce and Science College, Aurangabad.

Distribution — India (Aurangabad, Maharashtra).

Notes — An initial BLASTn similarity search using the LSU region sequence in the NCBI type sequences database showed the highest similarity to A. lign CBS 125.21 (GenBank MH866211; 98 % identity, 99 % query cover) followed by A. melanogenum strain CBS 105.22 (GenBank MH866219; 98 % identity; query coverage 97 %). The BLASTn similarity search in the NCBI type sequences database using the ITS sequence showed the highest similarity to Kabatiella bupleuri CBS 131304 (GenBank NR_121524; 95 % identity, 100 % query coverage) followed by Aureobasidium iranianum CCTU 268 (GenBank K093738; 95 % identity, 99 % query coverage) and A. melanogenum CBS 105.22 (GenBank NR_159598, 95 % identity, 99 % query coverage). The neighbour-joining (NJ) phylogenetic analyses of ITS and LSU RNA gene regions were done using sequences of other species of Aureobasidium. The phylogenetic tree topology clearly shows that the present strain UN-1 is novel and does not cluster with any known species of the genus. The phylogenetic analysis based on the ITS alignment shows that it forms a sister branch to A. thailandense NRRL 58543 (GenBank JX462675) and A. mangrovei IBRC-M-30266 (GenBank KY089087). In the phylogenetic analysis based on the LSU alignment, it does not group with known species but was placed at equal evolutionary distance with A. caulivorum CBS 242.64 (GenBank FJ150944).

Colour illustrations. India, Maharashtra. Aurangabad, Vivekanand Arts, Sardar DalipSingh Commerce and Science College, Aurangabad. Growth of A. tremulum on potato dextrose agar; light microscopic (LM) view of A. tremulum; Cryo Scanning Electron Microscopic (CSEM) image of A. tremulum. Scale bars = 5 µm (LM image), 1 µm (CSEM image).

Typus. India, Aurangabad, Maharashtra, laboratory contaminant, July 2016, A. Inamdar (holotype MCC 1683 preserved as metabolically inactive strain. ITS and LSU sequences GenBank MK503657 and MK503660, MycoBank MB829941).

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Backusella azygospora  T.R.L. Cordeiro, Hyang B. Lee & A.L. Santiago, sp. nov.

**Etymology.** Name refers to the production of azygosporas.

**Classification —** Backusellaceae, Mucorales, Mucoromycotina, Mucoromycota.

Mycelium hyaline. Rhizoids present, well branched, balled and matted. Sporangiophores arising directly from the substrate, curved when young and becoming erect in maturity, with smooth or slightly encrusted walls, up to 12 μm diam, constrictions below the sporangia; majority with simple or sympodial branches with long and short asymmetrical ramifications. Shorter branches may be circinate, usually supporting pedicels from which sporangiola originate. A septum observed near the point of azygosporangial formation or below the sporangia, and not always present. Sporangia yellowish, becoming light brown, globose or slightly flattened with short, hyaline and vitreous spines, and a deliquescent wall up to 70 μm diam. Columellae of sporangiophores hyaline, smooth or slightly encrusted, majority ellipsoid, cylindrical, ellipsoid to slightly piriform (18–)22–35–(42) × (19–)22–30–(35) μm, globose and subglobose, (14–)20–40–(50) μm diam. Collar evident with no needle-like spines. Sporangiola present, easily found after fifth day of inoculation, abundant when multispored and rarely unisporous, both with persistent, spinulose and vitreous walls, up to 40 μm diam. Columellae of sporangiophora hyaline, smooth-walled, globose, subglobose to 15 μm diam and subglobose to conical (7–)12 × 14–(20) μm. Sporangiospores globose and subglobose (4.5–)9–22–(30) μm diam, some irregular (14.5–)33 × 12–(18) μm, smooth-walled, hyaline. Azygosporangia up to 110 μm diam, initially hyaline or yellow, becoming dark brown to black, globose, some flattened, wall with conical projections. Azygosporas up to 50 μm diam, globose, smooth-walled. Suspensor cells up to 55 × 48 μm, heavily encrusted walls. Zygosporangia not observed.

**Culture characteristics and temperature tests** — Colony light grey, powdery in aspect (MP5 A7), exhibiting rapid growth (9 cm diam and 0.5 cm height) after 5 d in MEA, at 25 °C. Reverse yellow to cloudy amber (MP12 K3) on MEA (Maerz & Paul 1950). Azygosporangia visible to the naked eye. At 10 °C — lack of growth and sporulation. At 15 °C — slow growth (9 cm diam in 360 h); poor sporulation. At 20 °C — good growth (9 cm diam in 240 h); good sporulation. At 25 °C — better growth (9 cm diam in 96 h); excellent sporulation. At 30 °C — slow growth (9 cm diam in 360 h); poor sporulation. At 35 °C — lack of growth and sporulation. Backusella azygospora exhibited better growth and sporulation in MEA than in PDA at all tested temperatures.

**Typos, Brasil**, Salóq municipality, Pernambuco State, S09°00.418’ W036°46.896’, isolated from soil samples, 22 Nov. 2018, T.R.L. Cordeiro (holotype URM 92986, culture ex-type URM 8065, ITS and LSU regions.

**Notes** — Backusella azygospora differs from other species of the genus based on its morphological characters and the phylogenetic relationships established based on the ITS and LSU rDNA regions. Morphologically, B. azygospora is the only species of Backusella that produces azygosporangia and azygosporas. In the ITS-rDNA phylogenetic tree B. azygospora was nested near the B. lamprospora clade, and data provided by BLASTn revealed 84 % and 95 % (ITS and LSU rDNA, respectively) of similarity between both species. However, B. lamprospora is characterised by producing globular or oval hemispherical columellae, differing from those found in B. azygospora, which may be cylindrical, ellipsoid, ellipsoid to slightly pyriform, globose and subglobule to conical. Additionally, sporangiospores of B. azygospora are globose and subglobule, some irregular in size and shape, and larger than the subglobe sporangiospores of B. lamprospora (6.8–)8–13–(14.5) × (6.4–)7.6–13–(14) μm (Benny & Benjamyn 1975).

**Phylogenetic tree of Backusella conducted using the ITS rDNA sequences.** Rhizopus microsporus CBS 112285 was used as outgroup. Sequences are labelled with their database accession numbers. Support values are from maximum likelihood analyses and Bayesian inference (values above and below the branches, respectively). Bayesian inference and maximum likelihood analyses were performed with MrBayes (Ronquist & Huelsenbeck 2003) and PhyML (Guindon & Gascuel 2003), respectively, launched from TOPALi (Milne et al. 2004). The new species is in **bold**. Bootstrap support values above 80 % are indicated.

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**Boletus pseudopinophilus** A.R. Bessette, Bessette, J. Craine & J.L. Frank, sp. nov.

**Etymology.** A combination of the Latin pseudo = ‘not true, but similar to’ and pinophilus = ‘pine-loving’ referring to the close affinity to the pine-loving European species, *Boletus pinophilus*.

**Classification.** *Boletaceae, Boletales, Agaricomycetes.*

Medium-sized to large basidiocarps with pinkish brown to reddish brown caps, white tubes stuffed with hyphae when young becoming yellow to olive-yellow in age, whitish reticulated stipe darkening to light brown as it ages, and white unchanging flesh. *Pileus* 5–16 cm wide, rounded to convex at first, becoming broadly convex to nearly plane in age, margin incurved at first, with a narrow band of sterile tissue, becoming even or undulating at maturity; surface slightly viscid when fresh, becoming dry, submentosentous, smooth, pinkish brown to greyish brown when young, becoming reddish brown and finally dull reddish brown to yellowish brown in age. *Context* thick, firm white, pinkish brown under the pileipellis, unchanging when exposed; *odour* and *taste* not distinctive. *Hymenophore* whitish at first, becoming yellow to olive-yellow, finally brownish yellow, unchanging when bruised. *Pores* stuffed with white hyphae when young, angular, 2–3 per mm; tubes 8–20 mm long, depressed around the stalk in age. *Stipe* 6–12 cm long, 1.5–4 cm thick, club-shaped, enlarged downward, typically with a pinched base, and white basal mycelium. Surface whitish to pale brown at first, darkening in age, dry, conspicuously reticulate overall, reticulum delicate, whitish at the apex and over the upper one third or more, darkening downward toward the base in age or when bruised; negative with the application of NH₄OH. *Context* firm, solid, white, unchanging when exposed. Spores olive-brown in mass, 15.8 × 4.8 (14–18 × 4–6) µm, Q = 3.28, elliptic-fusiform to subfusiform, smooth, yellowish in KOH. Basidia clavate, (2–)4-spored; cheilocystidia not observed; pleurocystidia sparse, 42–60 × 7–9 µm, narrowly fusoid-ventricose, smooth, thin-walled, hyaline in KOH. Pileipellis a trichodermium of interwoven, thin-walled, non-encrusted hyphae, 4–12 µm wide, lacking clamp connections.

**Habit, Habitat & Distribution.** Solitary or scattered on the ground under Slash Pine (*Pinus elliottii*) and Longleaf Pine (*Pinus palustris*) along the coastal plains across the south-eastern United States from southern Virginia at lower elevations south and west into Texas. It seems to prefer younger forests and can be common in pine plantations. Fruit in summer and fall.

Typs. USA, Georgia, Elbert County, near Ruckersville Road, 15 Sept. 2014, A.R. Bessette (holotype ARB1267, FLAS, ITS and LSU sequences GenBank KX610682 and KX610680, MycoBank MBB829952).

Additional material examined. USA, Georgia, Gwinnett County, 11 June 2014, J. Craine MO167169 (FLAS), ITS sequence GenBank KX610683; Mississippi, Harrison County, Harrison Experimental Forest, 5 Dec. 1982, D. Lewis 3382 (F1132005); Texas, Tyler County, 19 Sept. 1980, D. Lewis 2318 (F1101782).

Notes — *Boletus pseudopinophilus* is included in Weber & Smith (1985) and in Bessette et al. (2000, 2007, 2016) as *Boletus pinophilus*, the European name that, prior to molecular studies, was misapplied in North America not only to this south-eastern portcini, but also to the Spring King (*B. rex-veris*) and to the Rocky Mountain Ruby-capped King (*B. rubriceps*) in the western United States. Molecular analysis of ITS rDNA data shows *Boletus pseudopinophilus* to be closely related to, but separate from, *B. pinophilus*, in a strongly supported clade that includes *B. subcaerulescens, B. regineus, B. subalpinus* and a taxon reported as ‘*Boletus cf. pinophilus*’ from Oaxaca Mexico, GenBank MG919994. *Boletus subcaerulescens* is very similar, but typically has more vinaceous tones on the pileus and stipe, a pore surface that stains bluish grey when bruised, a northerly distribution and typically grows with spruce and short-needle pines including Scots Pine (*Pinus sylvestris*), Pitch Pine (*Pinus rigida*) and Jack Pine (*Pinus banksiana*). *Boletus aurantioruber* has a darker, rusty orange pileus, and a pinkish cinnamon to rusty red or red-brown reticulum. It usually grows associated with two and three needle pines such as Jack Pine and Pitch Pine and is more northerly in its distribution, typically found in north-eastern North America. *Boletus separans* grows with oak, has a variable coloured cap that tends to be more vinaceous to pink when young, and a white, finely reticulated stipe. Lilac areas of the pileipellis and stipitipellis of *B. separans* stain aqumarine to deep blue with the addition of NH₄OH. The European *Boletus pinophilus* differs in having a darker reddish brown pileus and grows in coniferous or mixed forests in Europe, mycorrhizal with pines (*Pinus*) or spruce (*Picea*), but has not been verified to occur in North America.

Colour illustrations. Top and bottom right: MO167169 under *Pinus elliottii*, Gwinnett County, GA; bottom left: holotype ARB1267 under *Pinus elliottii* and *Pinus palustris*, Elbert County, GA, USA.

Maximum likelihood tree inferred from ITS nrDNA, using RAxML v. 8 (Stamatakis 2014), showing placement of *Boletus pseudopinophilus* in *Boletus* s.str. Bootstrap support values (> 50 % with 1000 replicates) are shown above branches.

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Botryotrichum foricae
**Botryotrichum foricae** Jurjević & Hubka, *sp. nov.*

*Etymology.* Refers to the restroom (forica) from where the sample was isolated.

*Classification.* Chaetomiaceae, Sordariales, Sordariomycetes.

*Micromorphology.* On malt extract agar (MEA): Hyphae hyaline to lightly yellow pigmented, 1.5–4.5 µm diam. Conidiophores hyaline to pale yellowish brown, produced laterally from hyphae, commonly sympodially branched, up to 35 µm long, 2–5 µm diam near the base. Conidiogenous cells terminal or intercalary, monoblastic or sympodially polyblastic, commonly cylindrical, occasionally with a broad denticle, 0–13 × 2–4 µm, occasionally swollen beneath the conidium. Sterile setae present only on potato carrot agar (PCA) after prolonged cultivation, absent on other media. Conidia single, rarely in chains of a few spores, globose to subglobose, occasionally pyriform, hyaline, with age becoming pale brown, smooth, rarely slightly roughened, (7–)8–13(–14.5) µm diam. Sexual morph unknown.

*Culture characteristics.* (in darkness, 25 °C after 7 d): Colonies on MEA (Oxoid) 22–23 mm diam, floccose, moderate deep sulphate, mycelium white to pinkish buff, good sporulation, (R29; Ridgway 1912), exudate absent; reverse warm buff to ochraceous-orange (R15). Colonies on MEA supplemented with 0.01 % chloramphenicol (HealthLink®, Jacksonville, FL) 44–47 mm diam, floccose, mycelium white, good sporulation, exudate absent; warm buff to ochraceous-orange (R15). Colonies on Czapek yeast autolysate agar (CYA) 58–61 mm diam, floccose, moderate deep to deep sulphate, mycelium white, exudate absent; reverse light orange-yellow to orange-buff (R3). Colonies on PCA 42–50 mm diam, floccose to lightly funicolose, mycelium white, good sporulation, exudate absent; reverse pale yellow-orange to light orange-yellow (R3). Colonies on corn meal agar (CMA) 30–32 mm diam, funicolose to floccose, mycelium white, exudate absent; reverse uncoloured to cream colour (R16). Colonies on modified cellulose agar (MCA) 47–49 mm diam, sub-surface or submerged, sporulation not observed. Colonies on oatmeal agar (OA) 45–47 mm diam, floccose to funicolose, mycelium white, exudate absent, reverse faint brown. Colony diam (in mm after 7 d) at 30 °C: MEA 18–20, MEA with chloramphenicol 30–32, CYA 51–54, PCA 29–31, CMA 29–31, MCA 48–50. No growth on MEA, CYA, PCA, CMA and MCA at 37 °C.

*Typus.* USA, New Jersey, Glenwood, restroom air, Feb. 2015, isol. Ž. Jurjević (holotype BPI 910933, culture ex-type CCF 5752 = EMSL 2683; ITS, LSU, SSU and β-tubulin sequences GenBank LR584032, LR584033, LR584031 and LR584034, MycoBank MB830668).

*Notes.* BLAST analysis with the ITS and β-tubulin sequences of *Botryotrichum foricae* with the reference sequences published by Wang et al. (2016, 2019) showed greatest similarity with *B. atrogriseum* (99.2 % and 95.4 %), *B. piluliferum* (99.2 % and 92.9 %) and *B. peruvianum* (99.4 % and 92.3 %).

*Botryotrichum foricae* produces on average smaller conidia, (7–)8–13(–14.5) µm diam, compared to *B. piluliferum*, (9–)11–17.5(–18.5) µm diam, *B. peruvianum*, (10–)12–16(–17.5) µm diam and *B. atrogriseum* 10–25 µm diam.

*Colour illustrations.* Air, restroom. 7-d-old cultures at 25 °C of *Botryotrichum foricae* (from left to right on MEA, CYA, PCA and OA); conidia and conidiophores on MEA. Scale bars = 10 µm.

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*[The figure of the phylogenetic tree showing the relationships of taxa within the genus *Botryotrichum* is not included in this text.]*
Cadophora helianthi
**Cadophora helianthi** L. Molinero-Ruiz, A. Martín-Sanz, C. Berlanas & Gramaje, *sp. nov.*

**Etymology.** Named after the host genus (*Helianthus annuus*), from which it was isolated.

**Classification.** *Ploettnerulaceae, Helotiales, Leotiomyctetes.*

**Mycelium.** Composed of branched, septate hyphae occurring singly or in bundles of up to 10; hyphae tuberculate with warts up to 2.5 µm diam, verruculose to smooth, olivaceous brown, 2.5–3.5 µm diam. **Conidiophores** mostly short, usually branched, arising from aerial or submerged hyphae, erect to flexuous, up to 6-septate, pale brown to brown, (9–)10.5–46 (–59) (av. = 23) µm long and 2–3.5 (av. = 2.5) µm wide. **Phialides** terminal or lateral, mostly monophialidic, smooth to verruculose, hyaline, with 1.5–3 µm long, 2–3 µm wide, mostly cylindrical collarettes, some elongate-ampulliform, attenuated at the base or navicular, (4–)6.5–12.5 (–14) × 1.5–3 (–4) (av. = 7.5 × 2.5) µm. **Conidia** hyaline, with up to 3 guttules, ovoid or oblong ellipsoidal, (3–)3.5–5.5 × 1.5–2.5 (av. = 4.5 × 2) µm, L/W = 2.0.

**Culture characteristics.** Colonies reached a radius of 14.5–17 mm after 8 d at 25 °C. The minimum temperature for growth was 5 °C, the optimum 20–25 °C and the maximum 30 °C. Colonies on MEA were flat, felty, with an even edge; after 16 d, white to grey olivaceous close to the centre an in reverse. Colonies on PDA were flat, felty, with an even edge; after 16 d, white to olivaceous buff close to the centre and in reverse. Colonies on OA were raised with striating furrows, woolly when close to the centre, with an even edge; after 16 d, they were olivaceous to olivaceous buff above. Colours rated according to Rayner (1970).

**Typus.** Ukraine, Uman, Cherkasi, isolated from necrotic tissues in stems of *Helianthus annuus* showing wilting, 2017, A. Martín-Sanz (holotype CBS H-23647, culture ex-type SR-03-16 = CBS 144752, ITS, LSU, beta-tubulin (*Btub*) and translation elongation factor 1-alpha (*tef1*) gene sequences GenBank MF962601, MK813837, MH733391 and MH719029, MycoBank MB827327).

**Notes.** — The genus *Cadophora* is characterised by having pale to hyaline phialidic collarettes with the vegetative hyphae more or less pigmented. The known *Cadophora* species and their relatives occur in many habitats such as decaying wood (Nilsson 1973, Blanchette et al. 2004), soil (Kerry 1990, Hujslová et al. 2010, Agustí-Brisach et al. 2013, Crous et al. 2017) or plants (Halleen et al. 2003, Di Marco et al. 2004, Gramaje et al. 2014, Travadon et al. 2015). *Cadophora helianthi* was previously identified as *C. malorum* based on *Btub* phylogenies, albeit with low statistical support (Martín-Sanz et al. 2018).

**Colour illustrations.** *Helianthus annuus* plants growing in a field in Montoro (Andalucía, Spain). 16-d-old colony on PDA; conidiophores and phialides; conidia. Scale bars = 10 µm.

**Maximum likelihood tree obtained from the ITS, *tef1* and *Btub* gene sequences of *Cadophora* species of our isolates and sequences retrieved from GenBank. The tree was built using MEGA v. 6.0. Bootstrap support values above 70 % are shown at the nodes. The species described here is printed in bold. The alignment and tree are available in TreeBASE (Submission ID 23150).**
Calonectria matogrossensis
**Calonectria matogrossensis** R.A. Fernandes, Alfenas & R.F. Alfenas, sp. nov.

**Etymology.** Name refers to the collection site of the fungus, Mato Grosso, a state in Brazil.

Classification — Nectriaceae, Hypocreales, Sordariomycetes.

**Sexual morph not observed.** Macroconidiophores consisting of a stipe bearing a penicillate arrangement of fertile branches, and stipe extension terminating in a vesicle; stipe septate hyaline, smooth, 113–214 × 2–5 μm; stipe extension septate, hyaline, straight to flexuous, 92–181 μm long, 2–4 μm wide at the apical septum, terminating in a vesicle ellipsoid to obpyriform, 6–9 μm diam, lateral stipe extensions (90° to main axis), septate, straight to flexuous, 77–180 μm long, 2–3 μm wide at the apical septum, terminating in a vesicle ellipsoid to obpyriform, 4–6 μm diam. **Conidiogenous apparatus** 33–100 μm long and 45–100 μm wide; primary branches aseptate, 17–30 × 3–6 μm; secondary branches, aseptate, 12–26 × 3–5 μm; tertiary branches, aseptate, 6–16 × 3–5 μm; additional branches 7–10 × 3–4 μm, each terminal branch producing 2–4 phialides, doliform to reniform, hyaline, aseptate, 10–17 × 3–5 μm, apex with minute pericentral thickening and inconspicuous collarette. **Macroconidia** cylindrical, rounded at both ends, straight, (42–)47–50 × (3.5–)4–5 μm (av. 47 × 4 μm), 1-septate, lacking a visible abscission scar, held in parallel cylindrical clusters by colourless slime. **Mega-** and **microconidia** not observed.

**Culture characteristics — Colonies** fast growing at 26 °C on MEA (50–55 mm after 7 d), producing abundant white mycelium and sporulating on the medium surface; culture with colour blight brown to dark brown after 7 d; chlamydospores abundant throughout the medium, forming microsclerotia.

**Typus.** **Brasil.** Mato Grosso, Primavera do Leste, on leaves of Eucalyptus urophylla clone 1144 (Myrtaceae), 2015, R.A. Alfenas (holotype UB24025, tef-1α, cmdA, his3 and tub2 sequences GenBank MH837659–MH837663, MH837653–MH837658, MH837648–MH837652 and MH837664–MH837669, MycoBank MB829570).

**Notes —** Calonectria matogrossensis is a new member of the Ca. candelabra complex (Alfenas et al. 2015). Morphologically and phylogenetically it can be distinguished from other species of the Ca. candelabra complex. Phylogenetically, Ca. matogrossensis forms a well-support clade (0.99 for Bayesian probability posterior and 96 % for maximum likelihood bootstrap support), closely related but separate from Ca. metrosideri, Ca. eucalyptica and Ca. pseudoscoparia. Morphologically, it differs from its nearest neighbours in having lateral stipe extensions. Calonectria piauienses is morphologically similar to Ca. matogrossensis, but it has smaller conidia, and the species are phylogenetically distant.

**Table** Distinctive morphological characters of Calonectria species closely related to C. matogrossensis.

| Species          | Conidiogenous apparatus | Stipe extension | Vesicle | Lateral vesicle | Macroconidia size (μm) | References                          |
|------------------|--------------------------|-----------------|---------|----------------|------------------------|------------------------------------|
|                  | Size Branches (μm)       | Diam (μm) Shape |         |                |                        |                                    |
| C. eucalypticola | 45–75 × 35–62            | 145–170 × 2–4   | 5–7     | ellipsoidal to obpyriform | absent                | (43–)49–52 (–55) × 3–5 Alfenas et al. (2015) |
| C. metrosideri   | 60–75 × 40–65            | 90–170 × 2–4    | 5–9     | spathulate to obpyriform | absent | (40–)44–46 (–51) × 3–5 Alfenas et al. (2013) |
| C. pseudoscoparia| 52–74 × 34–87            | 124–201 × 4–6   | 6–10    | obpyriform to ellipsoidal | absent | (41–)45–51 (–52) × 3–3 Lombard et al. (2010) |
| C. matogrossensis| 33–99 × 45–100           | 113–214 × 2–5   | 6–9     | ellipsoidal to obpyriform | present | (42–)47–50 (× 3.5–)4–5 This study |

**Colour illustrations.** Leaves of Eucalyptus urophylla. Calonectria matogrossensis (ex-type UB24025): macroconidiophores (scale bars = 50, 20, 20 μm); conidiogenous apparatus with conidiophore branches and phialides; macroconidia (scale bars = 20 μm); ellipsoidal to obpyriform vesicles (scale bars = 10 μm).
**Calvatia brasieliensis** R.J. Ferreira, R.L. Oliveira, B.D.B. Silva, M.P. Martin & Baseia, *sp. nov.*

*Etymology.* In reference to the country where this species was collected.

*Classification.* — Agaricales, Agaricales, Agaricomycetes. *Basidiomata* growing solitary or in small groups, pyriform to subglobule, 19−37 mm wide × 27−29 mm high. *Exoperidium* subtomentose, evanescent, greyish yellow (1B3 and 1B4, Körnerup & Wanscher 1978), at the base with sand encrusted at maturity. *Mesoperidium* papery, dark brown, greyish brown to violet brown (9F4, 9F6, 10E3, 10E4) at maturity. *Endoperidium* papyraceous in the outer surface and tomentose in the inner surface, fragile and dark brown to violet brown (6F4, 10F4, 10F5). *Rhizomorphs* brown (7E4) densely encrusted with sand. Sub gleba reduced, compact, occupying a third of the basidioma, when mature greyish yellow (4B3). *Gleba* lanose, greyish brown to violet brown (10E3, 10E4, 10F5), at maturity. *Exoperidium* composed of hyphae measuring 3.2−6.4 µm diam, with regular walls ≤ 1.0 µm thin, straight, septate and rarely branched, hyaline in 5 % KOH, and dextrinoid (low reaction). *Mesoperidium* pseudoparenchymatous composed of cells measuring 13−18 6 × 10.7−14.1 µm diam, with regular walls ≤ 0.56 thin, hyaline in 5 % KOH, and non-dextrinoid. *Endoperidium* with hyphae measuring 2.7−4.6 µm diam, with regular walls ≤ 0.8 µm thin, straight, branched, non-septate, brown in 5 % KOH, and non-dextrinoid; in the apical portion, mycosclereids globose, subglobule, pyriform, ovoid, ellipsoid or rectangular in shape, 13.5−42 µm × 7.4−15.7 µm diam, with regular walls ≤ 0.56 µm thin, straight, frequently branched, septate, with small and numerous circular pits, hyaline in 5 % KOH, dextrinoid (low reaction). *Basidiospores* globose to subglobule, equinulated, 5.8−6.6 × 5.2−6.5 µm (av. = 6.1 ± 0.3 × 5.9 ± 0.3; Qm (medium coefficient) = 1.04; n (measurement numbers) = 20), pedicels present in some spores, ≤ 0.89 µm, brown in 5 % KOH, non-dextrinoid and acyanophilic.

Habit & Habitat — Basidiomata growing solitary or in pairs on moist soil.

**Supplementary material**

FP913 ITS nrDNA phylogenetic tree obtained with MrBayes v. 3.1.2 (Huson beck & Ronquist 2001) under T92+G model for 5 M generations. The new species is marked with a rectangle. The posterior probabilities greater than 0.9 are indicated on the branches. *Bovista paludosa* was included as outgroup. Figtree v. 1.42 and Adobe Illustrator CS5 software were used to edit the final tree.

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Carcinomyces nordestinensis
Carcinomyces nordestinensis D.A. Andrade, C.R. Félix, F.S. Bomfim, R.P. Neves & Landell, sp. nov.

Etymology. Name refers to the Brazilian region, Nordeste (in Portuguese), where all yeast isolates were obtained.

Classification — Carcinomyctaceae, Tremellales, Tremellomyctes.

On YEPD agar after 3 d at 22–25 °C, cells are globose to sub-globose (3–5 × 1.5–3.5 μm), and colonies are cream to pale pink, mucoid and glistening. Vegetative reproduction is by multilobular budding. After 3 wk in Dalmau plate culture on corn-meal agar, pseudohyphae are formed. Sexual reproduction is not observed. Ballistoconidia production is absent. Fertmentation ability is negative. The following carbon compounds are assimilated: N-Acetyl-D-glucosamine, L-arabinitol, cellobiose, erythritol, galactose, melezitose, raffinose, soluble starch, sucrose, D-arabinose (slow), L-arabinose (slow), inulin (slow), galacturonate (slow), D-glucose (slow), glycerol (slow), lactose (slow), maltose (slow), D-mannitol (slow), melibiose (slow), myo-Inositol (slow), D-ribose (slow), trehalose (slow), xylitol (slow), D-xyllose (slow), galactitol (variable), D-glucitol, (variable), succinate (variable), L-rhamnose (weak). No assimilation of citrate, gluconate, DL-lactate, salicin, tween 20, tween 80. Assimilation of nitrogen compound are L-lysine (slow) and potassium nitrate (weak). No assimilation of sources nitrogen of creatine, creatinine, sodium nitrite, ethylamine and cadaverine. Growth at 22, 25 and 30 °C and no growth at 35 °C. Growth was observed not on YEPD with 50 % glucose, in the 10 % sodium chloride and 1 % in the acetic acid. After 21 d, growth was observed in the presence of 0.01 % cycloheximide and in 0.1 % no growth was observed. Urease activity and diazonium blue B reaction are positive. No stanch formation.

Typus. BRASIL, Santana do Ipanema municipality, Alagoas state, Private Reserve of Natural Heritage (59°21’14.9″W 37°14.5′S) as ephiphytic yeast on leaves of Bromelia anticaantha (Bromeliaceae), 11 Sept. 2017, C.R. Félix & M.F. Landell (holotype as metabolically inactive culture, UFMG-CM-Y6457, LSU and ITS sequences GenBank MH909022 and MK659873, MycoBank MB830322); iso-holotype as metabolically inactive culture URM 8088 = CBS 15981 = BRT 317.

Additional materials examined. BRAZIL, Recife municipality, Pernambuco state, Federal University of Pernambuco campus (38°03’02.30″W 34°56’54.41″) as endophytic yeast from the medicinal plant Handroanthus impetiginosus (Bignoniaceae), 20 Jan. 2013, F.S. Bomfim (cultures URM 7675, eURN: 7675, URM 7676, URM 7677 and isolate 20F, ITS sequences GenBank MK792995, MK792995, MK792960, MK792965, and LSU sequences GenBank MK792962, MK792963, MK800011, MK792964, respectively).

Notes — Carcinomyces nordestinensis is proposed as new species based on phylogenetic analysis, physiological and biochemical features. The strains had 100 % identity in the LSU and between 98–100 % in the ITS region (0–4 substitutions). Phylogenetic inferences of LSU (D1/D2 domain) and ITS rDNA sequences indicated Carcinomyces arundinariae (CBS 9931) as the closest species. According to BLASTn searches (9 Apr. 2019) the LSU rDNA sequences have 98.6 % identity to C. arundinariae (CBS 9931, GenBank NG_058990; 7 nucleotide substitutions), 97 % to sequences deposited as Carcinomyces sp. (BPT 70, GenBank KY305115; 19 nucleotide substitutions) 96.8 % to Bullera sp. (TO 115, GenBank KJ156986; 18 nucleotide substitutions), and 96.07 % to Bullera sp. (BI 335, GenBank EU679387; 17 nucleotide substitutions). The closest hits using ITS sequences are 95.1 % identity to C. arundinariae (CBS 9931, GenBank NR_077092; 22 nucleotide substitutions), 86.1 % to Bullera sp. (TO 115, GenBank KJ156987; > 50 nucleotide substitutions) and 85.8 % to Carcinomyces sp. (BPT 70, GenBank KY305146; 64 nucleotide substitutions). Carcinomyces nordestinensis differs physiologically and biochemically from C. arundinariae by inulin and glycerol assimilation and no assimilation of salicin and citrate (Kurtzman et al. 2011, Liu et al. 2015a).

Supplementary material

FP914-1 Phylogenetic placement of Carcinomyces nordestinensis was obtained by neighbour-joining (Kimura two-parameter distance method) analysis of the LSU (D1/D2 domains) rRNA gene using MEGA v. 7 (Kumar et al. 2016). Bootstrap support values higher than 50 % are shown (1000 replicates). The novel species is indicated in bold and type cultures with a superscript †. The tree was rooted to Rhodotorula glutinis. Bar = 0.02 substitutions per nucleotide position.

FP914-2 Phylogenetic placement of Carcinomyces nordestinensis was obtained by neighbour-joining (Kimura two-parameter distance method) analysis of the ITS region using MEGA v. 7 (Kumar et al. 2016). Bootstrap support values higher than 50 % are shown (1000 replicates). The novel species is indicated in bold and type cultures with a superscript †. The tree was rooted to Rhodotorula glutinis. Bar = 0.02 substitutions per nucleotide position.
Clavaria parvispora
**Clavaria parvispora** Kautman., Majerová & Olariaga, *sp. nov.*

**Etymology.** Name refers to the spore size, which is the smallest among pink-coloured *Clavaria* species.

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

*Basidiomata* gregarious or in small clumps of 2–5 basidiomata, rarely solitary, 5–20 (–30) mm long, simple, with well-delimited, but quite short stipe (up to 3 mm). *Clavula* 5–25 × 0.5–1.5 mm, cylindrical, smooth, tomentose, pale pink (Pantone 162UP), darkening upon drying (Pantone 190UP). Apex obtuse and paler, almost white in young basidiomata. *Stipe* 2–3 × 1–1.5 mm, cylindrical, smooth, silky, yellowish (Pantone 750BC) with white, tomentose basal mycelium. *Context* watery, yellowish, taste mild, smell indistinctive. Reaction with FeCl₃ positive, blackening, slow after 3–5 min. *Basidiospores* ellipsoid to broadly ellipsoid, thin-walled, smooth, hyaline, non-amyloid, usually with one big vacuole, 5.2–6.1 (–6.4) × 3.8–4.3 μm (Lm = 5.8; Wm = 4.0; Qm = 1.41). *Apiculus* short, up to 0.5 μm. Ornamentation of spores not observed. *Basidia* claviform, 4-spored, with a loop-like basal clamp, 28–35 × 2.5–4 μm. *Cystidia* absent. *Subhymenium* 25–35 μm thick, formed by densely interwoven hyphae, cylindrical to inflated, thin-walled, clampless, 2.0–3.5 μm broad. *Context* hyphae parallel, inflated, thin-walled, secondarily septate, hyaline, smooth, clampless, 10–20 μm wide, mostly (20–)70–100 μm long. Basal mycelium white, composed of interwoven hyphae, cylindrical, thick-walled, scarcely septate, hyaline, clampless, 1–2 μm wide.

**Distribution —** Known from Slovakia, Czech Republic and Norway, probably more widespread but overlooked. Preferred habitat is probably represented by bare soil and mosses under shrubs in outgrown pastures and semi-natural grasslands.

**Typus.** **Norway**, Oslo, Bygdøy, Dronningberget Nature Reserve, in deciduous trees and shrubs along the old outgrown forest road, in bare soil and mosses, N59.914164 E10.683094, alt. 10 m, 7 Sept. 2009, I. Kautmanová (holotype BRA CR13266, LSU sequence GenBank MH727523, MycoBank MB828502).

**Additional materials examined.** **Slovakia**, Považský Inovec Mts, Banka village, in shrubs (*Prunus spinosa, Crataegus sp., Corylus avellana*) in outgrown pasture, among mosses on bare soil, alt. 230 m, 26 Sept. 2014, V. Kučera, BRA CR21309, LSU sequence GenBank MH727524; Žilinská kotlina Basin, Žilina, in city park in meadow, alt. 450 m, 18 Oct. 2008, L. Jánošík, BRA CR16030, LSU sequence GenBank JQ415937; Podtatranská kotlina Basin, Hybe village, under shrubs (*Prunus spinosa, Rosa sp., Corylus avellana*) in old orchard, on bare soil, alt. 810 m, 15 Aug. 2008, I. Kautmanová, BRA CR16024, LSU sequence GenBank JQ15936; ibid., 12 Aug. 2011, I. Kautmanová, BRA CR16636, LSU sequence GenBank MH727522; Javoniky Mts, Trenčín, Zlatovec, in bare soil in shrubs (*Crataegus sp., Corylus avellana, Prunus spinosa*) in outgrown pasture, alt. 230 m, 17 Sept. 2014, V. Kautman, BRA CR21304, LSU sequence GenBank MH727520; ibid., 17 Sept. 2014, V. Kautman, BRA CR21311, LSU sequence GenBank MH727521.

**Notes —** *Clavaria parvispora* differs from other pink-coloured species of the *Clavaria* subg. *Holocoryne* by small broadly ellipsoid spores. *Clavaria mesapica* is characterised by much larger basidiomata (up to 7 cm tall), which are pale pink, drying to pale cream colour without pink tones, hymenial cystidia and ellipsoid to almost rhomboid spores 7.2 × 5.2 μm. Spore ornamentation frequently observed in *C. mesapica* and other pink *Clavaria* subg. *Holocoryne* species, was not found in any of the *C. parvispora* specimens.

In the ML tree based on the LSU alignment *C. parvispora* sequences are grouped in a well-supported clade, although showing a certain degree of sequence divergence. Other clades represent three species of the *Clavaria incarnata* complex, where *Clavaria* sp. 1 is probably an undescribed species characterised by big spores (up to 9.5 × 8.5 μm), *Clavaria* sp. 2 possesses typically a high proportion of ornamented spores and is probably conspecific with *Clavaria stellifera*, and the third species can be attributed to *C. incarnata* s.s.

Bayesian inference 50 % majority rule consensus phylogram of *Clavaria incarnata* group from LSU sequence data constructed by MrBayes 3.2.6 (Ronquist et. al. 2012). Bayesian posterior probabilities (PP) ≥ 95 % and Maximum Likelihood bootstrap values (ML-BP) ≥ 70 % are shown at the nodes (ML-BP / PP). Thickened branches received support by both analyses. The tree was rooted to *C. flavostellifera*.

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Colletotrichum feijoicola Guarnaccia & Damm, sp. nov.

Etimology. Name refers to feijoa, the host plant from which this fungus was collected.

Classification — Glomerellaceae, Glomerellales, Sordariomycetes.

Sexual morph not observed, but pale brown, subglobose, glabrous immature ascomata formed after > 3 wk on SNA, 20–65 μm diam. Asexual morph on SNA. Vegetative hyphae 1–8.5 μm diam, hyaline, smooth-walled, septate, branched. Chlamydospores not observed. Conidiomata absent, conidiophores and setae formed directly on hyphae. Setae not observed. Conidiophores hyaline, smooth-walled, cylindrical to clavate, sometimes flexuous, sometimes extending to form new conidiogenous loci, 5.5–21 × 3–4 μm, opening 1.5–2.5 μm diam, collarette 1–1.5 μm long, periclinal thickening distinct. Conidia hyaline, smooth-walled, septate, cylindrical, with round ends, already germinating and becoming septate after 10 d, (11.5–)12–14(–15) × (4.5–)5–5.5 μm, mean ± SD = 12.9 ± 0.9 × 5.1 ± 0.3 μm, L/W ratio = 2.5. Appressoria single or in loose groups, pale to medium brown, smooth-walled, bullet-shaped, navicular, subsphaerical, ovoidal to irregular in outline, with an entire, undulate to lobate margin; buff, pale luteous, saffron, apricot to dark brick, growth 27.5–32.5 mm in 7 d, L/W ratio = 1.4. No sporulation on Anthriscus stem or OA. Strain GMLC 1898 remained sterile.

Culture characteristics — (near UV light with 12 h photoperiod, 20 °C after 10 d): Colonies on SNA flat with entire margin, hyaline to saffron, filter paper partly pure yellow, filter paper and Anthriscus stem covered with white felt-like mycelium, reverse same colours; growth 23.5–28 mm in 7 d (34.5–39 mm in 10 d). Colonies on OA flat with entire to undulate margin; buff, pale luteous, saffron, apricot to dark brick, partly covered with white felt-like mycelium, reverse buff, pale luteous, saffron, cinnamon to dark brown, growth 27.5–32.5 mm in 7 d (37.5– ≥ 40 mm in 10 d). Conidia in mass not observed.

Typus. PORTUGAL, Azores Islands, Sao Miguel, from a leaf spot of Acca sellowiana (feijoa, Myrtaceae), 17 July 2017, V. Guarnaccia (GML-F116096 holotype, culture ex-type CBS 144633 = GMLC 1899 = CPC 34246; act, gapdh, ITS, LSU and tub2 sequences GenBank MK876466.1, MK876475.1, MK876413.1, MK876420.1 and MK876507.1, MycoBank MB830862).

Additional material examined. PORTUGAL, Azores Islands, Sao Miguel, from a leaf spot of A. sellowiana, 17 July 2017, V. Guarnaccia, GML-F116095, culture GMLC 1898 = CPC 34245; act, chs-1, gapdh, his3, ITS, LSU and tub2 sequences GenBank MK876465.1, MK876471.1, MK876474.1, MK876477.1, MK876414.1, MK876421.1 and MK876506.1.

Notes — Acca sellowiana is native to South America and is grown as an ornamental plant or for its tropical fruit production in Europe, where cultivation is affected by fungal pathogens such as Calonectria spp. (Guarnaccia et al. 2014). Colletotrichum feijoicola was found associated with reddish leaf spots of A. sellowiana cultivated in a small orchard in Sao Miguel, the main island of the Azores archipelago.

No Colletotrichum species has previously been described from Acca spp. and none was reported on Acca spp. in Europe (Farr & Rossman 2018). However, there are three previous reports of Colletotrichum spp. on A. sellowiana from other regions: C. gloeosporioides in Uruguay (Bettucci et al. 2004), C. siamense in Brazil (Fattim et al. 2017) and C. theobromicola in New Zealand (Weir et al. 2012); all of these species belong to the C. gloeosporioides species complex. However, the report of C. gloeosporioides in Uruguay is unreliable as the study was conducted prior to the revision of the C. gloeosporioides species complex (Weir et al. 2012), and could refer to probably any Colletotrichum species with cylindrical conidia and rounded ends including species e.g. in the C. boninense, C. gloeosporioides and C. orchidearum species complexes (Damm et al. 2012, 2019, Weir et al. 2012).

In contrast to these reports, BLASTn searches with ITS, LSU, act, tub2 and gapdh sequences of C. feijoicola in NCBI’s GenBank nucleotide database restricted to ex-type strains resulted in different species of the C. boninense species complex: 98 % similarity with C. oncidii and C. colombiense (CBS 129828 and CBS 129818; Damm et al. 2012) using ITS, 99 % with C. hippeastri (CBS 125376; Vu et al. 2019) using LSU, 96 % with C. camelliae-japonicae and C. anellatum (LC6416 and CBS 129826; Hou et al. 2016, Damm et al. 2012) using act, 97 % with C. anellatum (CBS 129826; Damm et al. 2012) using tub2 and 90 % with C. petchii (CBS 378.94; Damm et al. 2012) using gapdh.

Based on these results we regard the strains from A. sellowiana as a new species belonging to the C. boninense species complex. Several Colletotrichum species are known as pathogens of various plants mainly in tropical and subtropical regions of the world; some of them have recently been reported as pathogens of other tropical fruit trees in Europe (Guarnaccia et al. 2016). Thus, C. feijoicola should be considered as a potential threat for fruit production.
Coniochaeta dendrobiicola
Coniochaeta dendrobiicola Sujit Shah, sp. nov.

**Etymology**: Name reflects the host genus it was isolated from, *Dendrobium longicornu*.

**Classification** — Coniochaetaceae, Coniochaetales, Sordariomycetes.

Vegetative hyphae thin, septate, smooth 1.2–2.4 µm wide. Conidiogenous cells arising laterally from vegetative hyphae, broader at base tapering towards apex (1.4 µm at base and 0.67 µm at apex). Conidia hyaline, smooth, cylindrical to allantoid, variable in size, 4.35–11.28 × 1.2–2.3 µm. Sexual morph absent which is reported in *Coniochaeta velutina*, *C. prunicola*, *C. africana* isolated from *Prunus* (Damm et al. 2010, Weber 2002, Abdalla & Al-Rokibah 2003, Asgari & Zare 2006).

Cultural characteristics — *Coniochaeta dendrobiicola* was first isolated on Czapek-Dox agar (CDA). The shape of the colony was circular, with lemon yellow colour and pale regular margin with pale white band as growing zone. The surface was smooth with flat topography and submerged mycelium. Colonies reach 4.5 cm diam after 15 d of incubation, with 1–2 eccentric brown rings present.

On potato dextrose agar (PDA) the colony shape was circular with regular margin, lemon yellow with 1 cm thick white growing margin. The colony surface was smooth, shiny with flat topography and submerged mycelium. Colonies reach 4 cm diam after 15 d of incubation, with 2–3 concentric rings. On oatmeal agar (OA) the colony shape was circular with regular margin, lemon yellow with 1 cm thick white growing margin. The colony surface was smooth, shiny with flat topography and submerged mycelium. Colonies reach 4.5 cm diam after 15 d of incubation, with a single concentric brown ring present.

**Habitat** — Roots of *Dendrobium longicornu*, District Makwanpur, Nepal.

**Typus. Nepal.** District Makwanpur, roots of *Dendrobium lognicornu* (Orchidaceae), 25 May 2017, S. Shah (holotype culture and specimen, MCC1811, preserved as metabolically inactive, ITS and LSU sequences GenBank MK225602 and MK225603, MycoBank MB830652).

Notes — Phylogenetic trees of the ITS region was prepared using sequences of *C. dendrobiicola* and other *Coniochaeta* species obtained from GenBank. An NCBI BLASTn search of ITS sequences showed closest similarity to be 93 % with *C. africana* (CBS 120868, GenBank MH863095), 92 % with *C. velutina* (STE-U 8315, GenBank KY312638), 92 % with *Coniochaeta angustispora* (CBS 871.73, GenBank MH960816) and 92 % with *Coniochaeta nepalica* (NBRC 30584, GenBank LC146727).

**Phialoconidial stage**

Neighbour-Joining tree based on ITS sequences using MEGA v. 6.06, showing the phylogenetic position of the new species among closely related 11 Coniochaeta species whose sequences were retrieved from the NCBI database. *Coniochaeta dendrobiicola* (DLCCR7) clustered in a clade containing the majority of the Coniochaeta species with a bootstrap support value of 100 %. The analysis involved 15 nucleotide sequences with Chaetosphaeria garethjonesii and Phialoconidial obovatum as outgroups.

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Crepidotus tobolensis
**Crepidotus tobolensis** Kapitonov, Biketova & Zmitr., *sp. nov.*

**Etymology.** The name refers to a geographic area of the type locality, namely Tobol river and Tobolsk city (Russia, Tyumen Region).

**Classification —** *Crepidotaceae, Agaricales, Agaricomycetes.*

**Pileus** hygrophanous, soft and brittle, 7–43 mm wide, sessile to subpetiolate, reniform to ungulate or flabelliform, at first more or less hemispherical, then convex-plane, the upperside initially subtomentose then, starting from the attachment point, velutinous to glabrous with internal hygrophanous radially-fibrilllose texture and snow-white tomentum around the attachment point, luteous to honey-yellow and creamy-white at the margin, at maturity less bright, with orange-ochraceous tinges in median zone; *context* as a thin hygrophanous layer 1–2.8 mm thick, creamy-white. *Margin* straight, entire, crenate to crisped. *Gills* frequent, 1–3 mm wide, thin, not serrate, but serrulate in marginal zone, gradually narrowing downward on stipe, convergent under basidiomata fruit-body, soft-ceraceous, easily cracked, lanellulae in 3–4 ranks, ivory-white, staining yellowish ochraceous starting from attachment point (many gills are covered with rufous spots). *Stipe* absent. *Odour* and taste not distinctive. *Spore-print* brownish orange to yellowish brown. Spores (5.4–)5.9–7(–7.6) × (4.4–)4.6–5.6(–6.3) µm, av. = 6.5 ± 5.1 µm, Q = (1.11–)1.21–1.35(–1.44), Qav. = 1.28 (n = 100/1), ovoid to widely lacrymoid, slightly ventrally flattened, with a germ pore, hyaline to yellowish; exosporium warted, golden-brown, perispore hyaline, strictly follows the exosporium ornamentation. Basidica (19.8–)21–24.4(–25.1) × (6.1–)6.13–8.1–8.5) µm, av. = 22.3 × 7 µm (n = 13), sterigmata (2.3–)2.4–3.2(–3.6) µm long, av. = 2.9 µm (n = 17), 4-spored, clavate to subpendunculate, hyaline. *Cheilocystidia* numerous, (28–)33.2–45.2(–73) × (6.5–)6.9–11.2–12.8(–12.8) µm, av. = 41.1 × 8.8 µm (n = 15), variable in shape: fusiform, hyphoid, flexuose, clavate (often swollen to sphaeropedunculate), mostly branched, branches stramgulate or capitate. *Pleurocystidia* especially not differentiated. *Pileipellis* a trichoderma, transforming into the cutis when mature; cutis 45–100 µm, thin, repent hypheae 3–11.7 µm diam, hyaline; terminal cells resemble the pleurocystidia in shape and size. *Subpellis* lacking. *Pingment deposits* lacking. *Clamp connections* present in all tissues.

**Habitat & Distribution —** Growing gregarious on wood debris of *Populus tremula*. Uncommon in the studied area. So far known only from Russia.

**Colour illustrations.** Russia, Tyumen Region, Tobolsk city, Betuleto-Tremuletum variherbosum, where the holotype was collected. Young basidiomata (top range: isotype); mature basidiomata upperside (median range: holotype LE 287655/1, isotype right); mature basidiomata hypomenophore in field; bottom range: four various cheilocystidia; basidium in hymenium; basidia spores. Scale bars = 5 mm (basidiomata) and 5 µm (microstructures).

**Typus.** *RUSSIA*, Tyumen Region, Tobolsk city, Betuleto-Tremuletum variherbosum, on debris of *Populus tremula*, 28 Aug. 2018, V.I. Kapitonov (holotype LE 287655, isotype TCSS UB RAS 2732, ITS and LSU sequences GenBank MK522393 and MK560782, MycoBank MB829922).

**Additional materials examined.** Crepidotus tobolensis: *RUSSIA*, Tyumen Region, Tobolsk district, Priirtyshskyi vicinity, Betuleto-Tremuletum variherbosum, on debris of *Populus tremula*, 1 July 2018, V.I. Kapitonov (TCSS UB RAS 9477, ITS sequence GenBank MK522392).

**Notes —** As it is shown on the molecular phylogram, *C. tobolensis* represents a distinct species, sister to the South European *C. macedonicus*. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequences were *C. macedonicus* (GenBank MH780922.1 and MH780921.1; Identities = 671/683 (98 %), 4 gaps (0 %)) and *C. praecipuus* (GenBank KY827311.1; Identities = 716/763 (94 %), 20 gaps (2 %)). The closest hits using the LSU sequence were Crepidotus sp. PBM3237 (GenBank KT382279.1; Identities = 1367/1378 (99 %), no gaps) and *C. macedonicus* (GenBank MK277889.1; Identities = 1286/1290 (99 %), no gaps).

Two other closely related species are *C. lutescens* from China and *C. praecipuus* from New Zealand. The similarities and differences of the listed taxa are summarised in the supplementary table FP918-1.

**Crepidotus tobolensis** can be well distinguished only by a complex set of characters. As can be seen (supplementary table FP918-1), it is similar to the closely related *C. lutescens* and *C. praecipuus* by basidiomata size and rather intense yellow pigmentation, whereas in its spore quotient to *C. macedonicus*. The new species can be differentiated from these Chinese and New Zealand species by elongated spores resembling those of *C. macedonicus*. The new species differs from *C. macedonicus* by smaller basidiomata with more intensely-coloured pileus surface, paler gills when young and its ecological preferences. The convergent morpho-anatomical similarities of *C. tobolensis* should also be noted to the more phylogenetically distant European *C. cesatii* and North American *C. croceitectus* (supplementary table FP918-1).

**Supplementary material**

FP918-1 Table: Differentiating characters of closely related *Crepidotus* species.

FP918-2 Maximum likelihood tree of *Crepidotus tobolensis* sp. nov. and closely related species. Analysis of the nrDNA ITS region was conducted using RAxML v. 8.1.2 (Stamatakis 2014) implemented in raxmlGUI v. 1.5b2 (Silvestro & Michalek 2012). *Crepidotus parietalis* was chosen as outgroup. Bootstrap support values ≥ 50 % are given at the nodes. The new species is indicated in bold, holotype species indicated with asterisk (*).
Dendryphiella stromaticola
**Dendryphiella stromaticola** Cantillo, Gusmão & Madrid, sp. nov.

**Etymology** Name refers to the presence of stroma.

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

On natural substrate: Colonies superficial, effuse, dark brown, releasing a yellow pigment in the substrate. Mycelium immersed, composed of smooth, subhyaline, septate, branched, 3–4.5 μm diam hyphae. Stromata pseudoparenchymatous, intraepidermal to erumpent, convex, black, composed of cells with textura globosa. Conidiophores macronematous, mononematous, emerging through stroma in loose groups of 3–5(–7) conidiophores, brown, wider at the base, slightly paler at the apex, thick, smooth or verrucose, erect, straight or slightly flexuous, septate, sometimes branched, up to 250(–290) μm high, 3–7 μm wide. Conidiogenous cells polytretic, integrated, terminal and intercalary, verrucose near the geniculate conidiogenous zones, with 1–3 pores, 26–37 × 3–6(–7) μm. Ramoconidia rare, cylindrical with rounded ends, yellowish brown, verruculose, 1-septate, 22.5–35 × 4–6.5 μm. Conidia cylindrical with rounded apex, truncate or blunt at the base, (1–)3-septate, yellowish brown, verruculose to verrucose, forming short chains, 20–35 × 4–6.5 μm, constricted at septa when older; loci thickened, darkened and refractive.

**Culture characteristics** — Conidia germinated on Water Agar (WA) within 24 h, germ tubes produced from apical and/or basal ends, mycelium hyaline, sparse. Colonies on PDA reaching 60 mm diam after 7 d (25°C/daylight cycle), cottony, dark grey, with regular margins, reverse black; diffusible pigments absent.

**Phylogenetic tree** inferred from Maximum likelihood and Bayesian analysis based on LSU nrDNA sequence data. ML Bootstrap support ≥ 75 % and BI values ≥ 0.90 are shown at the nodes. The alignment was performed with MAFFT v. 7 and the General Time Reversible model with Gamma distribution and invariant sites (GTR+G+I) was used as the best nucleotide substitution model. *Dendryphiella stromaticola* is marked in red.

**Typus. Brazil.** Rio Grande do Norte, Portalegre, on small branches of unidentified plant, S6°01'W37°59', 30 Apr. 2016, T. Cantillo (holotype HUEFS 239363, culture ex-type LAMIC 90/16, ITS and LSU sequence GenBank MK829079 and MK156678, MycoBank MB828657).

**Notes** — In *Dendryphiella*, an accurate morphological differentiation of certain species is difficult due to overlapping sizes of reproductive structures and the apparent lack of other taxonomically informative traits. Some species previously identified as *Dendryphiella* has been segregated in two genera using ecological, molecular and morphological characters: *Paradendryphiella*, with marine species (Woudenberg et al. 2013) and *Neodendryphiella* (Iturrieta-González et al. 2018). The blast analysis of the ITS sequence indicates a relatively close affinity of *Dendryphiella stromaticola* with *D. fasciculata* (GenBank MF399213, Identities = 89 %, no gaps), *D. paravinosa* (GenBank NR_154012, Identities = 89 %, no gaps) and of the LSU sequence with *D. variabilis* (GenBank LT963454, Identities = 97 %, no gaps); morphological differences with these species are mainly in the size of conidia and conidiophores, conidiophore aggregation and the presence of stromata. *Dendryphiella stromaticola* is also morphologically similar to *D. eucalyptorum* and *D. vinosa*, which also produces mostly 3-septate conidia. *Dendryphiella eucalyptorum* can be differentiated from *D. stromaticola* based on its smooth and smaller conidia (20–23 × 5–7 μm) and larger conidiogenous cells (20–40 × 6–10 μm). Phylogenetically, *D. stromaticola* appears distinct from the ex-epitype sequence of *D. vinosa* (NBRC 32669), but based on morphological characters, both species share many features such as size, colour and conidial morphology, distinguished only by the longer conidiophores in the latter species and the absence of stromata. It has been suggested by Crous et al. (2014) that the type species, *D. vinosa*, probably represents a species complex, and Iturrieta-González et al. (2018) segregated a new species, *D. variabilis*, previously identified as *D. vinosa* based mostly on molecular characters and the number of septa. However, molecular data in *Dendryphiella* are still scarce and available only for a few species, and so this genus requires further phylogenetic and taxonomic revision.

**Colour illustrations.** Portalegre, Rio Grande do Norte. Colonies on natural substrate, conidiogenous cells and conidia. Scale bars = 0.5 mm (colonies in natural substrate), 30 μm (conidia and conidiogenous cell).
Diaporthe fructicola
**Diaporthe fructicola** Minosh., T. Ono & Hirooka, *sp. nov.*

**Etymology.** Name refers to fruit, the substrate from which the ex-type strain was isolated.

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

Only the asexual morph formed on the surface of post-harvest passion fruit (*Passiflora edulis* × *P. edulis f. flavicarpa*). Conidiomata pycnidial, scattered to aggregated in small groups including two or three conidiomata, ampulliform to ellipsoidal, up to 490 µm wide, black, lacking necks, exuding creamy droplets from central ostioles. Conidial walls c. 57–104 µm thick, consisting of two layers; outer layer dark brown, medium brown, c. 8–16 µm thick, cells forming *textura angulares*; inner layer ocharaceous c. 38–68 µm thick, cells forming *textura globosa*. Conidiophores hyaline, smooth, straight to slightly sinuous, unbranched, (8–)13.5–21(–26.5) µm long, c. 1–2(–3) µm in diam. Alpha conidia aseptate, hyaline, smooth, biguttulate, fusiform to ellipsoidal, base truncate, (6–)9–14.5(–16.5) µm long, (4–)8–16(–20) µm wide. Beta conidia not observed.

Diaporthe fructicola CBS 296.67*

**Colour illustrations.** Passion fruit (*Passiflora edulis* × *P. edulis f. flavicarpa*) growing in Hahajima. Fruit rot of passion fruit; conidiomata on fruit; conidiophore and conidiogenous cells; alpha conidia; gamma conidia; colonies on PDA, OA and MEA. Scale bars = 1 mm, 200 µm and 100 µm (conidiomata), 10 µm (conidiophore), 5 µm (conidia).

**Culture characteristics.** After 3 d at 25 °C, colonies 58.5–60.3 mm (av. 57.6 mm). Colony surface on PDA covering with floccose mycelium, white to buff, formed in rosetaceous. On MEA covering aerial mycelium thin, buff to yellow. On OA surface olivaceous grey to buff, central velvet.

**Notes.** Four species of *Diaporthe* and *Phomopsis*, i.e., *D. eres, D. passiflorae, D. passifloricola* and *Phomopsis tersa*, have been reported on *Passiflora* spp. (Farr & Rossman 2018). *Diaporthe fructicola* has alpha and gamma conidia, whereas *D. eres, D. passifloricola* and *P. tersa* produce only alpha conidia (Lutchmeah 1992, Udayanga et al. 2014, Crous et al. 2016). Of the four species, *Diaporthe fructicola* is morphologically quite similar to *D. passiflorae* (Crous et al. 2012). However, the alpha and gamma conidia of *D. fructicola* are much longer than those of *D. passiflorae*. Based on a MegaBLAST search of NCBI s, GenBank nucleotide database, the ITS sequence of *D. fructicola* is 99 % similar to *D. aspalathi* (GenBank KT669842), *D. endophytica* (GenBank NR_111847), *D. phaselorum* (GenBank KP182390, etc.), *D. maseirevic* (GenBank KY110888, etc.), *D. terebinthifoili* (GenBank NR_111862, etc.), *D. novem* (GenBank NR_111855, etc.), *D. schini* (GenBank MF185331, etc.) and *P. asparagi* (GenBank JQ613999). In our five-loci phylogeny, *D. fructicola* was clearly distinct from the four species as a fully supported monophyletic clade. The results therefore indicate that *D. fructicola* is a distinct species.

**Phylogenetic tree of the combined ITS, TEF, TUB, HIS and CAL sequences**

Culture characteristics — After 3 d at 25 °C, colonies 58.5–60.3 mm (av. 57.6 mm). Colony surface on PDA covering with floccose mycelium, white to buff, formed in rosetaceous. On MEA covering aerial mycelium thin, buff to yellow. On OA surface olivaceous grey to buff, central velvet.

**Phylogenetic tree of the combined ITS, TEF, TUB, HIS and CAL MAFFT-aligned datasets obtained using maximum likelihood.** A heuristic search was performed in RAxML v. 0.6.0 with support at the nodes calculated using bootstrap analyses with 100 replicates. The new species is indicated by **bold** text and highlight, *"* ex-type strain. The ML bootstrap values ≥ 75 % are indicated at the nodes. Fully supported branches are indicated with thickened lines. *Diaporthe ambigu* (CBS 114015) and *D. sclerotoides* (CBS 296.67) were used as outgroup.

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Fungal Planet description sheets 409
Entoloma nipponicum
Entoloma nipponicum T. Kasuya, Nabe, Noordel. & Dima, sp. nov.

Etymology: The epithet refers to Nippon (Japan), the origin of the new species.

Classification — Entolomataceae, Agaricales, Agaricomycetetes.

Basidiomata small, collybioid. Pileus 10–50 mm diam, initially hemispherical to hemispheric-convex expanding to convex to planoconvex with a depressed to umbilicate centre, not hygrophanous, not translucently striate, light orange to greyish red with a darker centre, often with lilac to dark blue tinge near margin, entirely fibrillose or minutely squamulose, sometimes radially splitting with age. Lamellae subdistant, white or cream-colour at first, then flesh coloured, edges serrulate and flocculose, concolorous or sometimes with dark blue tinge. Stipe 25–60 × 3–5 mm, almost cylindrical, sometimes slightly thickened at base, rarely somewhat twisted, pale orange or whitish to grey towards base, sometimes with slight blue-green tinge, smooth, almost polished, white tomentose at base. Context thin, concolorous with surface, odour and taste indistinct. Basidiospores 8–11(–12) × 6.5–8 μm (n = 50, mounted in water), Q = 1.07–1.42, 6–9-angled in side view. Basidia 25–39 × 7–10 μm (excluding sterigmata), clavate, 4-spored, without clamp connections. Lamella edge of serrulatum-type. Cheilocystidia 32–63 × 7–18 μm, clustered densely, cylindrical to subfusiform or sublageniform, sometimes septate, often with violaceous blue, granular intracellular pigment. Pleurocystidia absent. Pileipellis a trichoderm composed of hyphae 4–10 μm across with inflated terminal elements, 15–30 μm; intracellular pigments pink to brown with violet tinges. Stipitipellis a cutis of 4–8 μm wide hyphae, made up of cylindrical hyphae with granular dark blue intracellular pigment, terminal cells often differentiated, clavate, particularly in apical part. Clamp connections absent.

Habitat & Distribution — Growing solitary, scattered or gregarious on the ground among leaf litter or grass. Known only from Japan.

Typus. JAPAN, Hyogo Pref., Kobe-shi, Kita-ku, Yamada-cho, Shimo-tanigami, N34°46’2.89” E135°9’53.11”, among leaf litter in mixed forest of Cryptomeria japonica and Acer spp., 29 June 2016, M. Nabe (holotype TNS-F-70747, ITS and LSU sequences GenBank MK693223 and MK696392, MycoBank MB830303).

Additional material examined. JAPAN, Chiba Pref., Tonoshō-machi, Awano, among leaf litter in bamboo grove (Phyllostachys spp.), 7 July 2015, T. Kasuya, TNS-F-70748, ITS and LSU sequences GenBank MK693222 and MK696391; Kyoto Pref., Kyoto-shi, Kita-ku, Kyoto University Kamigamo Experimental Station, among leaf litter of Sequoia sempervirens, 13 June 2018, M. Nabe, TNS-F-70748; Nara Pref., Kashiwara-shi, Kashiwara-ji, among leaf litter in bamboo grove (Phyllostachys spp.), 17 June 2018, M. Nabe, TNS-F-70749; Okayama Pref., Shouo-cho, Oka, among grass, 8 July 2017, M. Nabe, TNS-F-70751.

Notes — Entoloma nipponicum forms a distinct clade in our phylogram where it clusters in the serrulatum clade of subg. Cyanula, together with species from Europe, China and North America. It is characterised by a serrulatum-type, blue pigmented lamella edge. Distinctive characters of E. nipponicum are the rather light coloured fruiting bodies with predominantly yellow-orange to greyish red pileus. As such it reminds of Entoloma catalaunicum from Europe, described with a pinkish red pileus and blue stipe, which, however, comes in a distant phylogenetic position outside the serrulatum clade. Blue tinges, so eminent in the European E. serrulatum and E. quercuddleda, are almost lacking in E. nipponicum. Entoloma subcaesiocinctum from China has a browner coloured pileus and a fibrous stipe (He et al. 2017). Entoloma subserrulatum from North America has a more yellowish grey pileus, and a pallid, almost white stipe (Noordeloos 2008).

Phylogenetic tree derived from Maximum Likelihood analysis based on nrITS1-5.8S-ITS2 data. Analysis was performed in PhyML v. 3.0 (Guindon et al. 2010) using the non-parametric Shimodaira-Hasegawa version of the approximate likelihood-ratio test (SH-aLRT) and the GTR+I+Γ model of evolution. ML bootstrap support values > 60 % are shown at the nodes. Sequences of the new species generated for this study are highlighted in bold.

Color illustrations. Japan, Hyogo Pref., Kobe-shi, Kita-ku, Yamada-cho, Shimosan-tanigami, type locality. Holotype TNS-F-70747: pileipellis; cheilocystidia; spores; basidiomata. Scale bars = 1 cm (basidiomata), 10 μm (pileipellis, spores and cheilocystidia).
Entoloma ekaterinae
Entoloma ekaterinae O.V. Morozova, Noordel., K. Nara, Dima & Brandrud, sp. nov.

**Etymology.** Named in honour of Ekaterina Malysheva, Russian agaricologist, known particularly as an investigator of the mycobiota of Far East and collector of the type specimen of this species.

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

**Basidiomata** small to medium-sized, collybioid. Pileus 10–25 mm diam, conico-convex soon expanding to plano-convex with flat to slightly depressed centre, with deflexed then straight margin, hygrophanous, translucently striate almost up to the centre, at first densely covered with dark blue squamules (20D5–7, 20E5–7, 21D5–7, 21E6–8; Komerup & Wanscher 1978), moving apart with age, showing light greyish blue background between them and stripes (21B3–4, 21C3–5). Lamellae moderately distant, adnate-meri margine, ventricose, whitish, becoming pink, with entire concolorous edge. Stereum 30–70 × 1.5–2 mm, cylindrical, smooth, polished, dark blue, concolorous with the pileus (20D5–7, 20E5–7, 21D5–7), white tomentose at base. Context white, greyish under the surface. Smell indistinct, taste not reported. Basidiospores 8–10(–11) × (5.5–)6.5–(7–8) μm, Q = (1.2–)1.4–1.5(–1.6), heterodiametrical, with 5–6 angles in side-view, relatively simple. Basidia 25–31 × 7.5–12.5 μm, 4-spored, narrowly clavate to clavate, clampless. Cheilocystidia 19–39 × 5–18 μm, broadly clavate, subglobose or sphaeropedunculate, sometimes septate, with several cylindrical or lageniform cells, not pigmented, forming sterile lamellae edge. Pileipellis cutis of cylindrical hyphae 2–7 μm broad with bundles of rising hyphae with globose to broadly clavate terminal elements (26–39 × 18–25 μm), forming squamules and central disk of pileus. Clamp connections absent.

**Habitat & Distribution —** In small groups on soil in Quercus mongolica forest and along the road in mixed forest of Quercus mongolica, Acer mono, Tilia amurensis, Pinus koraiensis, or in perennial herbaceous shrubs dominated by Fallopia japonica, some other Poaceae and Asteraceae plants. Known from Russia (Far East) and Japan.

**Typus.** Russia, Primorsky Krai, Sikhote-Alin Nature Reserve, vicinities of Blagodatnoye, N44.956033° E136.535133°, 15 Aug. 2013, E. Malysheva (holotype LE312053, ITS and LSU sequences GenBank MK693215 and MK733926, MycoBank MB830279).

**Additional materials examined.** Japan, Fuji Mt, Gotenba, Shizuoka prefecture, N35.339128° E138.791317°, 15 Sept. 2000, K. Nara (TNS-F-88377, as Entoloma sp. No242 (Kinoshita et al. 2012), ITS and LSU sequences GenBank AB692002 and AB692011). – Russia, Primorsky Krai, Sikhote-Alin Nature Reserve, vicinities of Maisa, N45.238833° E136.511117°, 22 Aug. 2013, O. Morozova (LE312054, LE312055, ITS and LSU sequences GenBank MK693216, MK693217 and MK733927, MK733928).

**Notes — Entoloma ekaterinae** is characterised by the entirely delicate-blue basidiomata, by the initially uniformly coloured pileus, which becomes distinctly translucently striate with dark squamules on a paler greyish blue background with age, and the trichodermal nature of the squamules, composed of globose elements. Microscopically, the sterile lamella edge composed of dense layer of clavate to subglobose and sphaeropedunculate cystidia is distinctive but, especially, in young specimens they can be mixed with cylindrical and lageniform cystidia. *Entoloma subcaesiellum*, described from the same region, is very similar morphologically, differing mainly in pileipellis structure. According to the molecular data, *Entoloma ekaterinae* belongs to the /chalybeum subclade of the /Cyanula clade.

Phylogenetic tree derived from a Maximum Likelihood analysis based on nrITS1-5.8S-ITS2 data. Analysis performed in PhyML v. 3.0 (Guindon et al. 2010) using the non-parametric Shimodaira-Hasegawa version of the approximate likelihood-ratio test (SH-aLRT) and the GTR+I+Γ model of evolution. ML bootstrap support values > 60 % shown at the nodes. Sequences of the new species generated for this study are highlighted in **bold**.

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Colour illustrations. Russia, Primorsky Territory, Sikhote-Alin Nature Reserve, Maisa River. Spores, cheilocystidia, basidiomata (from holotype); basidioma (LE312054). Scale bars = 1 cm (basidiomata), 10 μm (spores and cheilocystidia).

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Entoloma erhardii
Entoloma erhardii  Noordel., Dima, Svetash., Læssøe & Kehlet, sp. nov.

**Etymology.** Named in honour of Erhard Ludwig (1938–2019), mycologist and master painter, remembered for his monumental Pilzkompendium.

Classification — Entolomataceae, Agaricales, Agaricomycetes.

*Basidiomata* medium-sized, collybioid. *Pileus* 10–35 mm diam, conico-convex soon expanding to plano-convex with convex or slightly umbilicate centre, with deflexed then straight or reflected margin, not hygrophanous, not transluculently striate or in the cap margin only, initially uniformly coloured blackish blue, blackish indigo (19F6–7, 19F5–8; Kornerup & Wanscher 1978), discolouring to bluish grey (18E3–5, 19E3–5) or with a violet tinge, minutely radially fibroellipsoid-tomentose all over, metallic-shining when drying. *Lamellae* moderately distant, adnate-emarginate, segmentiform to narrowly ventricose, white, contrasting with the pileus surface, becoming pink, with irregular, concolous or brown edge. *Stipe* 30–70 × 1.5–3 mm, cylindrical, sometimes compressed with longitudinal groove, smooth, polished or minutely longitudinally striate, concolous with pileus or paler (up to 19D3–5, 19E5–7) or tinged in green, white tomentose at base. *Context* white, greyish under the surface. *Smiell* distinct, like flowers, pleasant, taste not reported. *Basidiospores* (9–)9.5–10(–12) × (5.5–)6–5.5(–7) µm, Q = (1.4–)1.5(–1.7), heterodiametrical, with 5–6 angles in side-view, relatively simple. *Basidia* 36–49.5 × 9.5–10.5 µm, 4-spored, narrowly clavate to clavate, clamped. *Cheilocystidia* 33–85 × 5–14.5 µm, cylindrical, lageniform, fusiform or irregularly clavate, sometimes septate with or without brown intracellular pigment. *Pileipellis* cutis with transition to a trichoderm of cylindrical to slightly inflated hyphae 10–20 µm wide with inflated terminal elements and dark intracellular pigment, brownish in KOH. *Caulocystidia* absent. *Clamp connections* absent.

**Habitat & Distribution** — In small groups on soil in alpine and subalpine grasslands and also in damp woodland on rich black soil. Known from Russia (Caucasus) and Denmark.

**Typus. Russia**, Karachevo-Cherkesia Republic, Teberda Nature Reserve, Klukhor pass, N43.252741° E41.857758°, asi ± 2700 m, 23 Aug. 2012, T. Svetasheva (holotype LE312051, ITS and LSU sequences GenBank MK693218 and MK733924, MycoBank MB830278).

**Additional materials examined. Denmark**, Sjælland, Eskebjerg Vester-lyng, Maereskov, 22 July 2012, T. Kehlet, DMS-450924, C, ITS sequence GenBank MK693220; Sjælland, Helvigstrup Skov, 1 Sept. 2014, T. Kehlet & T. Læssøe, DMS-675991, C, ITS sequence GenBank MK693221. — Russia, Karachevo-Cherkesia Republic, Malaya Khatipara Mt, N43.445828° E71.12153°, asi ± 2500 m, 16 Aug. 2009, O. Morozova, LE312052, ITS and LSU sequences GenBank MK693219 and MK733925.

**Colour illustrations.** Russia, Karachevo-Cherkesia Republic, Teberda Nature Reserve, Klukhor pass, type locality. Spores, cheilocystidia, basidiomata (from holotype; basidiomata (DMS-675991). Scale bars = 1 cm (basidiomata), 10 µm (spores and cheilocystidia).

Notes — *Entoloma erhardii* is nested within the *chalybeum* subclade of the Cyanula clade (data not shown). Members of the *chalybeum* subclade are characterised by the entirely blue basidiocarps with not or hardly striate pileus, lamellae with sterile edge, and polished or at most finely striate stipe. *Entoloma erhardii* is distinguished by rather uniformly coloured bluish black not transluculently striate pileus with contrasting white lamellae, concolous or greenish stipe and mostly sterile lamella edge with differentiated cheilocystidia. It can be distinguished from *E. chalybeum* by the darker basidiomata, white lamellae (lamellae of *E. chalybeum* are bluish), and smaller spores (Noordeloos 1992). The macro- and microscopical features of *E. erhardii* resemble those of *E. corvinum*, except for the smaller spores. Current research on the phylogeny of *Cyanula* species reveals that *E. corvinum* based on a morphological species concept covers several distantly related more or less cryptic taxa. *Entoloma porphyrogriseum* is almost pure black in youth, can be differentiated by the strong brownish or purplish brown discoloration when maturing, initially distinctly fibrillose stem (Noordeloos 1987), and is phylogenetically distant (data not shown).

See tree in Fungal Planet 922.
Hygrocybe rodomaculata
Hygrocybe rodomaculata A. Barili, C.W. Barnes & Ordoñez, *sp. nov.*

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

Classification — Hygrohoraceae, Agaricales, Agaricomycetes.

*Basidiomata* stipitate, pileus 45 mm diam, conical to flattened, with umbo, surface glabrous, dry, sericeous, margin entire, sinuose, undulate, rimose, fragile texture, whitish with orange and pink tones towards the centre. *Lamellae* broadly adnate, thick, ventricose, distant, with decurrent teeth or emarginate, anastomosed, sometimes forked, ochre yellow with whitish parts, edge entire. *Stipe* central, 120 × 10 mm, whitish with pink spots towards the apex, ochre at the centre and whitish at the base, cylindrical sinuose, hollow, fragile, glabrous. *Pileipellis* as a cutis, short cylindrical hyphae 52 × 8 µm with simple septa, *clamp connections* present. *Gill trama* irregular. *Basidia* 41–70 × 4–9 µm, claveate, very elongate, 4-spored, sometime with basal clamp, stigmata elongate 5.5–9.5 µm. *Basidiospores* 7.5–10 × 5–7 µm, mainly ellipsoid, some oblong, smooth, hyaline, cyanophilic, non-amyloid, weakly metachromatic. *Q* = 1.3–1.7.

**Habitat** — Gregarious on the ground in humid montane forest.

**Typus.** Ecuador, Zamora Chinchipe province, Yacuri National Park, alt. 3234 m, May 2015, A. Barili (holotype QCAM5904, ITS and LSU sequences GenBank MK684225 and MK684352, MycoBank MB830309).

Notes — *Hygrocybe rodomaculata* belongs to the section *Coccinea*, considering pink as a discolouration of the characteristic red pileic surface of the group, with a dry or somewhat viscid stipe (Boccardo et al. 2008). The closest species based on morphological characters, according to Boertmann (2008) and Boccardo et al. (2008), is *H. calyptriformis*. However, it differs from *H. rodomaculata* by the pointed umbo, absence of yellow colour of the stipe and is non-radicate. In addition, *H. calyptriformis* belongs to the section *Microspore* whose distinctive feature is spore dimensions below 9 µm, while *H. rodomaculata* exceeds this size. The closest species determined by DNA sequence analysis was *H. reidii*, which is distinguished mainly by not having an umbo, by the slightly felted, scaly and uniform colouration, gills more or less decurrent, a proportionally shorter stipe, slightly smaller basidiospores, and characteristic honey odour.

A megablast search of NCBI GenBank nucleotide database using the full ITS sequence showed that the holotype of *H. rodomaculata* was distinct from other species presently available for the genus. The first five hits were *Hygrocybe* aff. *reidii* (GenBank KF291196), *Hygrocybe* sp. (GenBank HM020688), *Hygrocybe* sp. (GenBank HM020687), *Hygrocybe* sp. (GenBank HM020686) and *H. pucicia* (GenBank HM020682); all with Identities = 564/627 (90 %) and 26 gaps (4 %). The top five sequences from the blast search aligned perfectly within the ITS region. The ITS phylogenetic tree includes the top 20 megablast hits for the *H. rodomaculata* sequence.

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 the Corrected Akaike Information Criterion (AICc). Hygrocybe reidii (GenBank KF291194) is the outgroup based on the megablast search results. Bootstrap support values > 70 % are given above branches. The phylogenetic position of *H. rodomaculata* is indicated in bold. The species name is followed by the GenBank accession number, and when the country of origin was indicated, the three letter United Nations country code was used, in order of appearance: USA: United States of America; ECU: Ecuador; GBR: United Kingdom. Samples ending with KEW are from Kew Royal Botanic Gardens, England.

**Colour illustrations.** Yacuri National Park, Ecuador. Basidiocarp; non-mature basidia with basal clamp; basidia. Scale bars = 10 µm.
Inocybe grammatoïdes

Etimology. Name refers to its resemblance to Inocybe grammata.

Classification — Incybaceae, Agaricales, Agaricomycetes.

Basidiomata agaricoid and stipitate. Pileus 15–55 mm, at first conical-campanulate, then convex to plano-convex, broadly umbo-borate to subumbonate, slightly hygrophanous; margin straight, regular to hardly wavy with age, fissurate at times, surface usually covered by a dense whitish velvellites; colour pinkish grey (Mu 5YR 5/2, 6/2) when young or moistened, to light grey or very pale brown (Mu 10YR 7/1-3) when drying; uniform; surface radially fibrillose, smooth, not rimose towards the margin, sticky when humid, often agglutinating soil remains. Lamellae moderately crowded (L = 34–40; I = 1–2), adnexed to emarginate, ventricose, initially whitish, becoming pale grey to beige, then light brown, edge paler to concolorous with age, finely crenulate. Stipe 30–65 × 5–10 mm, straight to curved towards base, cylindrical, clavate to subbulbous, but never distinctly bulbous to marginately bulbous; colour often distinctly pinkish (Mu 5YR 6/3–4) at the apex or upper half, whitish becoming beige to ochraceous (Mu 10YR 8/2; 7/3) towards the lower half with age or when handled; surface densely pruinose at the upper half, becoming sparsely pruinose towards the base. Cortina not seen. Context fibrose, whitish, pinkish at the upper part of the stipe. Smell intense and penetrating, aromatic, reminiscent of elder flowers (Sambucus nigra), sometimes with a subaspermic component, taste not recorded. Spores (7.3–)7.4–8.7–10.1–(10.8) × (4.5–)5.1–5.8–6.6–7.1 (µm), Qm = (1.2–)1.3–1.5–1.7–1.9 (n = 236 / N = 4), heterodiametric, polygonal-subrectangular under the optical microscope (‘entolomatoïd’), at times provided with 1–5 low knobs (0.5 µm high), yellowish, apicula distinct. Basidio 27–37 × 7.5–10 µm, 4-sored, rarely 2-sored, clavate, sterigmata 3.5–6 µm long. Lamella edge heterogeneous, composed by dispersed protruding chelioctydia mixed with abundant hyaline, clavate paracystidia. Pleurocystidia abundant. (49.1–)55.9–66.7–78–79 (–88) × (10.4–)11.2–16.3–22.3–25 µm, Qm = (2.67–)2.87–4.2–5.38–6.05 (n = 118 / N = 3), narrowly utriform to fusiform, rarely sublageniform, hyaline, base often pedicellate, crystalliferous at the apex, walls (1–)1.1–1.6–2.23–3.01 (µm thick, pale to moderately yellowish in 10 % NH4OH. Chelioctydia similar in size and shape to pleurocystidia. Stipitipellis a cutis bearing numerous caulocystidia, more scattered towards the base, similar in shape and size to hymenial cystidia, mixed with clavate to broadly clavate hyaline paracystidia. Pileipellis a cutis formed by parallel cylindrical cells, 3–8 µm wide, broader (~18 µm) towards a hardly differentiated subcutis, showing minute pale intracellular pigment, slightly gelified. Clamp connections abundant in all tissues.

Habitat & Distribution — Gregarious in both basic and acidic soils; found in natural environments, such as deciduous humid forests.

Colour illustrations. Spain, Asturias, Ribadeveda, Pimiangio, in Quercus ilex subsp. ilex forest, same locality as the holotype was collected. From top to bottom: basidiospores; pleurocystidia; caulocystidia; basidiomata (bottom right). Scale bars = 10 µm (spores), 50 µm (cystidia).

Notes — Colour codes are taken from Munsell (1994), terminology follows Kuyper (1886) and Vellinga (1988). Inocybe grammatoïdes differs from I. grammata in the absence of a marginate bulb in the stipe, which may be cylindrical, claviform or sometimes subbulbous; most collections of I. grammatoïdes show more slender cystidia (Qm = 4.2; Qm = 3.7 in I. grammata) with a thinner wall (e0 = 1.6; e2 = 2.5 in I. grammata); the sporal characteristics of both species appear overlapping. According to the data, I. grammatoïdes behaves as a mesopholic species, usually associated with Quercus (Fagaceae) and other broad-leaved trees in humid and warm environments; part of the records of I. albodisca in Moënne-Loccoz et al. (1990), seem to correspond to I. grammatoïdes (record n° 87114, Tab.151 bottom left). Inocybe grammata is a common species in boreal and circumboreal areas, associated with coniferous and birch forests in Europe and Eastern North America; it extends to the hyperhumid mountain enclaves of southern Europe, often associated with birch, but also with conifers. Inocybe albodisca, originally collected from coniferous forests in North Elba (Essex County, Eastern USA), appears to correspond morphologically to I. grammata (Moënne-Loccoz et al. 1990, Vauras 1997, Matheny pers. comm.).

Genetically, I. grammatoïdes is closely related (99 % ITS rDNA similarity) to the type specimen of I. acerifolia (WTU:AU10493, GenBank NR_153186), although it probably represents an independent taxon because of the lack of significant phylogenetic support for a monophyletic origin and, morphologically, by the different spores, the latter containing distinct knobs. In addition, I. grammatoïdes has a 98 % BLAST identity with European sequences of I. grammata (Osmundson et al. 2013, Vauras & Larsson 2016 unpubl. data, as well as those produced for the present work from specimens AH 22127, AH 15662 and AH 47717). The isotype of I. permutica and a paratype of I. grammata var. chamaesalicis are not significantly different from other sequences of I. grammata. Besides, several sequences of I. grammata coming from North America probably represent different species (see phylogram).

Supplementary material

FP925-1 Table: Collections used in the molecular phylogenetic analyses, with voucher information and GenBank accession numbers for ITS and LSU regions. The GenBank accessions of sequences generated in this study are in bold.

FP925-2 Collections studied by the authors are indicated in bold in the phylogenetic tree for ITS and LSU sequences; type collections are annotated. Country of origin for each collection is given using ISO 3166/2 country codes.

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Kazachstania molopis Gouliamova, R.A. Dimitrov, sp. nov.

Etymology. mo-lo-pis, referring to the host beetle Molops piceus (Carabidae) from which two new strains were isolated.

Classification — Saccharomycetaceae, Saccharomycales, Saccharomyces.

After 7 d at 25 °C in 5 % glucose broth, the cells are ovoid to ellipsoidal, 2–4 × 4–7 μm, occurring singly or in clusters. Asexual reproduction occurs by multilateral budding. Poorly developed pseudohyphae can be present. After 7 d at 25°C on YPGA (yeast extract, peptone, glucose agar) the colony is creamy, butyrous, glistening, convex and with an entire margin. Dalmau plate culture after 10 d on morphology agar did not show pseudohyphae or true hyphae. Sexual reproduction was detected on yeast extract, malt extract, peptone, glucose (YM) and McClary acetate agar. Conjugation between independent cells was observed. Ascii contained one to four globose ascospores.

Fermentation — Glucose and galactose are fermented. Sucrose, maltose, lactose and raffinose are not fermented.

Carbon assimilation — D-glucose, D-galactose, L-sorbosé, D-ribose, sucrose, maltose, α,α-trehalose, α-methyl-D-glucoside, cellobiose (delayed), salicin, arbutin (delayed), melezitose, soluble starch, glycerol, ribitol, D-gluclot, D-mannitol, D-glucono-1,5-lactone, 2-keto-D-gluconate (delayed), ethanol, quinic acid are assimilated. D-xylene, D-arabinose, D-glucosamine, L-arabinose, L-ribose, melibiose, melibiose, raffinose, lactose, inulin, meso-erythritol, myo-inositol, xylitol, D-glucanote, D-gluconate, D-galacturonate, succinate, citrate, DL-lactate, methanol, propane 1,2 diol, butane 2,3 diol, galactonic acid, galactitoll, galactonic acid and saccharate are not assimilated.

Nitrogen assimilation — Nitrate, nitrite, ethylamine, creatine, creatinine, L-lysine, cadaverine and imidazole are not assimilated.

Other tests — Starch formation test is negative. Growth in 10 % is negative. Growth in 0.01 % is negative. Growth in 50 % glucose is negative. Urea hydrolysis and DBB reaction tests are negative. Growth without all vitamins is test is negative. Growth at 25 °C is positive. Growth at 30 °C is negative.

Type species. BULGARIA, Nature park Zlatni Pyasatsi from the gut of the beetle Molops piceus (Carabidae, Coleoptera) collected in oak forest under fallen tree trunk, 23–24 Apr. 2009, D. Gouliamova (holotype IMB 4R preserved in metabolically inactive state, ex-type cultures NBIMCC 9029 and CBS 12448; ITS and D1/D2 LSU sequences GenBank KC118123 and KC578454, MycoBank MB802456).

Additional material examined. BULGARIA, same details as type, IMB4 = NBIMCC 9028 = CBS 12566, ITS and D1/D2 LSU sequences GenBank HM627145 and HM627092.

Colour illustrations. Krushuna Waterfalls, Bulgaria. Molops piceus (Photo credit: Ruslan Panin, http://carabidae.org); bottom to top: morphology of cells of Kazachstania molopis IMB4R in 5 % glucose broth after 1 wk; ascis with ascospores in YM agar. Scale bars = 5 μm (cell morphology), 10 μm (ascospores).

Notes — In our previous article we determined the lower and upper bounds for the range of species discrimination in the Kazachstania clade based on sequence identity value (SI) and distance between physiological profiles (DPP); SI (98.5–83.7 %) and DPP (8–18) (Dimitrov & Gouliamova 2019). A phylogenetic analysis of combined ITS and LSU sequences placed the new strain IMB 4R on a separate branch between K. vitcola and K. kunashirensis. Pairwise analysis of sequences in a multiple alignment showed that the new strains show 87.95 % identity (847 identical nt., 90 nt subst., 123 gaps) with K. kunashirensis and 85.49 % identity (884 identical nt., 137 subst., 138 gaps) with K. vitcola. The new strains can be differentiated from both K. kunashirensis and K. vitcola based on 14 common physiological characteristics. The new species can assimilate L-sorbosé, D-ribose, sucrose, maltose, α-methyl-D-glucoside, cellobiose, salicin, arbutin, melezitose, soluble starch, ribitol, D-gluclot, 2-keto-D-gluconate and quinic acid. It cannot grow in the presence of 10 % NaCl. In addition the new species can be differentiated from K. vitcola based on its ability to assimilate α,α-trehalose and its inability to assimilate D-gluconate and growth in the presence of 15 % NaCl. The new species differ from K. kunashirensis based on its inability to assimilate L-lysine. The obtained SI and DPP data for the new strain IMB 4R fall within the limits for species discrimination of the Kazachstania clade. Thus, based on our results we propose a new yeast species, Kazachstania molopis, to accommodate Bulgarian yeast strains IMB 4R and IMB 4 (100 % SI in both ITS and LSU sequences). So far, only three species of Kazachstania were isolated from insects. A strain of K. spencerorum was isolated from larva of a Psychidae moth (Lepidoptera) collected from an acacia tree (South Africa) (CBS database). Three strains of K. intestinalis were isolated from the gut of the passable beetle, O. disjunctus, collected from rotten oak tree (Virginia, USA) (Suh & Zhou 2011). Recently two strains of K. chrysolinae were isolated from the guts of Chrysolinae polita in Bulgaria (Gouliamova & Dimitrov unpubl. data).

Phylogenetic tree obtained by the analysis of combined ITS and LSU rDNA sequences of Kazachstania molopis IMB 4R and related species using a neighbour-joining method (Kimura two-parameter model; MEGA v. 7; 100 bootstrap replicates). Kazachstania humilis and K. pseudohumilis represent an outgroup species. GenBank accession numbers of ITS and LSU rDNA sequences are presented on the tree.

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Leucosporidium himalayensis S.M. Singh, Roh. Sharma & Shouche, sp. nov.

Etymology. Name reflects the Himalaya, the place where this fungus was collected.

Classification — Leucosporidiaeae, Leucosporidiales, Incertae sedis, Microbotryomycetes.

Yeast colonies on SD agar Petri dishes are creamy-white, raised, margin entire. In external appearance, the colonies have a glabrous texture. Cells are subglobose to ovoid, 2–5 µm, occurring singly and budding is mostly polar, occurring frequently and repeatedly from the site of the primary budding scar. Sexual reproduction was not observed. Pseudohyphae formation absent. Growth occurred at 15 °C which is very similar to the primary habitat of this strain. Optimum growth was observed after 10 d. The following compounds are not assimilated: D-lactose, D-maltose, D-saccharose, L-arabinose, Calcium-2-keto-gluconate. The following compounds are assimilated: D-xylitol, Adonitol, Methyl-Alpha-D-Glucopyranoside, D-cellobiose, D-galactose, D-raffinose, D-trehalose, Glycerol, Inositol, Sorbitol, Xylitol. Growth occurred at 15 °C which is very similar to the primary habitat of this strain. Optimum growth was observed after 10 d. The following compounds are not assimilated: D-lactose, D-maltose, D-saccharose, L-arabinose, Calcium-2-keto-gluconate. The following compounds are not assimilated: D-lactose, D-maltose, D-saccharose, L-arabinose, Calcium-2-keto-gluconate. The following compounds are not assimilated: D-lactose, D-maltose, D-saccharose, L-arabinose, Calcium-2-keto-gluconate. The following compounds are not assimilated: D-lactose, D-maltose, D-saccharose, L-arabinose, Calcium-2-keto-gluconate. The following compounds are not assimilated: D-lactose, D-maltose, D-saccharose, L-arabinose, Calcium-2-keto-gluconate.

Culture characteristics — On CMA the colonies are white, round, margin entire, ± 0.5 mm after 10 d.

Habitat — Powderly windblown dust on glaciers (Cryococietes).

Distribution — India (Chhota Shigiri glacier, Gramphu-Batal-Kaza Rd, Himachal Pradesh).

Typus. INDIA. Gramphu-Batal-Kaza Road, Chandra river basin, Pir Pinjal range, Lahul valley, Himachal Pradesh, cryocones, 4 Aug. 2015, P. Sharma & S.M. Singh MCC 1733 (holotype RNF079 as metabolically inactive culture, ITS and LSU sequences GenBank MK601695 and MK601698, MycoBank MB823364).

ITS

Leucosporidium himalayensis

Leucosporidium fragarium CBS 8620 (AF444629)
Leucosporidium creatinivorum CBS 5930 (AF444495)
Leucosporidium scottii CBS 6291 (AF444527)
Leucosporidium muscorum CBS 131409-E2A-C3-Il-lev (JN197600)
Leucosporidium fragarium CBS 6264 (AF444530)
Leucosporidium golubevii PYCC 5759T (AY129287)
Leucosporidium intermediate CBS 7226 (AF444564)
Leucosporidium kansaivy VKM Y 2837T (AY213000)
Rhodotorula nothofagi CBS 8166 (AF444537)

Notes — An initial BLASTn similarity search using the LSU sequence of the ex-type culture with the NCBI nucleotide database showed the highest similarity to Leucosporidium fragarium CBS 6254 (GenBank NG_058330; 99.5% identity, 97% query cover) followed by Sampaiozyma ingeniosa CBS 4240 (GenBank NG_058396; 96.60% identity, query coverage 96%). The BLASTn similarity search of the ex-type ITS sequence with NCBI database showed the highest similarity to Leucosporidium fragarium CBS 6254 (GenBank NR_073287; 94.45% identity, 99% query coverage) followed by Leucosporidium drummii CBS 11562 (GenBank NR_137036; 95.02% identity, 99% query coverage). The neighbour-joining (NJ) phylogenetic analyses of ITS and LSU rRNA regions was done using sequences of other species of Leucosporidium. The combine phylogenetic tree topology of both regions clearly showed that strain RNF079 is novel.

Phylogenetic relationship of Leucosporidium himalayensis with other members of the genus based on a neighbour-joining tree of ITS and LSU sequences using MEGA v. 7.0.21. The bootstrap values of above 50% are given at the nodes using 1,000 replications.

Colour illustrations. India, Himachal Pradesh, Chhota Shigiri glacier, Chandra river basin, Lahul valley. Yeast cells at 100× under phase contrast and light (CMA after 15 d); yeast cells at 40× (SDA after 15 d). Scale bars = 5 µm.
Lycoperdon vietnamense
**Fungal Planet 928 – 19 July 2019**

**Lycoperdon vietnamense** Rebriev, A.V. Alexandrova, sp. nov.

*Etymology.* Name refers to the country where the type specimen was collected.

*Classification.* Agaricaceae, Agaricales, Agaricomycetes.

Basidiomes turbinate, 0.5—1.5 cm high and 1.5—2.3 cm broad, with upper surface ± flattened, dehiscing by a ragged roundish or sometimes slit-like opening. *Exoperidium* of white crowded spines up to 0.5 mm in upper part united by their tips into persistent stellate groups, fine felty material present between the spines; spines falling away at maturity leaving an inconspicuous reticulate pattern on endoperidium. *Endoperidium* light-brown. *Gleba* brown or concolorous with subgleba. *Subgleba* prominent, cellular, olive-brown, occupying up to 1/2 of the basidiome, in age separated from the gleba by a line (an apparent diaphragm). *Diaphragm* well developed. *Basidiospores* globose, pale brown, 2.8—3.3 µm, verrucose in LM and with robust conic spines 0.3—0.5 µm in SEM, with stumps of a pedicel up to 1 µm. *Capillitium* abundant, 2.5—3.5(-4) µm diam, poorly branched, sometimes slightly swollen at rare septa, light brown, with pores up to 0.5 µm. *Paracapillitium* scanty developed.

*Ecology & Distribution.* The specimen was found on soil in tropical open deciduous forest, in group of three basidiomes. Until now the known distribution is restricted to Vietnam.

**Typh. VIETNAM, Đắk Lắk Province, Buôn Đôn District, Krông Na commune, Bản Đôn, Yok Đôn National Park, alt. 196 m, N12°56'24" E107°43'31", margin of tropical open deciduous forest, on soil, 10 May 2014, A.V. Alexandrova (holotype LE 314844, ITS sequence GenBank MH468767, MycoBank MB826727).

Notes — *Lycoperdon vietnamense* belongs to *Lycoperdon* subg. *Vascellum* by having a diaphragm. It is characterised by the verrucose spores, abundantly septate eucapillitium and stellate-echinulate exoperidium. Morphologically, it is close to *L. curtisi* (= *L. wrightii*) which has a stellate-echinulate exoperidium and spinulate spores, but the latter differs in having a poor capillitium. *Lycoperdon qudenii* differs in having larger spores with long pedicels as well as a furfuraceous exoperidium. The more common *L. pratense* has larger, finely ornamented spores, a poorly developed capillitium and a non-stellate exoperidium. Based on the ITS rDNA phylogenetic analyses, *L. vietnamense* clusters in the *Vascellum* clade, close to *L. pratense* and *L. curtisi*.

**Colour illustrations.** Vietnam, Yok Đôn National Park, tropical open deciduous forest. Matured basidiome; peridium with areolate pattern; basidiospores and capillitium with pores in LM; basidiospores and paracapillitium in SEM; basidiospores, capillitium and paracapillitium under SEM. Scale bars (from top to bottom) = 2 mm, 1 mm, 10 µm, 2 µm, 3 µm.

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**ITS rDNA phylogenetic tree obtained with MrBayes v. 3.2.6 under GTR+I+G model for 2 M generations.** The GenBank accession numbers are indicated before species names. Support values are indicated on the branches (posterior probabilities). The novel species is shown in blue text and *Bovistella radicata* was used as outgroup.
Fungal Planet 929 – 19 July 2019

**Marasmius lebeliae** Guard, sp. nov.

**Etymology.** Named for its delicate beauty and in acknowledgement of mycologist Teresa Lebel, for elevating the study of Australian *Marasmius* into the DNA Era of the 21st Century.

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

*Basidiomata* small, marasmioid. *Pileus* 5–12 mm, conico-convex when young to campanulate at maturity, cinnamon (10; Royal Botanic Garden Edinburgh 1969) to rusty tawny (14), centre darker and occasionally wrinkled, margins paler buff (52), dry, deeply sulcate, flesh thin, white. *Lamellae* free to adnexed, sparse, 7–11, with occasional lamellulae, narrow, off-white, margins non-coloured. *Stipe* central, wiry, 35–60 x < 0.5–0.5 mm, glossy, black to purplish chestnut (21) in lower half, dark brick (20) in mid stem, buff (52) in upper end, tiny basal pad present (hand lens required). *Spore* print white. *Basidiospores* (27.5–)34.5–38.5(–35.5) x 4.5–5.5 μm (av. 32 x 5 μm, Q = 5.1–6.9, Qn = 6.1 ± 0.4, n = 50), long, narrowly clavate, with widest diameter approximately 2/3 along scope of spore, hyaline, inamyloid. *Basidia* 25–30 x 11–13 μm, sterigmata average 5.4 μm long; occasional basidia up to 40 x 15.5 μm. *Cheilocystidia* present in two forms – constricted cylindrical cells, 29–33 x 5–9 μm, and occasional *Siccus*-type broom cells with cylindrical bodies 16–27 x 3.5–5.5 μm with apical digitate projections 3.3–5.5 x 0.7–0.9 μm. *Pleurocystidia* narrow, cylindrical with constrictions (moniliform), or narrow to broadly clavate with swollen mucronate apices 11–25(–29) x 3.5–6(–8) μm. *Pileipellis* is a hymeniderm composed of *Siccus*-type broom cells: 7–12(–20) x 7–12 μm, main body cylindrical to broadly clavate, occasionally branched, thin-walled at base and often thick-walled in upper third, projections digitate, nodulose, or obverse to subacute, thick-walled, 2.7–5.5 x 0.5–0.9 μm. Thick walled portion of broom cells is yellow-brown in KOH. *Caulocystidia* absent. *Stilipiellis* of parallel hyphae, dextrinoid in Melzers’.

Habit, Habitat & Distribution. — Fruits in troops in mid-summer after significant periods of rain, usually in deep leaf litter, with an apparent preference for *Casuarina* needles in forest that has been regenerating for 10–30 years. To date this species has only been found from four sites in privately conserved land on Dilkusha Nature Refuge, Maleny, Queensland. It is expected that the distribution is in fact much wider, but *Marasmius* species are frequently overlooked in fungal surveys.

**Notes** — *Marasmius lebeliae* is characterised by a small pale brown pileus, distant lamellae, very large basidiospores, strangulate pleurocystidia, and two types of cheilocystidia – common strangulate and common to uncommon *Siccus* type broom cells. These features in the absence of cauloxylicida and with a well-developed, non-collariate, non-insitious stipe place this species in sect. Globulares (group Siccii), subsect. Siccini, ser. Haematocephali.

*Marasmius lebeliae* is part of a small but well-supported clade that includes a strongly supported sister species, *Marasmius crinipes* described from Korea (Antonin et al. 2012). However, it differs significantly in having shorter spores (av. 22.8 x 4.3 μm), different coloured pileus (brownish orange), longer stipe and different type of cystidia. Another species similar in shape, size and habitat is *Marasmius bambusiformis*. It differs in being brighter orange, having more lamellae (10–16), which have a concolorous margin, significantly smaller spores (av. 16 x 4.3 μm) and lacking pleurocystidia (Singer 1976).

**Supplementary material**

*FP929* Bayesian (Mr Bayes v. 3.2.6) 50 % majority-rule consensus tree of the ITS-nrDNA for a selection of *Marasmius* species. Bold lines indicate PP support > 0.95. G - sect. Globulares; N - sect. Neossellae; L - sect. Leveil-leant; MM - sect. Marasmius subsect. Marasmius; MS - sect. Marasmius subsect. Sicciomorphes; S - sect. Siccii; SA - sect. Siccii ser. Atrorubentes; SL - sect. Siccii ser. Leoninii; SS - sect. Siccii ser. Spinulosi; SH - sect. Siccii ser. Haematocephali.

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Mariannaea terricola
Mariannaea terricola  A.L. Alves, A.C.S. Santos, R.N. Barbosa, Souza-Motta, P.V. Tiago, sp. nov.

**Etymology.** terricola, terri means soil, referring to substrate from which the fungus was isolated.

Classification — Nectriaceae, Hypocreales, Sordariomycetes.

On PDA: Hyphae 2–12 μm wide, septate, hyaline, smooth, thin-walled, branched. Conidiophores up to 575× 5–12 μm length/width at the base cell, macronematous, mononematous, erect, straight, smooth or verrucose, thin-walled, septate, hyaline, cylindrical, tapering with base cell wall slightly verrucose, bearing short branches in the upper part, with three phialides at each branch. Phialides 3–9 × 2–4 μm length/width, globose to fusoid, hyaline, thin-walled, smooth, aseptate, produced in imbricate chains. Chlamydospores single, globose when in a terminal position, 7.5–8 μm diam, and doliform when in an intercalary position, 7.5–20 × 4–10 μm length/width, hyaline, thick-walled. Ascomatal morph not observed.

Culture characteristics — (in the dark, 25 °C after 7 d): Colonies on PDA reaching 4–6 cm diam, at first white, rosy buff close to margins and honey to cinnamon at centre; zonate; reverse white close to margins to cinnamon at centre, becoming wine coloured after 14 d.

**Typus.** B R A Z I L, Pernambuco state, Mata São João, Paudalho, S7°57’09” W35°06’19”, isolated from soil, July 2017, A.L. Alves (holotype URM 92163, ex-type culture URM 8023, ITS and LSU sequences GenBank MK101011 and MK101012, MycoBank MB828377).

Notes — ITS and LSU sequences are important identification markers for Mariannaea. Based on the current phylogenetic analysis, the new species Mariannaea terricola represents a distinct lineage, clustering close to M. fusiformis and M. punicea. However, M. fusiformis is characterised by its hyphae, 2–8 μm wide, conidiophores up to 800 μm long, phialides 14–22 × 2–5 μm, smooth-walled or occasionally verrucose, conidia 5–10 × 3–4 μm, fusiform to subglobose, chlamydospores 8–10 × 5–7 μm, globose to subglobose. Mariannaea punicea is characterised by its conidiophores c. 160–300 μm long, 6–9 μm wide at the basal cell, conidia 4–7 × 2–3.5 μm, ellipsoidal to fusoid, chlamydospores yellow-brown, 6–10 μm diam (Hu et al. 2016). These two species also have red-purple colonies, but M. punicea differs from M. fusiformis in its conidial shape that is broadest at the 1/4 part from the apex (Samson 1974, Cai et al. 2010). The new species described here also differs in colony colour and zonation. Mariannaea terricola initially has white colonies, rosy buff close to margins and honey to cinnamon at centre, zonate. Mariannaea terricola was isolated from soil collected in the Brazilian Tropical Atlantic Forest, in the city of Paudalho, Pernambuco state.

Bayesian inference tree obtained by phylogenetic analyses of the combined ITS and LSU sequences conducted in MrBayes on XSEDE in the CIPRES science gateway. Bayesian posterior probability values and Maximum likelihood are indicated at the nodes. The new species is indicated in red face. Calonectria brassicae (CBS 111869) and C. ilicicola (CBS 190.50) were used as outgroup.

Colour illustrations. Atlantic forest's soil, isolation source of Mariannaea terricola. 7-d-old (left) and 14-d-old (right) colonies; conidiophores, conidia and chlamydospores from 7-d-old colonies on PDA. Scale bars = 10 μm.
Meliola gorongosensis
**Meliola gorongosensis** Iturr., Raudabaugh & A.N. Mill., *sp. nov.*

**Eymology.** Name refers to the locality in which it was collected, Gorongosa National Park.

**Classification — Meliolaceae, Meliolales, Sordariales, Sordariomycetes.**

**Mycelium** forming ovate to irregular black patches on both surfaces of leaflets, up to 10 mm diam, hyphae dark brown, 5–7 μm diam, thick-walled, wall 1 μm wide, septate, closely branched forming a dense network on the surfaces of the leaflet, bearing numerous short hyphopodia. **Hyphopodia** arranged in a variety of manners: on opposites sides of the hyphae or alternately or uniymmetrically on one side of the hyphae, arising from a single basal cell, 12–17 μm long, terminating in a swollen, rounded to slightly curved head, 7.6–10.3 × 8.8–11.6 μm. Setae arising from the hyphae, multiple, stiff, erect, dark-brown, septate, more than 1 mm high, tapering towards the apex, smooth-walled with walls equally thickened the entire length. **Ascomata** on both surfaces of leaves, numerous, black, lenticulo-spherical, 220 × 165 μm, arising from the hyphae. **Ascomatal wall of textura globulosa-angularis** in surface view, with a distinguishable pattern composed of groups of 4–5 dark brown cells each with a group circumscribed by a dark periphery, cells 10–11 μm, 3–4 layers thick, brown, outer cells dark-brown, isodiametric. **Asci** arranged in a basal layer, oblong when young, 53.5–80.4 × 31–36.3 μm, widening as they mature to become subspherical, with a short point of attachment, 71–75 × 34–51 μm, 3-spored with one aborted spore, evanescent when mature. **Ascospores** dark-brown when mature, thick-walled, broadly ellipsoidal, slightly curved, inequilateral, with one rounded end and the other end tapering or both ends tapering, 40–50(–55) × 14–22(–24) μm, with four very dark and thick-walled septa, sometimes constricted at the septa; with one large guttule per cell.

**Habitat —** On living and fallen, dead leaflets of *Philenoptera violacea*.

**Distribution —** Known only from Gorongosa National Park, Mozambique.

**Typus.** **Mozambique,** Sofala Province, Gorongosa National Park, Great Rift Valley of central Mozambique, road south of Chitengo base camp toward Punque River and Vinho community, mixed palm forest, on fallen, dead leaflets of *Philenoptera violacea* (Fabaceae), -18.9889S, 34.3525E, 40 m elev., 21 May 2016, T. Iturriaga MOZ 9 (holotype CUP 70689, isotype ILS 82564, ITS sequence GenBank MK802897, MycoBank MB830654).

**Additional material examined.** *Meliola carvalhoi* in foliis *Lonchocarpus cyanescens* (Papilionaceae), Africa orientalis (Portuguese East Africa): Larde, 30 Aug. 1946, T. Carvalho, IMI 16646 (typyus). *Meliola carvalhoi* Sydowia 5: 4. 1951.

**Notes** — The phylogenetic placement of *Meliola* has been the subject of debate for many years. Saenz & Taylor (1999) showed that Meliola belongs to the ‘ununicate pyrenomycetes’, today treated in the Meliolaceae (Sordariomycetes). The new species described here, *Meliola gorongosensis*, possesses the typical characters known for the genus: dark mycelium as a superficial mat of thick, dark-septate hyphae; hyphopodia, setae and ascomata superficial on the mycelium; ascomatal wall with thick-walled cells, with or without a pattern, and ascospores usually 4-septate with a thick dark-brown wall. Most species occur in tropical areas as highly specialised biotrophs on leaves of specific genera or species of higher plants. A ‘Beeli formula’ (Beeli 1920) is a numerical code traditionally used to characterise each species, in this case Beeli number 3113.4344. The type of *Meliola carvalhoi* (Deighton 1951) was compared to our material since it was described from the same plant genus *Philenoptera* (as Lonchocarpus cyanescens, a nomenclatural synonym of *Philenoptera cyanescens*), both in the family *Leguminosae* (Schrire 2000) and also both from Mozambique. Both species were collected in the same general area (-18.25S, 35.00E). *Meliola gorongosensis* differs from *M. carvalhoi* in that the former has an ascomatal wall with a defined cell pattern, whereas *M. carvalhoi* shows no specific pattern. *Meliola gorongosensis* has only one type of appressorium, while *M. carvalhoi* has two kinds of appressoria. In *M. carvalhoi* the appressorium terminal cell is rounded with a rugose cell wall. In *M. carvalhoi*, one type of appressoria terminal cell is also rounded, but with a smooth cell wall, while the second type of appressorium has mucronate apical cells. Ascospores of *M. gorongosensis* are ellipsoid and inequilateral, while those in *M. carvalhoi* are cylindrical to slightly ellipsoid and equilateral. Setae in *M. gorongosensis* are smooth-walled with walls equally thickened the entire length unlike those in *M. carvalhoi* with walls irregularly thickened. Deighton (1951) describes the setae in *M. carvalhoi* as being spiny, although we were not able to observe the spines in the material that we examined. The host of *M. gorongosensis* is *Philenoptera violacea*, while the host of *M. carvalhoi* is *Philenoptera cyanescens*.

**Colour illustrations.** Typical African savannah mixed with patches of forest in Gorongosa National Park, Mozambique. Fallen leaflet of *Philenoptera violacea* with blackened areas of *M. gorongosensis*; longitudinal section through ascus; erect and pointed setae on superficial hyphae; two young ascii with three ascospores each (in Congo Red); three dark brown 4-septate ascospores. Scale bars = 40 μm (ascomal section), 40 μm (setae), 20 μm (immature ascii), 10 μm (ascospores). Photo credits: T. Iturriaga, D. Raudabaugh.
Mollisia endocrystallina
**Mollisia endocrystallina** Matočec, I. Kušan, Jadan, Mešić & Tkaličec, sp. nov.

**Eymology.** Named after the crystalloid matter found in the ectal excipular and marginal cells.

**Classification —** Mollisiaceae, Helotiales, Leotiomycetes.

*Ascomata* apothecial, shallowly cupulate when young, then expanding to discoid or plate-shaped, becoming subpulvinate when fully mature, superficial, sessile, ± circular from the top view, ±0.6–1.3 mm diam, solitary or gregarious (up to few apo-
thecia). Hyphenum pale grey in young stage to pale lead-grey in maturity, not wrinkled; margin ± sharp and whitish but lowered down at full maturity, smooth, entire, not lobed, ex-rolled in maturity; excipular surface pale brownish grey from base almost to the margin, smooth. Basal hyphae macroscopically indistinct-
ly ignis. Asexual morph not seen. *Hymenium* ±95–125 µm thick. Asci cylindrical with conical-subtruncate apex, ±88.7–117 × (6.6–)7–8.1–(8.6) µm, ±64–73.5 × 5.7–6.5 µm, *pars sporifer*a ±24–34.6 µm, 8-spored, in living state protruding above paraphyses up to 20 µm, base cylindrical-truncate, containing cysto-
toplasmic refractive hyphal globule, arising from repetitive croziers, apical apparatus strongly refractive and visible already in water and especially in *KOH*, in Lugol’s solution (*IKI*) api-
cal ring medium to strongly amyloid (2-3bb) of *Calycina*-type. Ascospores ciborioid to villiform, with notably rounded poles, bilaterally symmetrical, 1-celled, (±6.8–7–8.4–11–(11.3) × (3.1–)3.3–3.7–4.3–(4.5) µm, *Q* = (1.8–1.9–2.5–2.9–(2,9–)3), hyaline, smooth, uncinulate, freshly ejected without sheath, biseriate inside *asci*, lipid bodies absent, *cystoplasm containing two*, rarely one, bipolar refractive vacuoles, ±0.9–3.3 µm diam; in *IKI* cystoplasm yellow, nucleus contrasted, bipolar vacuoles hya-
line and non-refractive; in brilliant crey blue (CRB) vacuoles greyish rose to pale purplish, disappearing after adding KOH.

*Paraphyses* cylindrocyst-obsolete to subclavate, apical cell *32.6–64 × 2.8–4.2–(5) µm, straight, simple, sometimes branched below apical cell, *containing single cylindrical strongly refractive vacuolar body* (*VB*), in some cells few *VBs* compacted next to each other, wall thin and hyaline; in KOH without yellow reac-
tion; in *IKI* VBs not stained, soon collapse, some yellow-orange particles remain peritunically; in CRB turquoise-blue to deep blue, immediately collapse after adding KOH. *Subhymenium* ±25–32 µm thick at the middle flank, hyaline, richly beset with highly repetitive croziers, composed of hyaline densely packed epidermoid and ± cylindrical cells *4.2–8.4 µm wide. Medullary excipulum* ±37–45 µm at the middle flank, composed of hyaline markedly gelatinised textura porrecta-intricata, cells *2.9–5.6 µm wide, outer cells somewhat swollen and perpendicularly oriented towards ectal excipulum, ±11.6–18.8 × 5.7–9.9 µm, thin-walled, occasionally with few lipid bodies, devoid of crys-
tals and KOH-soluble cystoplasmic bodies; in *CRB* intercellular spaces puprash. *Ectal excipulum* *33–44 µm thick at the middle flank, composed of textura globulosa-angularis, cells ±6–19.5 µm, ±4.6–15.3 µm wide, walls ochre-brown, ±0.7–0.9 µm thick, most cells in the cortical layer contain ± central, freely floating, hyaline and moderately refractive, rossetiform crystalloid bodies which are differentially stained in CRB and *IKI*, and soluble in KOH; 2) *sporoplasm regularly contains refractive vacuoles while true oil drops are missing; and 3) lack of VBs in the outermost cells of margin and ectal excipulum. *Mollisia rivularis* is KOH negative like *M. endocrystallina* but its spores contain oil drops while *M. usa* is KOH positive (unlike *M. endocrystallina*) and has eguttulate ascospores (unpubl. data). Furthermore, *M. rivularis* has nar-
rower spores: 1.8–2.4 µm in Krieglsteiner (2004) and 1.7–2 µm in *Svrček* (1987) vs 3.3–4.3 µm in *M. endocrystallina* and shorter asci, while *M. usa* has considerably more elongated spores *Q* = 2.9–3.6 vs 1.9–2.9 in *M. endocrystallina*. *Mollisia rivularis* and *M. usa* are found exclusively on hardwood (mostly Fagus) submersed in a creek (*Svrček* 1987, Krieglsteiner 2004, unpubl. data) while *M. endocrystallina* was found on *Picea* remnants in an air-humid environment in a hyperkarst waterless area. *Fisher* & *Webster* (1983) described *Mollisia gigantea* from a submerged *Picea* branch but contrary to the new species it is creamy to buff-coloured and has longer spores (10–12 vs 7–11 µm) without sporoplastic inclusions. Phylogenetically, close *M. caesia* is imperfectly known species found on smaller wood remnants of *Fagus*, *Salix* and *Alnus* with much longer spores (*e.g.*, 12–14 µm, see *Rehm* 1996).

Notes — According to our analysis (see Supplementary Fig. FP932) and recent molecular phylogenetic studies certain members of the asexual genera *Acephala*, *Acidomelanica*, *Barrenia*, *Cystodendron*, *Phialocephala* and *Trimmatastroma* (*Crous* et al. 2007, *Grüning* et al. 2009, *Walsh* et al. 2014, 2015, *Tanne* et al. 2016, *Hamm* et al. 2017) cluster with *Mollisia* sp. in a *Loramycetes-Vibrissea-Mollisia* clade (cf. *Wang* et al. 2006).

*Mollisia endocrystallina* displays certain similarity to *M. rivularis* and *M. usa* ss. auct. Certain critical microscopic characters found in *M. endocrystallina* are unique: 1) ectal excipular and marginal cells contain freely floating, hyaline and moderately refractive, rossetiform crystalloid bodies which are differentially stained in CRB and *IKI*, and soluble in KOH; 2) *sporoplasm regularly contains refractive vacuoles while true oil drops are missing; and 3) lack of VBs in the outermost cells of margin and ectal excipulum. *Mollisia rivularis* is KOH negative like *M. endocrystallina* but its spores contain oil drops while *M. usa* is KOH positive (unlike *M. endocrystallina*) and has eguttulate ascospores (unpubl. data). Furthermore, *M. rivularis* has nar-
rower spores: 1.8–2.4 µm in Krieglsteiner (2004) and 1.7–2 µm in *Svrček* (1987) vs 3.3–4.3 µm in *M. endocrystallina* and shorter asci, while *M. usa* has considerably more elongated spores *Q* = 2.9–3.6 vs 1.9–2.9 in *M. endocrystallina*. *Mollisia rivularis* and *M. usa* are found exclusively on hardwood (mostly *Fagus*) submersed in a creek (*Svrček* 1987, Krieglsteiner 2004, unpubl. data) while *M. endocrystallina* was found on *Picea* remnants in an air-humid environment in a hyperkarst waterless area. *Fisher* & *Webster* (1983) described *Mollisia gigantea* from a submerged *Picea* branch but contrary to the new species it is creamy to buff-coloured and has longer spores (10–12 vs 7–11 µm) without sporoplastic inclusions. Phylogenetically, close *M. caesia* is imperfectly known species found on smaller wood remnants of *Fagus*, *Salix* and *Alnus* with much longer spores (*e.g.*, 12–14 µm, see *Rehm* 1996).

Supplementary material

FP932 ML phylogenetic tree inferred from the dataset of ITS1-5.8S-ITS2 gene sequences from *Mollisia endocrystallina* and related species.
Naganishia indica
**Naganishia indica** Roh. Sharma, S.M. Singh & Shouche, *sp. nov.*

**Etymology** Name reflects the country from where it was isolated.

**Classification** — Tremellaceae, Tremellales, Tremellomycetes.

After 7–10 d at 15 °C on Sabouraud dextrose agar (SDA), the cells are ovoid to ellipsoidal, 3 × 5 μm (2.2–4.5 × 3.5–6.9 μm) occurring singly, single budding, sedimentation occurs. After 15 d at 15 °C on SDA medium only pseudohyphae are produced and no true hyphae are observed. On SDA, the colony of RNF072 is yellowish cream on the surface, and yellow in reverse, raised, smooth entire margin, > 1 mm after 10 d. No asc and ascospores were observed after 20 d of incubation on SDA medium as well as Corn Meal Agar (CMA). Assimilation of carbon compounds: D-xylene, D-maltose, D-saccharose, L-Arabinose, Calcium-2-keto-Gluconate, Methyl-Alpha-D-Glucopyranoside, D-melezitose were assimilated. D-galactose, D-raffinose, D-trehalose, Glycerol, Inositol, Sorbitol, Adonitol, D-cellobiose, Xylitol were not assimilated.

**Cultural characteristics** — On CMA the colonies are white, round, smooth margin, small, pointed > 0.1 mm after 10 d. The strain was grown at different temperatures from 5–25 °C and it showed optimal growth at 15 °C.

**Habitat** — Powdery windblown dust on snow/glaciers (Cryoconites).

**Notes** — The genus Naganishia was proposed to accommodate Naganishia albida with 15 species separated from Cryptococcus. Most of the species of Naganishia earlier belonged to the albida clade of Cryptococcus. Molecular phylogenetic analysis of the D1/D2 LSU rDNA and ITS regions placed strain RNF072 in the Naganishia clade. In terms of pairwise sequence divergence, strain RNF072 differed from other existing Naganishia species and showed highest similarity with the ex-type strains of Naganishia friedmannii CBS 7160° (GenBank KY108613) and Naganishia globosa CBS 5106° (GenBank KY108616). It differed from ex-type strains of N. friedmannii CBS 7160° and N. globosa CBS 5106° by 39 (4 %) and 43 (5 %) nucleotide substitution, respectively in the D1/D2 LSU rDNA region. A phylogenetic tree based on D1/D2 LSU rDNA gene was constructed by Neighbour-Joining. The tree discriminates the strain RNF072° from *N. bhutanensis* CBS 6294° and *N. antarctica* CBS 7687° indicating its novel stature. A phylogenetic tree was also constructed by Maximum Parsimony and Maximum Likelihood method using all the species of the genus Naganishia, but no difference was obtained in the topology of trees and position of the proposed novel species within the genus Naganishia. We propose this yeast isolate as a novel species which is supported by phylogenetic, morphological and physiological data. The morphological characteristics of *N. indica* RNF072° is in accordance with the genus Naganishia. Cell morphology is ovoid to ellipsoidal with well-developed pseudohyphae. The strain RNF072° proliferated by single budding. The novel yeast *N. indica* RNF072° is isolated from the cryoconites of Chhota Shigri glacier, Indian Himalayas. The present novel species shares similarity with its closest phylogenetic relatives *N. antarctica* and *N. bhutanensis* as all three are isolated from soils in extremely cold environments, but from different geographical regions, i.e., from India, Antartica and Bhutan.

**Neighbour-joining tree was constructed using MEGA7, based on the D1/D2 LSU rDNA region showing the position of Naganishia indica sp. nov. among related species within Naganishia. Bootstrap support values > 50 % are given at nodes based on 1000 replications. The scale bar represents 2 % sequence difference.**

![Neighbour-joining tree](image)

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Nakazawaea ambrosiae
**Fungal Planet 934 – 19 July 2019**

**Nakazawaea ambrosiae** Kachalkin, M.A. Tomashchevskaya, T.A. Kuznetsova & M.V. Vecherskii, *sp. nov.*

**Etymology.** Name refers to ambrosia beetles, the galleries and the larvae of which served as the source of the strains.

**Classification —** *Pichiaceae, Saccharomyctales, Saccharomycetes.*

On glucose peptone yeast extract agar (GPYA) and 5% malt extract agar (MEA), after 7 d at 22 °C, streak is white, glistening, smooth and butyrous, raised, with hyphal production at the lobed margin; the surface of the colony is rugose or smooth. Cells are globose, subglobose and ovoid, 3.0–4.5 × 1.5–2.5 µm, occur singly or in pairs, divide by multilateral budding, with one or two buds. Pseudo hyphae and true hyphae with subglobose and ovoid bostryconidia are formed. Ascospores have not been observed during 4 wk at 22 °C in culture (pure cultures and in mating test) grown on GPYA, MEA, potato dextrose agar (PDA), yeast nitrogen base with 0.5% glucose (YNB) agar, cornmeal agar and Gorodkowa agar. Glucose, trehalose, maltose (variable) and cellobiose (slowly and variable) are fermented, but galactose is not fermented. Glucose, galactose, L-sorbosé, sucrose, maltose, cellobiose, trehalose, raffinosé (weak and variable), melezitose, D-xylóse, L-arabinóse, D-arabinóse, D-ribose, L-rhamnóse, ethanol, glycerol, erythritóle (weak), ribitol, galactítol, D-mannitol, D-glucitóle, methyl alpha-D-glucoside, salicín, DL-lactic acid, citric acid (weak), D-gluconate (weak), D-glucosamine, and arbutin are assimilated; no growth occurs on lactosé, melibísé, inulín, soluble starch, myo-inositol, methanol, D-gluconórate, succinic acid, 2-keto-D-gluconate and 5-keto-D-glucóate. Nitrogen compounds: ammonium sulfate, potassium nitrate (variable), L-lysíne, D-glucosamine, creatíne (weak) and creatíne (weak) are assimilated. Growth on vitamin-free medium and on MEA with 10% NaCl is not present. Growth on 50% w/w glucose / yeast extract (0.5%) agar is positive. Growth with 0.01% cyclohexamíde and 0.1% cyclohexamíde is present. Starlike compounds are not produced. Diazonium blue B colour and urease reactions are negative. Maximum growth temperature is 41 °C.

**Type. Russia.** Moscow region, in the vicinity of Zvenigorod town, from the galleries of *Ips typographus* under the bark of the *Picea abies* (Pinaceae), Mar. 2017, A.V. Kachalkin UL1 (holotype KBP Y-6137 preserved in a metabolically inactive state, ex-type cultures VKN Y-3024 = DSM 106748 = CBS 15358, SSU, ITS-D1/D2 domains of LSU nrDNA, TEF1 and RPB1 sequences GenBank MK508964, MK508963, LRZ15815 and LRZ16143, MycoBank MB830277).

Additional materials examined. Russia, Moscow region, in the vicinity of Dmitrov town, from the galleries of *Ips typographus* under the bark of the *Pinus sylvestris*, Dec. 2017, A.V. Kachalkin, KBP Y-6306; Moscow region, in the vicinity of Ruza town, from *Ips typographus* larvae in the wood of the *Picea abies*, from the galleries of *Ips typographus* under the bark of the *Picea abies*, May 2018, K.B. Kachalkin, KBP Y-6362 and Y-6367, KBP Y-6378, KBP Y-6380. ITS sequences GenBank MK562506–MK562510.

**Colour illustrations.** Russia, Moscow region, spruce forest infected by bark beetles. Growth of yeast colonies on MEA; yeast cells and hyphal structures on MEA (after 7 d at 22 °C). Scale bars = 5 µm.

**Notes —** Analysis of the ITS region of the surveyed yeasts suggested that they were conspecific and represented a hitherto undescribed species of *Nakazawaea*. Based on the NCBI GenBank database, the best hits using the ITS sequence are *N. holsti* CBS 4140 (GenBank KY104365; 90% similar, 36 subst. and 15 gaps) and uncultured clone S57 from pine shoot beetle (*Tomicus piniperda*) in Finland, GenBank KJ512850 (99.8%, 1 subst.), using LSU these are *N. laoshanensis* NRRL-Y-63634 (GenBank NG_055166; 98% similar, 9 subst.) and some strains (with 1–2 subst.) from plum in China (GenBank KU240039), from bark beetles in Canada (GenBank AV761152), from gut of scolytid beetle in USA (Su et al. 2005; GenBank AY242329), from *Dendroctonus brescius* in USA (Davis et al. 2011; GenBank HQ413286), from associations with *Dendroctonus* spp. in USA and Mexico (Rivera et al. 2009; GenBank EF016026, EF016034, EF016040, EF016061), using SSU these are *N. pelletata* strain NRRL Y-6688 (GenBank EU011730; 99% similar, 16 subst. and 2 gaps) and strain Candida sp. from gut of scolytid beetle in USA (Su et al. 2005; GenBank AY242217; 98.8% similar, 3 subst.), using *TEF1* it is *N. anamitae* NRRL-Y-17641 (GenBank EU014758; 92% similar, 32 subst. and 2 gaps) and using *RPB1* it is *N. erubii* MUCU 30037 (GenBank EU344100; 81% similar, 122 subst. and 4 gaps). In compliance with a recent phylogenetic analysis of the genus (Polburee et al. 2017), the placement of the new species is demonstrated using the combined SSU and LSU rDNA phylogeny. *Nakazawaea ambrosiae* differ from the phylogenetically (by rDNA) closely related species by no galactose fermentation, no growth on soluble starch, growth at 41 °C (different from *N. holsti*, *N. laoshanensis*, *N. pelletata*) and pseudo hyphae and hyphae formation (different from *N. laoshanensis*, *N. pelletata*).

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Nigrospora brasiliensis
**Nigrospora brasiliensis** A.C.Q. Brito, C. Conforto, A.R. Machado, sp. nov.

**Etymology.** Name refers to the country where the species was collected, Brazil.

**Classification.** *Apiosporaceae, Xylariales, Sordariomycetes.*

*Hyphae* septe, hyaline to pale brown, branched, smooth, 2.6–5.2 μm diam. *Conidiophores* reduced to conidiogenous cells. *Hyaline vesicles* around the septum delimiting the conidia and their conidiogenous cells. *Conidiogenous cells* solitary, monoblastic, discrete, determinate, pale brown to dark brown, doliiform, ampulliform, subglobose or globose, 7.8–13 × 5.2–13 μm. *Conidia* solitary, acrogenous, smooth, aseptate, black, shiny, ovoid, subglobose or globose, 15.6–28.6 μm diam.

**Culture characteristics.** On PDA, the colonies are woolly, floccose, margin circular, white, reaching 9 cm diam at 25 °C in 12 d in the dark.

**Typus.** *Braz.* Pernambuco state, São João (S08°51'14.5" W36°22'43.7"), isolated from cladode brown spot of *Nopalea cochenillifera* (*Cactaceae*), 15 Aug. 2013, C. Conforto (holotype URM 93057, culture ex-type CMM 1214, ITS, TEF1-α and TUB2 sequences GenBank KY566929, MK753271 and MK720816, MycoBank MB850343).

**Additional material examined.** *Braz.* Pernambuco state, São João (S08°48'50" W36°26'42"), isolated from cladode brown spot of *N. cochenillifera*, 3 Sept. 2013, C. Conforto, CMM 1217, ITS, TEF1-α and TUB2 sequences GenBank KY566930, MK753272 and MK720817.

**Notes.** — The specimens obtained were identified causing initially brown and then black spots, circular or elliptical in shape, 1–3 cm diam on the cladodes of *Nopalea cochenillifera*. The lesions may extend from one side to the other of the cladodes, causing perforations due to the fall of the affected tissue. Such lesions can coalesce to form large necrotic areas which cause cladode drop. Based on metablast searches in GenBank, the *N. brasiliensis* ITS sequences have 98.46 % identity to *N. sphaerica* (LC6996; GenBank KX986085), while on TEF1-α sequences and TUB2 the percentage identity was 89.19 % to *N. sphaerica* (LC2840; GenBank K019318) and 91.55 % to *N. sphaerica* (LC7312; GenBank K019618), respectively. According to the phylogenetic analyses, *N. brasiliensis* is most closely related to *N. sphaerica*. Conidiophores in *N. brasiliensis* are reduced to conidiogenous cells, whereas in *N. sphaerica* conidiophores are micromatous or semi-macromatous, flexuous or straight, extensively branched, multi septate (Wang et al. 2017). The conidiogenous cells are also different, since in *N. sphaerica* they have a subspherical shape (Wang et al. 2017), but in *N. brasiliensis* they are doliiform, ampulliform, subglobose to globose. In *N. sphaerica* conidia are globose or subglobose (Wang et al. 2017), in *N. brasiliensis* they are subglobose to globose (in general) and ovoid. In addition, *N. brasiliensis* has slightly larger conidia. The additional material examined (CMM 1217) under the same conditions as the ex-type culture CMM 1214 (PDA, 12 d, 25 °C in the dark) shows a different colony appearance, white mycelium in the centre to greyish near the edge of the Petri plates, becoming black with time.

**Colour illustrations.** Cladode of *Nopalea cochenillifera* with brown spot in Pernambuco. Colony on PDA after 12 d at 25 °C in the dark; conidia; conidiophore and conidiogenous cell (indicated by arrow). Scale bars = 10 μm.

Bayesian inference tree was obtained by analysis of concatenated matrix of ITS, TEF1-α and TUB2 sequences in MrBayes v. 3.2.6 at CIPRES science gateway. The nucleotide substitution model used was SYM+Γ+I for ITS, HKY+Γ+Γ for TEF1-α and GTR+Γ+Γ for TUB2, selected separately by MrMODELTEST v. 2.3 according Akaike Information Criterion (AIC). Bayesian posterior probability values above 0.95 are indicated at the nodes. The new species is indicated in bold. (*) indicates the ex-type culture. *Arthrinium malaysianum* (CBS 102053) was used as outgroup. The alignment was deposited in TreeBASE (Submission ID 24256).

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Ossicaulis salomii
**Ossicaulis salomii** Siquier & Bellanger, *sp. nov.*

**Etymology.** Named in honour of the mycologist Joan Carles Salom, for his significant contribution to our knowledge of the Balearic Fungi.

**Classification — Lyophyllaceae, Agaricales, Agaricomycetes.**

*Pileus* up to 11 mm diam, soon flat-convex and somewhat depressed in the centre with involute margin for a long time; surface dry, with white rimoilose coating, cracked with time, exposing more or less clear caramel colour. Lamellae emarginate to slightly decurrent, somewhat ventricose, white at first, white cream when ageing or dehydrating. *Stipe* up to 19 × 1.5 mm, central, cylindrical, slightly thickened towards base, subpruinose o pruinose, especially in the upper zone and towards base, whitish to grey or slightly brownish with age. *Context* thin, whitish, with a strongly farinaceous *odour* and *taste*. *Spore* *print* white. *Basidiospores 4–5(–6) × 3–4 μm, *Q*: (1.33–)1.42–1.66, *Qp*: 1.4–1.6, ovoid to ellipsoidal, pruiniform or, very often, larniformal, with rounded to slightly conical base and rounded apex, not flattened, smooth, non-amyloid, non-dextrinoid and non-cyanophil, thin-walled and with the apicule somewhat marked. *Basidia* 20–25 × 4.5–5.5 μm, 4-spored, cylindrical and narrowly clavate, with sterigmata up to 4 μm, accompanied by some cylindrical hyphae, up to 3 μm, that are interspersed between the basidia and that undoubtedly correspond to terminations of the trama, which appears regular. *Cheilocystidia* and *pleurocystidia* not observed. *Pleilepils* a cutis composed by cylindrical hyphae up to 5 μm wide, from parallel to more or less interwoven, with obtuse extremities, not so apparent, with few emerging elements, of greater calibre in the area of the subcuts; brownish parietal pigment slightly encrusting and intracellular pigment of ochraceous colour. *Stipitipellis* a cutis of parallel hyphae with rare cylindrical and very thin hairs. *Clamp connections* abundant and present in all tissues.

**Distribution & Habitat —** Spain, Balearic Islands, on dead and very wet remains of *Juncus sp.* or of *Posidonia oceanica*, in the dune zone next to the sea.

**Notes —** Initially these samples were determined as *Clitocybe augeana sensu* Kuyper (Siquier et al. 2015), but recent molecular investigations revealed that the species actually belongs to *Lyophyllaceae*, in the vicinity of the genus *Ossicaulis*, and that it is so far not represented in the fungal sequence databases (GenBank & UNITE). This small genus introduced in 1985 currently includes the two European species *O. lignatilis* (Redhead & Ginns 1985) and *O. lachnopus* (Contu 2007), as well as *O. yunnanensis* recently described from China (Yang et al. 2018). Based on LSU, *O. salomii* is closest to *O. yunnanensis* (seven substitutions + three indels, 98.8 % identity) but using TEF1 sequences, the species is closer to *O. lignatilis* than *O. yunnanensis*, with quite an important phylogenetic distance to these two species though (87.2 % vs 84.7 % identity, respectively). The ITS rDNA analysis confirms the extent of molecular divergence of *O. salomii* within the genus, as it differs from sequences in the clad by 9.6 % to 11.4 %. The new species occupies a basal position in the ITS phylogeny, which may support a dedicated genus. However, in addition to the LSU data, the gross morphology, anatomy, organoleptic features and ecology of the Balearic collections, fit well with the classic delineation of *Ossicaulis* (Holec & Kolářík 2013). With *O. lachnopus*, *O. salomii* shares the shape, but not the size, of the spores; with *O. lignatilis*, spore calibre but not the shape. The new species differs from all *Ossicaulis* species known to date, by its unique ecology and the absence of cystidia.

**Colour illustrations.** Dune area where the samples were found, in the Arenal de Son Bou (Minorca Island, Spain). Basidiomata in situ; basidiospores in congo red; basidia; clamp connections; elements of stipitipellis; elements of pleilepils. Scale bar = 10 mm (basidiomata), 10 μm (microstructures).

**Typhus.** Swan, Balearic Islands, Minorca, Alaior, Arenal de Son Bou, 2 m asl, 16 Nov. 2011, J.L. Siquier, JLS 3421 (holotype MA-FUNG! 91823 in Herbarium Real Jardín Botánico de Madrid, isotype AB 14-04-02 in personal herbarium of A. Bidaud, ITS, LSU and TEF1 sequences GenBank MK650044, MK650043 and MK644259, MycoBank MB830239).

**ITS phylogeny of *Ossicaulis*.** Maximum likelihood phylogenetic analysis of 25 ITS rDNA sequences belonging to the genus *Ossicaulis*, including the newly generated sequence from *O. salomii* sp. nov., performed on phylogeny.fr. Branch support is assessed by the SH-aLRT, significant when > 81 %.

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Penicillium americanum
**Penicillium americanum** Jurjević, G. Perrone, S.W. Peterson, D. Magistà, *sp. nov.*

**Etymology.** Named for USA, where the culture was isolated.

**Classification.** *Aspergillaceae, Eurotiales, Eurotomyces.*

Micromorphology (on malt extract agar; MEA): Conidiophores borne on surface, occasionally on aerial hyphae, (100–)150–350 (–375) × (3–)4–5 (–6) μm, with smooth, occasionally finely roughened walls, bearing terminal biverticillate or terverticillate penicillin; rami commonly with divergent asymmetric branching 2–3 (–4), (8–)10–25 × 4–5 μm; (3–)5–9 (–11) metulae in verticils, (6–)7–12 (–14) × 3–4 (–4.5) μm; phialides (3–)5–9 (–11) per metula, ampulliform, 7–9 (–9.5) × (2–)2.5–3.5 μm, with short collarettes. Conidia spherical to subospheral, occasionally broadly ellipsoidal, 2.5–3.5 (–5) × 2.5–4.5 μm, with smooth to finely roughened walls. Borne in long, loose to unordered chains.

**Culture characteristics.** — (in darkness, 25 °C after 7 d): Colonies on MEA 11–12 mm diam, colony texture velutinous to floccose centrally, rising c. 3 mm, mycelium white, visible at margins, sporulation heavy, conidia *en masse*, Medici blue to deep green-blue grey (R48; Ridgway 1912), exudate absent, soluble pigments yellow ochre (R15) to primuline yellow (R16), reverse wax to yellow to straw yellow (R16). Colonies on Czapek yeast autolysate agar (CYA) 12–13 mm diam, colony texture velutinous to rudimentally floccose centrally, rising c. 4 mm, mycelium white, mainly visible at margins, sporulation heavy, conidia *en masse*, greyish greenish blue (Medici blue to dark Medici blue, R48), exudate abundant, mustard yellow to wax yellow (R16), at the centre of the colony c. 5 mm diam, soluble pigments mustard yellow to mustard yellow to primuline yellow (R16), reverse wax yellow to straw yellow (R16), near straw yellow marginally. Colonies on potato dextrose agar (PDA) 11–12 mm diam, colony texture velutinous to rudimentally floccose centrally, rising c. 3 mm, mycelium white, sporulation heavy, conidia *en masse*, Medici blue to deep green-blue grey (R48), exudate barium yellow to wax yellow, abundant (R16), soluble pigments mustard yellow (R16) to honey yellow (R30), reverse wax yellow to straw yellow (R16). Colonies on Czapek yeast agar with 20 % sucrose (CY20S) 10–11 mm diam, colony texture velutinous, mycelium white, very sporulation, conidia *en masse*, pale light dull glacous-blue to greenish glacous-blue (R42), exudate absent, soluble pigments absent, reverse uncoloured to cuticle surface (R30). Colonies on dichloran-glycerol agar (DG18) 14–15 mm diam, colony texture velutinous, centrally rising c. 3 mm, and c. 4 mm diam, button-like, mycelium white, mainly visible at margins c. 2 mm diam, very heavy sporulation, conidia *en masse*, greyish greenish blue (Medici blue to dark Medici blue, R48), exudate absent, soluble pigments absent, reverse cuticle surface (R30) to pale glass green (R31). Colonies on CYA with 5 % NaCl (CYAS) 17–18 mm diam, colony texture velutinous to rudimentally floccose, centrally rising c. 4 mm, radially moderate to deep sulcate, mycelium white, sporulation heavy, conidia *en masse*, greyish greenish blue (light Medici blue to deep Medici blue, R48), exudate absent, soluble pigments absent, reverse cuticle surface to colonial buff, near reed yellow (R30). Colonies on oatmeal agar (OA) 9–10 mm diam, colony texture velutinous, centrally rising c. 2 mm, button like, mycelium white, visible at margins c. 2 mm diam, sporulation heavy, conidia *en masse*, greyish greenish blue (Medici blue to dark Medici blue, R48), exudate clear to brown, soluble pigments absent, reverse in pale brown shades. Colonies on creatine succore agar (CREA), 4–5 mm diam, no acid production, poor growth. On CYA/MEA (colony diam in mm) at 15 °C 11–13/13–24; 20 °C 18–19/19–20; no growth at 5 °C, 30 °C or 37 °C.

**Typus.** USA, Colorado, Medicinal Marijuana greenhouse, air, 22 July 2011, Ž. Jurjević (holotype BPI 910642, culture ex-type NRRL 66819 = ITEM 17520 = ESMLE1473, ITS, β-tubulin (Bera) and calmodulin (CaM) sequences GenBank MK791278, MK803427 and MK803428, MycoBank MB830667).

Notes — BLAST searches of the sequences of *Penicillium americanum* sp. nov. showed a β-tubulin similarity to *P. soppii* GenBank MF351761 (90.65 %) and a calmodulin similarity to *P. lenticrescens* GenBank KJ775404 (91.06 %). The ITS barcode was 98.72 % similar to *P. soppii* GenBank MF303707 and *P. lenticrescens* GenBank KJ775675 (98.53 %).

*Penicillium americanum* produces conidiophores (100–)150–350 (–375) μm long, while sclerotal production is not observed, compared to *P. soppii* which produces abundant sclerotia and conidiophores up to 500 μm long (Raper & Thom 1949); *Penicillium lenticrescens* produces conidiophores 150–415 μm long (Visagie et al. 2014a).

**Supplementary material**

FP937 Maximum likelihood tree of *Penicillium americanum* sp. nov. and closely related species (30 strains in total) of the Sections Ramosa and Brevicompacta based on concatenated BenA, CaM, ITS DNA sequences give evidence of net separation of this new species from the other well-resolved branch. All positions with less than 90 % site coverage were eliminated, i.e., fewer than 10 % alignment gaps, missing data, and ambiguous bases were allowed at any position (partial deletion option); 1141 positions were used in the final dataset. The evolutionary history was inferred by using the Maximum Likelihood method and Kimura 2-parameter model as implemented in MEGA X (Kumar et al. 2018). The tree with the highest log likelihood (−7673.46) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Support values at branches were obtained from 1000 bootstrap replicates. Bootstrap support values greater than 70 % are shown.
Penicillium minnesotense
**Penicillium minnesotense** Jurjević, G. Perrone, S.W. Peterson, D. Magistà, *sp. nov.*

**Etymology.** Named for state Minnesota, where the culture was isolated.

**Classification.** Aspergillaceae, Eurotiales, Eurotiomycetes.

**Micromorphology.** On malt extract agar (MEA): Conidiophores borne on the surface or from aerial hyphae, (8–)25–80(–130) × 2.5–3.5 µm, with smooth to finely roughened walls, apically swollen up to 7 µm diam, bearing a terminal whorl of (2.5–) 11(–13) ampulliform phialides, (7.8–) 12(–17) × 2.5–3.5 µm, occasionally finally roughened. Conidia subspherical to spherically to broadly ellipsoidal, occasionally nearly pyriform, (2.8–) 4.5(–9) × (2.2–) 4.5(–5) µm, with smooth to finely roughened walls. Borne in short disordered chains.

**Culture characteristics.** (in darkness, 25 °C after 14 d): Colonies on MEA 17–20 mm diam, colony texture velutinous, rising c. 4 mm, radially moderate deep to deep sulcate, mycelium white to carafe buff (R30), sporulation heavy, conidia en masse, pale glaucous-green to glaucous-green (R33; Ridgway 1912), exudate absent, soluble pigments neutral red to vinaceous-purple (R38), strong, soluble pigments on MEA with chloramphenicol not observed, reverse brick red (R13) to vinaceous-rufous (R14). Colonies on Czapek yeast autolysate agar (CYA) 18–20 mm diam, colony texture velutinous, abruptly rising c. 5–6 mm, centrally concave 5–9 mm diam, radially deep sulcate near wrinkled, mycelium white occasionally with laelia pink near euptoparian purple (R38) spots, sporulation heavy, conidia en masse, pale glaucous-green to glaucous-green (R33), exudate when present vinaceous, soluble pigments absent to feint purplish red; reverse dark vinaceous-brown to deep brownish vinaceous (R39). Colonies on potato dextrose agar (PDA) 15–16 mm diam, colony texture velutinous, abruptly rising c. 5–6 mm, centrally concave 5–8 mm diam, radially deep sulcate near wrinkled, mycelium white to light laelia pink, near vinaceous-purple (R38), sporulation very good, conidia en masse, pale glaucous-green to glaucous-green (R33), exudate when present vinaceous, soluble pigments daphne red to vinaceous-purple (R38); reverse brownish vinaceous to vinaceous-brown (R39). Colonies on Czapek yeast agar with 20% sucrose (CY20S) 14–15 mm diam, colony texture velutinous, mycelium white to carafe buff (R30), good sporulation, conidia en masse, pale glaucous-green to glaucous-green (R33), exudate absent, soluble pigments absent; reverse uncoloured to pale ochraceous-salmon (R15). Colonies on dichloran-glycerol agar (DG18) 20–21 mm diam, colony texture velutinous, centrally rising c. 4–5 mm, radially and concentrically moderate deep to deep sulcate, mycelium white nearly inconspicuous, sporulation heavy, conidia en masse, glaucous green to Niagara green (R33), exudate absent, soluble pigments Pompeian red to Vandyke red (R13), reverse English red to mahogany red (R2). Colonies on CYA with 5% NaCl (CYAS) 30–31 mm diam, colony texture velutinous, rising c. 5 mm, centrally concave, radially and concentrically deep sulcate near wrinkled, mycelium white, inconspicuous, sporulation heavy, conidia en masse, glaucous green to celandine green (R47), exudate absent, soluble pigments faint red; reverse walnut brown to vinaceous-russet (R28). Colonies on oatmeal agar (OA) 20–21 mm diam, colony texture velutinous, rising c. 3–4 mm, radially light to moderate sulcate, mycelium white to vinaceous lilac (R44), sporulation very good, conidia en masse, court grey to gnaphalium green (R47), exudate clear to light vinaceous lilac (R44), soluble pigments vinaceous laundering to purple (R44), reverse dull violet-black to vinaceous-purple (R44). Colonies on creatine sucrose agar (CREA) 14–15 mm diam, no acid production, good growth. On CYA/MEA (colony diam in mm after 14 d) at 5 °C 3–4/3–4; 15 °C 18–20/13–18; 20 °C 25–27/20–25; no growth at 30 °C or 37 °C.

Typus. USA, Minnesota, Air, outside, 10 Aug. 2012, Z. Jurjević (holotype BPBI, culture ex-type NRRL 7175 = ISU 19150 = MFLUCC 16407 = CBS 138075 = IMI 328898 = Type A & B = Goma & MFLUCC 90/0702). The species is closely related to *Penicillium salmoniflumine* GenBank KF932928 (98.81%), calmodulin similarity to *P. salmoniflumine* GenBank KF932945 (98.12%), RNA polymerase II second largest subunit (RPB2) sequences GenBank MK791277, MK803429, MK803430 and MK796158, MycoBank MB830666.

Notes. — BLAST searches of the sequences of *Penicillium minnesotense* sp. nov. showed β-tubulin similarity to *P. salmoniflumine* GenBank KF932928 (98.81%), calmodulin similarity to *P. salmoniflumine* GenBank KF932945 (98.12%), RNA polymerase II second largest subunit similarities to *P. salmoniflumine* GenBank KF932999 (98.43%). The ITS barcode was 100% similar to *P. salmoniflumine* GenBank NR 137849.

*Penicillium minnesotense* produces shorter conidiophores, on average (8–)25–80(–130) µm, than *P. salmoniflumine*, 15–250 µm long; also *P. minnesotense* produces larger conidia on average; subspherical to spherically to broadly ellipsoidal, occasionally nearly pyriform (2.8–)3–4.5(–9) µm, in short disordered chains, with smooth to finely roughened walls, in contrast to *P. salmoniflumine* with conidia ellipsoidal to spherical (2–)2.5–3.5(–6) µm, in loose to well-defined columns, with smooth to finely roughened walls (Peterson et al. 2015).

**Supplementary material.** FP938 Maximum likelihood tree of *Penicillium minnesotense* sp. nov. and closely related species (19 strains in total) based on concatenated *BeriA*, CaM, ITS and RPB2 DNA sequences give evidence of net separation of this new species from the other well-resolved branch. All positions with less than 90% site coverage were eliminated, i.e., fewer than 10% alignment gaps, missing data, and ambiguous bases were allowed at any position (partial deletion option); 2144 positions were used in the final dataset. The evolutionary history was inferred by using the Maximum Likelihood method and Tamura 3-parameter model as implemented in MEGA X (Kumar et al. 2018). The tree with the highest log likelihood (−11093.69) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Support values at branches were obtained from 1000 bootstrap replicates. Bootstrap support values greater than 70% are shown.

**Fungal Planet description sheets**

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Penicillium alagoense L.O. Ferro, A.D. Cavalcanti, O.M.C. Magalhães, Souza-Motta & J.D.P. Bezerra, sp. nov.

Etymology. The name refers to the Brazilian state, Alagoas, where this fungus was found.

Classification — Aspergillaceae, Eurotiinae, Eurotomiaceae.

On malt extract agar (MEA), conidiophores varying in length, erect not ramified, 70–300 × 2.5 μm; stipes septate with wall echinulate and apice enlarged (4 μm); asymmetric penicilli, monovercillate, occasionally with branch, biverticillate, lightly echinulate, spathulate, 10.5–15.5 × 2–2.5 μm; phialides ampulliform, 3–4(–5) phialides per metulae, 7.5–10 × 2–2.5 μm; conidia smooth to echinulate, globose, greenish, 2–3.5 μm.

Culture characteristics (25 °C, 7 d, darkness) — On Czapek Yeast extract Agar (CYA): colonies slightly raised, texture velvety, radially sulcate, slow sporulation, centrally purplish grey, hyaline mycelium with whitish margin, exudate and pigment absent; reverse cream. On MEA: colonies low, plane, texture velvety, light sporulation, greyish green to greenish glaucous, hyaline mycelium with whitish margin, exudate and pigment absent; reverse brownish to umber. On Yeast Extract Sucreose agar (YES): colonies slightly raised, texture velvety radially sulcate, slow sporulation, centrally purplish grey, hyaline mycelium with whitish margin, exudate and pigment absent; reverse brownish to yellowish. On oatmeal agar (OA): colonies low, plane, texture velvety, greenish olivaceous, hyaline mycelium with whitish margin, aerial mycelium centrally observed, exudate and pigment absent; reverse whitish. On Dichloran 18 % Glycerol agar (DG18): colonies low, plane, texture velvety, greyish to centrally greenish olivaceous, hyaline mycelium with whitish margin, exudate and pigment absent; reverse cream to yellowish. On Czapek Yeast Agar (CREA): weak growth and very weak or no acid production. Colony diam, in mm, after 7 d, darkness — CYA: 15 °C 13–15, 25 °C 26–28, 30 °C 19, 37 °C no growth; MEA: 15 °C 18, 25 °C 35–43, 30 °C 31, 37 °C no growth; YES: 15 °C 13–14, 25 °C 19–21, 30 °C 18–19, 37 °C no growth; AO: 15 °C 13–14, 25 °C 32–37, 30 °C 35–38, 37 °C no growth; DG18: 15 °C 5, 25 °C 23–24, 30 °C 19–29, 37 °C no growth; CREA: 15 °C 8, 25 °C 5–7, 30 °C 3, 37 °C no growth.

Typus. BRAZIL, Alagoas state, Quebrangulo, Pedra Talhada Biological Reserve, S09°15′26.8″ W36°25′53.7″, as endophyte from leaves of Miconia sp. (Melastomataceae), July 2018, L.O. Ferro (holotype URM 93058, culture ex-type URM 8086, ITS, BenA, CaM and RPB2 sequences GenBank MK804503, MK802333, MK802336 and MK802338, MycoBank MB830760).

Additional materials examined. BRAZIL, Alagoas state, Quebrangulo, Pedra Talhada Biological Reserve, S09°14′47.0″ W36°25′15.0″, as endophyte from leaves of Miconia sp., July 2018, L.O. Ferro, URM 8087, ITS, BenA, CaM and RPB2 sequences GenBank MK804502, MK802332, MK802335 and MK802337, Alagoas state, Quebrangulo, Pedra Talhada Biological Reserve, S09°14′47.0″ W36°25′15.0″, as endophyte from leaves of Handroanthus albus (Bignoniaceae), July 2018, A.D. Cavalcanti, B17B, BenA sequence GenBank MK802334.

Notes — Penicillium alagoense exhibits phylogenetic and morphological similarities to P. skrjabinii. Penicillium alagoense differs from P. skrjabinii by the numbers and size of phialides (6–8 per metulae, 7.7–10.5 × 2.3–3 μm), metulae (26.4–32 × 2.4–3.5 μm) and by the production of conidia that are ellipsoidal, globose or subglobose (3.5–5 × 1.8–2.4 μm) (Ramirez 1982). In addition, P. alagoense differs from P. skrjabinii by macroscopic characteristics presenting lower growth in the colonies and no growth at 37 °C.

P. alagoense displays distinctive colony characteristics and morphological features that differ from those of P. skrjabinii. The new species is characterized by smaller phialides, differing in size and shape, and a distinct growth pattern in various media.

Notes — Penicillium alagoense exhibits phylogenetic and morphological similarities to P. skrjabinii. Penicillium alagoense differs from P. skrjabinii by the numbers and size of phialides (6–8 per metulae, 7.7–10.5 × 2.3–3 μm), metulae (26.4–32 × 2.4–3.5 μm) and by the production of conidia that are ellipsoidal, globose or subglobose (3.5–5 × 1.8–2.4 μm) (Ramirez 1982). In addition, P. alagoense differs from P. skrjabinii by macroscopic characteristics presenting lower growth in the colonies and no growth at 37 °C.
Penicillium lunae
**Penicillium lunae** Visagie & Yilmaz, sp. nov.

**Etymology.** Latin, *luna*, named after Luna Visagie. This species was isolated from a banana was about to eat.

**Classification — Aspergillaceae, Eurotiales, Eurotiumycetes.** Conidiophores monoverticillate, minor portion biverticillate; stipes smooth-walled, 13–60 × 2–3 (3.5) μm; vesicle 5–7 μm; metulae two when present, 18–30 × 2–3 (3.5) μm; phialides ampulliform, 10–20 per vesicle, (7.5–)18–10 × 2–3 μm (8.8 ± 0.8 × 2.5 ± 0.4); average length metula/phialide 2.5: conidia smooth-walled, subglobose to broadly ellipsoid, 2–3 (–3.5) × 1.5–2 (–2.5) μm (2.2 ± 0.4 × 1.8 ± 0.2), average width/length = 1.2, n = 70.

Culture characteristics (25 °C, 7 d) — On Czapek yeast autolysate agar (CYA): Colonies low, slightly radially sulcate, sunken in centrally; margins low, wide (3 mm), entire; mycelia white; texture floccose; sporulation moderately dense, conidia *en masse* greyish to dull green (26B3–C3–D4); soluble pigments absent; exudates clear, minute droplets; reverse pale to light yellow (3A3–4). On dichloran 18 % glycerol agar (DG18): Colonies low, plain, sunken in centrally; margins low, wide (3 mm), entire; mycelia white; texture floccose, loosely funiculose; sporulation moderately dense, conidia *en masse* greyish to dull green (26B3–C3–D4); soluble pigments absent; exudates clear, minute droplets; reverse greyish white (30A2), yellowish white to pale yellow (2A2–3). Colony diam (in mm): CYA 34–36; CYA 30 °C 28–29; CYA 37 °C no growth; CYAS 33–35; MEAbl 25–26; DG18 24–25; YES 34–35; OA 28; PDA 29–30.

**Notes** — A BLAST search against an ex-type reference sequence dataset placed the new species in *Penicillium* sect. *Cinnamopurpurea* (Visagie et al. 2014b). A multigene phylogeny based on ITS, *BenA*, *CaM* and *RPB2* resolves *Penicillium lunae* as sister to *P. chermesinum*. All four genes can be used to make an identification. Morphologically, the new species is easily distinguished from *P. chermesinum* based on the absence of sclerotia and no growth on CYA at 37 °C. Microscopically, they are very similar except for *P. lunae* producing longer phialides ((7.5–)8–10 vs 7–8 μm) (Pitt 1980).

**Colour illustrations.** Luna Visagie with her banana. Colonies on CYA: colonies on MEA; colony texture on MEA; conidiophores. Scale bars = 10 μm.

Combined phylogeny of sect. *Cinnamopurpurea* based on ITS, *BenA*, *CaM* and *RPB2*. Aligned datasets were analysed in IQ-tree v. 1.6.8. Bootstrap support values (≥ 80 %) are given above branches. The new species is indicated by bold text, *t* = ex-type strain. GenBank accession numbers are given between square brackets (ITS = green, *BenA* = blue, *CaM* = red, *RPB2* = orange). The tree is rooted to *P. charlesi*.
Phialemonium guarroi
Phialemonium guarroi Rodrigues, Cano & Stchigel, sp. nov.

Etymology. In honour of the mycologist Josep Guarró Artigas.

Classification. Cephalothecaceae, Sordariaceae, Sordariales, Moniliomycetes.

Myeloma composed of septate, hyaline, smooth- and thin-walled hyphae, 1.5–2 μm wide, becoming cinnamon and moniliform in old cultures, whose cells reach up to 10 μm diam. Conidiophores absent or poorly differentiated, often consisting in single lateral phialides and adelophialides borne directly from aerial hyphae, occasionally composed of a short stipe of up to 15 μm long and bearing 1–3 phialides in an irregular arrangement. Phialides abundant, hyaline, smooth-walled, flask-shaped, with more or less inflated at the base and tapering towards the top, 12–15 × 1.5–2 μm, percurrently proliferating to form long chains in old cultures. Adelophialides hyaline, smooth-walled, cylindrical but slightly tapering towards the top, 12–15 × 1.5–2 μm. Conidia hyaline, aseptate, lemon-shaped, 3–3.5 × 1.5–2 μm, smooth-walled, produced in chains of up to 25 conidia, with a cylindrical-truncate scar at both ends. Chlamydospores and sexual morph not observed.

Culture characteristics. Colonies on OA reaching 9–10 mm diam after 2 wk at 25 °C, flattened, velvety, grey (6B1; Kornev & Wanscher 1978), margins regular, sporulation sparse, exudate absent; reverse pale yellow (3A3), diffusible pigment absent. Colonies on PCA attaining 10–11 mm diam after 2 wk at 25 °C, flattened, velvety, white (4A2), margins regular, sporulation abundant, exudate absent; reverse yellowish grey (3B2), diffusible pigment absent. Colonies on PDA of 12–13 mm diam after 2 wk at 25 °C, elevated, velvety to floccose, margin irregular, yellowish brown (SE4) at centre and yellowish grey (GB2) at edge, exudate absent, sporulation abundant; reverse olive brown (4E6) at centre and white (4A1) at edge, diffusible pigments absent. Minimum, optimal and maximum temperature of growth (on PDA): 15 °C, 25 °C and 30 °C, respectively.

Type. Spain, Canarias, Santa Cruz de Tenerife province, La Palma, Punta Gorda, isolated from soil, Aug. 2009, A.M. Stchigel & M. Calduch (holotype CBS H-23924, cultures ex-type FMR 17080 = CBS 145626; ITS and LSU GenBank LT633912, identities = 94/535 (92%), 10 gaps (1%)), and the production of phialides which proliferate percurrently to form long chains (feature not reported in P. inflatum) and the production of smaller conidia than those of P. inflatum. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hit using the ITS sequence is the ex-type strain of P. inflatum CBS 259.39 (GenBank LT633912; Identities = 490/535 (92%), 10 gaps (1%)); using the LSU sequence was the same ex-type strain of P. inflatum (GenBank LT633912; Identities = 845/857 (99%), no gaps). The ITS-LSU phylogenetic tree corroborated the placement of our isolate as a new species of Phialemonium, being located phylogenetically close to P. inflatum.

Notes. Phialemonium guarroi was recovered from a soil sample collected in Punta Gorda, La Palma, Canary Islands, Spain. The genus Phialemonium was established by Gams & McGinnis (1983). Phialemonium contains seven accepted species, mostly isolated from environmental sources and human specimens (Rivero et al. 2009, Perdomo et al. 2011, Guarro 2012, Crous et al. 2015b), Phialemonium guarroi is morphologically similar to Phialemonium inflatum. However, the new species can be distinguished from the latter due to the production of phialides which proliferate percurrently to form long chains (feature not reported in P. inflatum) and the production of smaller conidia than those of P. inflatum. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hit using the ITS sequence is the ex-type strain of P. inflatum CBS 259.39 (GenBank LT633912; Identities = 490/535 (92%), 10 gaps (1%)); using the LSU sequence was the same ex-type strain of P. inflatum (GenBank LT633912; Identities = 845/857 (99%), no gaps). The ITS-LSU phylogenetic tree corroborated the placement of our isolate as a new species of Phialemonium, being located phylogenetically close to P. inflatum.

Colour illustrations. Typical vegetation of La Palma island, Canary Islands archipelago, Spain (Photo credit: A. Decort). Moniliform cells, adelophialides, phialides and conidia. Scale bars = 10 μm.

Fungal Planet description sheets

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Phylllosticta longicauda
**Phyllosticta longicauda** Mapperson, Bransgr., R.G. Shivas & Dearnaley, *sp. nov.*

**Etymology.** Name refers to the long apical appendages on the conidia.

**Classification.** *Phyllostictaceae, Botryosphaeriales,* Dothideomycetes.

**Conidiomata.** Produced on PDA after 4 wk at 23 °C. Pycnidia black, abundant and aggregated on surface of agar, unilocular, subglobose, up to 500 μm diam; wall dark reddish brown. Conidiophores subcylindrical, up to 3-septate, 10–40 × 2–6 μm, subhyaline to hyaline, sometimes branched, often with a swollen basal cell up to 12 μm diam. Conidiogenous cells terminal, hyaline, smooth, subcylindrical, 10–20 × 2–4 μm. Conidia subglobose, broadly ellipsoidal or obovoid, with a truncate base and rounded apex, hyaline, 6–12 × 6–8 μm, aseptate, smooth, with a large subglobose vacuole, enclosed in an inconspicuous mucilaginous sheath, with an inconspicuous apical tapered hyaline appendage up to 30 μm long. Sexual morph not seen.

**Culture characteristics.** Colonies on PDA up to 3 cm diam after 1 mo at 23 °C, flattened, without aerial mycelium, margins irregular, surface grey in the central part, pale yellow in the outer part, reverse buff becoming lighter towards the margin; up to 5 cm diam after 6 mo, surface and reverse dark grey to black, margins coralloid to irregular, subhyaline conidial ooze on parts of surface.

**Typus.** AUSTRALIA, Queensland, Mt Kingsthorpe, Kingsthorpe, next to walking track at top of mountain, S27°28'48" E151°49'55", alt. 620 m, isolated as an endophyte from healthy leaves of *Eustrephus latifolius* (Asparagaceae), 8 June 2010, R.R. Mapperson RMEVL3.21 (holotype BRIP 66984, ITS sequence GenBank MH971220, MycoBank MB828031).

**Notes.** *Phyllosticta* is a large genus of foliar Dothideomycetes with more than 3,000 epithets currently listed in MycoBank. *Phyllosticta* contains many significant plant pathogenic species as well as saprobic and endophytic species (Van der Aa & Vaney 2002, Glienke et al. 2011, Wikke et al. 2013). Recent studies of rainforest plants in southern and northern Queensland (Mapperson 2014, Bransgrove unpubl.) indicated that there were many undescribed species of *Phyllosticta* that occurred as endophytes. Based on ITS sequence BLAST searches against the GenBank database, *P. longicauda* has 96 % identity to a number of fungal taxa including *P. cordylinophila* (582/604; GenBank AB454357) and *P. aristolochiicola* (580/604; GenBank NR111791). Morphologically, *P. longicauda* has larger pycnidia than *P. cordylinophila* (80–160 μm diam in *P. cordylinophila*) and longer conidial appendages than *P. aristolochiicola* (3–7 μm long in *P. aristolochiicola*). Phylogenetically, *P. longicauda* was sister to a clade containing *P. alliacea*, *P. fallopii*, *P. paracapitalesis* and *P. capitalesis*.

A Bayesian inference tree of selected *Phyllosticta* taxa based on the alignment of ITS (ITS1-5.8S-ITS2) sequences. Analyses were done with MrBayes v. 3.2.6 (Huelsenbeck & Ronquist 2001) on the Geneious v. 9.1.8 platform (Biomatters Ltd.) based on the GTR substitution model with gamma-distribution rate variation. The scale bar represents expected substitutions per site. Posterior probability values are indicated on the nodes. *Phyllosticta citricarpa* was used as the outgroup. The new species proposed in this study is indicated in **bold**.
Pluteus ludwigii


**Pluteus ludwigii** Ferisin, Justo & Dovana, *sp. nov.*

*Etymology.* Named in honour of the famous German mycologist Erhard Ludwig.

*Classification —* *Pluteaceae, Agaricales, Agaricomycetes.*

*Basidiomata medium-sized, agaricoid. Pileus* 20–30 mm, hemispherical at first, then plano-concave to concave, with straight margin sometimes reflexed, not hygrophanous, dark brown at centre, pallescent towards margin to light brown, surface glabrous, weakly to strongly venous at centre, surface occasionally cracked demonstrating whitish context underneath. *Lamellae* moderately crowded, free, slightly ventricose, up to 4 mm broad, first whitish later pink with flocculose edge. *Stipe* 30–45 × 2–4 mm, cylindrical, bulbous, pubescent, white all over, sometimes grey at the base. *Context white. Smell and taste* not distinctive. *Basidiospores* (5.3–)5.5–6.6–(6.9) × (4.9–)5.2–5.7–(6) µm, Q = (1.02–)1.09–1.21–(1.29), subglobose to broadly ellipsoid, thick-walled, non-amyloid, cyanophilous. *Cheilocystidia* 50–77 × 19–25 µm, abundant, thin-walled, hyaline, variable in shape, fusiform, narrowly utriform, subcapitate to subagulate, so numerous as to make the lamellar edge sterile. *Pileipellis* 70–90 × 22–32 µm, thin-walled, hyaline; shape variable from fusiform to clavate. *Pileipellis* a hymeniderm made up of broadly clavate or sphaeropedunculate elements, some mucronate, 33–51 × 20–30 µm, pigment intracrucial (vacuolar), light brown or brown. *Stipitipellis* a cuts of light brown, 4–10 µm wide hyphae. *Caulocystidia* present only in apical part of the stipe, clavate. *Clamp connections* absent in all tissues.

*Habitat & Distribution —* Solitary, on twigs of broadleaved trees. So far only known from the type locality.

*Typus.* Slovenia, Nova Gorica, Panovec Park, on twigs of broadleaved trees, in wet shady places, 9 Sept. 2018, G. Ferisin (holotype MCVE30136, ITS and LSU sequences GenBank MK834525 and MK834527, MycoBank MB830756).

*Additional material examined.* Slovenia, Nova Gorica, Panovec Park, on twigs of broadleaved trees, in wet shady places, 12 May 2018, G. Ferisin, MCVE30137. ITS sequence GenBank MK834526.

*Notes —* Terminology for descriptive terms is according to Vellanga (1988). Maximum-likelihood analysis of the ITS region was performed with RAxML v. 8.2.1 (Stamatakis 2014) using the GTR+G model as implemented in Geneious v. 8.2.1. Only ML bootstrap values ≥ 70% are indicated on the nodes (1,000 bootstraps).

The ITS phylogenetic tree was inferred using the Maximum likelihood (ML) method based on the GTR+G model in RAxML v. 8.2.1. Only bootstrap values ≥ 70% are indicated on the nodes (1,000 bootstraps).

The ITS phylogenetic tree was inferred using the Maximum likelihood (ML) method based on the GTR+G model in RAxML v. 8.2.1. Only bootstrap values ≥ 70% are indicated on the nodes (1,000 bootstraps).

*Colour illustrations.* Panovec Park, Nova Gorica, Slovenia. *Pluteus ludwigii* basidiomata in habitat; basidiospores; pileipellis elements; pleurocystidia and cheilocystidia. Scale bars = 10 µm.

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Podosordaria nigrobrunnea
**Podosordaria nigrobrunnea** R.F.R. Melo & A.C.S. Silva, *sp. nov.*

*Etymology.* *nigrobrunnea* refers to the colour of the stroma, dark brown to black.

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

On dung of unknown origin: Stromata erect, monopodial, dichotomously branched to finally antler-like, straight to tortuous, with one to three branching points, 46–59 mm long, 3.5–4 mm diam; stipe cylindrical near the base, eventually flattened near the first branching point, glabrous to slightly pilose at the base, dark brown to black, with surface composed of parallel to anastomosing ridges, with *ectostromal* surface cracking in a somewhat reticulated pattern towards its tip, 39–42 mm; conidigenous part usually with thin to flabelliform branches, occasionally interlaced at the tip, greyish to yellowish white, finally pale yellow, with surface composed by a powdery to fibrillose mass of mature conidia, 15–17.5 mm. *Conidiophores* formed at the stromatal branches, from the first branching point up to most tips, with a supporting hyphae branching near base to form a subhyaline to pale brown nodulisporium-like palisade, smooth, up to 90 mm long. *Conidiogenous cells* solitary, hyaline, smooth, terminal, tightly clustered, cylindrical or obconical due to the occasional swelling at its tip, weakly to non-cyanophilous, smooth, up to 90 mm long, to form a subhyaline to pale brown nodulisporium-like palisade, smooth, up to 90 μm long. *Conidiogenous part of the stromata*; conidiogenous nodulisporium-like cells, with visible denticles; conidia. Scale bars = 10 mm (stromata), 10 μm (conidiogenous part of the stromata and conidia), 5 μm (conidiogenous nodulisporium-like cells).

*Notes.* — Based on a megablast search of NCBI’s GenBank nucleotide database using the ITS sequence, the closest species (91 %) was *Podosordaria tulasnei* (GenBank AY572970.1 and KT281902.1). The MAFFT alignment consisted of 39 sequences, mainly species of *Xylarioidae*, which includes *Podosordaria, Cainia graminis* (GenBank KR092793.1) was elected as outgroup. Maximum Likelihood (ML) and Bayesian Inference (BI) analyses were constructed on the CIPRES Science Gateway portal using the RAxML-HPC BlackBox v. 8.2.10 and MrBayes v. 3.2.6, respectively. The ML phylogenetic tree is shown with both Bayesian posterior probability and maximum likelihood bootstrap support values. The sequence clustered with the *Podosordaria tulasnei* and *Xylaria vaporaria* sequences. This grouping was well supported by the BI analysis (0.99), but had low bootstrap support in the ML analysis (47 %), which may be due the limited number of *Xylariaceae* sequences in the database. Species of *Poronia* and *Podosordaria* are usually coprophilous representatives of *Xylariaceae*. The material presented here shows that both a geniculosporium-like as a nodulisporium-like asexual morph can be observed in *Podosordaria*. Stromata of *P. nigrobrunnea* were collected directly on herbivore dung at field. Although phylogenetically closely related to *P. tulasnei*, the conidial morph of *P. nigrobrunnea* presents larger (11–12.5 × 4.5–7.5 μm), variously shaped conidia, in contrast with the minute, ovate-globose conidia of *P. tulasnei*.

*Typus.* Brazil, Paraíba, Cabedelo, S7°3′58.3″ W34°51′16.39″, on dung, 2015, A. de Meiras-Ottoni (holotype URM 92162, ITS sequence GenBank MK049926, MycoBank MB829271).

*Colour illustrations.* Floresta Nacional da Restinga de Cabedelo, Paraíba State. Fresh stromata in situ; dry stromata; conidigenous part of the stroma; conidigenous nodulisporium-like cells, with visible denticles; conidia. Scale bars = 10 mm (stromata), 10 μm (conidigenous part of the stroma and conidia), 5 μm (conidigenous nodulisporium-like cells).

Maximum Likelihood tree inferred with RAxML-HPC BlackBox v. 8.2.10 from the ITS region. Bootstrap support (BS) values ≥ 50 % and Bayesian posterior probabilities (PP) ≥ 0.5 are displayed at the nodes as BS/PP. GenBank accession numbers are indicated behind the species names. Bar represents the expected substitutions per site. Type strains are indicated with superscript †. The novel species is indicated in **bold**. Alignment and tree in TreeBASE under 23082.

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Saitozyma wallum
**Saitozyma wallum** Gogorza Gondra, J. Kruse, McTaggart, Boekhout & R.G. Shivas, *sp. nov.*

**Etymology.** Derived from the word ‘wallum’, which in the Kabi Kabi language is the name for *Banksia aemula*, the plant species from which this fungus was isolated in the Sunshine Coast, Australia.

**Classification.** *Trimorphomycetaceae, Tremellales, Tremellomycetes.*

On MYPGA (Malt 0.3 %, Yeast 0.3 %, Peptone 0.5 %, Glucose 1 %, Agar 1.5 %), after 5 d at 25 °C, colony is raised, smooth, glossy, cream to white, 1–1.5 mm with an entire margin; cells are subglobose to ellipsoidal, 2–5 × 1.5–3.5 μm, occurring singly or in small clusters and proliferating by polar budding on a narrow base. Sexual spores, pseudohyphae or hyphae were not observed. Fermentation and assimilation of carbon compounds – see MycoBank MB827331.

**Typus.** AUSTRALIA, Queensland, Bribie Island, S27°00'11.3" E153°07'14.1", on leaves of *Banksia aemula* (Proteaceae), 21 Feb. 2018, R.A. Gogorza Gondra, N.V. Wolter, M.D.E. Shivas & R.G. Shivas (holotype preserved as metabolically inactive culture BRIP 66859; culture ex-type BRIP 66859, ITS and LSU sequences GenBank MH793357 and MH793355, MycoBank MB827331).

**Notes.** *Saitozyma wallum* is the fifth species described in this genus of basidiomycetous yeasts and filamentous fungi (Liu et al. 2015a). *Saitozyma* was proposed for yeasts in the *flavus* clade *sensu* Liu et al. (2015b), which is equivalent to the *podzolicus* clade *sensu* Boekhout et al. (2011). *Saitozyma* contains species formerly assigned to *Cryptococcus* and *Bullera*, namely *C. flavus*, *C. paraflavus*, *C. podzolicus* and *B. ninhibinhensis*. *Saitozyma wallum* was isolated using a spore fall technique (Pennycook & Newhook 1978) from the abaxial surface of a leaf of *Banksia aemula*, collected in wallum heathland on Bribie Island. The wallum heathland is floristically diverse and endemically rich, restricted to coastal parts of southern Queensland and northern New South Wales (Keith et al. 2014).

*Saitozyma wallum* had high sequence identity to *S. podzolica* (GenBank NR_073213, 451/483 base pairs, 93 % in the ITS region; GenBank NG_058283.1, 847/894 base pairs, 95 % in the LSU region) and *S. ninhibinhensis* (GenBank AB261011, 541/583 base pairs, 93 % in the LSU region) in a BLAST search against sequences from ex-types. *Saitozyma wallum* was sister to *S. podzolica* (CBS 6819) and an as yet unpublished *Saitozyma* species (GenBank AB720988) isolated from the bark of a cinnamon tree in India. There was intraspecific diversity within *S. wallum* as evidenced by two SNPs in the ITS region of three specimens.
**Spegazzinia bromeliacearum** S.S. Nascimento & J.D.P. Bezerra, *sp. nov.*

*Etymology.* The name refers to the host plant family, Bromeliaceae.

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

*Hyphae.* Hyaline when young and becoming brown to dark brown with age, smooth to slightly verrucose, 2–3 μm wide. *Conidiophores* straight or flexuous, smooth to slightly verrucose, pale brown, 0–(2)-septate, 17–32 × 2–3 μm. *Conidiogenous cells* monoblastic, ampulliform, smooth to slightly verrucose, (6.5–)7–8.5(–14) × (3–)4–5 μm. *Conidia* globose, initially hyaline to pale brown, becoming brown to dark brown with age, 4-celled, crossed-septate, (7.5–)11.5–19(–26.5) μm diam excluding the spines; old conidia conspicuously spinulate, with spines measuring up to 5 μm long, globose, (21–)26.5–28(–30.5) μm diam. *Fertile coils* observed.

*Culture characteristics.* Colonies at 25 °C for 7 d in darkness. On PDA, colonies reaching 5 cm diam, flat, lightly velvety, surface smooth, Olivaceous and reverse olivaceous to black, with whitish margins. On MEA, colonies growing up to 6 cm diam, greenish olivaceous, with whitish margins, flat, velvety, moderately dense, reverse brownish olivaceous to black. Conidia forming before 7 d.

*Typus.* *Brazil*, Pernambuco state, Buíque, Catimbau National Park (S8°36’35” W37°14’40”), as endophyte from leaves of *Tilandsia catimbauensis* (Bromeliaceae), June 2015, K.T.L.S. Freire (holotype URM 93059, culture ex-type URM 8084, ITS and LSU sequences GenBank MK804501 and MK809513, MycoBank MB830761).

*Notes.* The genus *Spegazzinia* was introduced by Saccardo (1880) and currently 27 records are listed in Index Fungorum and MycoBank (Feb. 2019). BLASTn searches using the ITS rDNA sequence from *S. bromeliacearum* demonstrated 92.41 % identity to *S. intermedia* (CBS 249.89, GenBank MH873861.1) and 88.52 % to *S. tessarthra* (MFLUCC 17-2249, GenBank MH071193.1), amongst others. The LSU rDNA sequence is 99.23 % identical to *Spegazzinia* sp. isolated as endophyte from *Camellia sinensis* var. assamica in Thailand (CMU328, GenBank MH734521.1) and 98.07 % to *S. intermedia* (CBS 249.89, GenBank MH873861.1). Morphologically, *S. bromeliacearum* resembles *S. intermedia*, but differs from it by the size of its conidiophores (up to 30 μm long and 1–4 μm wide) and conidia (18–28 μm diam) (Ellis 1976). The production of fertile coils in *S. bromeliacearum* has never been reported in any species of *Spegazzinia*.
Sugiyamaella trypani
Sugiyamaella trypani A. Gęsiorska & J. Pawłowska, sp. nov.

Etymology. The specific epithet ‘trypani’ was derived from the name of azo dye – trypan blue – from which the novel yeast strain was isolated.

Classification — Trichomonascaceae, Saccharomycetales, Saccharomyces.

On maltose extract agar (MEA) after 14 d at 17 °C, colony is raised, cream, cerebriform, with undulate margin. After 3 d of growth at 17 °C on 10 % ME broth, cells are sphaerical, ovoid, oblong. 1–3 × 2–8 μm, occurring singly, in pairs, in chains or in small clusters, and proliferating by multilateral budding. Pseudohyphae and hyphae formation confirmed on MEA, potato glucose agar (PGA), glucose yeast peptone agar (GYPA) and in ME broth. Blastospores on hyphae are formed on short denticles. No sexual reproduction was detected.

Typus. POLAND, Warsaw, Pole Mokotowskie Park, from soil submerged in trypan blue solution, 16 Nov. 2017, J. Pawłowska (holotype WA67193, culture ex-type CBS 15876, ITS and LSU sequences GenBank MK388412 and MK387312, MycoBank MB829450).

Notes — The genus Sugiyamaella was delimited by Kurtzman & Robnett (2007) to accommodate ascosporic yeasts which are characterised by the production of globose to elipsoidal asci with an apical cell or with a short protuberance and common formation of pseudohyphae. The genus belongs to the family Trichomonascaceae (Sena et al. 2017). The genus presently accommodates 27 species. The majority of described species was isolated from rotting plant materials or soil (Urbina et al. 2013). Representatives of this genus are known to assimilate D-xylene (Morais et al. 2013). The strain WA67193 was isolated from trypan blue solution remains after grass roots dyeing. Phylogenetic analyses using an alignment of concatenated sequences of the LSU and ITS regions showed that it represents a novel yeast species, closely related to S. valenteae and S. ayubii (85 % sequence similarity on ITS region in both cases). Physiological profiles (see MycoBank MB829450) further supported the delimitation of a new species distinct from S. valenteae and S. ayubii. The new species can be distinguished from S. valenteae and S. ayubii by its ability to grow on Sucrose, Melezitose and Glycerol as a sole carbon source; in contrast to these species it is unable to grow on Xylitol. Similar to S. ayubii, the isolate is unable to grow at 37 °C.

Colour illustrations. Pole Mokotowskie Park, Warsaw, Poland where the sample was collected. Budding cells, pseudohyphae and blastospores formation; hyphae; colony on SDA after 14 d at 20 °C; colony on water agar with 1 % trypan blue solution after 30 d at 20 °C. Scale bar = 20 μm (others), 10 μm (hyphae).
Suillus gastroflavus
Suillus gastroflavus Zvyagina, Rebriev, Sazanova & E.F. Malysheva, sp. nov.

Etymology. ‘gastro’ refers to the artificial genus Gastro suillus; ‘flavus’ refers to similarity with Suillus flavus.

Classification — Suilleaceae, Boletales, Agaricomycetes.

Mature basidiomata epigeous or subhypogeous, secotioid, 1.5–3.3 cm broad, 1.5–2.7 cm high in dry specimens and 3–5 cm broad, 5–7 cm high when fresh. Pileus completely enclosing the gleba, adpressed, subseriophobia to slightly irregular with margin fused with stipe and partial veil. Surface mucous and pale yellow in wet weather, yellow-brown in herbarium, covered by scales of yellowish brown stuck hairs. Context partly hygrophanous, fleshy, white in central part, yellowish or with brown context in KOH, arranged in fascicles. Stipe rudimental, conical, more or less centrally attached, in central part 0.5–0.8 cm long and 0.2–0.5 cm broad in herbarium specimen, 1–3 cm long and 1–1.5 cm broad when fresh, concolorous or lighter than pileus, covered by yellowish brown hairs. Context hygrophanous, white in young specimens and yellowish to lighter than pileus, covered by yellowish brown hairs.

Mature basidiomata — Peridium. Stipe rudimental, conical, more or less centrally attached, in central part 0.5–0.8 cm long and 0.2–0.5 cm broad in herbarium specimen, 1–3 cm long and 1–1.5 cm broad when fresh, concolorous or lighter than pileus, covered by yellowish brown hairs. Context hygrophanous, white in young specimens and yellowish to lighter than pileus, covered by yellowish brown hairs.

Pileus — Pileipellis disorganised, angular, big and different in size, fused with stipe and partial veil, surface mucous and pale yellow in wet weather, yellow-brown in herbarium, covered by scales of yellowish brown stuck hairs. Context partly hygrophanous, fleshy, white in central part, yellowish or with brown context in KOH, arranged in fascicles. Stipe rudimental, conical, more or less centrally attached, in central part 0.5–0.8 cm long and 0.2–0.5 cm broad in herbarium specimen, 1–3 cm long and 1–1.5 cm broad when fresh, concolorous or lighter than pileus, covered by yellowish brown hairs. Context hygrophanous, white in young specimens and yellowish to lighter than pileus, covered by yellowish brown hairs.

Notes — The greyish hymenophore and scales on the pileus indicate that our taxon belongs to a group of closely related species in Suillus viscidos s.lat. The main microscopic difference of the new species from another species of this group is in spore size and form. Suillus gastroflavus has broader spores, the majority having a narrowed and elongated apiculus. Suillus gastroflavus clearly differs from another known secotioid Suillus spp. by a greyish hymenophore. According to phylogenetic analysis, the nearest species for the new taxon is Suillus viscidos s.lat. Differences from other secotioid Suillus spp. ranged 8–12 %. Suillus gastroflavus is a third known secotioid Suillus species and first secotioid Suillus taxon in Eurasia.

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Talaromyces pernambucoensis
Talaromyces pernambucoensis R. Cruz, C. Santos, Houbraken, R.N. Barbosa, Souza-Motta, sp. nov.

Etymology. *pernambucoensis*, refers to the Brazilian State of Pernambuco (Brazil), which is the geographical location of the ex-type strain of this species.

Classification — *Trichocomaceae, Eurotiellales, Eurotiomycetes*.

On MEA: *Stipites* hyaline, smooth, (30–)50–130(–140) × 2.5–3(–3.5) μm; conidiophores symmetrical biverticillate; *metulae* generally in numbers of five, measuring (8–)10–15 × (2–)2.5–3(–3.5) μm; *phialides* acerose, (8–)10–21 × (2–)2.5–3(–3.5) μm; *conidia* globose occasionally subglobose, rough-walled to spinose, *en masse* green, 2.5–3 μm diam including ornamentation. Ascomata not observed.

Culture characteristics — MEA: Colonies 32–35 mm diam, plane, raised at centre, *conidia en masse* blue to dark green, sporulation strong, mycelium white to yellow, colony texture floccose, exudate absent, soluble pigments absent, reverse orange. CYA 25 °C, 7 d, in darkness: Colonies 17–25 mm diam, flat, mycelium greyish green, colony texture velutinous to slightly floccose, exudate redish to brown, soluble pigments absent, reverse brown to dark brown. OA 25 °C, 7 d, in darkness: Colonies 30–32 mm diam low, plane, colony texture velutinous; margins low, entire; mycelium yellowish white and white; sporulation moderate at centre; exudates absent, soluble pigments absent, reverse light yellow to white. No growth on CYAS and CREA. MEA 15 °C, 7 d, in darkness: Colonies 20–25 mm diam, plane, raised at centre, *conidia en masse* green, sporulation strong, mycelium white to yellow, colony texture floccose, exudate absent, soluble pigments absent, reverse orange. CYA 15 °C, 7 d, in darkness: Colonies 10–15 mm diam, flat, *conidia en masse* green, sporulation strong, mycelium greyish green, colony texture velutinous to slightly floccose, exudate redish to brown, soluble pigments absent, reverse brown to dark brown. MEA 37 °C, 7 d, in darkness: Colonies 25–30 mm diam, plane, raised at centre, *conidia en masse* green, sporulation strong, mycelium white to yellow, colony texture floccose, exudate absent, soluble pigments absent, reverse orange. CYA 37 °C, 7 d, in darkness: Colonies 15–20 mm diam, flat, *conidia en masse* green, sporulation strong, mycelium greyish green, colony texture velutinous to slightly floccose, exudate redish to brown, soluble pigments absent, reverse brown to dark brown.

Notes — Talaromyces pernambucoensis was isolated from soil in a Brazilian dry forest (Caatinga). Various other species are reported from this soil that seems to contain a high number of *Talaromyces*, *Penicillum* and *Aspergillus* diversity (Cruz et al. 2013, Barbosa et al. 2016). ITS, *BenA*, *RPB2* and *CaM* are commonly used to study the phylogenetic relationships within *Talaromyces* (Yilmaz et al. 2014, Chen et al. 2016, Barbosa et al. 2018). The phylogenetic relationship of *T. pernambucoensis* with other members of section *Trachysperm* is difficult to determine using single-gene phylogenies. Based on the combined dataset, consisting of ITS, *BenA*, *CaM* and *RPB2* sequences, *T. pernambucoensis* belongs to the same clade as *T. aerius* and *T. solicola*. *Talaromyces pernambucoensis* can be distinguished from *T. aerius* and *T. solicola* by its ability to grow on CYA incubated at 37 °C (15–20 mm vs no growth).

**Colour illustrations.** Catimbau National Park. Colony on MEA and CYA after 7 d at 25 °C; conidiophores and conidia. Scale bar = 10 μm.

Phylogeny based on the combined ITS, *BenA*, *CaM* and *RPB2* sequence dataset for species classified in *Talaromyces* sect. *Trachysperm* conducted in MrBayes on XSEDE and RAxML-HPC BlackBox in the CIPRES science gateway. Bayesian posterior probability and RAxML bootstrap support values are indicated at the nodes. The new species is indicated in **bold.** *Talaromyces purpurogenus* CBS 286.36 was chosen as outgroup.
Xylobolus brasiliensis
**Fungal Planet 950 – 19 July 2019**

**Xylobolus brasiliensis** Chikowski, C.R.S. de Lira, Gibertoni & K.H. Larss., *sp. nov.*

*Etymology.* Name refers to the country where the fungus was collected.

*Classification.* — *Stereaceae, Russulales, Agaricomycetes.*

*Basidiomata* perennial, stratified in several layers, resupinate to effused reflected, 1–2 mm thick, corky to woody, separated in small irregular patches (0.6–3 × 2.5–10 mm), slightly niphose. *Abhyomenial surface* glabrous, dark brown (cigar brown 16). *Context and margin* concolorous with the abhyomenial surface. *Hymenial surface* greyish brown (Clay buff 32) (Watting 1969), glabrous, smooth to slightly pilose. *Hyphal system* monomitic to pseudodimictic due to the acanthohyphidia, vertically arranged, *Hyphae* clamped.

*Notes.* Morphologically, *X. brasiliensis* is quite similar to *X. frustulatus*, but the latter has shorter acanthohyphidia (25–30 × 4–5 µm) and basidiospores (4.5–5 (–5.5) × 3–3.2 (–3.5) µm), rare pseudocystidia and elongated basidia (25–30 × 4–5 µm) (Hjortstam et al. 1988).

Based on a BLASTn search of NCBIs GenBank database, the closest hits using the ITS sequence are *X. subpileatus* (GenBank KX578084; *Identities* = 559/634 (88 %), 27 gaps (4 %)), *X. subpileatus* (GenBank KX578082; *Identities* = 558/633 (88 %), 27 gaps (4 %)) and *X. subpileatus* (GenBank KX578080; *Identities* = 558/634 (88 %), 27 gaps (4 %)). Using the LSU sequence, the closest hits are *Acanthophysium lividocaerulescens* (GenBank AY039314; *Identities* = 929/947 (98 %), 3 gaps (0 %)), *X. subpileatus* (GenBank AY039309; *Identities* = 927/947 (98 %), 4 gaps (0 %)) and *X. subpileatus* (GenBank AY039307; *Identities* = 927/947 (98 %), 3 gaps (0 %)).

Although genetically close to *X. subpileatus*, this species differs by effused-reflexed basidiomata, tuberculated hymenium when young, smaller, acute to subclindrical acanthohyphidia (20–30 × 4–5 µm) and longer basidia (20–30 × 4–5 µm) (Bernicchia & Gorjón 2010).

*Typus.* *BraziL, Paraíba,* Areia, Reserva Estadual Mata do Pau-Ferro, S6°59’ W35°45’, on decaying wood, Apr. 2013, R.S. Chikowski & G. Gibertoni 553 (holotype URM 93051, isotype in O, ITS and LSU sequences GenBank MK491193 and MK491189, MycoBank MB830132).

*Additional materials examined.* *BraziL,* Alagoas, Pilar, RPNN Fazenda de São Pedro, on decaying wood, Nov. 2001, T.B. Gibertoni TBG 106, URM 77155; Paraíba, Areia, Reserva Estadual Mata do Pau-Ferro, on decaying wood, Apr. 2013, C.R.S. Lira CL 619, URM 93052, Pernambuco, Jaqueira, Reserva Particular do Patrimônio Natural Frei Caneca, S08°42’41” W35°50’30”, on decaying wood, June 2012, R.S. Chikowski RC 71, URM 85814; ibid., Mar. 2013, R.S. Chikowski RC 552, URM 85815; ibid., Mar. 2013, R.S. Chikowski, RC 553, URM 85818; ibid, Apr. 2013, R.S. Chikowski RC 659, URM85817.

*Notes.* — *Xylodendron tingitans* can be distinguished from *X. brasiliensis* by a more concolorous hymenium, a more sapropelic context, shorter basidioles and shorter basidiospores. The latter species is characterized by a yellow-brown hymenium, a yellow context, yellow-brown spore masses, and subglobose to ellipsoid, white basidiospores. *X. brasiliensis* is characterized by a greyish brown hymenium, a greenish context, greyish brown spore masses, and subglobose to ellipsoid, yellowish-brown basidiospores. *X. brasiliensis* is also distinguished from *X. frustulatus* by its larger basidiospores (4.5–5.5 × 3–3.2(–3.5) µm) and its shorter acanthohyphidia (25–30 × 4–5 µm) (Hjortstam et al. 1988).
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