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Key words

ITS nrDNA barcodes
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Abstract Novel species of fungi described in this study include those from various countries as follows: **Antarctica**, *Cladosporium arenosum* from marine sediment sand. **Argentina**, *Kosmimatamyces alatophylus* (incl. *Kosmimatamyces* gen. nov.) from soil. **Australia**, *Aspergillus banksianus*, *Aspergillus kumbius*, *Aspergillus luteorubrus*, *Aspergillus malvicolor* and *Aspergillus nanangensis* from soil, *Erysiphe medicaginis* from leaves of *Medicago polymorpha*, *Hymenotorrendiella communis* on leaf litter of *Eucalyptus bicostata*, *Lactifluus albopicri* and *Lactifluus austropiperatus* on soil, *Macalpinomyces collinsiae* on *Eriachne benthamii*, *Marasmius vagus* on soil, *Microdochium dawsoniorum* from leaves of *Sporobolus natalensis*, *Neopestalotiopsis nebuloides* from leaves of *Sporobolus elongatus*, *Pestalotiopsis etonensis* from leaves of *Sporobolus jacquemontii*, *Phytophthora personensis* from soil associated with dying *Grevillea mccutcheonii.* **Brazil**, *Aspergillus oxumiae* from soil, *Calvatia baixaverdensis* on soil, *Geastrum calycicoriaceum* on leaf litter, *Greeneria kielmeyerae* on leaf spots of *Kielmeyera coriacea*. **Chile**, *Phytophthora aysenensis* on collar rot and stem of *Aristotelia chilensis.* **Croatia**, *Mollisia gibbospora* on fallen branch of *Fagus sylvatica.* **Czech Republic**, *Neosetophoma hnaniceana* from *Buxus sempervirens.* **Ecuador**, *Exophiala frigidotolerans* from soil. **Estonia**, *Elaphomyces bucholtzii* in soil. **France**, *Venturia paralias* from leaves of *Euphorbia paralias.* **India**, *Cortinarius balteatoindicus* and *Cortinarius ulkhagarhiensis* on leaf litter. **Indonesia**, *Hymenotorrendiella indonesiana* on *Eucalyptus urophylla* leaf litter. **Italy**, *Penicillium taurinense* from indoor chestnut mill. **Malaysia**, *Hemileucoglossum kelabitense* on soil, *Satchmopsis pini* on dead needles of *Pinus tecunumanii.* **Poland**, *Lecanicillium praecognitum* on insects' frass. **Portugal**, *Neodevriesia aestuarina* from saline water. **Republic of Korea**, *Gongronella namwonensis* from freshwater. **Russia**, *Candida pellucida* from *Exomias pellucidus*, *Heterocephalacria septentrionalis* as endophyte from *Cladonia rangiferina*, *Vishniacozyma phoenicis* from dates fruit, *Volvariella paludosa* from swamp. **Slovenia**, *Mallocybe crassivelata* on soil. **South Africa**, *Beltraniella podocarpi*, *Hamatocanthoscypha podocarpi*, *Coleophoma podocarpi* and *Nothoseiridium podocarpi* (incl. *Nothoseiridium*

Abstract (cont.)

gen. nov.) from leaves of *Podocarpus latifolius*, *Gyrothrix encephalarti* from leaves of *Encephalartos* sp., *Paraphyton cutaneum* from skin of human patient, *Phacidiella alsophilae* from leaves of *Alsophila capensis*, and *Satchmopsis metrosideri* on leaf litter of *Metrosideros excelsa*. **Spain**, *Cladophialophora cabanerensis* from soil, *Cortinarius paezii* on soil, *Cylindrium magnoliae* from leaves of *Magnolia grandiflora*, *Trichophoma cylindrospora* (incl. *Trichophoma* gen. nov.) from plant debris, *Tuber alcaracense* in calcareus soil, *Tuber buendiae* in calcareus soil. **Thailand**, *Annulohypoxylon spougei* on corticated wood, *Poaceascoma filiforme* from leaves of unknown *Poaceae*. **UK**, *Dendrostoma luteum* on branch lesions of *Castanea sativa*, *Ypsilina buttingtonensis* from heartwood of *Quercus* sp. **Ukraine**, *Myrmecridium phragmiticola* from leaves of *Phragmites australis*. **USA**, *Absidia pararepens* from air, *Juncomyces californiensis* (incl. *Juncomyces* gen. nov.) from leaves of *Juncus effusus*, *Montagnula cylindrospora* from a human skin sample, *Muriphila oklahomaensis* (incl. *Muriphila* gen. nov.) on outside wall of alcohol distillery, *Neofabraea eucalyptorum* from leaves of *Eucalyptus macrandra*, *Diabolocovidia claustri* (incl. *Diabolocovidia* gen. nov.) from leaves of *Serenoa repens*, *Paecilomyces penicilliformis* from air, *Pseudopezicula betulae* from leaves of leaf spots of *Populus tremuloides*. **Vietnam**, *Diaporthe durionigena* on branches of *Durio zibethinus* and *Roridomyces pseudoirritans* on rotten wood. Morphological and culture characteristics are supported by DNA barcodes.

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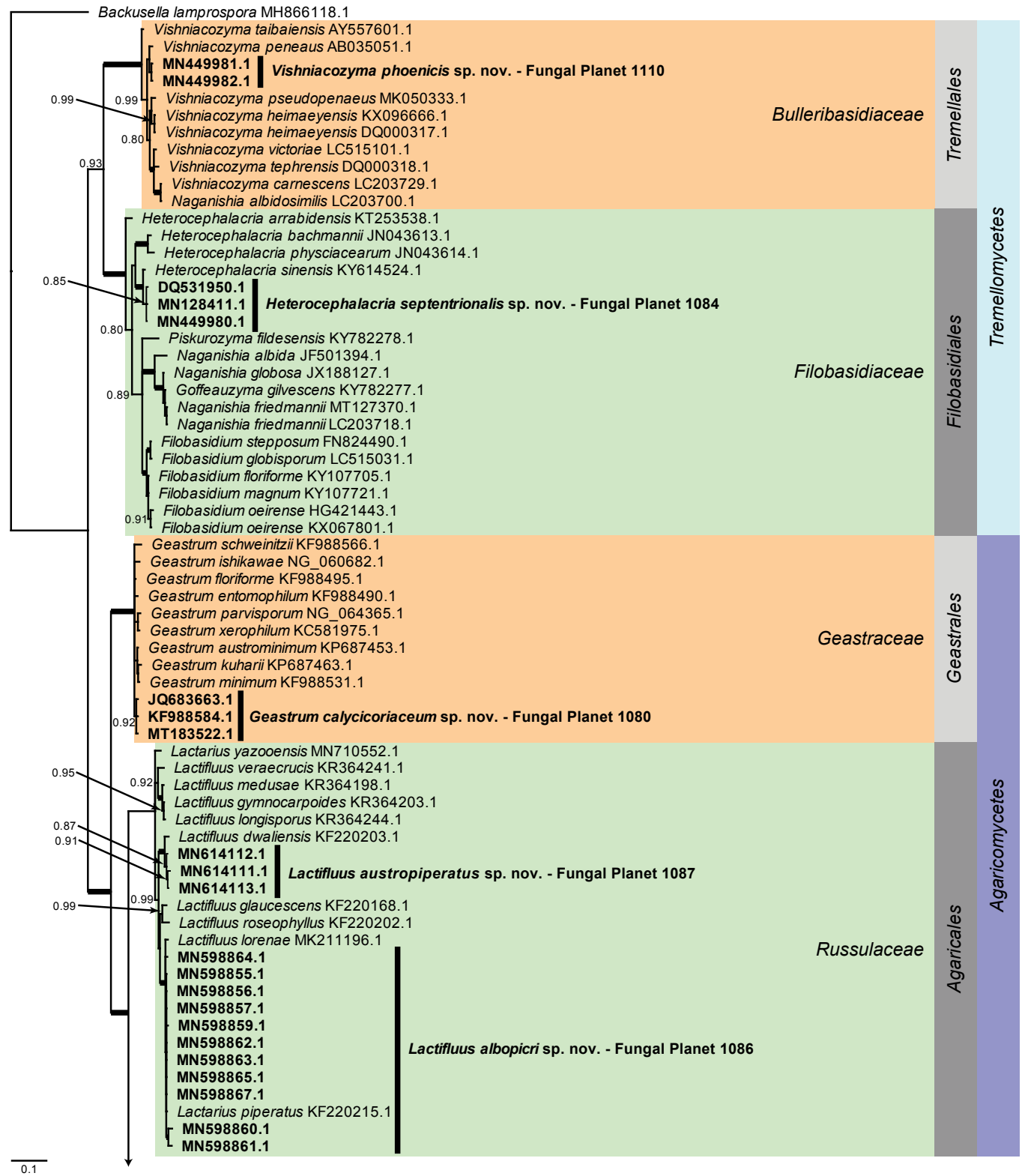
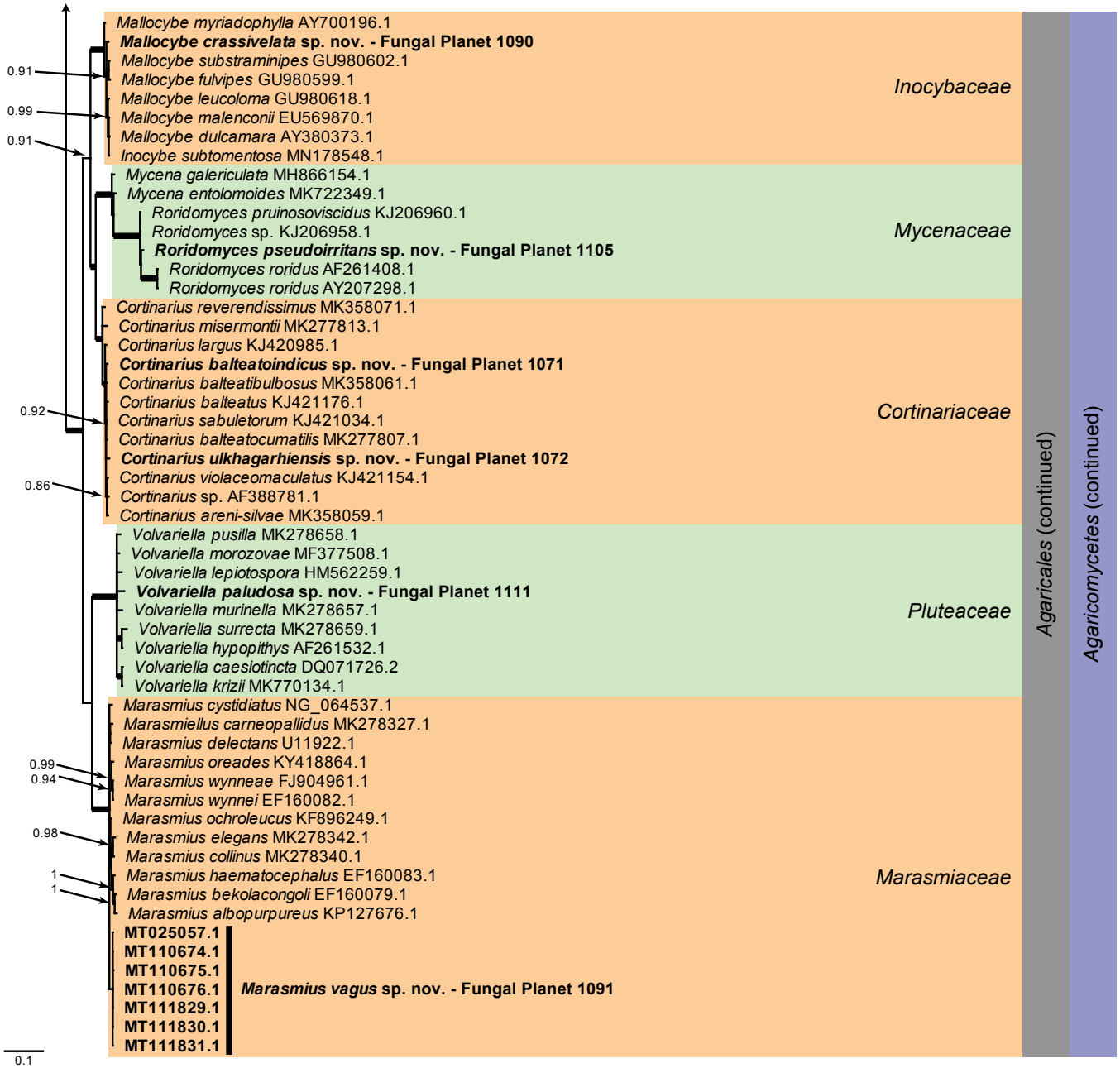
Vitelli and colleagues was supported by AgriFutures Australia, through funding from the Australian Government Department of Agriculture, Water and the Environment as part of its Rural R&D for Profit program (PRJ 15-02-005) and Queensland Department of Agriculture and Fisheries, New South Wales Department of Primary Industries, NSW Weed Biocontrol Taskforce, Bundaberg Regional Council, Gladstone Regional Council and HQPlantations Pty Ltd. Peter Johnston was supported through the Manaaki Whenua Systematics Portfolio with funding from the Science and Innovation Group of the New Zealand Ministry of Business, Innovation and Employment.

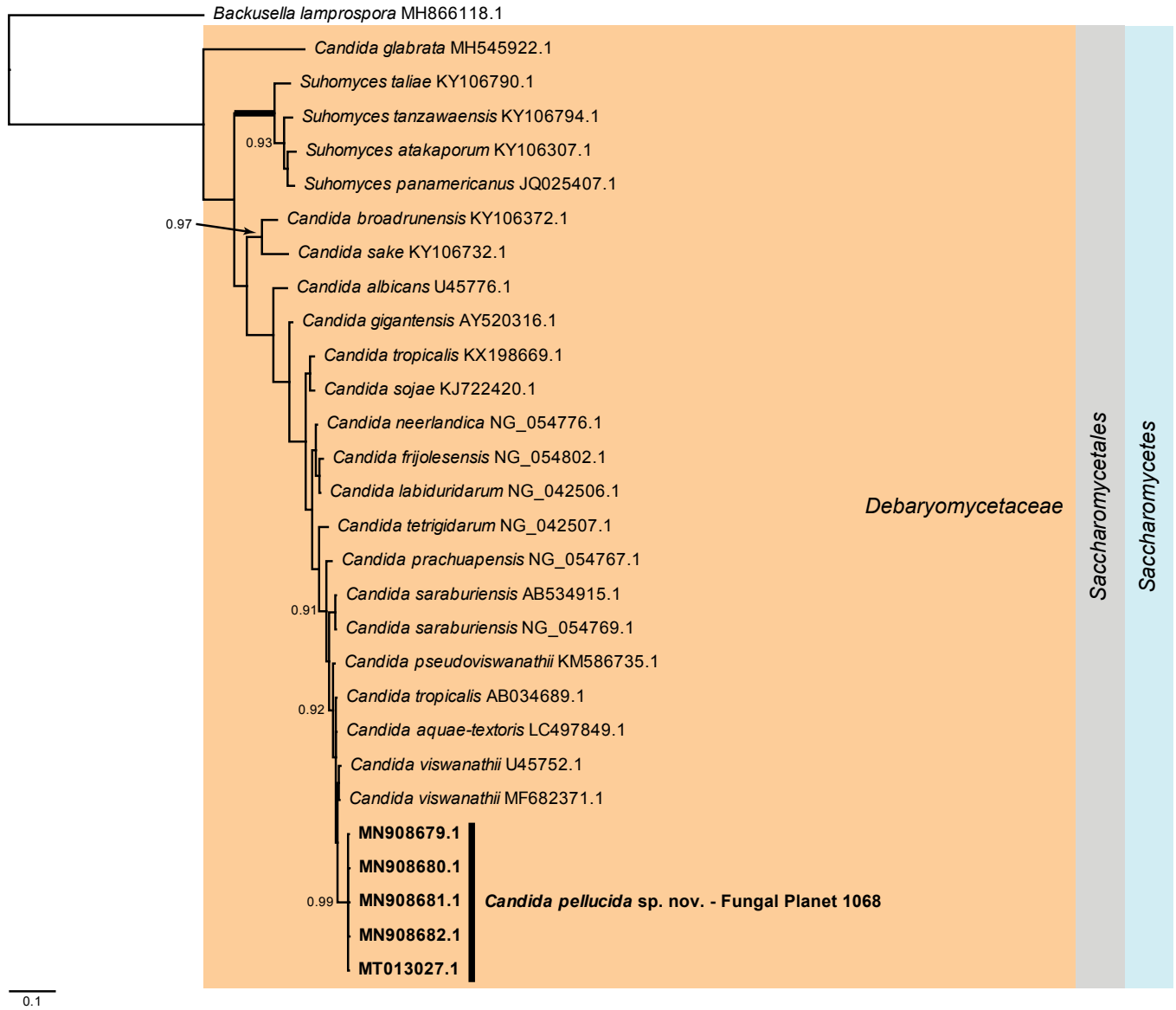


Overview *Tremellomycetes* and *Agaricomycetes* phylogeny part 1

Consensus phylogram (50 % majority rule) of 416252 trees resulting from a Bayesian analysis of the LSU sequence alignment (122 sequences including outgroup; 745 aligned positions; 487 unique site patterns) using MrBayes v. 3.2.7a (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 and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Backusella lamprospora* (GenBank MH866118.1) 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 S26166).

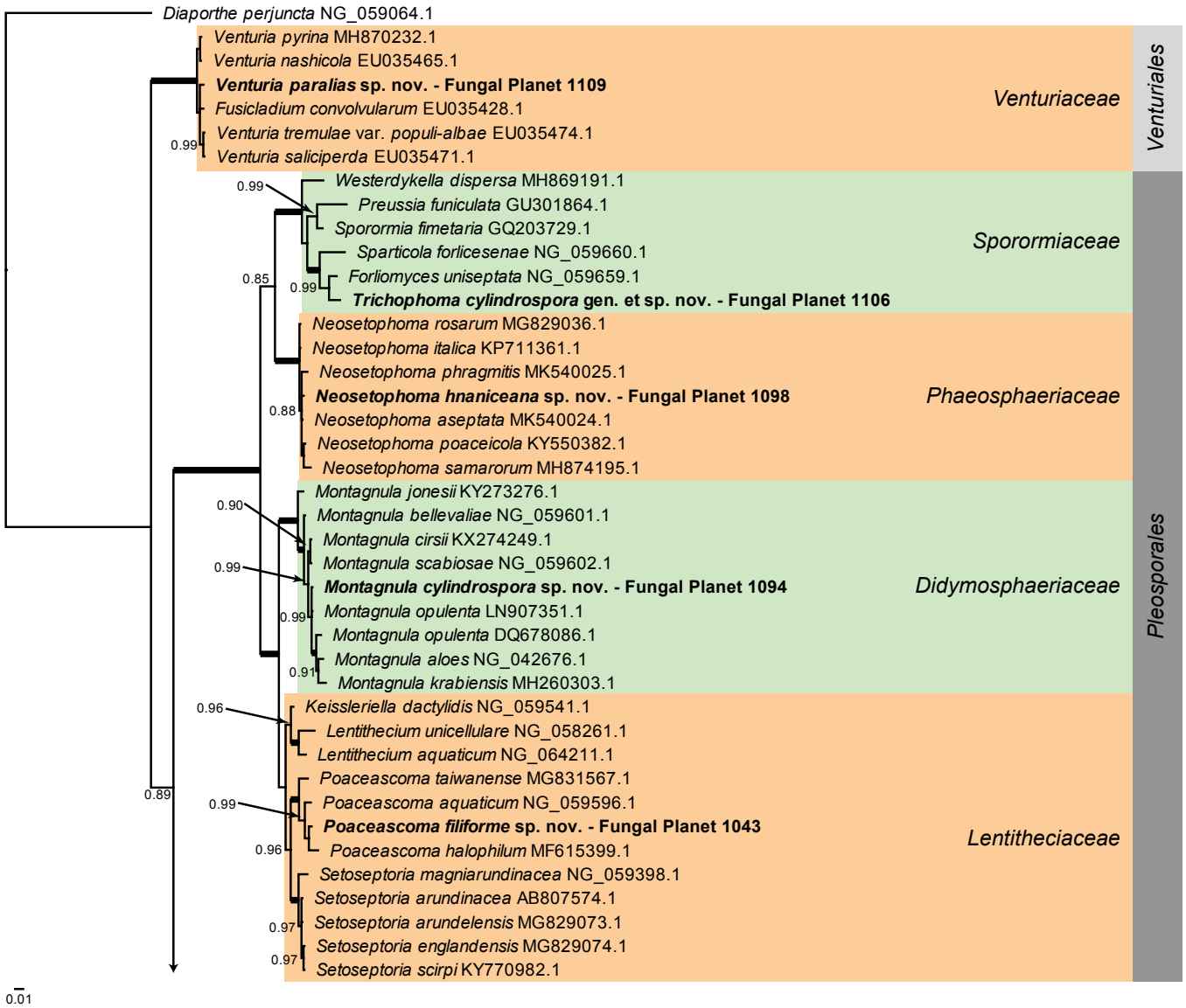


Overview *Tremellomycetes* and *Agaricomycetes* phylogeny (cont.) part 2



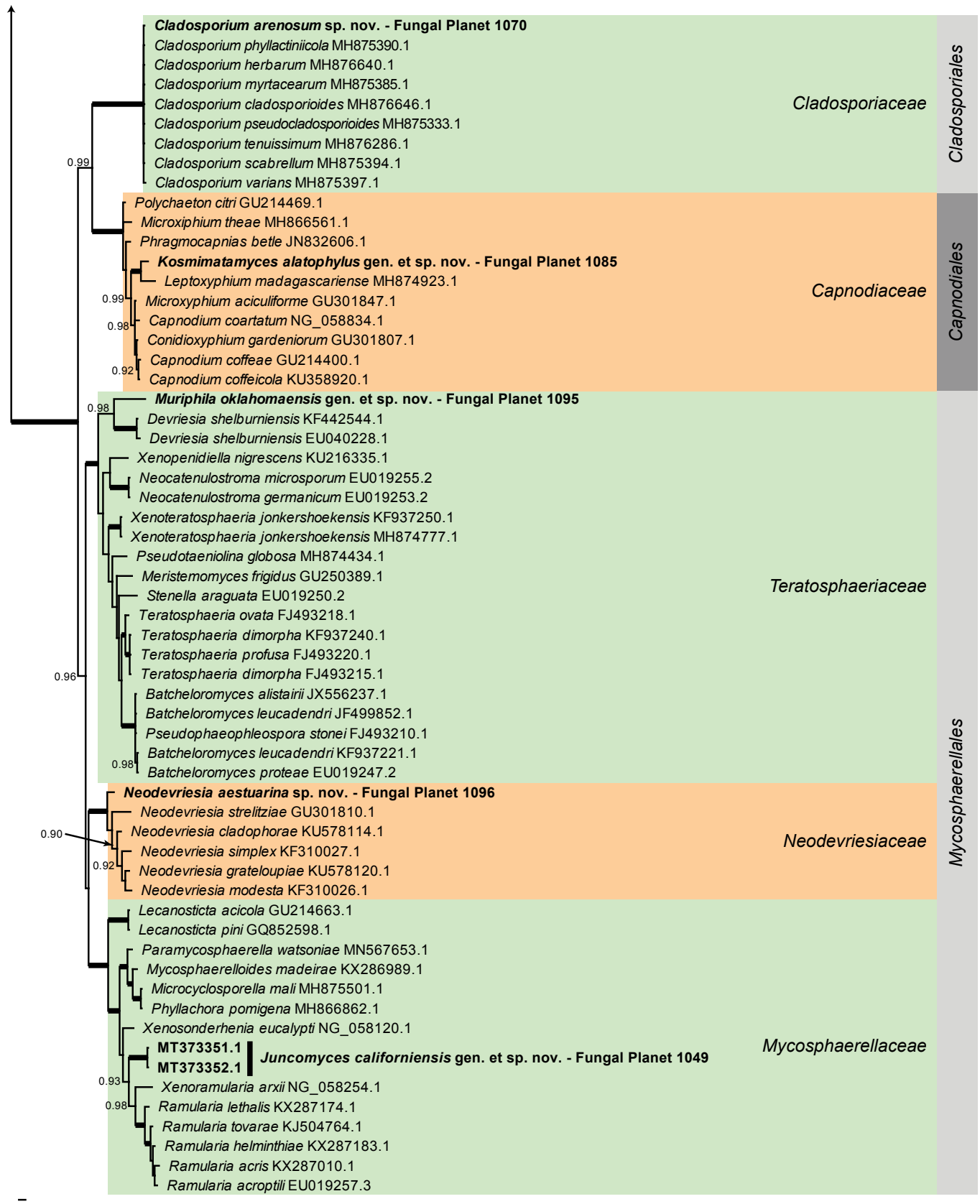
Overview *Saccharomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 198751 trees resulting from a Bayesian analysis of the LSU sequence alignment (29 sequences including outgroup; 520 aligned positions; 197 unique site patterns) using MrBayes v. 3.2.7a (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. The family, order and class 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 *Backusella lamprospora* (GenBank MH866118.1) 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 S26166).

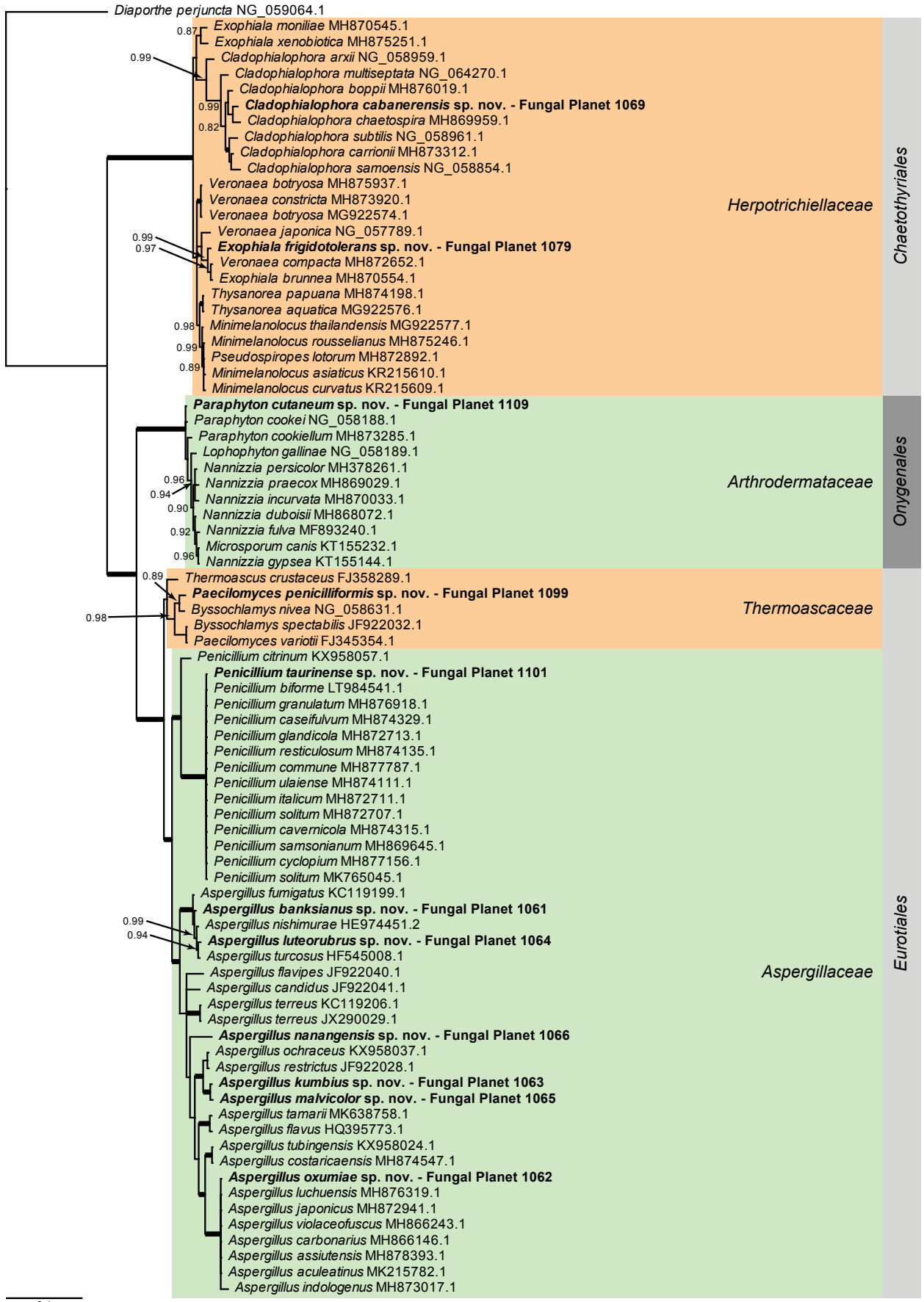


Overview *Dothideomycetes* phylogeny part 1

Consensus phylogram (50 % majority rule) of 138002 trees resulting from a Bayesian analysis of the LSU sequence alignment (101 sequences including outgroup; 816 aligned positions; 351 unique site patterns) using MrBayes v. 3.2.7a (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 *Diaporthe perjuncta* (GenBank NG_059064.1) 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 S26166).

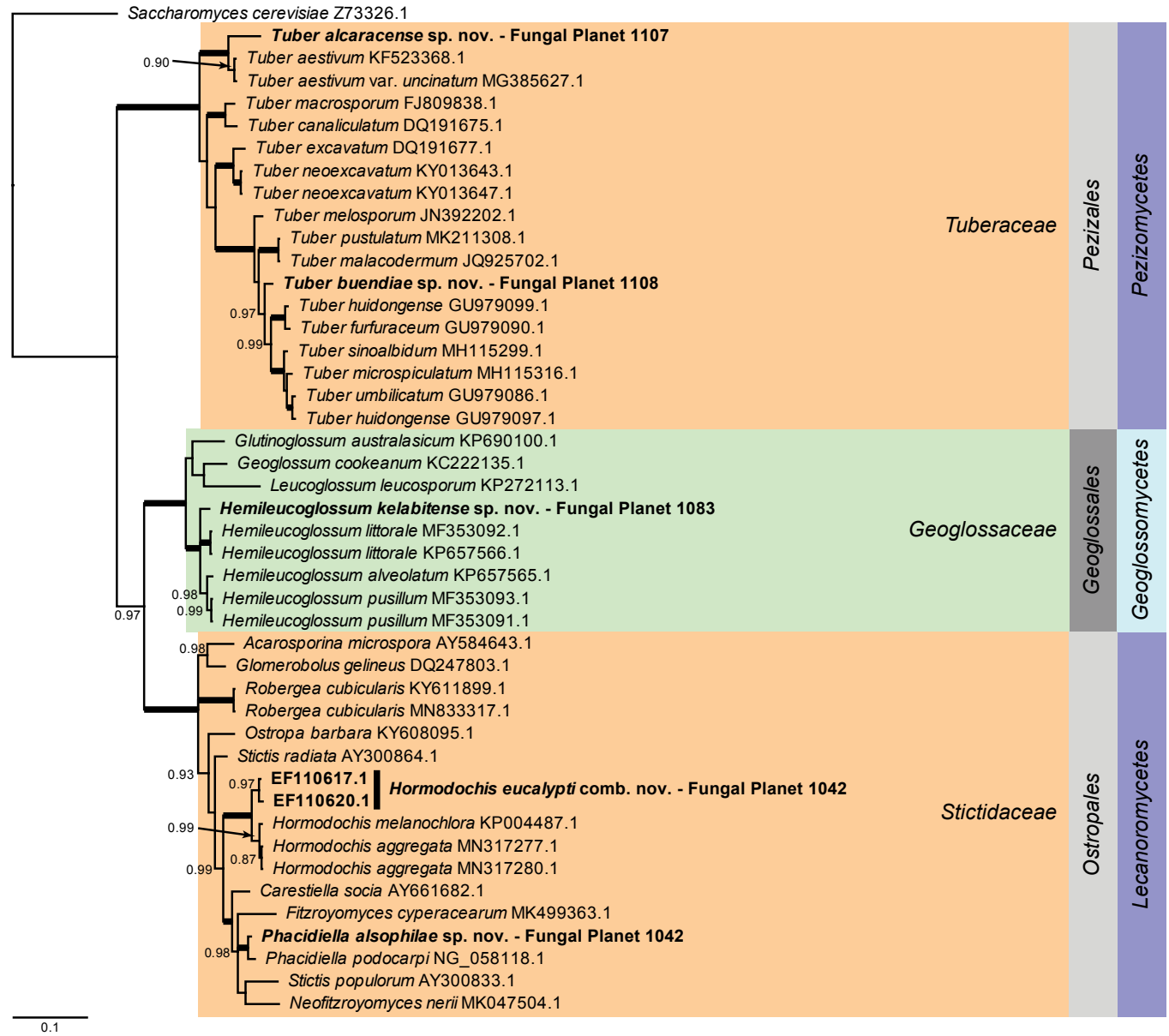


Overview *Dothideomycetes* phylogeny (cont.) part 2



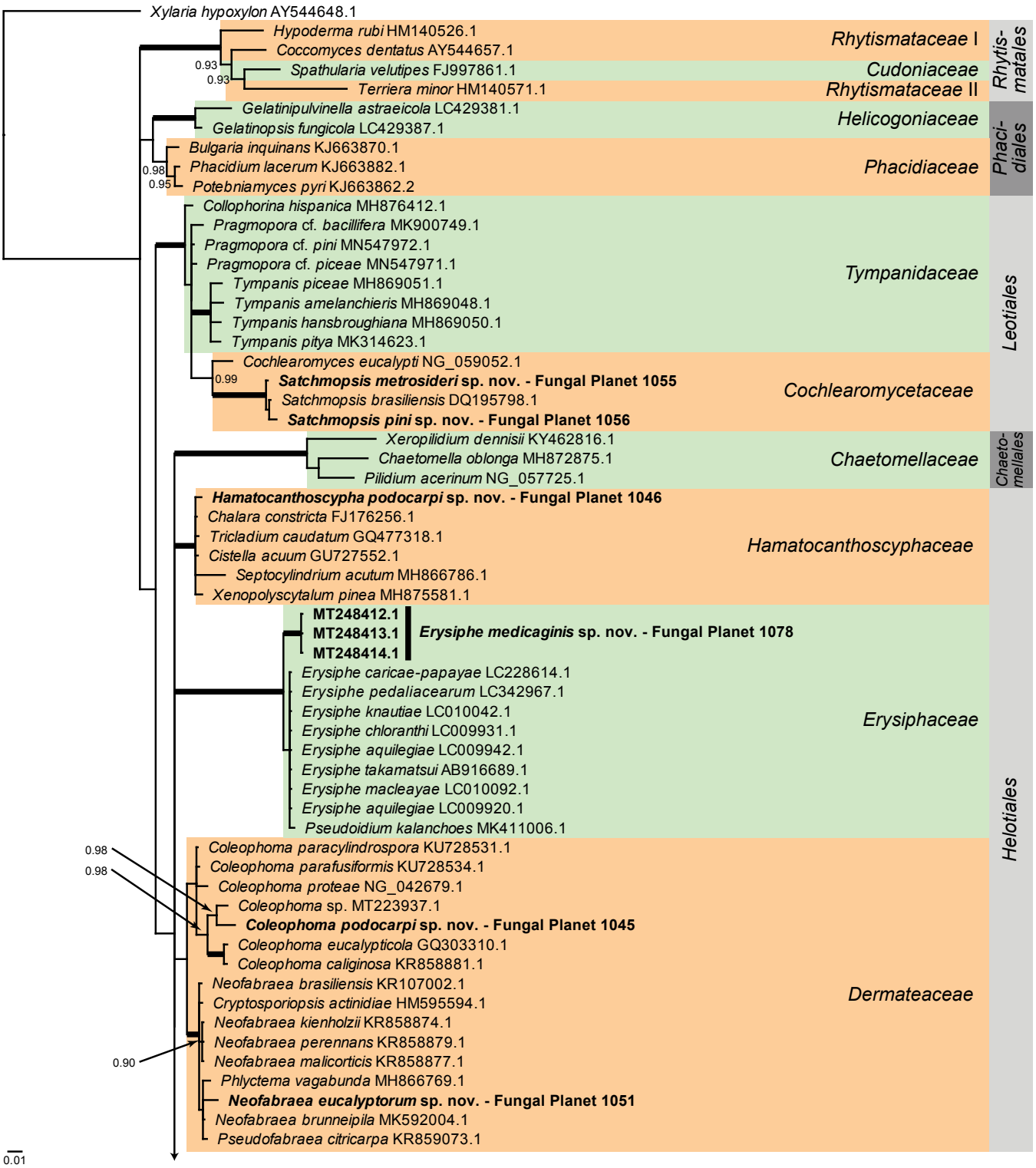
Overview *Eurotiomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 109 502 trees resulting from a Bayesian analysis of the LSU sequence alignment (82 sequences including outgroup; 826 aligned positions; 273 unique site patterns) using MrBayes v. 3.2.7a (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 *Diaporthe perjuncta* (GenBank NG_059064.1) 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 S26166).



Overview *Geoglossomycetes*, *Lecanoromycetes* and *Pezizomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 21 002 trees resulting from a Bayesian analysis of the LSU sequence alignment (45 sequences including outgroup; 784 aligned positions; 310 unique site patterns) using MrBayes v. 3.2.7a (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 *Saccharomyces cerevisiae* (GenBank Z73326.1) 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 S26166).



Overview *Leotiomycetes* phylogeny part 1

Consensus phylogram (50 % majority rule) of 634 502 trees resulting from a Bayesian analysis of the LSU sequence alignment (116 sequences including outgroup; 839 aligned positions; 328 unique site patterns) using MrBayes v. 3.2.7a (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 or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Xylaria hypoxylon* (GenBank AY544648.1) 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 S26166).

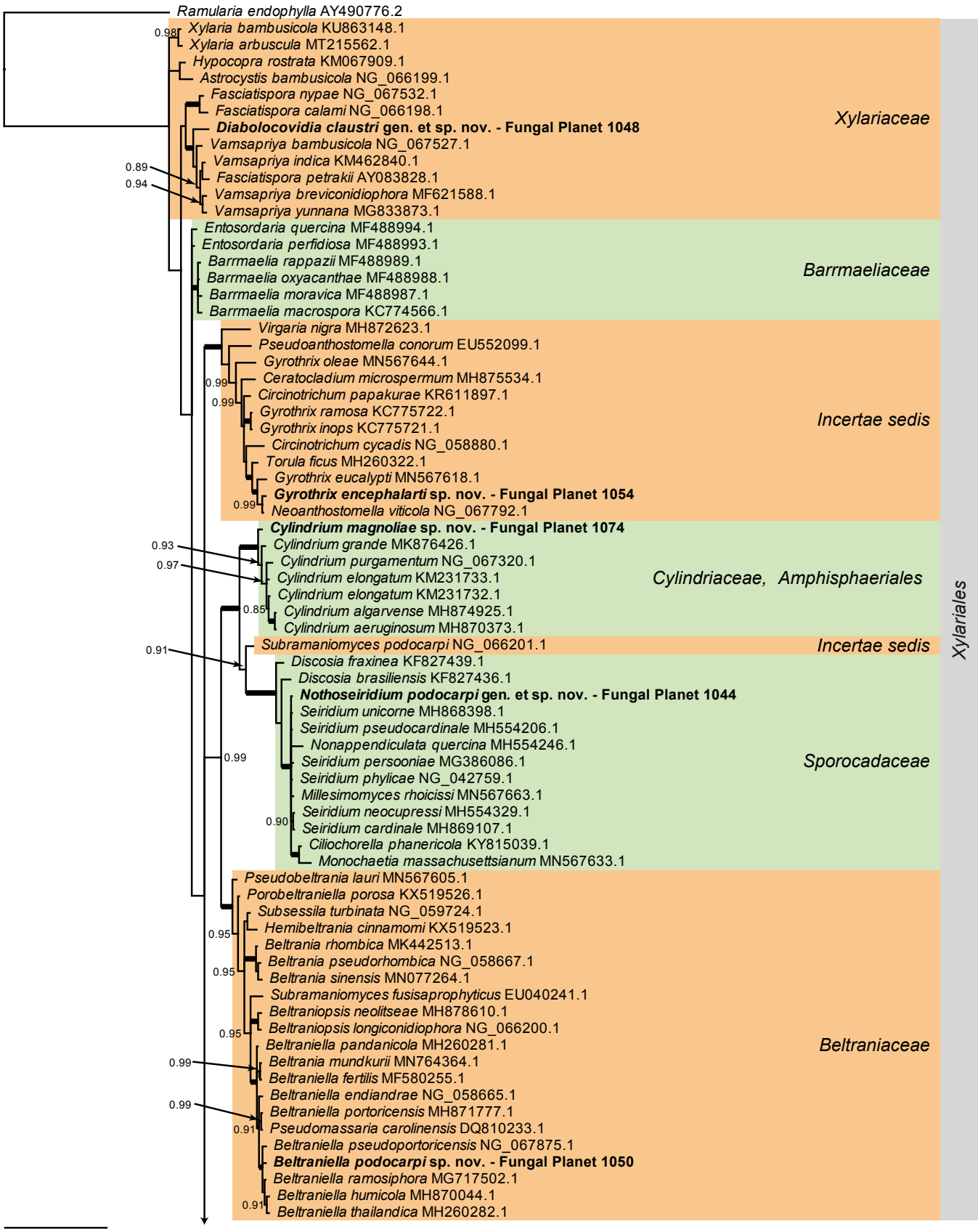
Overview *Leotiomycetes* phylogeny part 2

Overview *Cunninghamellaceae* phylogeny

Consensus phylogram (50 % majority rule) of 97 502 trees resulting from a Bayesian analysis of the LSU sequence alignment (18 sequences including outgroup; 616 aligned positions; 278 unique site patterns) using MrBayes v. 3.2.7a (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. The higher order taxonomic classification is 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 *Chytridium lagenaria* (GenBank FJ804156.1) 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 S26166).

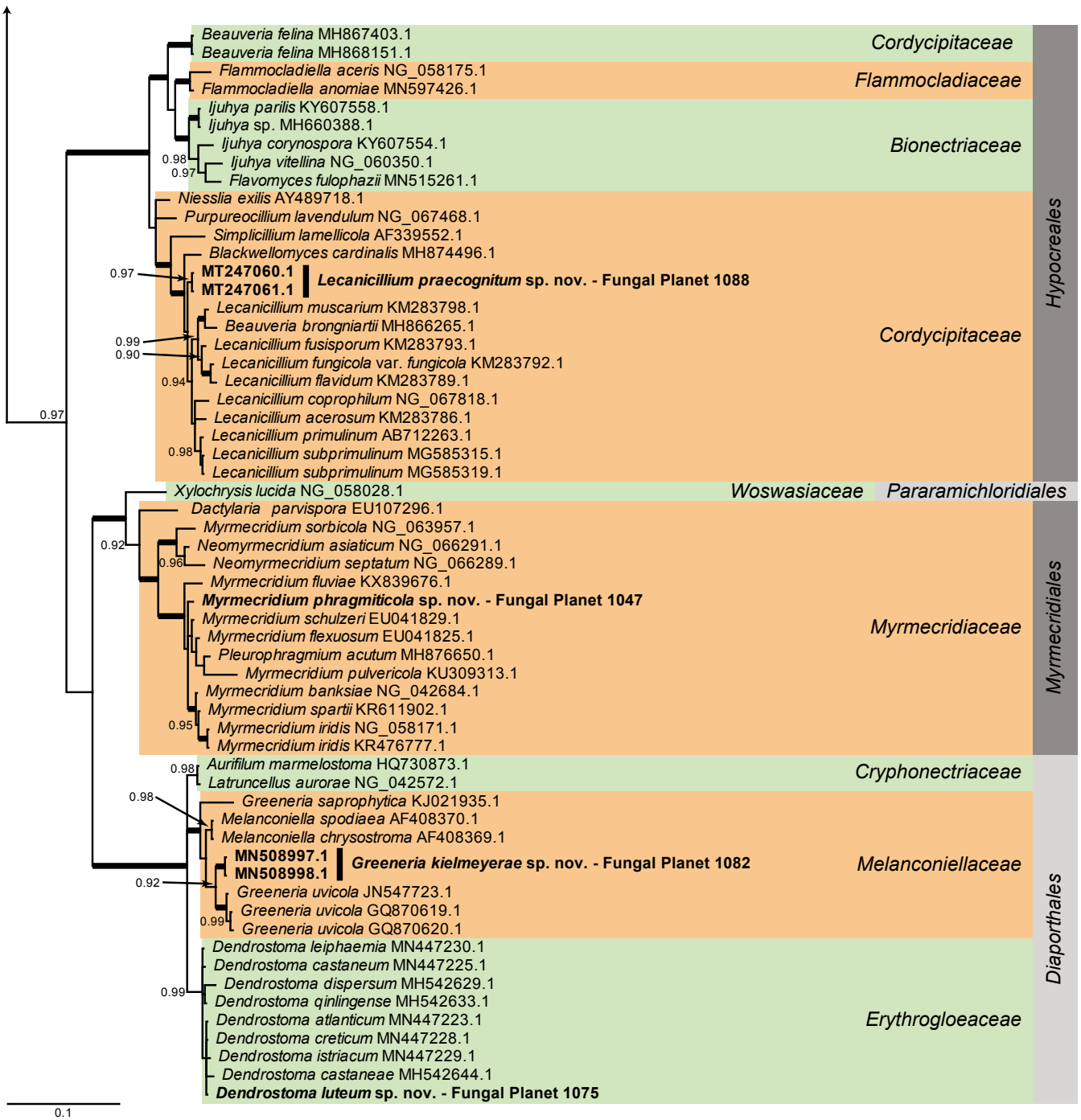
Overview *Phytophthora* phylogeny

Consensus phylogram (50 % majority rule) of 337 502 trees resulting from a Bayesian analysis of the LSU sequence alignment (19 sequences including outgroup; 1 284 aligned positions; 63 unique site patterns) using MrBayes v. 3.2.7a (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. The higher order taxonomic classification is 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 *Absidia panacisoli* (GenBank NG_063948.1) 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 S26166).



Overview *Sordariomycetes* phylogeny part 1

Consensus phylogram (50 % majority rule) of 684 002 trees resulting from a Bayesian analysis of the LSU sequence alignment (132 sequences including outgroup; 786 aligned positions; 296 unique site patterns) using MrBayes v. 3.2.7a (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 AY490776.2) 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 S26166).



Overview *Sordariomycetes* phylogeny (cont.) part 2


Phacidiella alsophilae

Fungal Planet 1042 – 29 June 2020

Phacidiella alsophilae Crous, *sp. nov.*

Etymology. Name refers to the host genus *Alsophila* from which it was isolated.

Classification — *Stictidaceae*, *Ostropales*, *Lecanoromycetes.*

Conidiomata pycnidial, erumpent, hyaline on SNA and OA, solitary or aggregated, globose, up to 300 µm diam; wall of 3–6 layers of hyaline *textura angularis*; exuding a creamy conidial mass. *Conidiophores* lining the inner cavity, subcylindrical, smooth, hyaline, 0–1-septate, giving rise to 1–2 conidiogenous cells, 4–10 × 2–3 µm. *Conidiogenous cells* terminal, smooth, subcylindrical to doliiform, proliferating sympodially at apex, 5–10 × 2–3 µm. *Conidia* solitary, hyaline, smooth, subcylindrical, flexuous, apex obtuse, base truncate, (60–)90–135(–150) × (2–)2.5(–3) µm, 15–25-septate, disarticulating into phragmospores, cylindrical with truncate ends, 4–7 µm long; flexuous conidia enclosed in mucoid sheath, 1–1.5 µm diam.

Culture characteristics — Colonies flat, spreading, surface folded, with sparse to moderate aerial mycelium and smooth, even margin, reaching 25 mm diam after 2 wk at 25 °C. On MEA surface cinnamon, reverse sepia. On PDA surface buff, reverse cinnamon. On OA surface buff.

Typus. South Africa, Western Cape Province, Knysna, on leaves of *Alsophila capensis* (= *Cyathea capensis*) (*Cyatheaceae*), Nov. 2018, *M.J. Wingfield*, HPC 2701 (holotype CBS H-24233, culture ex-type CPC 37041 = CBS 146134; ITS and LSU sequences GenBank MT373361.1 and MT373344.1, MycoBank MB835393).

Notes — *Phacidiella alsophilae* is related to *P. podocarpi* (conidia 1-septate, (7–)8–10(–12) × (2–)2.5(–3) µm; Crous et al. 2014), although they are morphologically distinct. Because the type species of *Phacidiella*, *P. salicina* (conidia aseptate, on twigs of *Salix viminalis*, Finland), is presently not known from culture, the phylogenetic relationships between species in the genus remains unresolved. *Phacidiella alsophilae* and *P. podocarpi* are thus tentatively retained in *Phacidiella*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Phacidiella podocarpi* (strain CBS 138904, GenBank NR_137934.1; Identities = 558/614 (91 %), 10 gaps (1 %)), *Fitzroyomyces cyperi* (strain CBS 143170, GenBank MG386047.1; Identities = 626/729 (86 %), 18 gaps (2 %)), and *Fitzroyomyces cyperacearum* (voucher MFLU 18-0695b, GenBank MK499349.1; Identities = 626/731 (86 %), 22 gaps (3 %)). Closest hits using the **LSU** sequence were *Phacidiella podocarpi* (strain CBS 138904, GenBank NG_058118.1; Identities = 904/930 (97 %), 10 gaps (1 %)), *Stictis radiata* (voucher Palice (ESS 21520), GenBank AY300864.1; Identities = 754/783 (96 %), no gaps), and *Carestiella socia* (strain GG2437a, GenBank AY661682.1; Identities = 793/826 (96 %), 3 gaps (0 %)).

Colour illustrations. Unfolding leaf of *Alsophila capensis*. Conidiomata on OA; conidiogenous cells giving rise to conidia. Scale bars = 10 µm.

Hormodochis eucalypti (Crous) Crous, *comb. nov*.

MycoBank MB835394.

Basionym. *Phacidiella eucalypti* Crous, Fungal Diversity 25: 30. 2007.

Description & Illustration — Crous et al. (2019b).

Typus. South Africa, Western Cape Province, Stellenbosch Mountain, on *Eucalyptus* sp., 10 Jan. 2006, *P.W. Crous* (holotype CBS H-19768, cultures ex-type CBS 120255 = CPC 12745, CPC 12746, 12747; ITS-LSU sequence GenBank EF110617.1).

Notes — The genus *Hormodochis* was resurrected by Crous et al. (2020a) to accommodate taxa with erumpent, globose pycnidial conidiomata with aseptate conidia, arranged in cylindrical chains, olivaceous brown, smooth, subcylindrical to somewhat doliiform, with truncate ends. Morphologically and phylogenetically, *Phacidiella eucalypti* is better accommodated in *Hormodochis* than *Phacidiella*, as the latter has hyaline conidia (Sutton 1980). Another genus to consider with subhyaline conidia is *Trullula*, which differs in mode of conidiogenesis and conidium morphology (see Crous et al. 2020a).

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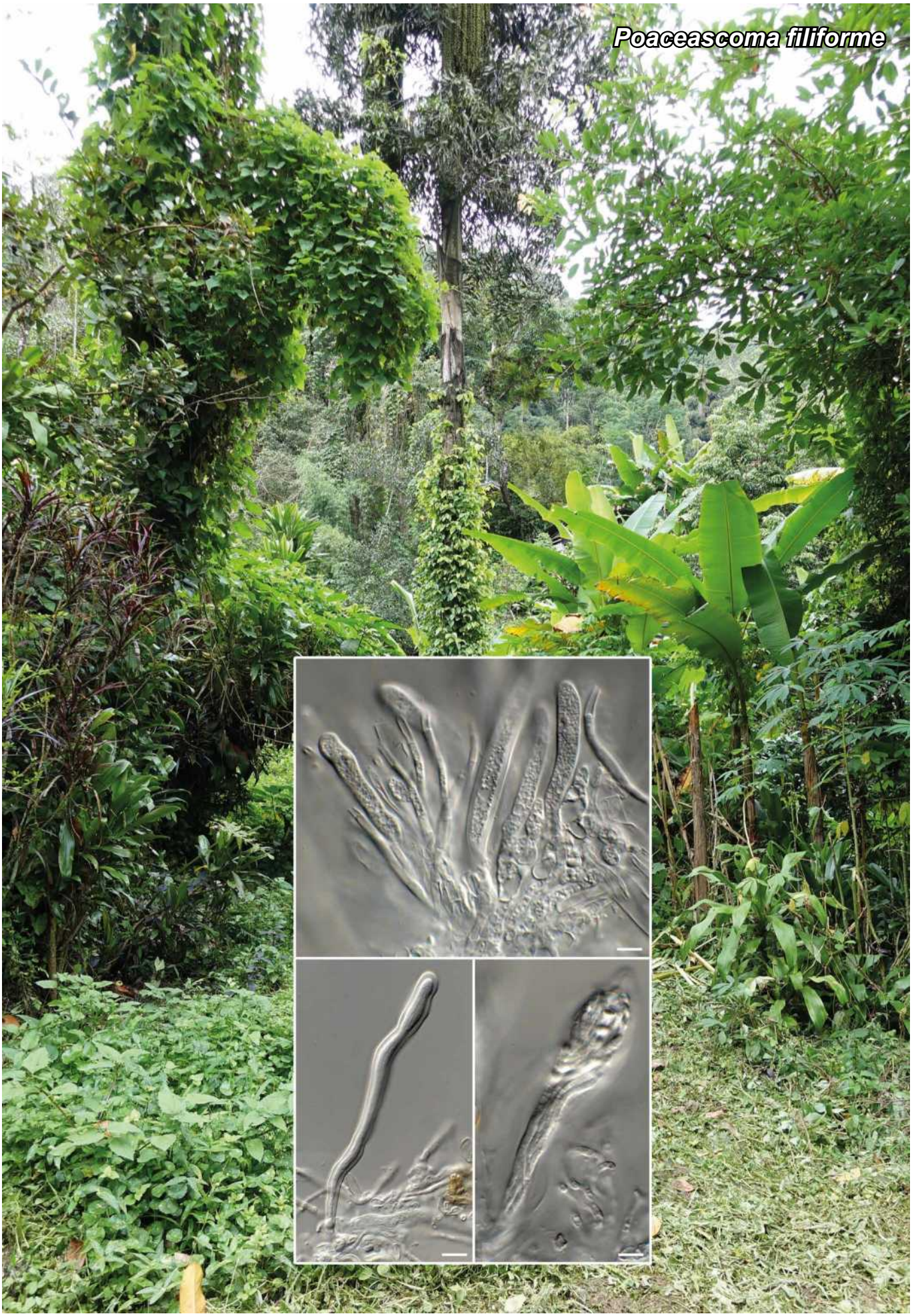
Poaceascoma filiforme

Fungal Planet 1043 – 29 June 2020

Poaceascoma filiforme Crous, *sp. nov.*

Etymology. Name refers to its characteristic filiform ascospores.

Classification — *Lentitheciaceae*, *Pleosporales*, *Dothideomycetes.*

Ascomata developing on OA, immersed in agar, globose, brown, 80–140 µm diam, with smooth wall and central ostiole; wall of 2–4 layers of brown *textura angularis*. *Pseudoparaphyses* intermingled among asci, hyphae-like, hyaline, smooth, septate, anastomosing, 2–3 µm diam. *Asci* bitunicate, subcylindrical, apex obtuse with small apical chamber, base truncate, stipitate, 80–140 × 8–10 µm. *Ascospores* multiseriate in asci, spirally twisted, hyaline, smooth, filiform, subcylindrical with obtuse ends, guttulate, 70–120 × 2–2.5 µm.

Culture characteristics — Colonies spreading, with moderate aerial mycelium and even, lobate margin, covering dish after 2 wk at 25 °C. On MEA and PDA surface and reverse olivaceous grey. On PDA surface isabelline.

Typus. Thailand, Chiang Mai, Unknown *Poaceae*, 2008, *P.W. Crous* (holotype CBS H-24361, culture ex-type CPC 33467 = CBS 146689; ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MT373362.1, MT373345.1, MT375098.1, MT375108.1 and MT375118.1, MycoBank MB835395).

Notes — *Poaceascoma* was introduced by Phookamsak et al. (2015) to accommodate a genus of saprobic ascomycetes on *Poaceae* with setose ascomata and filiform ascospores. Although *P. filiforme* lacks setae, its spirally twisted, filiform ascospores are a good fit for the genus.

Based on a megablast search of NCBIs GenBank nucleotide database, the **ITS** sequence had distant, partial hits to *Poaceascoma taiwanense* (strain MFLUCC 18-0083, GenBank MG831569.1; Identities = 269/299 (90 %), 6 gaps (2 %)), *Setoseptoria phragmitis* (strain CBS 114966, GenBank KF251250.1; Identities = 346/388 (89 %), 8 gaps (2 %)), and *Setoseptoria englandensis* (strain MFLUCC 17-0778, GenBank MG828963.1; Identities = 342/383 (89 %), 9 gaps (2 %)). Closest hits using the **LSU** sequence are *Poaceascoma aquaticum* (strain MFLUCC 14-0048, GenBank NG_059596.1; Identities = 864/872 (99 %), 1 gap (0 %)), *Poaceascoma halophilum* (strain MFLUCC 15-0949, GenBank MF615399.1; Identities = 854/864 (99 %), 3 gaps (0 %)), and *Poaceascoma taiwanense* (strain MFLUCC 18-0083, GenBank MG831567.1; Identities = 837/849 (99 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Poaceascoma aquaticum* (strain MFLUCC 14-0048, GenBank KT373846.1; Identities = 798/875 (91 %), no gaps), *Poaceascoma helicoides* (strain MFLUCC 11-0136, GenBank KP998460.1; Identities = 728/833 (87 %), no gaps), and *Wettsteinina lacustris* (strain AFTOL-ID 1592 = CBS 618.86, GenBank DQ677972.1; Identities = 741/889 (83 %), 5 gaps (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Darksidea zeta* (strain CBS 135640, GenBank KP184191.1; Identities = 324/407 (80 %), 24 gaps (5 %)), *Darksidea beta* (strain CBS 135637, GenBank KP184189.1; Identities = 323/406 (80 %), 25 gaps (6 %)), and *Darksidea gamma* (strain CBS 135633, GenBank KP184187.1; Identities = 315/396 (80 %), 25 gaps (6 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Pleurophoma acaciae* (strain CPC 29188, GenBank KY173612.1; Identities = 520/649 (80 %), 35 gaps (5 %)), *Crassiclypeus aquaticus* (strain KH 185, GenBank LC312616.1; Identities = 425/539 (79 %), 32 gaps (5 %)), and *Flabellascoma minimum* (strain KT 2040, GenBank LC312620.1; Identities = 424/540 (79 %), 36 gaps (6 %)).

Colour illustrations. Rainforest in Chiang Mai. Asci with spirally twisted ascospores. Scale bars = 10 µm.

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Nothoseiridium podocarpi

Fungal Planet 1044 – 29 June 2020

Nothoseiridium Crous, *gen. nov.*

Etymology. Name refers to the fact that it is related to *Seiridium*, but morphologically distinct from that genus.

Classification — *Sporocadaceae*, *Xylariales*, *Sordariomycetes.*

Plant pathogenic. *Conidiomata* black, round, flattened, acervular; wall of several layers of brown *textura epidermoidea*. *Conidiophores* reduced to conidiogenous cells, arising from basal layers of stroma, hyaline, smooth, subcylindrical to ampulliform, annellidic. *Conidia* fusoid, slightly curved, smooth-walled, guttulate, pale brown, unequally 4-euseptate; basal cell obconic with truncate hilum, hyaline; median cells pale brown; apical cell obtuse, hyaline; apical and basal appendage filiform, flexuous, unbranched, excentric.

Type species. Nothoseiridium podocarpi Crous.
MycoBank MB835396.

Nothoseiridium podocarpi Crous, *sp. nov.*

Etymology. Name refers to the host genus *Podocarpus* from which it was isolated.

Associated with brown leaf spots. *Conidiomata* (on *Podocarpus* leaves and on SNA), black, round, flattened, acervular, 300–400 µm diam; wall of several layers of brown *textura epidermoidea*, splitting open all along outer margin, appearing saucer-shaped on leaf. *Conidiophores* reduced to conidiogenous cells, arising from basal layers of stroma, hyaline, smooth, subcylindrical to ampulliform, annellidic, 5–10 × 2.5–3 µm. *Conidia* fusoid, slightly curved, smooth-walled, guttulate, pale brown, unequally 4-euseptate; basal cell obconic with truncate hilum, hyaline; median cells pale brown; apical cell obtuse, hyaline. Apical cell 2.5–4 µm long; second cell 2.5–4 µm long; third cell 4–5 µm long; fourth cell 12–14 µm long; basal cell 3–4 µm long; conidia (22–)24–25(–27) × (2.5–)3 µm; apical appendage filiform, flexuous, unbranched, excentric, 7–10 µm long; basal appendage filiform, flexuous, unbranched, excentric, 6–7 µm long.

Culture characteristics — Colonies spreading, with moderate aerial mycelium and smooth, lobate margin, covering dish after 2 wk at 25 °C. On MEA surface smoke grey, reverse olivaceous grey. On PDA surface and reverse olivaceous grey. On OA surface pale olivaceous grey.

Typus. South Africa, Western Cape Province, Knysna, on leaf spots of *Podocarpus latifolius* (*Podocarpaceae*), Nov. 2018, *M.J. Wingfield*, HPC 2710 (holotype CBS H-24362, culture ex-type CPC 36967 = CBS 146690; ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MT373363.1, MT373346.1, MT375099.1, MT375109.1 and MT375119.1, MycoBank MB835397).

Notes — *Seimatosporium* and allied genera have recently been revised (Bonthond et al. 2018, Liu et al. 2019), with 23 genera being accepted in *Sporocadaceae*. *Nothoseiridium podocarpi* is allied to *Seiridium* (5-septate, appendaged conidia) and *Nonappendiculata* (3-septate, non-appendaged conidia), but is distinct in having 4-septate, fusoid conidia with unbranched, excentric apical and basal appendages. *Nothoseiridium* is further characterised by forming submerged acervuli that break through the epidermis with a saucer-like appearance, being associated with prominent leaf spots. It is not possible to distinguish *Nothoseiridium* from *Seiridium* based on LSU sequence data.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Seimatosporium lichenicola* (as *Discostroma fuscellum*; strain GSAA-0182, GenBank JF320818.1; Identities = 542/571 (95 %), 7 gaps (1 %)), *Sporocadus rosarum* (as *Seimatosporium pseudorosarum*; strain MFLUCC 14-0466, GenBank KT284775.1; Identities = 561/592 (95 %), 4 gaps (0 %)), *Seimatosporium lichenicola* (strain CBS 160.25, GenBank MH854829.1; Identities = 561/592 (95 %), 6 gaps (1 %)) and *Millesimomyces rhoicissi* (strain CPC 35297, GenBank NR_166350.1; Identities = 566/598 (95 %), 12 gaps (2 %)). Closest hits using the **LSU** sequence are *Seiridium unicorne* (strain CBS 320.51, GenBank MH868398.1; Identities = 870/870 (100 %), no gaps), *Seiridium pseudocardinale* (strain CBS 122613, GenBank MH554206.1; Identities = 834/834 (100 %), no gaps), and *Seiridium phylicae* (strain CPC 19962, GenBank NG_042759.1; Identities = 870/871 (99 %), 1 gap (0 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Seiridium cardinale* (strain CPC 23791, GenBank LT853119.1; Identities = 721/838 (86 %), no gaps), *Seiridium unicorne* (strain CBS 143873, GenBank MK058478.1; Identities = 636/741 (86 %), no gaps), and *Seiridium aquaticum* (voucher MFLU 18-1627, GenBank MN156531.1; Identities = 642/748 (86 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Seiridium marginatum* (strain CBS 140403, GenBank LT853199.1; Identities = 344/417 (82 %), 30 gaps (7 %)), *Seiridium papillatum* (strain CBS 340.97, GenBank LT853200.1; Identities = 332/404 (82 %), 22 gaps (5 %)), and *Seiridium podocarpi* (strain CBS 137995, GenBank LT853198.1; Identities = 331/403 (82 %), 31 gaps (7 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Seiridium cupressi* (strain CBS 224.55, GenBank LT853230.1; Identities = 652/791 (82 %), 46 gaps (5 %)), *Seiridium papillatum* (strain CBS 340.97, GenBank LT853250.1; Identities = 636/771 (82 %), 31 gaps (4 %)), and *Seiridium podocarpi* (strain CBS 137995, GenBank LT853248.1; Identities = 638/777 (82 %), 39 gaps (5 %)).

Colour illustrations. Leaf spot on *Podocarpus latifolius* with *Nothoseiridium podocarpi* and *Coleophoma podocarpi*. Conidioma on PNA; conidioma on OA; conidiogenous cells; conidia. Scale bars: conidiomata = 400 µm, all others = 10 µm.

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Coleophoma podocarpi

Fungal Planet 1045 – 29 June 2020

Coleophoma podocarpi Crous, *sp. nov.*

Etymology. Name refers to the host genus *Podocarpus* from which it was isolated.

Classification — *Dermateaceae*, *Helotiales*, *Leotiomycetes.*

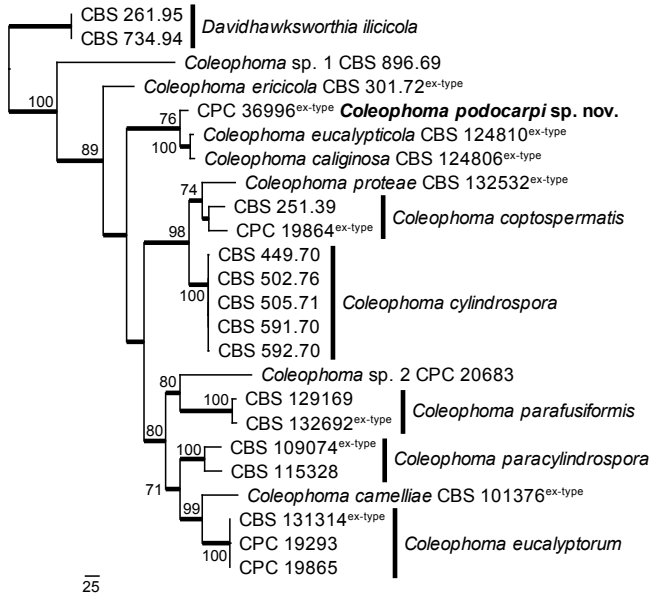
Associated with prominent brown leaf spots. *Conidiomata* pycnidial, grey-brown, 200–300 µm diam, with central ostiole. *Conidiophores* lining the inner cavity, intermingled among paraphyses, 0–2-septate, 20–35 × 5–7 µm, or reduced to conidiogenous cells, hyaline, smooth, guttulate, doliiform to ampulliform, 7–10 × 3–4 µm. *Paraphyses* intermingled among conidiophores, hyaline, smooth, cylindrical, aseptate, 3–4(–6) µm diam, up to 30 µm long, with age becoming multiseptate and with intercalary conidiogenous cells. *Conidiogenous cells* hyaline, smooth, guttulate, doliiform to ampulliform, 7–10 × 3–4 µm, phialidic, with minute periclinal thickening. *Conidia* aseptate, hyaline, smooth, guttulate, subcylindrical to fusoid to irregular, straight to somewhat curved, apex subobtuse, base truncate, (9–)14–22(–25) × (3.5–)4–5(–7) µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and feathery, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA and PDA surface brick, reverse vinaceous with diffuse vinaceous pigment. On OA surface brick.

Typus. South Africa, Western Cape Province, Knysna, on leaf spots of *Podocarpus latifolius* (*Podocarpaceae*), Nov. 2018, *F. Roets*, HPC 2697 (holotype CBS H-24347, culture ex-type CPC 36996 = CBS 146625; ITS, LSU, *tef1* and *tub2* sequences GenBank MT373364.1, MT373347.1, MT375110.1 and MT375120.1, MycoBank MB835398).

Notes — *Coleophoma* includes species that are plant pathogenic or saprobic, occurring on a wide range of plant hosts (Crous et al. 2019b, 2020b). The genus was revised by Crous & Groenewald (2016), and shown to reside in the *Dermateaceae* (*Leotiomycetes*), with morphologically similar taxa also clustering in *Dothideomycetes*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Coleophoma parafusiformis* (strain CBS 132692, GenBank NR_154807.1; Identities = 525/550 (95 %), 3 gaps (0 %)), *Coleophoma ericicola* (strain CBS 301.72, GenBank NR_154805.1; Identities = 523/549 (95 %), no gaps), and *Coleophoma xanthosiae* (strain CPC 29214, GenBank NR_154838.1; Identities = 512/543 (94 %), 2 gaps (0 %)). Closest hits using the **LSU** sequence are *Coleophoma paracylindrospora* (strain CBS 109074, GenBank KU728531.1; Identities = 847/864 (98 %), no gaps), *Coleophoma parafusiformis* (strain CBS 132692, GenBank KU728534.1; Identities = 846/864 (98 %), no gaps), and *Coleophoma proteae* (strain CBS 132532, GenBank NG_042679.1; Identities = 845/864 (98 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Coleophoma ericicola* (strain CBS 301.72, GenBank KU728566.1; Identities = 428/500 (86 %), 22 gaps (4 %)), *Coleophoma parafusiformis* (strain CBS 132692, GenBank KU728573.1; Identities = 411/489 (84 %), 30 gaps (6 %)), and *Coleophoma eucalyptorum* (strain CPC 19865, GenBank KU728569.1; Identities = 402/483 (83 %), 31 gaps (6 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Coleophoma xanthosiae* (strain CPC 29214, GenBank KY173598.1; Identities = 399/449 (89 %), 2 gaps (0 %)), *Coleophoma ericicola* (strain KU728605.1, GenBank KU728605.1; Identities = 383/439 (87 %), 5 gaps (1 %)), and *Coleophoma proteae* (strain CBS 132532, GenBank KU728613.1; Identities = 384/442 (87 %), 9 gaps (2 %)).



The first of two equally most parsimonious trees obtained from a phylogenetic analysis of the *Coleophoma* ITS/*actA*/*tef1*/*tub2* alignment (24 strains including the outgroup; 1 324 characters including alignment gaps analysed: 766 constant, 126 variable and parsimony-uninformative and 432 parsimony-informative). PAUP v. 4.0b10 (Swofford 2003) was used to analyse the data. The novel species was added to the alignment of Crous & Groenewald (2016), where also the GenBank accession numbers of the reference sequences can be found. The tree was rooted to two strains of *Davidhawksworthia ilicicola* and the scale bar indicates the number of changes. Parsimony bootstrap support values higher than 70 % are shown at the nodes (PBS/NJBS) and the novel species is highlighted in **bold**. Type status is indicated in superscript. Branches present in the strict consensus tree are thickened. Tree statistics: TL = 1501, CI = 0.640, RI = 0.745, RC = 0.477. The alignment and tree were deposited in TreeBASE (Submission ID S26166).

Colour illustrations. Knysna forest with waterfall. Conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

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Hamatocanthoscypha podocarpi

Fungal Planet 1046 – 29 June 2020

Hamatocanthoscypha podocarpi Crous, *sp. nov.*

Etymology. Name refers to the host genus *Podocarpus* from which it was isolated.

Classification — *Hamatocanthoscyphaceae*, *Helotiales*, *Leotiomycetes.*

Mycelium consisting of hyaline, branched, 1.5–2 µm diam hyphae. *Conidiophores* smooth, pale to medium brown, erect, solitary or in clusters, subcylindrical, branched below, 0–4-septate, 12–60 × 3–5 µm. *Conidiogenous cells* 13–40 × 3–4 µm, integrated, terminal and intercalary, subcylindrical, pale brown, smooth, base tapering to long cylindrical, apical venter, 3–9 µm long, slightly flared or not, 2–3 µm diam. *Conidia* in long unbranched chains, aseptate, hyaline, smooth, guttulate, subcylindrical with truncate ends, (6–)7–8(–9) × (1.5–)2 µm.

Culture characteristics — Colonies flat, spreading, with folded surface, moderate aerial mycelium and smooth, lobate margin, reaching 20 mm diam after 2 wk at 25 °C. On MEA surface honey, reverse cinnamon. On PDA surface honey with isabelline in outer region, reverse isabelline. On OA surface honey.

Typus. South Africa, Western Cape Province, Knysna, on leaf spots of *Podocarpus latifolius* (*Podocarpaceae*), Nov. 2018, *M.J. Wingfield*, HPC 2710 (holotype CBS H-24349, culture ex-type CPC 37055 = CBS 146626; ITS, LSU, *actA* and *rpb2* sequences GenBank MT373365.1, MT373348.1, MT375095.1 and MT375100.1, MycoBank MB835399).

Notes — The genus *Chalara* as circumscribed by Nag Raj & Kendrick (1976) is polyphyletic and awaits revision. *Hamatocanthoscypha podocarpi* is phylogenetically allied to the type species of *Hamatocanthoscypha*, *H. laricionis* (Svrček 1977), and placed in this genus based on DNA similarity. Several species of '*Chalara*' have been described from *Podocarpus*, namely *C. brevipes* (conidia (6–)8.9(–12) × 1.5–2 µm), *C. novaezelandiae* (conidia (5–)6.4(–8) × 1–1.5 µm), *C. cylindrosperma* (conidia (5.5–)11(–17) × (1.5–)1.9(–2.5) µm), *C. fusidioides* (conidia (4.5–)7.7(–12) × (1.5–)2.1(–3.5) µm), *C. acuaria* (conidia (12–)16(–20) × (2–)2.7(–3.5) µm) and *C. bicolor* (conidia 7-septate, (45–)50–60(–71) × 5.5–6 µm) (Nag Raj & Kendrick 1975). Of these, *H. podocarpi* is most similar to *C. brevipes*, but can be distinguished in having smaller conidiogenous cells, and conidiophores that are aggregated in clusters.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to numerous sequences wrongly labelled as '*Infundichalara microchona*' (e.g., strain KRP75-5, GenBank HM036588.1; Identities = 531/537 (99 %), 2 gaps (0 %)), *Chalara holubovae* (strain CCF 3978, GenBank NR_154760.1; Identities = 483/501 (96 %), 3 gaps (0 %)), and *Hamatocanthoscypha laricionis* (voucher TNS-F13530, GenBank JN033441.1; Identities = 540/567 (95 %), 4 gaps (0 %)). Closest hits using the **LSU** sequence are *Leptodontidium beauverioides* (strain CBS 672.76, GenBank MH872794.1; Identities = 836/840 (99 %), no gaps), *Tricladium caudatum* (strain CCM F-13498, GenBank GQ477318.1; Identities = 833/837 (99 %), no gaps), and *Chalara constricta* (strain CBS 248.76, GenBank FJ176256.1; Identities = 825/829 (99 %), no gaps). No significant hits were obtained when the ***actA*** and ***rpb2*** sequences were used in blastn and megablast searches.

Colour illustrations. Walkway in the Knysna forest. Conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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Myrmecridium phragmiticola

Fungal Planet 1047 – 29 June 2020

Myrmecridium phragmiticola Crous & Akulov, *sp. nov.*

Etymology. Name refers to the host genus *Phragmites* from which it was isolated.

Classification — *Myrmecridiaceae*, *Myrmecridiales*, *Sordariomycetes.*

On SNA: *Mycelium* consisting of hyaline, smooth, branched, septate, 2–3 µm diam hyphae. *Conidiophores* unbranched, erect, straight, medium brown, thick-walled, 2–4-septate, up to 70 µm tall, 3–3.5 µm diam; basal cell 4–6 µm diam. *Conidiogenous cells* terminal, integrated, subcylindrical, 25–35 µm long, pale brown, forming a rachis with pimple-shaped denticles less than 1 µm long and 0.5 µm diam; slightly thickened. *Conidia* solitary, aseptate, pale brown, thin-walled, smooth, guttulate, with or without a wing-like gelatinous sheath, ellipsoid to fusoid, (7–)8–9 × (2.5–)3 µm; hilum unthickened nor darkened, 0.5 µm diam.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface isabelline, reverse hazel. On PDA surface and reverse greyish sepia. On OA surface isabelline.

Typus. Ukraine, Sumy region, bank of Vorskla river, NNP Hetmanskyi, Klymentove village, on leaves of *Phragmites australis* (*Poaceae*), 5 Aug. 2018, *A. Akulov*, HPC 2554, AS 6809 (holotype CBS H-24351, culture ex-type CPC 36367 = CBS 146628; ITS and LSU sequences GenBank MT373366.1 and MT373349.1, MycoBank MB835400).

Notes — Arzanlou et al. (2007) established the genus *Myrmecridium* to accommodate taxa with hyaline mycelium, pigmented, solitary conidiophores with pimple-like denticles, and 0–1-septate, ellipsoid conidia with a mucoid sheath. *Myrmecridium phragmiticola* should be compared to *M. phragmites* (*Phragmites australis*, Netherlands), which has 0–1-septate conidia, (6.5–)7–8(–9) × (2.5–)3(–3.5) µm (Crous et al. 2011). Although the conidia are similar in size, those of *M. phragmiticola* are aseptate.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Myrmecridium phragmitis* (strain CBS 131311, GenBank NR_137782.1; Identities = 531/552 (96 %), 6 gaps (1 %)), *Myrmecridium spartii* (strain CBS 140006, GenBank NR_155376.1; Identities = 523/543 (96 %), 4 gaps (0 %)), and *Myrmecridium banksiae* (strain CBS 132536, GenBank NR_111762.1; Identities = 522/546 (96 %), 4 gaps (0 %)). Closest hits using the **LSU** sequence are *Myrmecridium schulzeri* (strain CBS 188.96, GenBank EU041829.1; Identities = 855/860 (99 %), no gaps), *Myrmecridium banksiae* (strain CBS 132536, GenBank NG_042684.1; Identities = 862/870 (99 %), no gaps), and *Myrmecridium flexuosum* (strain CBS 398.76, GenBank EU041825.1; Identities = 852/860 (99 %), no gaps).

Colour illustrations. *Phragmites australis* along the bank of the Vorskla river. Conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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Diabolocovidia claustri

Fungal Planet 1048 – 29 June 2020

Diabolocovidia Crous, *gen. nov.*

Etymology. This fungus was described during the coronavirus pandemic, April 2020. Name composed of *diabolicus* = devilish and covid, referring to COVID-19.

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

Mycelium consisting of branched, septate, hyaline to pale brown, smooth to finely roughened, hyphae. *Conidiophores* solitary, erect, flexuous, mostly reduced to a terminal conidiogenous cell. *Conidiogenous cells* pale brown, smooth, subcylindrical to slightly clavate, proliferating via single apical blastic locus, and remaining attached to acropetal chain of conidia that remain attached to one another via narrow isthmus. *Conidia* brown, thin-walled, smooth, guttulate, granular, ellipsoid to obovoid; conidia remaining attached in chains of propagules, disarticulating at maturity into single propagules or shorter chains.

Type species. Diabolocovidia claustri Crous.
MycoBank MB835401.

Diabolocovidia claustri Crous, *sp. nov.*

Etymology. Name refers to the closure or lockdown experienced in many countries during the COVID-19 pandemic.

Mycelium consisting of branched, septate, hyaline to pale brown, smooth to finely roughened, 2–3 µm diam hyphae. *Conidiophores* solitary, erect, flexuous, mostly reduced to a terminal conidiogenous cell. *Conidiogenous cells* pale brown, smooth, subcylindrical to slightly clavate, 8–10 × 3–4 µm, proliferating via single apical blastic locus, and remaining attached to acropetal chain of conidia that remain attached to one another via narrow isthmus. *Conidia* brown, thin-walled, smooth, guttulate, granular, ellipsoid to obovoid, (7–)8–9(–11) × (4–)5–6(–7) µm; conidia remaining attached in chains of 8–12 propagules, disarticulating at maturity into single propagules or shorter chains.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium and feathery, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface and reverse cinnamon. On PDA surface and reverse hazel to brown vinaceous. On OA surface hazel.

Typus. USA, Florida, Gainesville, on leaves of *Serenoa repens* (*Arecaceae*), 28 Feb. 2018, *M.J. Wingfield*, HPC 2792 (holotype CBS H-24353, culture ex-type CPC 37593 = CBS 146630; ITS and LSU sequences GenBank MT373367.1 and MT373350.1, MycoBank MB835402).

Notes — *Diabolocovidia* is reminiscent of genera such as *Ampullifera* (but conidiophores different and hyphopodia present) and *Junctospora* (but conidiophores sparingly branched, subhyaline; Seifert et al. 2011). Phylogenetically, it is allied to *Vamsapriya*, which is characterised by having brown, synnematous conidiophores, mono- to polytretic conidiogenous cells, and dark brown, septate conidia arranged in acropetal chains (Dai et al. 2014). Based on these differences, *Diabolocovidia* is herewith introduced as a new genus.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Vamsapriya khunkonensis* (voucher MFLU 13-0367, GenBank NR_154499.1; Identities = 427/464 (92 %), 5 gaps (1 %)), *Didymobotryum rigidum* (strain JCM 8837, GenBank LC228650.1; Identities = 517/561 (92 %), 7 gaps (1 %)), and *Vamsapriya bambusicola* (voucher MFLU 13-0368, GenBank NR_154500.1; Identities = 533/605 (88 %), 37 gaps (6 %)). Closest hits using the **LSU** sequence are *Vamsapriya bambusicola* (strain MFLUCC 11-0477, GenBank NG_067527.1; Identities = 849/864 (98 %), no gaps), *Fasciatispora petrakii* (strain HKUCC 207, GenBank AY083828.1; Identities = 832/848 (98 %), 1 gap (0 %)), and *Vamsapriya indica* (strain MFLUCC 12-0544, GenBank KM462840.1; Identities = 815/831 (98 %), no gaps).

Colour illustrations. Leaves of *Serenoa repens*. Conidiophores with conidiogenous cells giving rise to chains of conidia. Scale bars = 10 µm.

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Juncomyces californiensis

Fungal Planet 1049 – 29 June 2020

Juncomyces Crous, *gen. nov.*

Etymology. Name refers to the host genus *Juncus* from which it was isolated.

Classification — *Mycosphaerellaceae*, *Mycosphaerellales*, *Dothideomycetes.*

Mycelium consisting of brown, smooth to warty, septate, branched. *Conidiophores* solitary, subcylindrical, mostly unbranched, erect, thick-walled, brown, verruculose, warty, multiseptate, rarely forming from a brown stroma, with a few fasciculate conidiophores. *Conidiogenous cells* integrated, terminal, straight to geniculate-sinuous, proliferating sympodially with several apical loci, flattened, thickened, darkened, and refractive. *Conidia* solitary, acicular to slightly obclavate, mostly thick-walled, verruculose, guttulate, apex subobtuse, base truncate, thickened, darkened and refractive, septate.

Type species. Juncomyces californiensis Crous.
MycoBank MB835403.

Juncomyces californiensis Crous, *sp. nov.*

Etymology. Name refers to the state of California, where it was collected.

Mycelium consisting of brown, smooth to warty, septate, branched, 2–3 µm diam hyphae. *Conidiophores* solitary, subcylindrical, mostly unbranched, erect, 80–180 × 5–7 µm, thick-walled, brown, verruculose, warty, multiseptate, rarely forming from a brown stroma, up to 120 µm diam, with 1–3 fasciculate conidiophores, up to 60 µm tall. *Conidiogenous cells* integrated, terminal, straight to geniculate-sinuous, 35–60 × 5–7 µm; proliferating sympodially with several apical loci, flattened, thickened, darkened, and refractive, 4.5–5.5 µm diam. *Conidia* solitary, acicular to slightly obclavate, mostly thick-walled, verruculose, guttulate, apex subobtuse, base truncate, 4.5–5 µm diam, thickened, darkened and refractive, 3(–6)-septate, (65–)70–85(–90) × (7–)8(–9) µm.

In vivo: *Conidiophores* on culms erect, solitary, rarely in fascicles of 2–3, straight, 2–6-septate, subcylindrical, rejuvenating percurrently, 50–110 × 5–7 µm, arising from immersed, brown, weakly developed stroma, 20–40 µm diam. *Conidiogenous cells* integrated, terminal and intercalary, medium brown, smooth, 10–45 × 5–6 µm with one to several loci, round, thickened, refractive, 3–4 µm diam. *Conidia* solitary, arranged in clusters on conidiophores, obclavate, slightly curved to straight, apex subobtuse, base truncate, 3–7-septate, at times constricted at some of the septa, thick-walled, medium brown, verruculose, hilum thickened, darkened, refractive, 4–5 µm diam, (45–)55–70(–75) × (6–)7(–8) µm.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium and smooth, feathery, even margin, reaching 12 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface olivaceous grey, reverse iron-grey.

Typus. USA, California, UC Davis, on leaves of *Juncus effusus* (*Juncaceae*), 3 Apr. 2019, *P.W. Crous*, HPC 2894 (holotype CBS H-24363, culture ex-type CPC 37989 = CBS 146682; ITS and LSU sequences GenBank MT373368.1 and MT373351.1, MycoBank MB835405).

Additional material examined. USA, California, UC Davis, on leaves of *J. effusus*, 3 Apr. 2019, *P.W. Crous*, HPC 2895, culture CPC 37993 = CBS 146631; ITS, LSU and *rpb2* sequences GenBank MT373369.1, MT373352.1 and MT375101.1.

Notes — *Juncomyces* is closely related to *Graminopassalora*, which was introduced to accommodate *Passalora graminis*, a widespread pathogen occurring on a broad range of grass (*Poaceae*) hosts (Videira et al. 2017). *Juncomyces* differs from *Graminopassalora* by chiefly having solitary conidiophores (rarely fascicles of 2–3), and multiseptate, obclavate conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 37989 had highest similarity to *Graminopassalora graminis* (strain CBS 113303, GenBank GU214666.1; Identities = 474/538 (88 %), 18 gaps (3 %)), *Mycosphaerella fimbriata* (strain CBS 120736, GenBank NR_137553.1; Identities = 465/526 (88 %), 16 gaps (3 %)), and *Zasmidium corymbiae* (strain CBS 145049, GenBank MK047423.1; Identities = 476/542 (88 %), 21 gaps (3 %)). The ITS sequences of CPC 37989 and 37993 are 100 % (528/528 bp) identical. Closest hits using the **LSU** sequence of CPC 37989 are *Xenosonderhenia eucalypti* (strain CBS 138858, GenBank NG_058120.1; Identities = 773/799 (97 %), 2 gaps (0 %)), *Ramularia lethalis* (strain CPC 25910, GenBank KX287174.1; Identities = 780/808 (97 %), no gaps), and *Ramularia acris* (strain CBS 109794, GenBank KX287010.1; Identities = 780/808 (97 %), no gaps). The LSU sequences of CPC 37989 and 37993 are 100 % (808/808 bp) identical. Closest hits using the ***rpb2*** sequence of CPC 37993 had highest similarity to *Ramularia gei* (strain CBS 344.49, GenBank KX288570.1; Identities = 637/840 (76 %), 14 gaps (1 %)), *Ramularia unterseheri* (strain CBS 124884, GenBank KP894709.1; Identities = 636/849 (75 %), 8 gaps (0 %)), and *Ramularia heraclei* (strain CPC 11507, GenBank KX288584.1; Identities = 634/848 (75 %), 6 gaps (0 %)).

Colour illustrations. *Juncus effusus* growing in California. Conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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Beltraniella podocarpi

Fungal Planet 1050 – 29 June 2020

Beltraniella podocarpi Crous, *sp. nov.*

Etymology. Name refers to the host genus *Podocarpus* from which it was isolated.

Classification — *Beltraniaceae*, *Xylariales*, *Sordariomycetes*.

Setae solitary to aggregated, erect, flexuous, arising from a lobate basal cell, 15–25 µm diam, dark brown, warty, chiefly unbranched, up to 20-septate, thick-walled with large central guttules, tapering in upper part to acute apex, 120–300 × 5–8 µm. *Conidiophores* arranged in dense clusters around the base of setae, brown, smooth, subcylindrical, frequently branched at basal cell, 1–2-septate, 10–30 × 6–8 µm. *Conidiogenous cells* integrated, terminal and intercalary, 7–12 × 6–7 µm, pale brown, smooth, obclavate, tapering toward 1–3 denticulate loci, 1–1.5 µm long, 1 µm diam. *Separating cells* clavate to fusoid-ellipsoid, pale brown, smooth, finely guttulate, tapering toward long basal stalk and short apical locus, 17–21 × 4–5 µm. *Conidia* obovoid to narrowly turbinate, tapering toward base, apex rounded to subtruncate, aseptate, finely verruculose, guttulate, pale brown, (25–)27–28(–33) × (7–)8 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and feathery, lobate margin, covering dish after 2 wk at 25 °C. On MEA surface olivaceous grey, reverse honey with olivaceous grey margin. On PDA surface olivaceous grey, reverse iron-grey. On OA surface iron-grey with dirty white margin.

Typus. South Africa, Western Cape Province, Knysna, on leaves of *Podocarpus latifolius* (*Podocarpaceae*), 30 Nov. 2018, *M.J. Wingfield*, HPC 2710 (holotype CBS H-24354, culture ex-type CPC 36783 = CBS 146633; ITS and LSU sequences GenBank MT373370.1 and MT373353.1, MycoBank MB835406).

Notes — *Beltraniella* is characterised by brown, unbranched setae, setiform conidiophores, polyblastic, denticulate conidiogenous cells, and turbinate conidia with a distinct hyaline transverse band (Rajeshkumar et al. 2016). *Beltraniella podocarpi* is closely related to several species that tend to have some overlap in conidial length, but have narrower conidia (Rajeshkumar et al. 2016, Crous et al. 2019a).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Beltraniella portoricensis* (strain BCRC 34590, GenBank GU905993.1; Identities = 479/487 (98 %), 6 gaps (1 %)), *Beltraniella ramosiphora* (strain LCG 10-2, GenBank MG717500.1; Identities = 527/536 (98 %), 4 gaps (0 %)), and *Beltraniella pseudoportoricensis* (strain CBS 145547, GenBank NR_165552.1; Identities = 578/591 (98 %), 5 gaps (0 %)). Closest hits using the **LSU** sequence are *Beltraniella pseudoportoricensis* (strain CBS 145547, GenBank NG_067875.1; Identities = 821/825 (99 %), no gaps), *Beltraniella acaciae* (strain CPC 29498, GenBank NG_066374.1; Identities = 786/790 (99 %), no gaps), and *Beltraniella portoricensis* (strain CBS 856.70, GenBank MH871777.1; Identities = 842/848 (99 %), 1 gap).

Colour illustrations. Rainforest in Knysna, South Africa. Setae and conidiophores on PNA; dichotomously branched seta; conidiophores with conidiogenous cells; conidia with separating cell. Scale bars = 10 µm.

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Neofabraea eucalyptorum

Fungal Planet 1051 – 29 June 2020

Neofabraea eucalyptorum Crous, *sp. nov.*

Etymology. Name refers to the host genus *Eucalyptus* from which it was isolated.

Classification — *Dermateaceae*, *Helotiales*, *Leotiomycetes*.

Associated with brown, amphigenous leaf spots, 3–5 mm diam. *Conidiomata* 200–300 µm diam, acervular, erumpent, associated with dark brown, amphigenous leaf spots. *Conidiophores* hyaline, smooth, branched, septate, subcylindrical, phialidic, up to 80 µm long, 3–5 µm diam. *Conidiogenous cells* hyaline, smooth, subcylindrical, terminal and intercalary with visible periclinal thickening, 10–18 × 3–4 µm. *Conidia* subcylindrical to fusoid-ellipsoid, variously curved, hyaline, smooth, guttulate, apex subobtuse, base with flattened hilum, aseptate, but becoming up to 3-septate in older cultures, (25–)30–35(–40) × (6.5–)7–8(–9) µm.

Culture characteristics — Colonies spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 22 mm diam after 2 wk at 25 °C. On MEA surface buff, reverse cinnamon. On PDA surface honey, reverse hazel. On OA surface honey.

Typus. USA, California, UC Davis, on leaves of *Eucalyptus macrandra* (*Myrtaceae*), 30 Apr. 2019, *P.W. Crous*, HPC 2889 (holotype CBS H-24355, culture ex-type CPC 37985 = CBS 146634; ITS, LSU and *tub2* sequences GenBank MT373371.1, MT373354.1 and MT375121.1, MycoBank MB835407).

Notes — The *Neofabraea* generic complex was revised by Chen et al. (2016), and *Neofabraea eucalypti* was subsequently placed in *Coleophoma* (Crous & Groenewald 2016). *Neofabraea eucalyptorum* is thus the first confirmed species of the genus associated with leaf spots on *Eucalyptus* (Crous et al. 2019b).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neofabraea alba* (strain UASWS0614, GenBank HQ166388.1; Identities = 485/499 (97 %), 3 gaps (0 %)), *Neofabraea brunneipila* (voucher MFLU 15-0231, GenBank MK584984.1; Identities = 490/505 (97 %), 1 gap (0 %)), and *Neofabraea inaequalis* (strain CBS 326.75, GenBank NR_155470.1; Identities = 490/505 (97 %), 1 gap (0 %)).Closest hits using the **LSU** sequence are *Neofabraea brasiliensis* (voucher CNPUV499, GenBank KR107002.1; Identities = 857/865 (99 %), no gaps), *Pseudofabraea citricarpa* (strain CBS 130297, GenBank KR859073.1; Identities = 844/852 (99 %), no gaps), and *Neofabraea kienholzii* (strain CBS 318.77, GenBank KR858874.1; Identities = 854/863 (99 %), no gaps). No significant hits were obtained when the ***tub2*** sequence was used in blastn and megablast searches.

Colour illustrations. Leaf spots on *Eucalyptus macrandra*. Conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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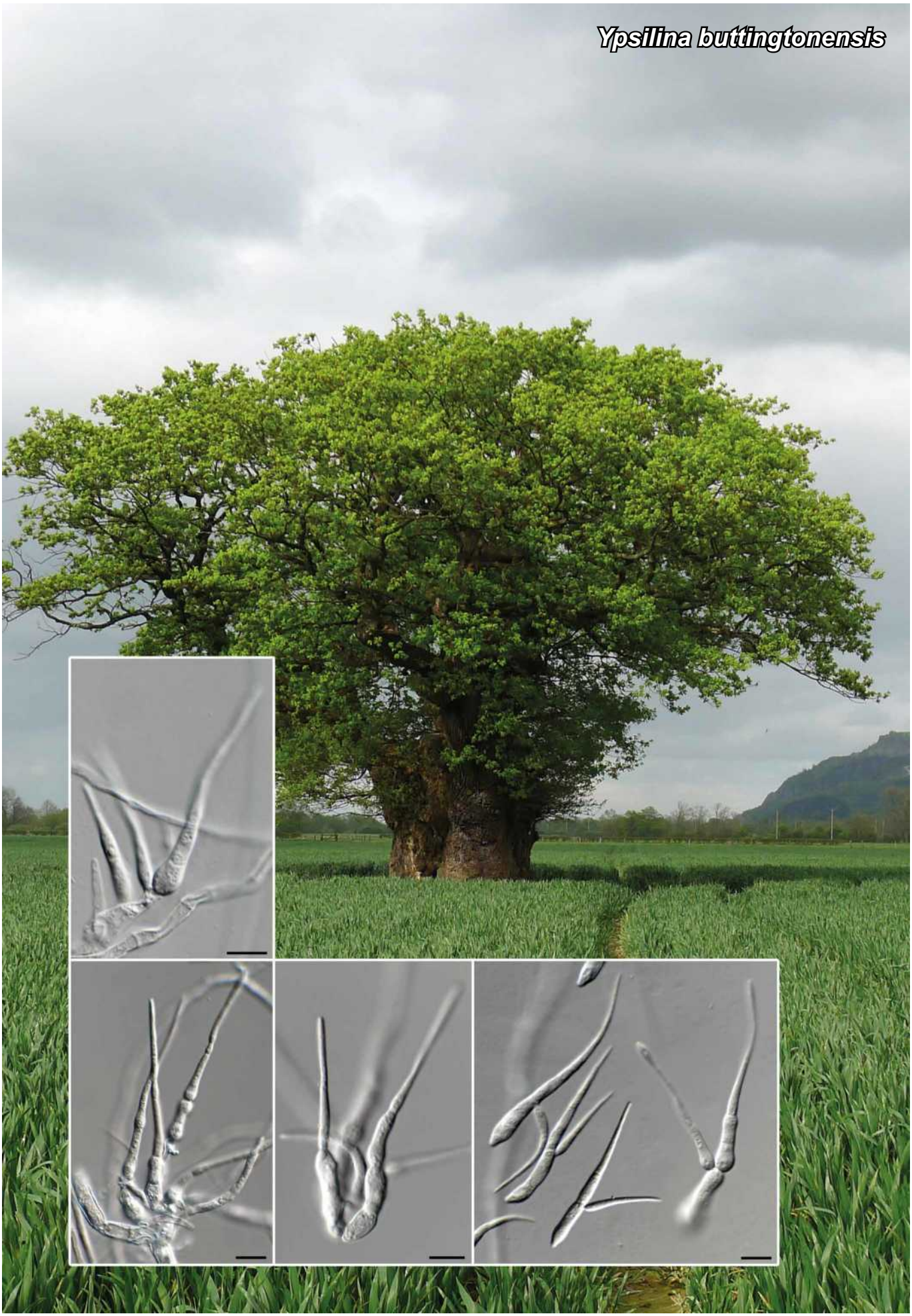
Ypsilina buttingtonensis

Fungal Planet 1052 – 29 June 2020

Ypsilina buttingtonensis Crous, Wainhouse & Brian Douglas, *sp. nov.*

Etymology. Name refers to the collection site, Buttington, Wales, UK, where it was collected.

Classification — *Ploettnerulaceae*, *Helotiales*, *Leotiomycetes.*

Mycelium consisting of hyaline, smooth, branched, septate, 2–3 µm diam hyphae. *Conidiophores* integrated, subcylindrical, hyaline, smooth, septate, sparingly branched, mostly terminal on hyphal ends, 30–100 × 4–6 µm. *Conidiogenous cells* integrated, terminal and intercalary, subcylindrical, smooth, 12–25 × 4–6 µm; proliferating sympodially. *Conidia* solitary but aggregating in mucoid mass, Y-shaped, smooth, hyaline; central cell obclavate, base with truncate hilum, 2 µm diam, apex subobtuse, 2–4-septate, (35–)40–50(–60) × (3–)4–5(–6) µm, with 1–2 lateral branches inserted below the median, pointing upwards, aseptate, obclavate, apex subobtuse, (8–)15–20(–25) × 2(–2.5) µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and folded surface (on MEA), with smooth, lobate margin, reaching 12 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface dirty white, reverse ochreous.

Typus. UK, Wales, Buttington, from heartwood of 1 000-yr-old *Quercus* sp. (*Fabaceae*), 14 Mar. 2018, *M. Wainhouse* (holotype CBS H-24356, culture ex-type B0.01.30 = CPC 39109 = CBS 146635; ITS and LSU sequences GenBank MT373372.1 and MT373355.1, MB835408).

Notes — Although the ecology of *Ypsilina* remains unknown, *Y. graminea* has been isolated from freshwater foam, roots and leaves of various plants (Descals et al. 1998). *Ypsilina buttingtonensis* was isolated from an ancient pedunculate oak *Quercus robur* in Buttington, Wales (longitude and latitude: 52.678236, -3.1108743). The tree, known as the Buttington Oak, was an open-grown lapsed pollard. At the time when the tree fell in February 2018, it had a trunk girth of 11.03 m at breast height and was believed to be the second oldest oak tree in Wales. The tree had a 1.5 m diam hollow through centre where brown cubical rot could be seen, attributed to *Fistulina hepatica*. The significance of the tree was realised in 2009 when it was 'discovered'.

Cores of wood were extracted from the tree with a 5.5 mm increment bore. Wood chips were taken from the 30 cm cores at 1 cm intervals and placed on low pH 2 % malt agar Petri dishes and incubated at 20 °C in the dark. *Ypsilina buttingtonensis* was cultured from a chip 30 cm into the heartwood.

In addition to *Ypsilina buttingtonensis*, *Fistulina hepatica*, and eight species of ascomycete were also cultured from the wood chips including *Cryphonectria radicalis*, a close relative of the aggressive canker pathogen *Cryphonectria parasitica*, responsible for chestnut blight.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Helgardia anguioides* (strain CBS 496.80, GenBank NR_158522.1; Identities = 522/533 (98 %), no gaps), *Oculimacula acuformis* (strain CBS 495.80, GenBank MH861289.1; Identities = 516/535 (96 %), 2 gaps (0 %)), and *Oculimacula aestiva* (strain CBS 114730, GenBank MG934454.1; Identities = 516/535 (96 %), 2 gaps (0 %)). Closest hits using the **LSU** sequence are *Ypsilina graminea* (strain CBS 114630, GenBank MH874529.1; Identities = 877/880 (99 %), 1 gap (0 %)), *Helgardia anguioides* (strain CBS 496.80, GenBank MH873055.1; Identities = 876/880 (99 %), no gaps), and *Rhynchosporium orthosporum* (strain 04CH-Bar-A.1.1.3, GenBank KU844335.1; Identities = 870/874 (99 %), no gaps).

Colour illustrations. The Buttington Oak (background photo credit: @thetreehunter Rob McBride). Conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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Pseudopezicula betulae

Fungal Planet 1053 – 29 June 2020

Pseudopezicula betulae Crous, *sp. nov.*

Etymology. Name refers to *Betula*.

Classification — *Discinellaceae*, *Helotiales*, *Leotiomycetes.*

Conidiomata sporodochial, superficial, round, 200–300 µm diam, white, composed of tightly aggregated conidiophores. *Conidiophores* hyaline, smooth, subcylindrical, extensively branched, septate, 3–4 µm diam, up to 90 µm long. *Conidiogenous cells* hyaline, smooth, phialidic, subcylindrical to fusoid, apex with periclinal thickening, at times with percurrent proliferation and indistinct flared collarette (2–3 µm long), 4–13 × 2–5 µm. *Conidia* solitary, aseptate, guttulate, hyaline, smooth, aggregating in mucoid mass, subcylindrical, straight to curved, apex obtuse, base truncate, with minute marginal frill, (5–)7–10(–17) × 2–2.5 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface cinnamon, reverse sepia. On PDA surface buff, reverse cinnamon with buff in outer region. On OA surface buff.

Typus. USA, California, Yosemite, on brown, amphigenous leaf spots of *Populus tremuloides* (*Salicaceae*), 2019, *S. Denman* (holotype CBS H-24357, culture ex-type CPC 36499 = CBS 146683; ITS, LSU, *rpb2*, and *tef1* sequences GenBank MT373373.1, MT373356.1, MT375102.1 and MT375116.1, MycoBank MB835409).

Pseudopezicula tracheiphila (Müll.-Thurg.) Korf & W.Y. Zhuang, Mycotaxon 26: 464. 1986

Basionym. *Pseudopeziza tracheiphila* Müll.-Thurg., Centralbl. Bakteriol. Parasitenk., 1. Abt. 10: 57. 1903.

Synonyms. *Botrytis tracheiphila* Sacc. & D. Sacc., Syll. Fung. (Abellini) 18: 157. 1906.

Phialophora tracheiphila (Sacc. & D. Sacc.) Korf, Mycotaxon 26: 464. 1986.

Typus. Neotype: Switzerland, Seemühle, Walenstadt, on leaves of *Vitis vinifera* cv. 'Blauburgunder', *H. Schüepp & M. Bodmer*, CUP-061784 (designated in Korf et al. 1986). Epitype: Luxembourg, on leaf of *Vitis vinifera*, coll. Sept. 1985, *R. Pearson*, isol. *W.-Y. Zhuang* (epitype designated here CUP 61766, MBT392064, culture ex-epitype CBS 308.86; ITS and LSU sequences GenBank MT373374.1 and MT373357.1).

Notes — *Pseudopezicula* accommodates two species of apothecial ascomycetes that cause angular leaf scorch on *Vitis vinifera*. An epitype is here designated for one of these, namely *P. tracheiphila.* In culture they produce phialophora-like asexual morphs (Korf et al. 1986), that resemble the phialidic asexual morph isolated in the present study. Although *Pseudopezicula betulae* was associated with prominent leaf spots, its occurrence was inconsistent, and therefore it is unknown whether it is a primary pathogen.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Gyoerffyella entomobryoides* (strain CBS 268.63, GenBank NR_145302.1; Identities = 512/529 (97 %), 1 gap (0 %)), *Gyoerffyella rotula* (strain 272Jb14, GenBank KU516477.1; Identities = 514/533 (96 %), 1 gap (0 %)), and *Fontanospora eccentrica* (strain UMB-881.11, GenBank KF730812.1; Identities = 495/514 (96 %), 2 gaps (0 %)). Closest hits using the **LSU** sequence are *Lemonniera aquatica* (strain CBS 167.46, GenBank MH867676.1; Identities = 831/837 (99 %), no gaps), *Margaritispora aquatica* (strain CBS 603.66, GenBank MH870561.1; Identities = 836/843 (99 %), 1 gap (0 %)), and *Gyoerffyella entomobryoides* (strain CBS 268.63, GenBank MH869886.1; Identities = 833/842 (99 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Gyoerffyella rotula* (strain CCM F-400, GenBank MK241434.1; Identities = 704/863 (82 %), 2 gaps (0 %)), *Lachnum virgineum* (strain AFTOL-ID 49 = voucher OSC 100002, GenBank DQ470877.1; Identities = 705/880 (80 %), 13 gaps (1 %)), and *Lachnellula hyalina* (strain CBS 185.66, GenBank XM_031145866.1; Identities = 699/877 (80 %), 11 gaps (1 %)). No significant hits were obtained when the ***tef1*** sequence was used in blastn and megablast searches.

Colour illustrations. Amphigenous leaf spots on *Populus tremuloides*. Conidiomata on PDA; conidiophores with conidiogenous cells; conidia. Scale bars = 300 µm (conidiomata), 10 µm (all others).

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Gyrothrix encephalarti

Fungal Planet 1054 – 29 June 2020

Gyrothrix encephalarti Crous, *sp. nov.*

Etymology. Name refers to the host genus *Encephalartos* from which it was isolated.

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

Culture sterile, morphology based on sporulation on dead leaf spots. *Mycelium* consisting of brown, smooth, septate, branched, 1.5–2 µm diam hyphae. *Setae* erect, 80–130 µm long, 3–4 µm diam, brown, multiseptate, thick-walled, verrucose, subcylindrical with apical taper, base bulbous, 5–6 µm diam, apex spirally twisted with twisted lateral branches in apical region. *Conidiophores* reduced to conidiogenous cells around base of setae, ampulliform to subcylindrical, pale brown, smooth, 6–10 × 3–4 µm, proliferating percurrently at apex. *Conidia* hyaline, smooth, aseptate, fusoid, inaequilateral, inner plane flat, outer plane convex, apex subobtuse, base truncate, (7–)10–12(–14) × 3(–3.5) µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 55 mm diam after 2 wk at 25 °C. On MEA surface buff, reverse cinnamon. On PDA surface buff, reverse rosy buff. On OA surface rosy buff.

Typus. South Africa, Northern Province, Tzaneen, on leaves of *Encephalartos* sp. (*Zamiaceae*), 2015, *P.W. Crous*, HPC 2486 (holotype CBS H-24364, culture ex-type CPC 35966 = CBS 146684; ITS, LSU and *tef1* sequences GenBank MT373376.1, MT373358.1 and MT375117.1, MycoBank MB835410).

Notes — *Gyrothrix encephalarti* is closely related to *G. eucalypti* (*Eucalyptus* sp., South Africa; conidia (8–)10–13(–15) × (2–)2.5 µm, setae 100–180 µm tall, 4–5 µm diam at base; Crous et al. 2019c), but has wider conidia and shorter setae. DNA sequences of *G. eucalypti* and *G. encephalarti* are related to the type sequence deposited for *Neoanthostomella viticola* (NG_067792.1), which has a completely different asexual morph.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neoanthostomella viticola* (strain MFLUCC 16-0243, GenBank NR_165511.1; Identities = 503/537 (94 %), 22 gaps (4 %)), *Gyrothrix eucalypti* (strain CPC 36066, GenBank NR_166315.1; Identities = 540/581 (93 %), 8 gaps (1 %)), and *Calceomyces lacunosus* (strain CBS 633.88, GenBank KY610397.1; Identities = 524/588 (89 %), 22 gaps (3 %)). Closest hits using the **LSU** sequence are *Gyrothrix eucalypti* (strain CPC 35992, GenBank MN567618.1; Identities = 869/880 (99 %), no gaps), and *Torula ficus* (strain MFLUCC 18-0112, GenBank MH260322.1; Identities = 792/803 (99 %), no gaps). Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Gyrothrix ramosa* (strain MUCL54061, GenBank KJ476975.1; Identities = 447/472 (95 %), no gaps), *Gyrothrix inops* (strain BE108, GenBank KJ476974.1; Identities = 447/472 (95 %), no gaps), and *Metarhizium globosum* (strain ARSEF 2596, GenBank EU248846.1; Identities = 438/470 (93 %), no gaps).

Colour illustrations. Leaves of *Encephalartos* sp. Setae and conidiogenous cells; conidia. Scale bars = 10 µm.

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Satchmopsis metrosideri

Fungal Planet 1055 – 29 June 2020

Satchmopsis metrosideri Crous, *sp. nov.*

Etymology. Name refers to the host genus *Metrosideros* from which it was isolated.

Classification — *Cochlearomycetaceae*, *Leotiales*, *Leotiomycetes*.

Conidiomata cupulate, superficial, 100–140 µm diam at apex, 130–180 µm deep, dark brown, attached to a basal stroma of dark brown cells that occupy the stomatal chamber; wall consisting of two regions, the lower region having thick-walled dark brown cells up to 5 layers thick; upper region on thin-walled paler cells, cylindrical, 10–17 × 3–4 µm, with even, smooth flat edge. In culture conidiomata are paler in colour and much larger, flattened, cupulate, and margins have cells that are lobate due to expanding growth (not flat as *in vivo*). *Conidiogenous cells* restricted to lower part of basal wall, 3–7 × 2–3 µm, doliiform to lageniform, phialidic with periclinal thickening, hyaline with indistinct collarette. *Conidia* hyaline, smooth, aseptate, guttulate, subcylindrical, predominantly straight with obtuse ends, (15–)16–17(–19) × 1–1.5 µm.

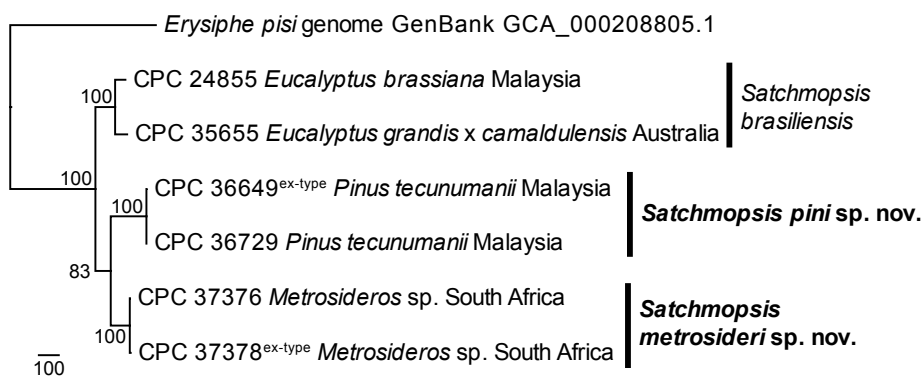
Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and feathery, lobate margin, reaching 60 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface umber with patches of sepia, reverse umber.

Typus. South Africa, Eastern Cape Province, Haga Haga, Amathole, on leaf litter of *Metrosideros excelsa* (*Myrtaceae*), 2015, *M.J. Wingfield*, HPC 2754 (holotype CBS H-24359, culture ex-type CPC 37378 = CBS 146686; ITS, LSU, *actA*, *rpb2*, *tef1* and *tub2* sequences GenBank MT373377.1, MT373359.1, MT432194.1, MT375103.1, MT375111.1 and MT375122.1, MycoBank MB835411).

Additional material examined. South Africa, Eastern Cape Province, Haga Haga, Amathole, on leaf litter of *M. excelsa*, 2015, *M.J. Wingfield*, HPC 2754, culture CPC 37376; ITS, *actA*, *rpb2*, *tef1* and *tub2* sequences GenBank MT432187.1, MT432188.1, MT432189.1, MT432190.1 and MT432190.1.

Notes — The genus *Satchmopsis*, based on *S. brasiliensis* (*Eucalyptus paniculata*, Brazil; conidia 11.5–15.5 × 1–1.5 µm) (Sutton 1975) was introduced for a genus of cupulate coelomycetes with aseptate conidia. *Satchmopsis* is commonly isolated from eucalypt leaf litter in South America (Crous et al. 2006). The present collection, from *Metrosideros excelsa* leaf litter collected in South Africa, differs from *S. brasiliensis* in being phylogenetically distinct, and also having longer conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Satchmopsis brasiliensis* (strain CPC 11017, GenBank DQ195786.1; Identities = 506/507 (99 %), no gaps), *Capturomyces luteus* (strain CBS 144839, GenBank NR_165905.1; Identities = 474/511 (93 %), 12 gaps (2 %)), and *Capturomyces funiculosus* (strain CBS 144840, GenBank NR_165904.1; Identities = 471/512 (92 %), 13 gaps (2 %)). Closest hits using the **LSU** sequence are *Satchmopsis brasiliensis* (strain CPC 11017, GenBank DQ195798.1; Identities = 857/858 (99 %), no gaps), *Cochlearomyces eucalypti* (strain CBS 142622, GenBank NG_059052.1; Identities = 828/862 (96 %), 4 gaps (0 %)), and *Pallidophorina paarla* (strain GLMC 791, GenBank MK314612.1; Identities = 824/863 (95 %), 10 gaps (1 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Chlorociboria spathulata* (strain D1822, GenBank JN985530.1; Identities = 695/887 (78 %), 8 gaps (0 %)), *Moellerodiscus lentus* (strain 10544, GenBank MH729344.1; Identities = 693/887 (78 %), 18 gaps (2 %)), and *Microscypha ellisii* (voucher KUS-F52489, GenBank JN086863.1; Identities = 687/890 (77 %), 16 gaps (1 %)). No significant hits were obtained when the ***actA***, ***tef1*** and ***tub2*** sequences were used in blastn and megablast searches. The ITS, *actA*, *rpb2* and *tef1* sequences of CPC 37378 and 37376 were identical; ITS: 508/508, *actA*: 644/644, *rpb2*: 911/911, and *tef1*: 552/552; and *tub2* almost identical: 695/701.



The single most parsimonious tree obtained from a phylogenetic analysis of the *Satchmopsis* ITS/*actA*/*rpb2*/*tef1*/*tub2* alignment (7 strains including the outgroup; 3220 characters including alignment gaps analysed: 1911 constant, 935 variable and parsimony-uninformative and 374 parsimony-informative). PAUP v. 4.0b10 (Swofford 2003) was used to analyse the data. The tree was rooted to *Erysiphe pisi* (genome GenBank GCA_000208805.1) and the scale bar indicates the number of changes. Parsimony bootstrap support values higher than 49 % are shown at the nodes and the novel species are highlighted in **bold**. Type status is indicated in superscript. Tree statistics: TL = 1572, CI = 0.964, RI = 0.880, RC = 0.849. The alignment and tree were deposited in TreeBASE (Submission ID S26166).

Colour illustrations. Beach area in Haga Haga, with *Metrosideros* in background. Conidioma on OA; conidioma on SNA; conidiomatal wall; conidia. Scale bars = 140 µm (conidiomata), 10 µm (all others).

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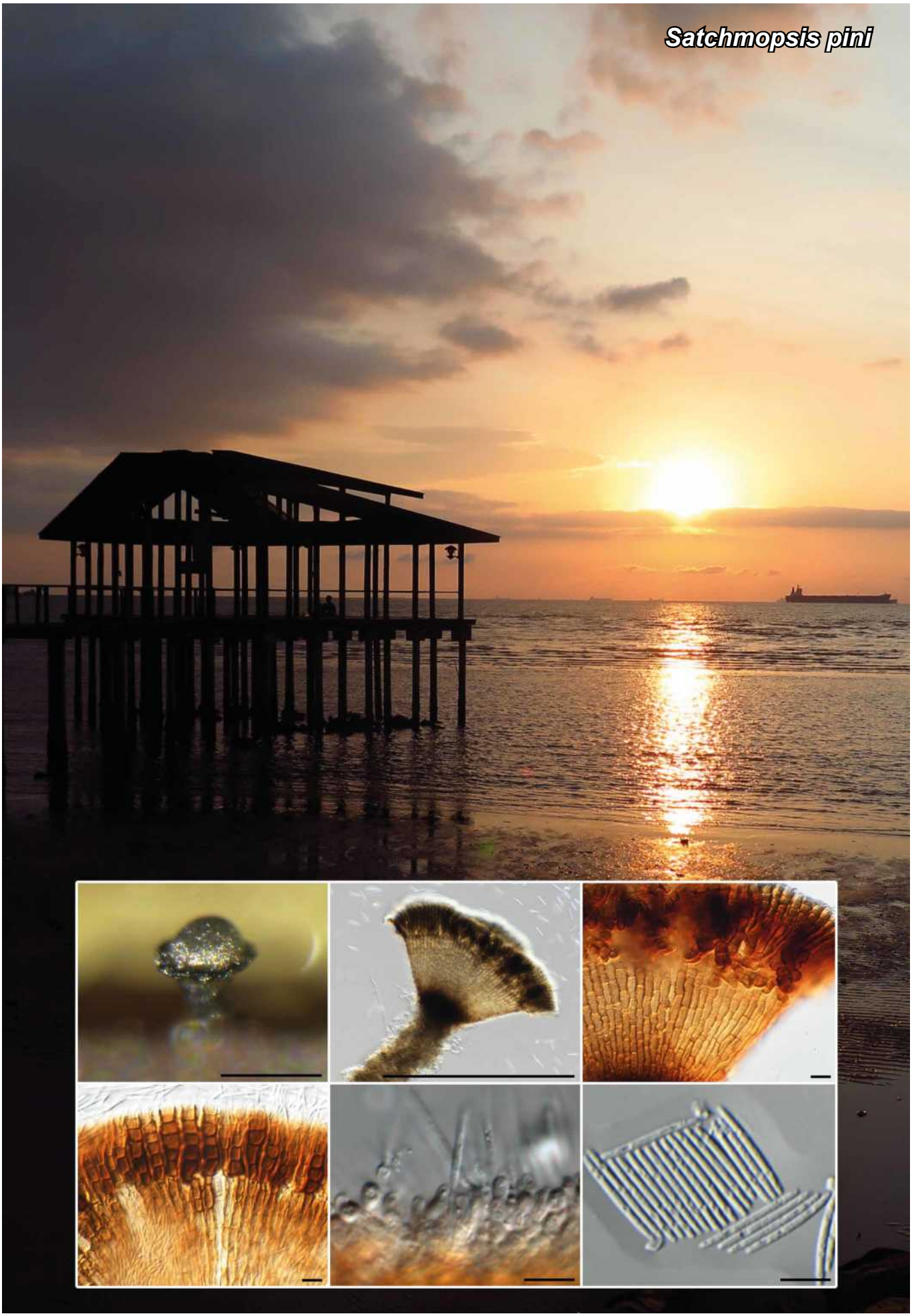
Satchmopsis pini

Fungal Planet 1056 – 29 June 2020

Satchmopsis pini Crous, *sp. nov.*

Etymology. Name refers to the host genus *Pinus* from which it was isolated.

Classification — *Cochlearomycetaceae*, *Leotiales*, *Leotiomycetes*.

Conidiomata cupulate, superficial, 140–200 µm diam, and 120–160 µm deep, dark brown, attached centrally to a brown stroma via a dark brown stalk, up to 150 µm tall, 50 µm wide; conidiomatal wall of two regions, the lower region of brown cells, the upper region of cylindrical cells with flat to obtuse edge, 3–7 × 4–7 µm; terminal 5–13 cell layers are prominently thick-walled, darker brown, and can give rise to hyphal outgrowths on outside of conidiomatal margin. *Conidiogenous cells* restricted to lower part of basal wall, 4–10 × 2–3 µm, doliiform to lageniform, phialidic with periclinal thickening, hyaline with indistinct collarette. *Conidia* hyaline, smooth, aseptate, guttulate, subcylindrical, straight with obtuse ends, (11–)12–14(–15) × 1–1.5 µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and feathery, lobate margin, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface umber with patches of sepia, reverse umber.

Typus. Malaysia, on dead needles of *Pinus tecunumanii* (*Pinaceae*), 31 Oct. 2010, *M.J. Wingfield*, HPC 2657 (holotype CBS H-24360, culture ex-type CPC 36649 = CBS 146687; ITS, LSU, *actA*, *rpb2*, *tef1* and *tub2* sequences GenBank MT373378.1, MT373360.1, MT375096.1, MT375104.1, MT375112.1 and MT375123.1, MycoBank MB835412).

Additional material examined. Malaysia, on dead needles of *P. tecunumanii*, 31 Oct. 2010, *M.J. Wingfield*, HPC 2657, culture CPC 36729; ITS, *actA*, *rpb2* and *tef1* sequences GenBank MT373379.1, MT375097.1, MT375105.1 and MT375113.1.

Notes — *Satchmopsis pini* is morphologically distinct from *S. brasiliensis* and *S. metrosideri* in having cupulate conidiomata with a prominently thick-walled, darker brown upper region, giving rise to hyphal outgrowths on outside of conidiomatal margin. Furthermore, conidiomata are centrally attached to a brown stroma via a long, dark brown stalk, which is absent in *S. brasiliensis* and *S. metrosideri*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Satchmopsis brasiliensis* (strain CBS 420.93, GenBank DQ195784.1; Identities = 507/507 (100 %), no gaps), *Massarina corticola* (strain 4607, GenBank FR668004.1; Identities = 420/451 (93 %), 9 gaps (1 %)), and *Capturomyces luteus* (strain CBS 144839, GenBank NR_165905.1; Identities = 473/510 (93 %), 11 gaps (2 %)). Closest hits using the **LSU** sequence are *Satchmopsis brasiliensis* (strain CBS 420.93, GenBank DQ195796.1; Identities = 873/873 (100 %), no gaps), *Cochlearomyces eucalypti* (strain CBS 142622, GenBank NG_059052.1; Identities = 840/877 (96 %), 4 gaps (0 %)), and *Pragmopora* cf. *bacillifera* (voucher G.M. 2019-04-30.1, GenBank MK900749.1; Identities = 843/883 (95 %), 10 gaps (1 %)). No significant hits were obtained when the ***actA***, ***rpb2***, ***tef1*** and ***tub2*** sequences were used in blastn and megablast searches. The ITS, *actA*, *rpb2* and *tef1* sequences of CPC 36649 and 36729 were identical; ITS: 507/507, *actA*: 596/596, *rpb2*: 879/879 and *tef1*: 405/405.

Colour illustrations. Beach area in Malaysia. Conidioma on OA; conidioma on SNA; conidiomatal wall; conidiogenous cells; conidia. Scale bars = 200 µm (conidiomata), 10 µm (all others).

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Hymenotorrendiella communis

Fungal Planet 1057 & 1058 – 29 June 2020

Hymenotorrendiella communis Crous & P.R. Johnst., *sp. nov.*

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

Classification — *Helotiaceae*, *Helotiales*, *Leotiomycetes.*

Apothecia scattered on leaves, at times aggregated in clusters of 2–3, erumpent, stipitate, arising from a subepidermal brown stroma. *Disc* plane to convex, greyish brown to olivaceous, smooth, 0.4–1.0 mm diam. *Receptacle* cupulate, usually darker than the hymenium, bearing dark brown setae. *Stipe* central, smooth, brown, 0.2–0.6 mm high, 180–200 µm diam. *Setae* 40–100 per apothecium, 150–300 µm long, smooth, dark brown, thick-walled, multiseptate, tip subobtusely rounded (2.5–3 µm diam), swollen at base, 9–15 µm diam. *Asci* cylindrical-clavate, apex conical-rounded, apical mechanism bluing slightly in Melzer's reagent, croziers present, 8-spored, 90–115 × 7–9 µm. *Ascospores* fusoid, aseptate, tapering towards ends, guttulate, hyaline with mucoid caps at each end, (16–)20–21(–22) × (3.5–)4 µm. *Paraphyses* simple or branched near base, obtuse, hyaline, somewhat inflated, 2.5–3 µm diam at apex.

Culture characteristics — Colonies flat, spreading, with even smooth margin and sparse to moderate aerial mycelium, covering dish after 2 wk at 25 °C. On MEA surface cinnamon with patches of hazel, reverse sienna to umber. On PDA surface amber to ochreous, reverse amber. On OA surface ochreous with patches of cinnamon.

Typus. Australia, New South Wales, La Trobe State Forest, on leaf litter of *Eucalyptus bicostata* (*Myrtaceae*), 30 Nov. 2015, *P.W. Crous*, HPC 1871 (holotype CBS H-24367, culture ex-type CPC 32835 = CBS 146703; ITS sequence GenBank MT373382.1, MycoBank MB835413).

Notes — The phylogeny and morphology of *Torrendiella* and *Hymenotorrendiella* was discussed in detail by Johnston et al. (2014). Although the name *Torrendiella eucalypti* has commonly been used for the species occurring on *Eucalyptus* leaf litter (Crous et al. 2006), Johnston et al. (2014) showed that the type of *T. eucalypti* occurred on fallen phyllodes of an *Acacia* sp. (Tasmania, Australia), which then became the type species of the new genus *Hymenotorrendiella.* However, this resulted in the common endophyte and saprobe occurring on eucalypt leaf litter not having a name. Several collections from *Eucalyptus* leaf litter were investigated in the present study, and two taxa were found to be present. The first, described here as *H. communis*, occurred in a clade with isolates from Australia, Colombia, Spain, and South Africa. Morphologically, however, the South African isolates differ from others in this clade based on macromorphology. Apothecia have shorter stalks, 100–200 µm high; setae vary from 60–80 per apothecium, but are much shorter, and wider that those from other collections in this clade, being 70–150 µm long, with obtuse apices, 4(–5) µm diam, and slightly inflated bases, 4–7 µm diam. Asci are similar however, being 85–110 × 6–8 µm, as well as ascospores, (15–)19–21(–23) × (3.5–)4 µm. *Hymenotorrendiella communis* can be distinguished from the second species, *H. indonesiana* (ascospores 17–25 × 3–4 µm), which occurs in Indonesia, by its shorter and wider ascospores.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Hymenotorrendiella indonesiana* (as *Torrendiella eucalypti*; strain 4876, GenBank FR668015.1; Identities = 522/527 (99 %), 5 gaps (0 %)), *Hymenotorrendiella andina* (as *Torrendiella andina*; strain PRJ SA193, GenBank KJ606682.1; Identities = 447/459 (97 %), no gaps), and *Hymenotorrendiella madsenii* (as *Torrendiella madsenii*; voucher PDD 58572, GenBank AY755336.1; Identities = 420/433 (97 %), 1 gap (0 %)).

Colour illustrations. *Eucalyptus* along roadside in La Trobe State Forest, where *H. communis* was collected. Apothecia with setae; cupulate receptacle with setae; asci; seta; ascus; ascospores. Scale bars: cupulate receptacle = 200 µm, all others = 10 µm.

Hymenotorrendiella indonesiana Crous & P.R. Johnst., *sp. nov.*

Etymology. Name refers to Indonesia, the country from which it was collected.

Description, Illustration & Discussion — See Crous et al. (2006), Stud. Mycol. 55: 61. 2006.

Typus. Indonesia, on *Eucalyptus urophylla* leaf litter, Mar. 2004, *M.J. Wing-field* (holotype CBS H-18041, single-ascospore cultures ex-type, CPC 11049 = CBS 115326, CPC 11050–11051; ITS, LSU and SSU sequences GenBank DQ195787.1–DQ195789.1, DQ195799.1–DQ195800.1 and DQ195810.1–DQ195811.1, MycoBank MB835414).

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 11049 had highest similarity to *Hymenotorrendiella andina* (as *Torrendiella andina*; strain PRJ SA193, GenBank KJ606682.1; Identities = 480/501 (96 %), 7 gaps (1 %)), *Hymenotorrendiella eucalypti* (voucher PDD 70105, GenBank MH578483.1; Identities = 470/495 (95 %), 7 gaps (1 %)), and *Hymenotorrendiella cannibalensis* (as *Torrendiella cannibalensis*; strain ICMP 18818, GenBank JN225947.1; Identities = 475/502 (95 %), 9 gaps (1 %)). The ITS sequences of CPC 11049, 11050 and 11051 are identical (498/498 bp). Closest hits using the **LSU** sequence of CPC 11049 are *Endoscypha perforans* (voucher PDD 102231, GenBank MK039717.1; Identities = 851/860 (99 %), no gaps), *Hymenotorrendiella madsenii* (as *Torrendiella madsenii*; strain PRJ D672, GenBank KJ606676.1; Identities = 817/829 (99 %), no gaps), and *Roesleria subterranea* (strain CBS 201.25, GenBank MH866343.1; Identities = 839/853 (98 %), no gaps).

Supplementary material

FP1057 & 1058-1 Additional materials examined - ***Hymenotorrendiella communis***

FP1057 & 1058-2 Additional materials examined - ***Hymenotorrendiella indonesiana***

FP1057 & 1058-3 The first of 28 equally most parsimonious trees obtained from a phylogenetic analysis of the *Hymenotorrendiella*

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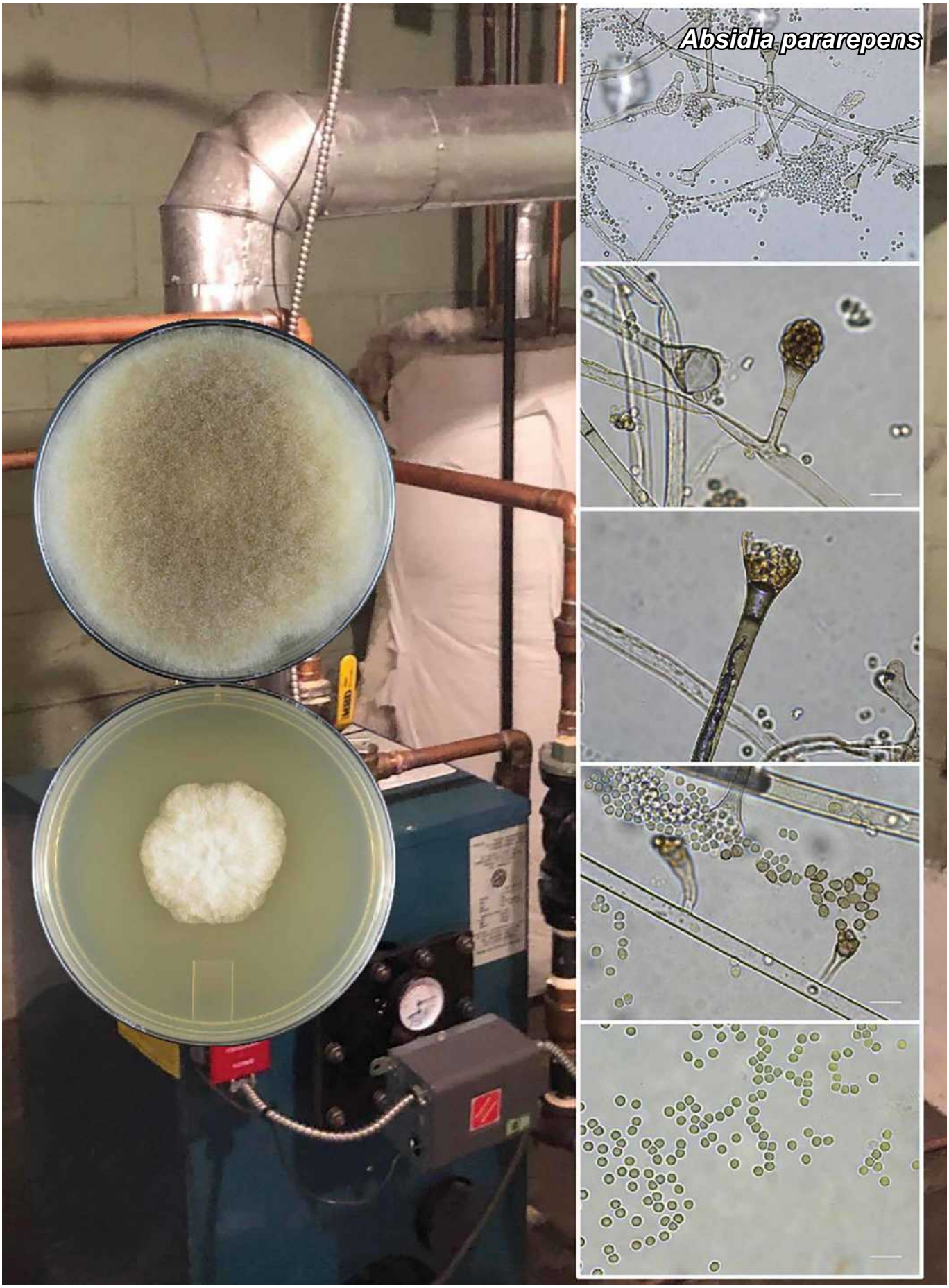
Absidia pararepens

Fungal Planet 1059 – 29 June 2020

Absidia pararepens Jurjević, M. Kolařík & Hubka, *sp. nov*.

Etymology. Refers to the phylogenetic proximity and phenotypic similarity to *A. repens*.

Classification — *Cunninghamellaceae*, *Mucorales*, *Mucoromycotina.*

Micromorphology (on malt extract agar; MEA): *Hyphae* hyaline to brownish, coenocytic, smooth, finely roughened to definitely roughened near crustaceous, 3–13 µm diam. *Sporangiophores* hyaline to brown near dark brown, simple or branched, arising solitarily, occasionally in pairs, never grouped in whorls, arising from aerial hyphae or substrate, most commonly 10–150 × 3–6 µm; smooth, finely roughened to definitely roughened near crustaceous walls, with a single septum below the sporangium and rarely with additional septum at the base. *Sporangia* hyaline to brown to dark greyish brown, most commonly pyriform, (10–)14–24(–26) µm diam, smooth-walled. *Apophyses* funnel-shaped, smooth-walled. *Columellae* globose, hemispherical, with a short collarette, occasionally with one projection, smooth-walled, (6–)12–17(–22) µm diam. *Sporangiospores* of two types: sub-globose to globose, hyaline, smooth-walled, and oval, occasionally slightly irregular, brown, rough-walled (formed in the different sporangia), (3.3–)3.5–5(–9) × (3.3–)3.5–6 µm. *Chlamydospores* (terminal and intercalary) occasionally present in the aerial mycelia. *Zygospores* not observed.

Culture characteristics — (in darkness, 25 °C after 3 d / 7 d): Colonies on MEA 39–45/>90 mm diam, cottony, mycelium at first white, then becoming grey to grey-brown (light mouse grey to mouse grey, R51; Ridgway (1912)), abundant sporulation, reverse colonial buff to deep colonial buff (R30), smooth and wavy zonate. Colonies on potato dextrose agar (PDA 39–44/>90 mm diam, cottony, mycelium at first white, then becoming grey to grey-brown [R51), very good sporulation, reverse grey to grey with buckthorn brown shades (R15), radially sulcate. Colonies on OA 35–40/>90 mm diam, cottony, mycelium at first white, then becoming light mouse grey to mouse grey (R51), good sporulation. Colony diam at 30 °C (in mm after 7 d): MEA 4–37; PDA 4–48; OA 5–48. No growth on MEA, PDA and OA at 32 °°C.

Typus. USA, New York, Jericho, bathroom, air, 12 Dec. 2015, *Ž. Jurjević* (holotype BPI 911217, cultures ex-type CCF 6352 = CBS 146002 = EMSL 3235; ITS and LSU sequences GenBank MT193669 and MT192308, MycoBank MB834983).

Additional materials examined. USA, Maryland, Parkton, bedroom, air, 16 Nov. 2015, *Ž. Jurjević*, culture CCF 6351 = EMSL 3145 (ITS and LSU sequences GenBank MT193670 and MT192307); New Jersey, Tinton Falls, basement, air, 08 Mar. 2016, *Ž. Jurjević*, culture CCF 6353 = EMSL 3556 (ITS sequence GenBank MT193671); New York, Massapequa Park, basement, swab, 09 Aug. 2016, *Ž. Jurjević*, culture CCF 6354 = EMSL 3570 (ITS sequence GenBank MT193672); Ohio, hospital, air, 26 Sept. 2016, *Ž. Jurjević*, culture CCF 6355 = EMSL 3656 (ITS sequence GenBank MT193673); New Jersey, Marlton, basement, concrete floor, swab, 04 Apr. 2017, *Ž. Jurjević*, culture CCF 6356 = EMSL 4142 (ITS sequence GenBank MT193674).

Colour illustrations. House basement. Seven-day-old cultures of *Absidia pararepens* on MEA (top to bottom 25 °C, 30 °C); sporangiophores, sporangiospores, and chlamydospores on MEA. Scale bars = 10 µm.

Notes — BLAST analyses with the ITS and LSU sequences of *A. pararepens* showed greatest similarity with *A. repens* ex-type CBS 115583 (~87 % and ~95 % similarity, respectively). The American isolates KAS 3611 (GenBank FJ849793), FSU 939 (GenBank AY944891), CBS 101.32 = FSU 5891 (GenBank EF030527), CBS 102.32 = FSU 5892 (GenBank EF030528), NRRL 1336 (GenBank AF113448) and 14849A (GenBank AY234881) also represent *A. pararepens*, while European isolates CBS 115583 (GenBank EU484281, HM849706) and FSU 4726 (GenBank EU484288) represent *A. repens* s.str. However, this geographic pattern should be confirmed by analysis of additional strains.

Hesseltine & Ellis (1966) invalidly designated a neotype for *A. repens*. In conflict with Art. 8.4 (Turland et al. 2018), the authors selected a living culture, NRRL 1336. This culture originated from a collection of A.F. Blakeslee, and was probably isolated in America. However, as pointed out by Hoffmann et al. (2009) and Hoffmann (2010), there are large genetic differences between European and American isolates of '*A. repens*'. Consequently, the neotype of *A. repens* should be selected from among European strains in accordance with the original description of Van Tieghem (1878), who collected *A. repens* on fruit of *Bertholletia excelsa* lying on a layer of moist *Sphagnum* in France. The specimen CBS 115583 originating from England, UK, was mentioned as isotype of *A. repens* by Hoffmann et al. (2009) and Hoffmann (2010), but formal typification has never been published.

To formalize the typification, we designate here a lectotype of *A. repens* (illustration from the original material): pl. 12, f. 55–63 (not paginated) in P. van Tieghem, *Annales des Sciences Naturelles Botanique* Ser. 6, Vol. 4. 1878 [1876]. MycoBank typification no. is MBT392665. Epitype designated here: specimen CBS 115583 (preserved in metabolically inactive state), ex-epitype culture CBS 115583. MycoBank typification no. is MBT392666).

Absidia pararepens has on average shorter sporangiophores (10–150 × 3–6 µm), and larger sporangiospores ((3.3–)3.5–5(–9) × (3.3–)3.5–6 µm) than the closely related *A. repens* ((50–)140–250(–450) × 2.5–6 µm), and (2.8–5.5(–6.5) × 2–3 µm), respectively.

Supplementary material

FP1059 A best scoring maximum likelihood tree based on the ITS region sequences shows the relationships of *Absidia pararepens* sp. nov. with other species.

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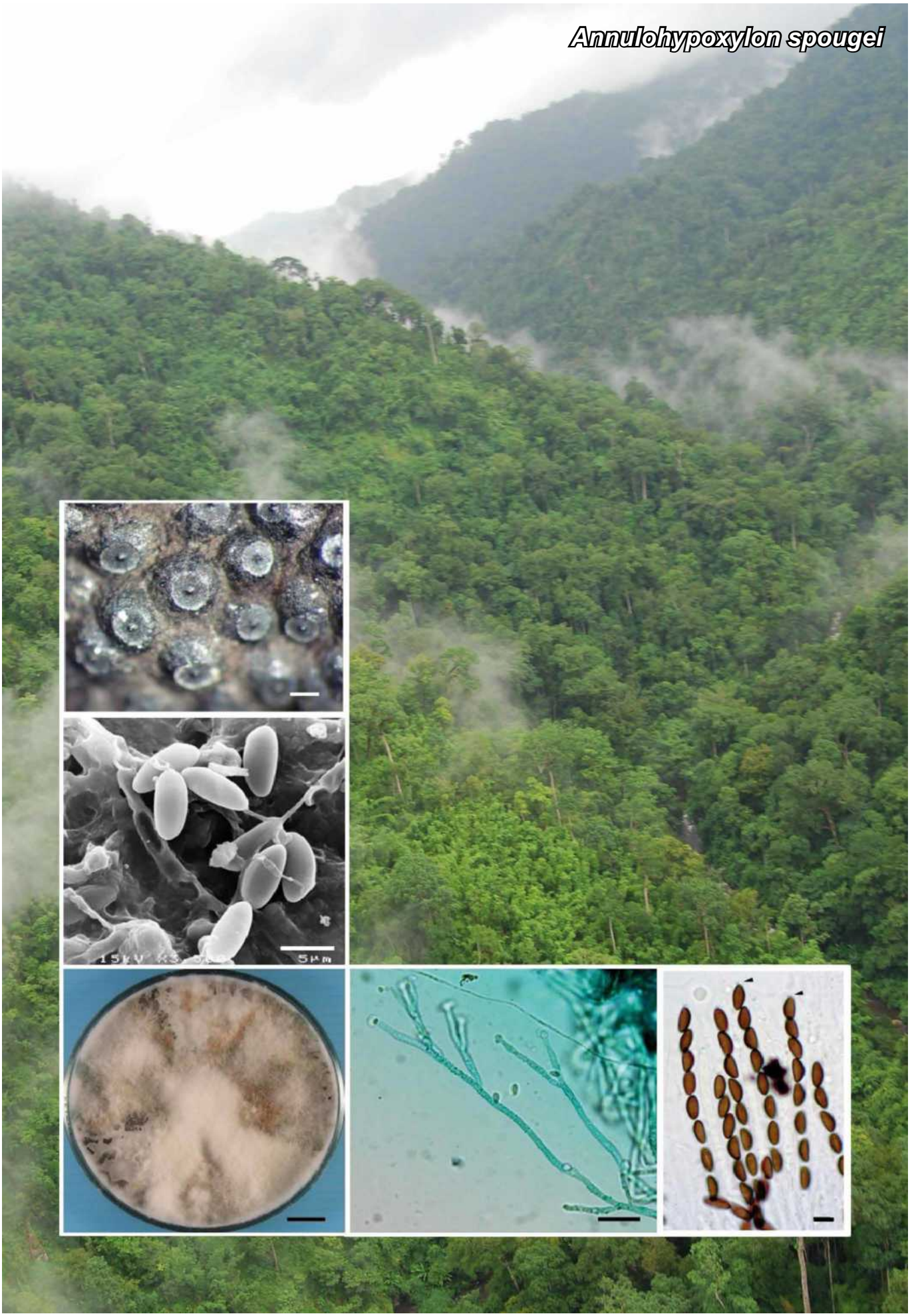
Annulohypoxylon spougei

Fungal Planet 1060 – 29 June 2020

Annulohypoxylon spougei Suwannasai, M.P. Martín, Phosri & Whalley, *sp. nov.*

Etymology. Named after the American bioinformatician John L. Spouge who contributed to the discovery of this species, and for his efforts to implement tools for DNA barcoding analyses within the genus *Annulohypoxylon*.

Classification — *Hypoxylaceae*, *Xylariales*, *Sordariomycetes*.

Stromata glomerate to hemispherical, effused-pulvinate, with perithecial mounds 1/4 to 2/3 exposed and not covered by the outermost stromatal layer, 0.3–6 cm long × 0.3–3 cm broad and 1–1.6 mm thick; surface dark brown vinaceous, becoming black with reddish brown hues, finally black and shiny; black granules immediately below the surface, KOH pigments green olivaceous. *Perithecia* spherical, 0.5–0.7 mm diam. *Ostioles* conical papillate, surrounded by a flattened *bovei*-type disc, 0.2–0.5 mm diam. *Asci* 62–114 × 4–4.5 µm, the spore bearing parts 64–73 µm long with stipes 20–32(–46) µm long, with apical ring bluing in Melzer's iodine reagent, discoid 0.7 µm high × 1.5–2 µm broad. *Ascospores* pale brown, unicellular, ellipsoid-inequilateral with narrowly rounded ends, 6–10.5 × 3–4.5(–5.5) µm with straight germ slit along the full length of the spore; perispore dehiscent in 10 % KOH, epispore smooth.

Culture characteristics — Colonies on potato dextrose agar (PDA) covering Petri dish in 2 wk, at first white, becoming hazel to dull green, azonate, with diffuse margins, with scattered black patches; reverse dull green to dark brown. *Conidiogenous structure* nodulisporium-like, brown. *Conidia* hyaline, smooth, ellipsoid, 3.5–4.5 × 2–3 µm.

Typus. Thailand, Phitsanoluk, Khao KraYang Forest Planation, on corticated wood, Sept. 2006, *C. Phosri & N. Suwannasai* H099 (holotype SWUF-H099; ITS, α-actin and β-tubulin sequences GenBank FN252419, FR875158 and KP134519, MycoBank MB811164).

Additional materials examined. Herbarium number is indicated, as well as the ITS, α-actin, β-tubulin and *EF1-α* GenBank sequences between brackets, absent sequences are indicated with '–'. ***Annulohypoxylon spougei***: Thailand, Phitsanulok Province, *Dipterocarpaceae* forest, Sept. 2006, *C. Phosri & N. Suwannasai* SWUF-H087 (FN252418, KP134506, FR875164, –); SWUF-H181 (FN252420, KP134507, KP134520, –); SWUF-H203 (FN252421, FR875159, FR875165, –); SWUF-H215 (FN252422, KP134508, KP134521, –); SWUF-H254 (FN252423, FR875160, FR875166, –); Nakhon Ratchasima Province, *Dipterocarpaceae* forest, July 2003, *N. Suwannasai* SUT081 (DQ322105, –, –, –); Trad Ratchasima Province, *Dipterocarpaceae* forest, Aug. 2003, *C. Phosri & N. Suwannasai* SUT236 (DQ322106, –, –, –); SUT242 (DQ322107, –, –, –); SUT244 (DQ322108, –, –, –); SUT251 (DQ322109, –, –, –); Kanchanaburi Province, *Dipterocarpaceae* forest, Aug. 2003, *N. Suwannasai* SUT285 (DQ322110, –, –, –); Chaiyaphum Province, *Dipterocarpaceae* forest, June 2009, *C. Phosri & N. Suwannasai* PK09007 (KP134526, KP134509, KP134522, KP134499); PK09026 (KP134527, KP134510, –, KP134500); PK09027 (KP134528, KP134511, –, KP134500); PK09029 (KP134529, KP134512, –, –). ***Annulohypoxylon nitens***: Thailand, Chiang Rai Province, *Dipterocarpaceae* forest, Sept. 2006, *C. Phosri & N. Suwannasai* SWUF-H154 (FM209453, FR875161, KP134513, –); SWUF-H157 (FM209455, FR875162, KP134514, –); Phitsanulok Province, *Dipterocarpaceae* forest, Sept. 2006, *C. Phosri & N. Suwannasai* SWUF-H189 (FM209459, KP134502, FR875167, –); SWUF-H197 (FM209461, FR875163, KP134515, –); Chaiyaphum Province, *Dipterocarpaceae* forest, June 2009, *C. Phosri & N. Suwannasai* PK121044 (KP134523, KP134503, KP134516, KP134496); PK121063 (KP134524, KP134504, KP134517, KP134498); PK121086 (KP134525, KP134505, KP134518, KP134497).

Notes — During extensive studies of the *Hypoxylaceae* in Thailand over a period of almost 20 yr, problems were encountered in the identification of several taxa, especially *A. nitens.* A previous study on species of *Hypoxylon* and *Annulohypoxylon* using morphology and ITS nrDNA sequences (Suwannasai et al. 2013) indicated that this taxon was not monophyletic but could be separated into *A. nitens* and another species. Twenty-eight fungal specimens of *A. nitens* and a cryptic species collected from Thailand, previously named '*A. nitens*' in our study (Suwannasai et al. 2013), were carefully re-analysed based on morphological and asexual morph characters. The comparison of morphological characters between *A. nitens* and a cryptic species showed unclear distinction of these species. The cryptic species, here named as *A. spougei* possesses spherical perithecia (0.5–0.7 mm diam), which are slightly narrower than those of *A. nitens* described by Ju & Rogers (1996) ((0.4–)0.5–1(–1.2) mm). The ostiolar discs of both species groups are *bovei*-type and have the same dimensions of 0.2–0.5 mm. Ascospore sizes of *A. nitens* and the cryptic species are 7.5–9 × 2.8–4.2 µm and 6–10.5 × 3–4.5(–5.5) µm, respectively. These are similar to the species description for *A. nitens* (as *H. nitens*) (6.5–10(–11) × 3–4.5 µm) from Ju & Rogers (1996). The cultural and asexual morph characters were observed from both PDA and oatmeal agar. Colonies of *A. spougei* are white at first becoming hazel and dull green with scattered black patches. The asexual morph is nodulisporium-like and conidial size (3.5–4.5 × 2–3 µm) is similar to *A. nitens* (4–5 × 2.5–3 µm). With those similar features, it is very difficult to separate the *A. spougei* from *A. nitens* by using only morphological and asexual morph characters. However, although morphological data for all of the collections initially identified as *A. nitens* failed to provide clear separation of the two entities, there are clear supporting DNA data for their separation. In the present study based on α-actin, β-tubulin and elongation factor 1-α sequences, we confirm the separation of two taxa mentioned in Suwannasai et al. (2013).

Colour illustrations. Thailand, Chaiyaphum Province, Phu Khiao Wildlife Sanctuary, where the specimens were collected. From top to bottom: stromata with ostiolar discs (SWUF-H099); ascospores under SEM (SWUF-H099); fungal culture on PDA (SWUF-H099); nodulisporium-like anamorph (SWUF-H099); ascospores with apical apparatus (SWUF-H099). Scale bars = 0.5 mm (stromata), 5 µm (ascospores SEM), 1 cm (fungal culture), 15 µm (asexual morph), 5 µm (ascospores)

Supplementary material

FP1060 UPGMA reconstruction based on K2P distances of α-actin, β-tubulin and *EF1-α* sequences of *Annulohypoxylon nitens* and *A. spougei* specimens using PAUP* v. 4.0b10 (Swofford 2003).

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Aspergillus banksianus

Fungal Planet 1061 – 29 June 2020

Aspergillus banksianus Pitt, *sp. nov*.

Etymology. Named for the Australian endemic tree *Banksia integrifolia*, from the rhizosphere of which this species was isolated.

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

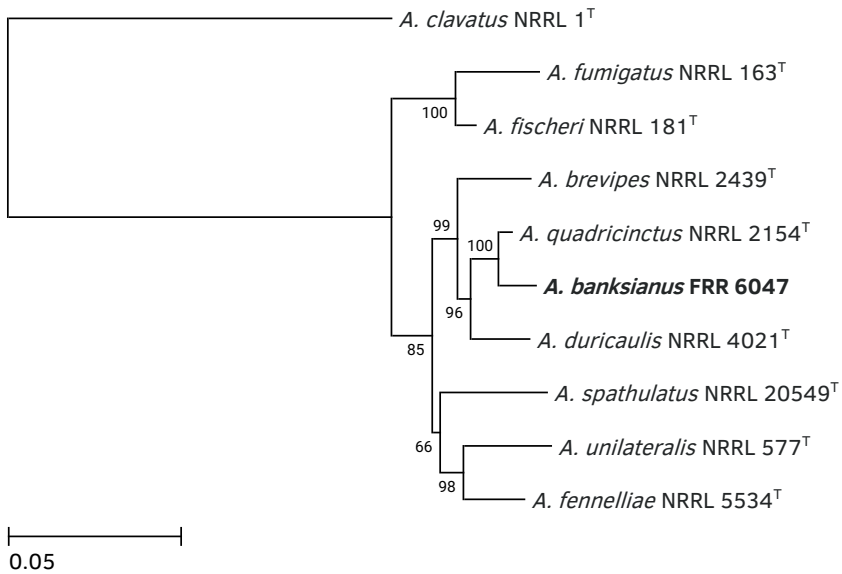
Culture characteristics — Czapek yeast extract agar (CYA), 25 °C, 7 d: Colonies 25–30 mm diam, low and dense, plane or irregularly wrinkled, with narrow margins of white mycelium; conidiogenesis moderate to heavy, dark grey to dark grey blue (M. 24–25D–E2–3); exudate absent, soluble pigment brown; reverse Deep Green (M. 29F3–4). MEA, 25 °C, 7 d: Colonies 40–45 mm diam, low and plane, with wide uncoloured margins, light to heavily sporing, coloured as on CYA or slightly greener (M. 26D3); exudate and soluble pigment absent; reverse centrally Dark Green (M. 27F5), paler towards the margins. 25 % Glycerol nitrate agar (G25N), 25 °C, 7 d: Colonies up to 5 mm diam, of white mycelium. 37 °C, CYA, 7 d: Colonies 40–45 mm diam, heavily sporing, dull green to grey green; reverse dark green, greyish green or black.

Conidiophores borne from aerial hyphae, sometimes unbranched, and then (5–)50–120 × 2.5–3 µm, sometimes bearing a short lateral stipe 10–40 µm long as well; broadening slowly to spathulate vesicles, 5–15 µm diam, fertile area characteristically hemispherical but sometimes asymmetrical to give a 'nodding' appearance. *Phialides* short and stout, 3.5–6 × 2.5–3 µm, with narrow bases and very short narrow necks, sometimes almost ellipsoidal. *Conidia* 2.5–3 µm diam, smooth to finely roughened, borne in short disordered chains, separating in wet mounts.

Media formulations are from Pitt & Hocking (2009); (M.) colours are from Kornerup & Wanscher (1978).

Typus. Australia, New South Wales, Collaroy, from rhizosphere soil beneath a specimen tree of the endemic species *Banksia integrifolia* (*Proteaceae*), 2004, *A.-L. Markovina* (holotype DAR 85042, cultures ex-type FRR 6047 = MST FP2248; ITS, *BenA*, *CaM* and *RPB2* sequences GenBank MH280013, MT184780, MT184786, MT184792, MycoBank MB835223).

Notes — *Aspergillus banksianus* clusters in *Aspergillus* subgenus *Fumigati*, in a small clade that includes *A. brevipes* and *A. duricaulis*, with which it shares slow growth at 25 °C, green conidial colouration and intermittent production of asymmetrical fruiting structures. Colonies of *A. banksianus* on CYA have a deep green reverse colour, in contrast with *A. duricaulis*, 'colorless to pinkish drab' or *A. brevipes* 'becoming purple-red' (Raper & Fennell 1965). Molecularly, *A. banksianus* is particularly close to *A. quadricinctus*, from which the most obvious difference is lack of the *Neosartorya* sexual morph. *Aspergillus banksianus* when grown on agar, liquid media or grain, displays a unique chemotaxonomic profile comprising banksialactones A-I, and banksiamarins A and B, which are not present in the closely related species *A. quadricinctus* and *A. duricaulis* (Chaudhary et al. 2018). *Aspergillus banksianus* also produces known metabolites clearanol and dothideomynone A, together with the pigments endocrocin and questin previously reported from other *Aspergillus* species.



A maximum likelihood tree inferred from the combined ITS, *BenA*, *CaM* and *RPB2* sequences of taxa within *Aspergillus* sect. *Fumigati*. The combined sequence alignment was partitioned by marker; substitution models for each partition were chosen according to the Bayesian Information Criteria using ModelTest-NG v. 0.1.6 (Darriba et al. 2020). The TrN+I model was used for ITS sequences, K80+G4 for *BenA*, TrNef+G4 for *CaM* and TIM2ef+I+G4 for *RPB2*. The tree was constructed using RAxML-NG v. 0.9.0 (Kozlov et al. 2019). Bootstrap support values are derived from 1 000 bootstrap replicates. Alignment available in TreeBASE (study S25912).

Colour illustrations. A specimen tree of the endemic species *Banksia integrifolia*, planted on a street in Collaroy, NSW, from under which a soil sample included *A. banksianus*. Colonies grown on CYA (upper) and malt extract agar (MEA) (lower) for 7 d at 25 °C; fruiting structures and conidia. Scale bars = 10 µm (fruiting structures) and 5 µm (conidia).

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Aspergillus oxumiae

Fungal Planet 1062 – 29 June 2020

Aspergillus oxumiae C.N. Figueiredo, L.S. Sales, Y.F. Figueiredo, J.P. Andrade & J.T. De Souza, *sp. nov*.

Etymology. *oxumiae*, in honour of Oxum, a female African deity from the Yoruba religion.

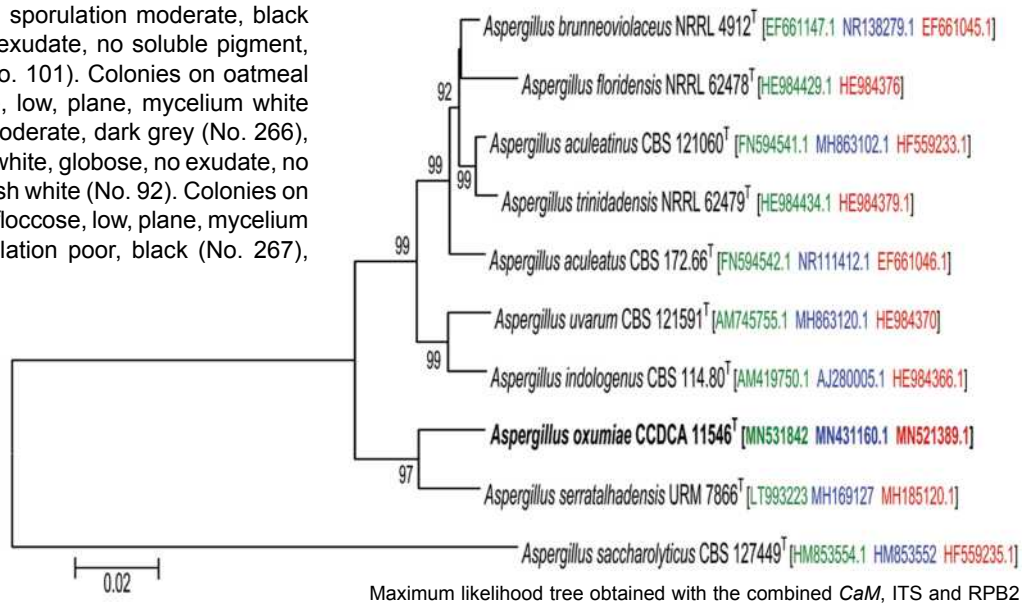
Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetes*.

Conidial heads radiate. *Conidiophores* uniseriate. *Stipes* smooth, frequently septate 48–890(–931) × 2–5(–7) µm, sometimes with subterminal branches and mycelial coils occasionally present. *Vesicles* pyriform to subglobose, pigmented, 8–20(–30) × 6.5–21(–30) µm (av. 12 ± 3.6 × 11 ± 3.2), phialides 4–13(–20) × 2–8 µm (av. 8 ± 2.7 × 4 ± 1.0) covering half to upper half of vesicle. *Conidia* globose to subglobose, 3–7 × 3.5–7 µm (av. 5 ± 0.77 × 5 ± 0.81), brown to greyish brown, with coarsely roughened to echinulate surface, average width/length = 1 ± 0.03, n = 74. *Sclerotia* observed.

Culture characteristics — Colonies on Czapek yeast autolysate agar (CYA 46–47 mm diam at 25 °C in 7-d-old, lanose to floccose, radially and concentrically wrinkled, mycelium white (ISCC-NBS No. 263), sporulation poor to abundant, dark greyish yellowish brown (No. 81) to black (No. 267), sclerotia abundant, white, globose, no exudate, no soluble pigment, reverse brownish pink (No. 33), yellowish white (No. 92), dark greyish olive (No. 111). Colonies on Blakeslee's malt extract agar (MEAbl) 53–54 mm, floccose, radially and concentrically wrinkled, mycelium white (No. 263), sporulation moderate to abundant, dark olive brown (No. 96), olive black (No. 114), sclerotia moderate, white, globose, no exudate, no soluble pigment, reverse pale yellow (No. 89), greyish yellow (No. 90). Colonies on yeast extract sucrose agar (YES) 27–28 mm, lanose, irregularly wrinkled, mycelium white (No. 263), sporulation moderate, black (No. 267), sclerotia absent, no exudate, no soluble pigment, reverse light greenish yellow (No. 101). Colonies on oatmeal agar (OA) 46–48 mm, floccose, low, plane, mycelium white (No. 263), sporulation poor to moderate, dark grey (No. 266), black (267), sclerotia abundant, white, globose, no exudate, no soluble pigment, reverse yellowish white (No. 92). Colonies on Czapek's agar (CZ) 50–52 mm, floccose, low, plane, mycelium yellowish white (No. 92), sporulation poor, black (No. 267), sclerotia absent, no exudate, no soluble pigment, reverse yellowish white (No. 92). Colonies on CYA with 5 % NaCl (CYAS) 23–25 mm, floccose, irregularly wrinkled, mycelium white (No. 263), sporulation poor to abundant, dark yellowish brown (No. 78), sclerotia absent, no exudate, no soluble pigment, reverse pale yellow (No. 89), dark greyish yellow (No. 91). Colonies on creatine sucrose agar (CREA) 19–22 mm, moderate mycelial growth, sclerotia absent, no acid production. The isolate did not grow in CYA at 10, 37 and 42 °C, but grows at 15 °C 20–22 mm, 20 °C 33–34 mm, 30 °C 32–33 mm and 33 °C 29–31.

Typus. Brazil, Bahia, municipality of Campo Formoso, S10°30' W40°19', in soil cultivated with *Agave sisalana*, 20 Oct. 2007, *J.R.Q. Silva* (holotype HURB 22369 - dried culture on MEAbl; culture ex-type CCDCA 11546 = UFLA115; ITS, LSU, *CaM*, *ben*A and *RPB2* sequences GenBank MN431160.1, MN508996, MN531842, MN521388 and MN521389, MycoBank MB832766).

Notes — *Aspergillus oxumiae* is phylogenetically related to the species *A. serratalhadensis* included in sect. *Nigri*, but it is clearly a different species. The morphological characteristics distinguishing *A. oxumiae* from *A. serratalhadensis* are: *A. oxumiae* grows slower on CYA and YES 25 °C and grows faster on OA 25 °C. *Aspergillus oxumiae* does not produce acid on CREA, the stipes and phialides are bigger and the vesicles are smaller. All macroscopic and microscopic measurements were done twice, independently, for isolate CCDCA 11546.



Maximum likelihood tree obtained with the combined *CaM*, ITS and RPB2 sequences from *A. oxumiae* and phylogenetically related species in section *Nigri* performed in MEGA v. 6.06 software (Tamura et al. 2013) employing the TN93+G model with 1000 bootstrap re-samplings. Bootstrap support values (BS > 80 %) are presented at the nodes. *Aspergillus saccharolyticus* CBS 127449^{T} was used as outgroup. The new species is presented in **bold** font (^{T} = ex-type). GenBank accession numbers are given after each strain (*CaM* = green, ITS = blue and *RPB2* = red).

Colour illustrations. *Agave sisalana*. Seven-day-old colonies growing at 25 °C, top row left to right, obverse CYA, MEAbl and CREA; bottom row left to right, reverse CYA, MEAbl and obverse OA; conidiophores, conidia and coiling of mycelia. Scale bars = 10 µm.

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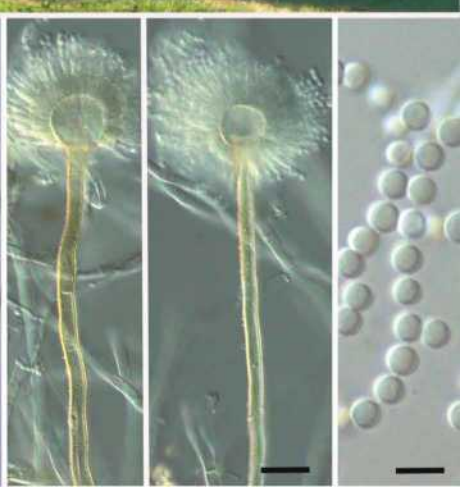
Aspergillus kumbius



Fungal Planet 1063 – 29 June 2020

Aspergillus kumbius Pitt, *sp. nov*.

Etymology. Named for the small town of Kumbia, South Burnett District, Queensland, Australia, near where this species was collected.

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

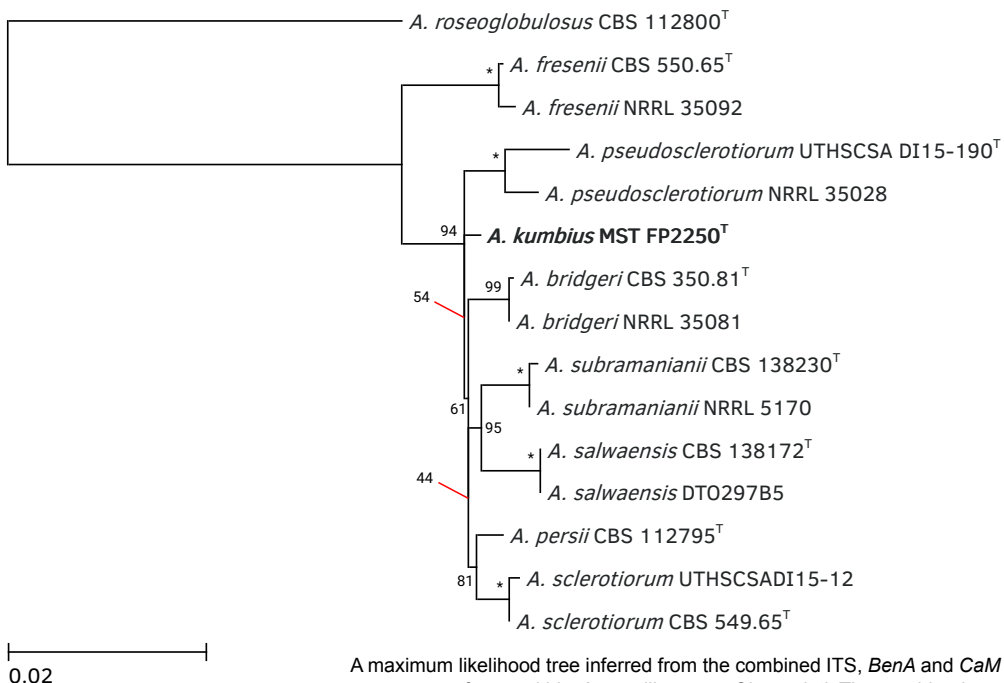
Conidiophores borne from aerial hyphae, stipes 300–400(–600) × 5–6 µm, uncoloured to pale brown, smooth walled. *Vesicles* spherical, 15–25 µm diam, fertile over the upper hemisphere or two thirds; metulae 6–8 × 2.5–3.0 µm; phialides acerose, 7–8 × 2.0–2.2 µm. *Conidia* spherical, 2.2–2.5 µm diam, walls smooth to finally roughened, borne in disordered chains.

Culture characteristics — Czapek yeast extract agar (CYA), 25 °C, 7 d: Colonies 45–50 mm diam, plane, low and relatively sparse, lightly sulcate, velutinous; margins entire, wide; mycelium white to pale yellow; abundant sclerotia borne on the agar surface, white at first, at maturity pale orange to orange grey (M. 5A–B3), spherical or near, 400–800 µm diam; conidial production sparse, pale yellow brown (M. 4–5A3); clear to pale brown exudate produced; soluble pigment absent; reverse pale yellow. Malt extract agar (MEA), 25 °C, 7 d: Colonies 50–55 mm diam, low, plane, sparse and velutinous; margins subsurface, entire; mycelium inconspicuous, white to pale yellow brown; sclerotia moderately abundant, as on CYA except sometimes enveloped in fine white hyphae; conidial production light, yellow brown (M. 4A–B3), exudate and soluble pigment not produced; reverse uncoloured to pale orange. 25 % Glycerol nitrate agar (G25N), 25 °C, 7 d: Colonies 26–30 mm diam, of white mycelium; reverse uncoloured. 37 °C, CYA, 7 d: Colonies 6–12 mm diam, of white mycelium, reverse pale.

Media formulations are from Pitt & Hocking (2009); (M.) capitalised colours and notations are from Kornerup & Wanscher (1978).

Typus. Australia, Queensland, Kumbia, from rhizosphere soil beneath pasture, 2004, *J.I. Pitt* (holotype DAR 85044, cultures ex-type FRR 6049 = MST FP2250 = CBS 146722; ITS, *BenA*, *CaM* and *RPB2* sequences GenBank MT179307, MT184782, MT184788 and MT184794, MycoBank MB835225).

Notes — *Aspergillus kumbius* belongs in *Aspergillus* subgenus *Circumdati* sect. *Circumdati*. Molecularly, it is very close to *Aspergillus bridgeri* and *A*, *subramanianii*. It is distinguished by rapid growth at 25 °C with abundant buff coloured spherical sclerotia. When grown on agar, liquid media or grain, *A. kumbius* displays a unique chemotaxonomic profile including kumbicins A–D, which are not present in the closely related species *A. bridgeri*, *A. subramanianii*, *A. salwaensis*, *A. persii* or *A. sclerotiorum*. *Aspergillus kumbius* also produces known metabolites asterriquinol D dimethyl ether, petromurins C and D, aspochracin, JBIR-15, and neohydroxyaspergillic acid, compounds previously reported from other *Aspergillus* species.



A maximum likelihood tree inferred from the combined ITS, *BenA* and *CaM* sequences of taxa within *Aspergillus* sect. *Circumdati*. The combined sequence alignment was partitioned by marker; substitution models for each partition were chosen according to the Bayesian Information Criteria using ModelTest-NG v. 0.1.6 (Darriba et al. 2020). The HKY model was used for ITS sequences, K80+G4 for *BenA* and K80 for *CaM*. The tree was constructed using RAxML-NG v. 0.9.0 (Kozlov et al. 2019). Bootstrap support values are derived from 1 000 bootstrap replicates. Alignment available in TreeBASE (study S25913).

Colour illustrations. A scene of pasture near Kumbia, Queensland, similar to the one from which this species was described. Colonies grown on CYA (left) and MEA (right) for 7 d at 25 °C; fruiting structures and conidia. Scale bars = 20 µm (fruiting structures) and 5 µm (conidia).

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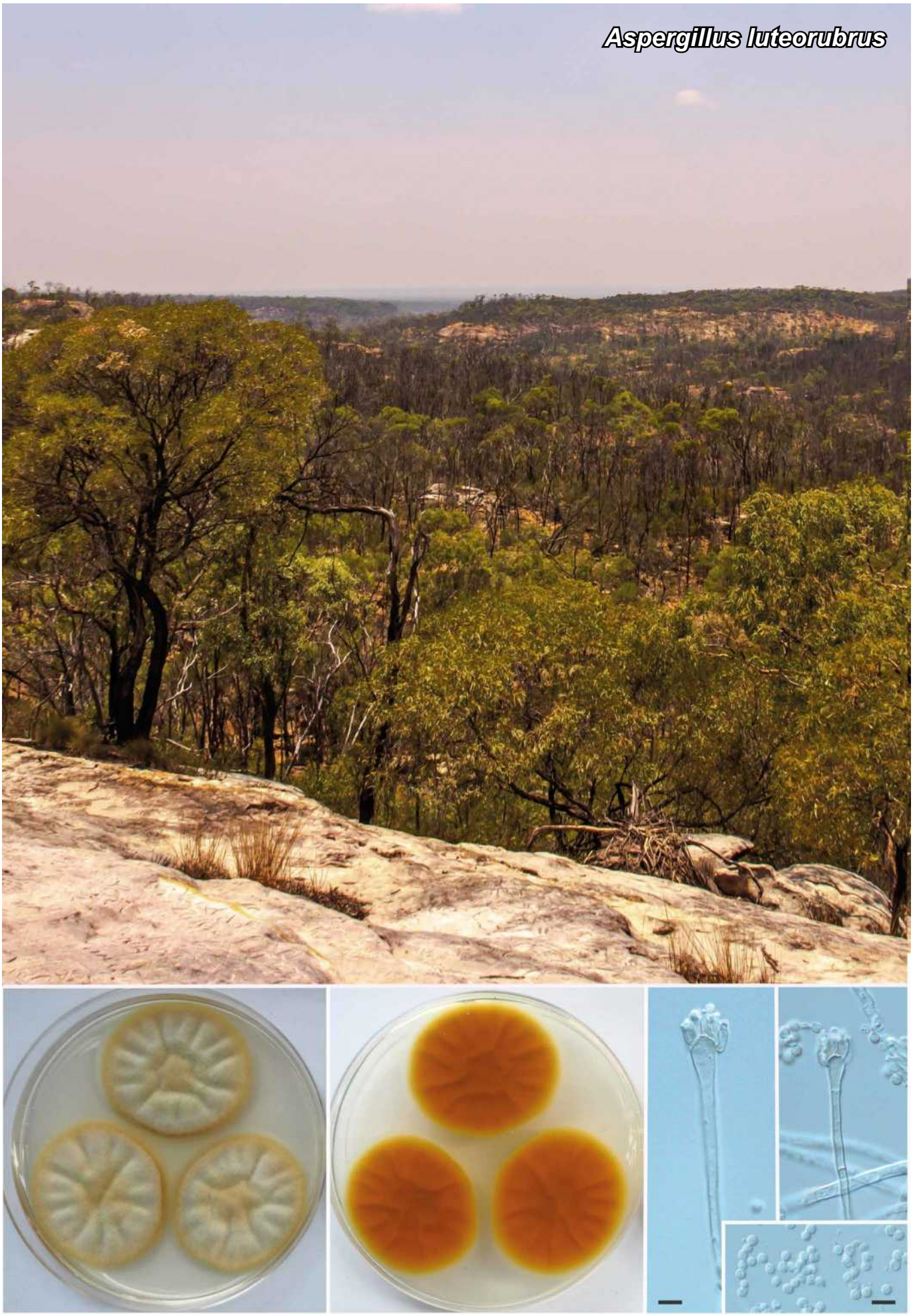

Aspergillus luteorubrus

Fungal Planet 1064 – 29 June 2020

Aspergillus luteorubrus Pitt, *sp. nov*.

Etymology. Named for the colony colours on CYA plates: Latin *luteus*, yellow and *ruber*, red.

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

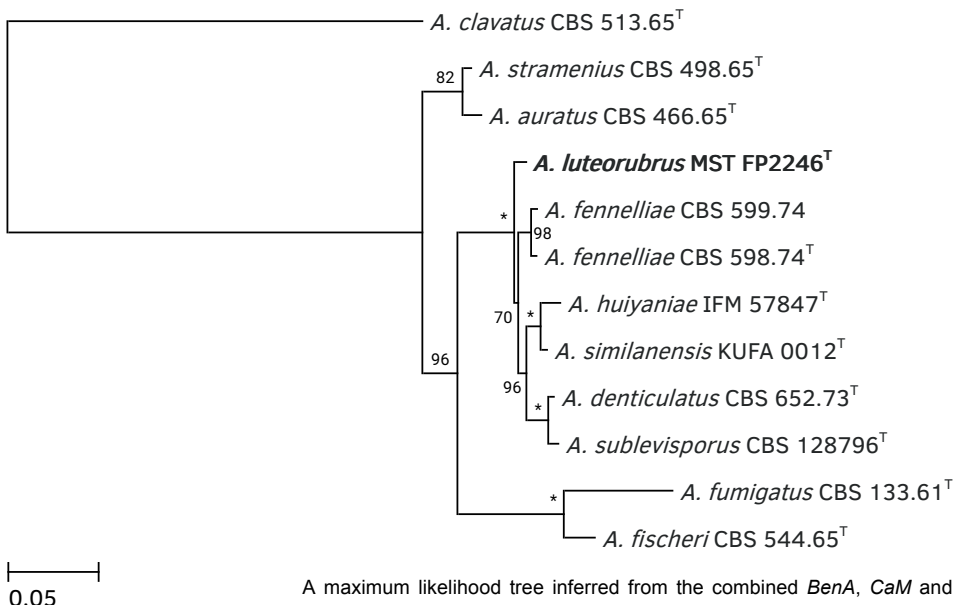
Conidiophores borne from aerial hyphae, slender, (40–)100–200(–300) × 2–2.5 µm, with thin smooth walls, enlarging slowly to very small spathulate vesicles, 4–6(–7) µm diam; bearing few short phialides, 5–7 × 2.5–3 µm. *Conidia* spherical, 2–2.5 µm diam, smooth-walled, borne in short disordered chains.

Culture characteristics — Czapek yeast extract agar (CYA), 25 °C, 7 d: Colonies 38–42 mm diam, dense and velutinous, plane or lightly wrinkled; margins low to moderately deep, entire; mycelium pale yellow (M. 3–4A2–3); sporulation very light, inconspicuous or pale brown (M. near 4B3); exudate absent, soluble pigment sometimes produced, pale yellow; reverse bright yellow at the margins, otherwise intensely coloured, Cadmium Orange to Brownish Red (M. 5–8A–C8). Malt extract agar (MEA), 25 °C, 7 d: Colonies 50–60 mm diam, plane, dense and velutinous to floccose; mycelium white to very pale yellow, in age becoming bright yellow (M. 4A3) centrally; sporulation inconspicuous; exudate and soluble pigment absent; reverse centrally Cadmium Orange (M. 5–6A–B7–8), paler yellow (M. 4A4–4A8) towards the margins. 25 % Glycerol nitrate agar (G25N), 25 °C, 7 d: Colonies 10–12 mm diam; pale yellow. 37 °C, CYA, 7 d: Colonies 55–60 mm diam, of white or pale yellow mycelium; reverse Amber to Yolk Yellow (M. between 3 and 4B7–8).

Media formulations are from Pitt & Hocking (2009); (M.) capitalised colours and notation are from Kornerup & Wanscher (1978).

Typus. Australia, Queensland, White Mountains National Park, from soil in a dry creek bed, 2004, *J.I. Pitt* (holotype DAR 85045, cultures ex-type FRR 5427 = MST FP2246 = CBS 146723; ITS, *BenA*, *CaM* and *RPB2* sequences MT179305, MT184781, MT184787 and MT184793, MycoBank MB835226).

Notes — *Aspergillus luteorubrus* clusters in *Aspergillus* subg. *Fumigati*, near *A. fennelliae*. This heterothallic species produces cleistothecia and ascospores characteristic of the sexual genus *Neosartorya*. As only a single strain of *A. luteobrunneus* is known, it is not clear whether this is an asexual species or, perhaps more likely, heterothallic. *Aspergillus luteorubrus* differs from this and other closely related species in colony colours, conidial size, shape and ornamentation. Differences also exist in molecular phylogeny and chemistry (unpubl. data).



A maximum likelihood tree inferred from the combined *BenA*, *CaM* and actin sequences of taxa within *Aspergillus* sect. *Fumigati*. The combined sequence alignment was partitioned by marker; substitution models for each partition were chosen according to the corrected Information Criteria using ModelTest-NG v. 0.1.6 (Darriba et al. 2020). The K80+G4 was used for *BenA* sequences, K80+G4 for *CaM* and TPM+I for actin. The tree was constructed using RAxML-NG v. 0.9.0 (Kozlov et al. 2019). Bootstrap support values are derived from 1 000 bootstrap replicates. Alignment in TreeBASE (study S25915).

Colour illustrations. View out over White Mountains National Park. Colonies of *Aspergillus luteorubrus* grown on CYA, left obverse, right reverse, for 7 d at 25 °C; fruiting structures and conidia. Scale bar = 5 µm.

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Aspergillus malvicolor

Fungal Planet 1065 – 29 June 2020

Aspergillus malvicolor A.D. Hocking, *sp. nov*.

Etymology. Named for the distinctive colour of the conidia. Latin *malvicolor*, mauve.

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

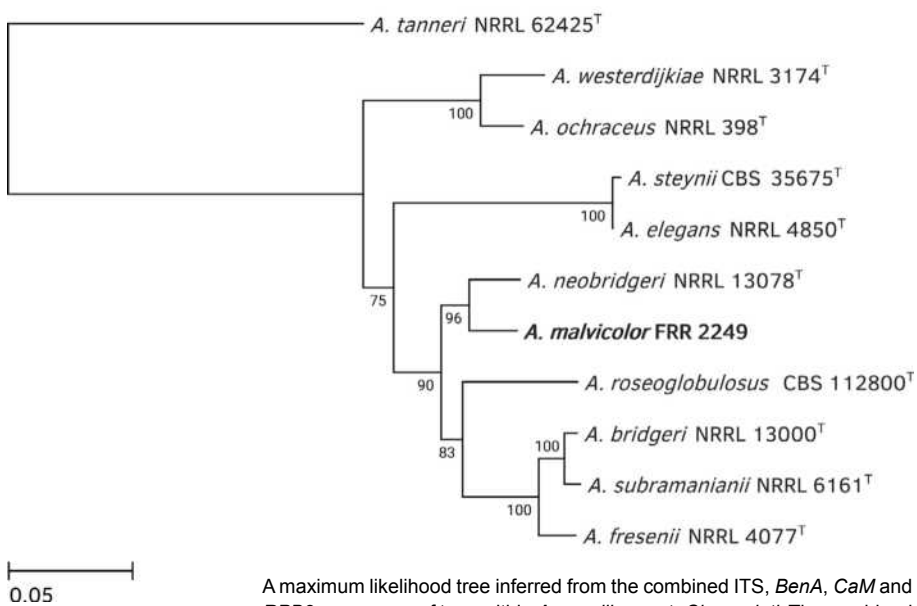
Conidiophores borne from subsurface or surface hyphae, stipes non-septate, 700–1000 × 8–10 µm, with thick, pale brown walls, often finely roughened, with small and undistinguished footcells. *Vesicles* 35–50 µm diam, sometimes with pinkish walls, bearing metulae and phialides over the entire surface area. *Metulae* mostly 8–10(–20) × 3–3.5(–5) µm; phialides closely packed, acerose, 8–10 × 2–2.5 µm. *Conidia* spherical, small, 2–2.2(–2.5) µm diam, with smooth to finely roughened walls, borne in radiate heads.

Culture characteristics — Czapek yeast extract agar (CYA), 25 °C, 7 d: Colonies 35–40 mm diam, plane or lightly radially sulcate, low to moderately deep; margins low, entire; mycelium inconspicuous; conidiogenesis heavy, coloured pink at the margins, grading to Greyish Magenta (M. 13C3) at the centres; colourless exudate sometimes produced; soluble pigment absent; reverse brown or pinkish brown. Malt extract agar (MEA), 25 °C, 7 d: Colonies 50–55 mm diam, low, plane and relatively sparse; margins subsurface to entire, low; mycelium pink or brown; sporulation heavy, coloured as on CYA; exudate and soluble pigment absent; reverse yellow brown. 25 % Glycerol nitrate agar (G25N), 25 °C, 7 d: Colonies 20–25 mm diam, low and dense, mycelium inconspicuous, moderately sporing in pink shades, reverse pinkish brown. 37 °C, CYA, 7 d: Colonies 15–20 mm diam, of pinkish brown mycelium, reverse pale to brown.

Media formulations are from Pitt & Hocking (2009); (M.) colour is from Kornerup & Wanscher (1978).

Typus. Australia, Queensland, Kingaroy, from rhizosphere soil beneath a commercial crop of peanuts (*Arachis hypogaea*), 1979, *A.D. Hocking* (holotype DAR 85046, cultures ex-type FRR 2383 = MST FP2244 = CBS 146724; ITS, *BenA*, *CaM*, *RPB2* sequences GenBank MT179308, MT184784, MT184790, MT184796, MycoBank MB835227).

Notes — *Aspergillus malvicolor* clusters in *Aspergillus* subg. *Circumdati*, sect. *Circumdati*, where it is related to *A. ochraceus*. It differs from all described species of *Aspergillus* by the mauve colour of its conidia. Phylogenetically, the nearest related species is *A. neobridgeri*, from which it is distinguished by conidial colour, by growth rate at 37 °C, and in metabolite production (unpubl. data).



A maximum likelihood tree inferred from the combined ITS, *BenA*, *CaM* and *RPB2* sequences of taxa within *Aspergillus* sect. *Circumdati*. The combined sequence alignment was partitioned by marker; substitution models for each partition were chosen according to the Bayesian Information Criteria using ModelTest-NG v. 0.1.6 (Darriba et al. 2020). The TrNef+I model was used for ITS sequences, K80+G4 for *BenA*, TrNef+G4 for *CaM* and *RPB2*. The tree was constructed using RAxML-NG v. 0.9.0 (Kozlov et al. 2019). Bootstrap support values are derived from 1 000 bootstrap replicates. Alignment available in TreeBASE (study S25914).

Colour illustrations. A commercial peanut crop, near Kingaroy, Queensland, similar to the one from under which this species was described. Colonies grown on CYA (left) and MEA (right) for 7 d at 25 °C; fruiting structures and conidia. Scale bars = 50 µm (fruiting structures) and 5 µm (conidia).

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Aspergillus nanangensis

Fungal Planet 1066 – 29 June 2020

Aspergillus nanangensis Pitt, *sp. nov*.

Etymology. Named for the town of Nanango, South Burnett District, Queensland, Australia, near which this species was collected.

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

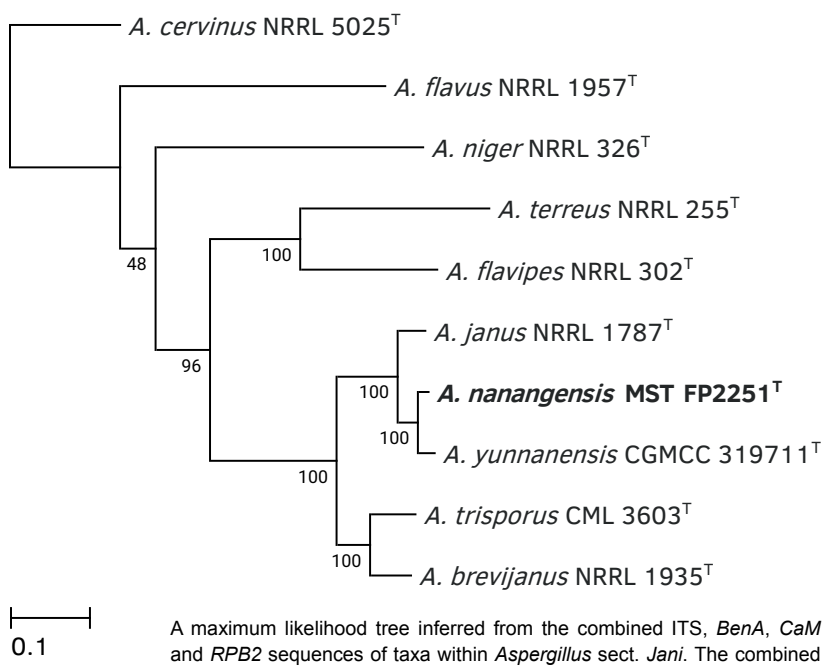
Conidiophores borne from surface hyphae, 200–400 × 7–9 µm, with thick, smooth, pale yellow walls, bearing very small vesicles. *Vesicles* 9–12 µm diam, ellipsoidal to somewhat irregular, bearing metulae and phialides over almost all of the vesicle surface, but sometimes bent to form only a hemispherical head; metulae 7–8 × 2.2–2.5 µm; phialides ampulliform 7–8 × 2.2–2.5 µm. *Conidia* spherical, 2.8–3.5 µm diam, with walls varying from almost smooth to conspicuously spiny, borne in compact spherical heads, even at age.

Culture characteristics — Czapek yeast extract agar (CYA), 25 °C, 7 d: Colonies growing slowly, 13–17 mm diam, rather sparse, lightly floccose; margins narrow and entire; mycelium white to off white; conidial production light, pale greenish grey (M. 25–26C3); exudate and soluble pigment absent; reverse greyish orange (M. 5B3–4). Malt extract agar (MEA), 25 °C, 7 d: Colonies growing slowly, 10–14 mm diam, low, dense and velutinous; margins narrow, entire; mycelium white; conidial production heavy, dark green near Bottle Green (M. 26F3–4); exudate and soluble pigment absent; reverse brownish orange (M. 5C3). 25 % Glycerol nitrate agar (G25N), 25 °C, 7 d: Colonies 3–5 mm diam, of white mycelium only. 37 °C, CYA, 7 d: No growth.

Media formulations are from Pitt & Hocking (2009); (M.) colours are from Kornerup & Wanscher (1978).

Typus. Australia, Queensland, Nanango, from undisturbed forest soil, 2004, *J.I. Pitt* (holotype DAR 84903, cultures ex-type CBS 146238 = FRR 6048 = MST FP2251; ITS, *BenA*, *CaM* and *RPB2* sequences GenBank MK979278, MT184783, MT184789 and MT184795, MycoBank MB836001).

Notes — *Aspergillus nanangensis* clusters in *Aspergillus* clade *Jani*, a small clade within *Aspergillus* subg. *Circumdati*, but is molecularly distinct. It is close to *Aspergillus janus* and *Aspergillus brevijanus*, but differs from both by lack of the larger white conidial heads that characterise these species. Culturally, growth rates of *A. nanangensis* on standard media are much slower. Microscopically, *A. nanangensis* produces smaller vesicles, fertile over a reduced area. When grown on agar, liquid media or grain, *A. nanangensis* displays a unique chemotaxonomic profile comprising isonanangenine B and D, nanangelenin, nanangenic acid, nanangenines A–H and nanoxepin not present in the closely related species *A. janus* and *A. brevijanus* (Lacey et al. 2019). *Aspergillus nanangensis* also produces known metabolites asperphenamate, benzomalvin B and C, cytochalasin E and WIN 66306, compounds previously reported from other *Aspergillus* species.



A maximum likelihood tree inferred from the combined ITS, *BenA*, *CaM* and *RPB2* sequences of taxa within *Aspergillus* sect. *Jani*. The combined sequence alignment was partitioned by marker; substitution models for each partition were chosen according to the Bayesian Information Criteria using ModelTest-NG v. 0.1.6 (Darriba et al. 2020). The TPM2uf+G4 model was used for ITS sequences, K80+I+G4 for *BenA*, TrNef+G4 for *CaM* and *RPB2*. The tree was constructed using RAxML-NG v. 0.9.0 (Kozlov et al. 2019). Bootstrap support values are derived from 1 000 bootstrap replicates. Alignment available in TreeBASE (study S25916).

Colour illustrations. Woodland near Nanango, Queensland, dominated by *Eucalyptus* species showing undisturbed soil from which *A. nanangensis* was collected. Colonies grown on CYA (left) and MEA (right) for 7 d at 25 °C; fruiting structures and conidia. Scale bars = 10 µm (fruiting structures) and 5 µm (conidia).

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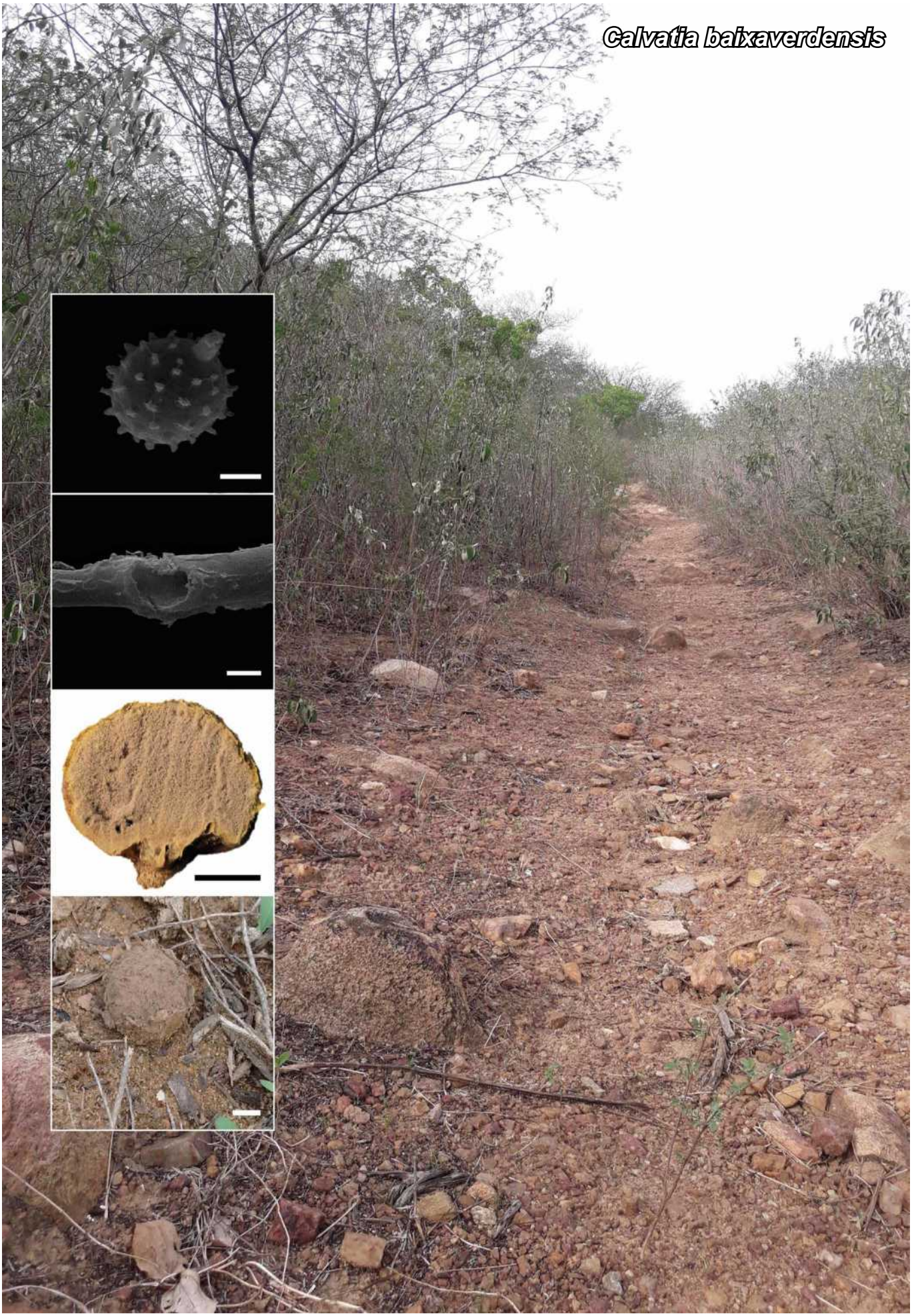
Calvatia baixaverdensis

Fungal Planet 1067 – 29 June 2020

Calvatia baixaverdensis R.L. Oliveira, R.J. Ferreira, P. Marinho, M.P. Martín & Baseia, *sp. nov.*

Etymology. In reference to the region where this species was collected, Baixa Verde, João Câmara, RN, Brazil.

Classification — *Agaricaceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata growing solitary, epigeous, incrustations in the rooting base, subglobose and 31–36 mm wide × 16–28 mm high. *Exoperidium* < 0.1 mm thin, fragile, slightly tomentose, evanescent, white to yellowish white (3A1, 3A2; Kornerup & Wanscher 1978). *Mesoperidium* < 0.1 mm thin, fragile, membranaceous, persistent at the base, smooth with senescence, greyish brown to brown (4C4, 6D3, 6E4, 7F4). *Endoperidium* < 0.3 mm thin, fragile and brittle at the apex, resistant and persistent at the base, papyraceous, olive brown to brown (4D6, 6E4). *Rhizomorphs* not seen. *Subgleba* reduced, woolly, compact, brownish beige (6E3). *Gleba* powdery, not persistent, brownish beige, brown to dark brown (6E3, 6E4, 6F4), at maturity. *Exoperidium* hyphalic, 2.0–5.3 µm diam, intertwined, frequent and non-regular septa, double V branching, walls ≤ 1.1 µm thin, straight for curves, hyaline, dextrinoid, low reaction and cyanophilic. *Mesoperidium* compacted, collapsed, hyaline, not dextrinoid and cyanophilic. *Endoperidium* apical composed of two layers of hyphae continuous, all brown, not dextrinoid and cyanophilic, hyphae 2.4–6.6 µm diam, frequent and non-regular true septa, double V branching, and mycosclereids globose, subglobose, pyriform, ovoid, ellipsoid, or rectangular, 15.4–60.3 µm high × 4.6–57.6 µm diam, weakly interconnected, branched, breaking in the septa, regular and thick walls ≤ 1.4 µm thin and straight for curves. *Endoperidium* basal hyphalic, 1.9–3.9 µm diam, rare and non-regular true septa, V-shaped branches, single and double, and in T, walls < 1.0 µm thin, tortuous and regular, brown, dextrinoid, and cyanophilic. *Subgleba* hyphalic, 1.5–3.8 µm diam, rare true septa, branching V, single and double, and T, cyanophilic nodes frequent, regular walls ≤ 1.0 µm thin, straight for curves, reddish brown, not dextrinoid and cyanophilic. *Paracapillitium* absent. *Capillitium Calvatia*-type, 1.9–3.5 µm diam, hyaline to light brown, dextrinoid and cyanophilic; septa frequent and non-regular, V-branching, single and double, and in T, fragmenting in any part of the capillitium or frequent in the septa; walls ≤ 0.8 µm thin and regular, straight, with large and numerous conspicuous pits (1–3 µm wide). *Basidiospores* globose to subglobose, 3.4–5.3 µm wide × 3.3–5.0 µm high (χ = 4.1 ± 0.3 × 3.9 ± 0.3; Q_m (medium coefficient) = 1.05; n (measurement numbers) = 30), verrucose, ornamentation < 1 µm length; pedicels present in some basidiospores ≤ 0.7 µm in length.

Habit & Habitat — Basidiomata growing solitary on moist soil.

Typus. Brazil, Rio Grande do Norte, João Câmara, Serra do Torreão, 17 Feb. 2017, *R.L. Oliveira* (holotype UFRN-Fungos 3027; ITS sequence GenBank MT152990, MycoBank MB827690).

Additional materials examined. Brazil, Rio Grande do Norte, João Câmara, Serra do Torreão, 17 Feb. 2017, *R.L. Oliveira* (UFRN-Fungos 3027); ibid., 17 Feb. 2017, *R.L. Oliveira* (UFRN-Fungos 3028); ibid., 5 Mar. 2019, *R.L. Oliveira* (UFRN-Fungos 3117); ibid., 5 Mar. 2019, *R.L. Oliveira* (UFRN-Fungos 3118).

Notes — *Calvatia baixaverdensis* is morphologically related to species of sect. *Calvatia*: *C. craniiformis*, *C. subtomentosa*, *C. rugosa*, *C. nodulata*, and *C. holothurioides*. *Calvatia craniiformis*, *C. rugosa* and *C. subtomentosa* have a capillitium with large conspicuous pits (1–3 µm wide) similar to *C. baixaverdensis*. However, *C. craniiformis* presents subglobose to globose basidiospores with punctate ornamentation, and well-developed cellular subgleba. *Calvatia rugosa* has exoperidium granulose, furfuraceous to subvelutinous, endoperidium smooth, membranous, very thin (< 0.5 mm), subgleba well-developed and lanose to cellular (Reid 1977). *Calvatia subtomentosa* has basidiospores 3.6–4.4 µm diam, and capillitium 3.6–5.8 µm, branched, septate, rather short fragments (Dissing & Lange 1962), but is easily distinguished from *C. baixaverdensis* in the ornamentation of the basidiospores, equinulate, and in the absence of pedicels, besides the absence of large pits in the capillitium and nodules in the hyphae of subgleba in *C. subtomentosa*. *Calvatia nodulata* and *C. holothurioides* are other morphologically close species to *C. baixaverdensis* mainly by the basidiospores 3–5 µm diam and capillitium 2–4 µm diam; however, *C. nodulata* has exoperidium granulose to pilose, subgleba occupying half of the basidiomata, and capillitium with spaced nodules (Alfredo et al. 2014), and *C. holothurioides* has subgleba prominent, cellular, capillitium with pores up to 2 µm diam (Rebriev 2013).

Colour illustrations. Brazil, Rio Grande do Norte, João Câmara, Serra do Torreão, where the specimens were collected. From bottom to top: mature basidiome *in situ*; longitudinal section through mature basidiome; capillitium under SEM; basidiospores under SEM. Scale bars = 10 mm (basidiomes), 1 mm (SEM photos).

Supplementary material

FP1067 The ITS nrDNA consensus phylogenetic tree was obtained with a Bayesian analysis using MrBayes v. 3.2.7a (Ronquist & Huelsenbeck 2003) under T92+G+I evolutionary for 5 M generations.

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Candida pellucida

Fungal Planet 1068 – 29 June 2020

Candida pellucida A.M. Glushakova, M.A. Tomashevskaya & Kachalkin, *sp. nov.*

Etymology. The name refers to *Exomias pellucidus* from which the ex-type strain was isolated.

Classification — *Debaryomycetaceae*, *Saccharomycetales*, *Saccharomycetes*.

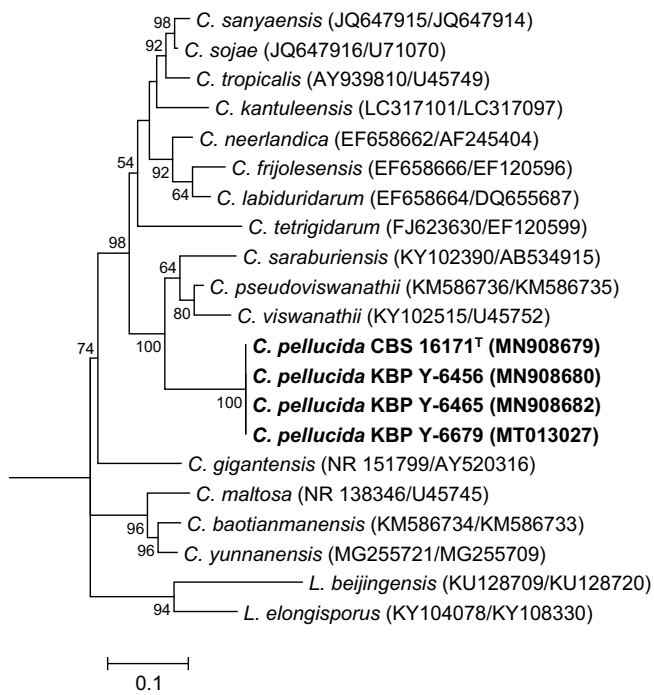
On glucose peptone yeast extract agar (GPYA) and 5 % malt extract agar (MEA), after 7 d at 25 °C, streak is white-cream, semi-glistening, with a smooth surface and entire margin. Cells are ovoid to elongate (2–6 × 5–8 µm) and occur singly or in pairs, dividing by polar and multilateral budding. Rare pseudohyphae are produced on potato dextrose agar (PDA) and cornmeal agar (CMA). *Ascospores* and *true hyphae* have not been observed during 4 wk at 10 and 25 °C in culture (pure cultures and in mating test) grown on GPYA, MEA, PDA, CMA and yeast nitrogen base with 0.5 % glucose (YNB) agar. Fermentation of glucose, galactose (delayed weak), trehalose and maltose (delayed) are positive, but negative for sucrose, lactose and raffinose. Glucose, sucrose, galactose, maltose, cellobiose, trehalose, melezitose, methyl alpha-D-glucoside, D-xylose, L-arabinose, D-glucosamine, ethanol, glycerol (weak), ribitol, D-mannitol, D-glucitol, salicin (weak), DL-lactic acid (weak), succinic acid (weak), citric acid, 2-keto-D-gluconate, arbutin are assimilated; no growth occurs on lactose, melibiose, raffinose, soluble starch, inulin, D-arabinose, D-ribose, L-sorbose, L-rhamnose, galactitol, erythritol, *myo*-inositol, 5-keto-D-gluconate, D-glucuronate and methanol. Nitrogen compounds: ammonium sulfate, potassium nitrate (weak), creatinine, creatine, L-lysine, D-glucosamine (weak) are assimilated. Growth on vitamin-free medium, on MEA with 10 % NaCl and on 50 % w/w glucose / yeast extract (0.5 %) agar is positive. Growth with 0.01 % and 0.1 % cycloheximide is weak. Starch-like compounds are not produced. Gelatin liquefaction and casein hydrolysis tests are positive. Diazonium blue B colour and urease reactions are negative. Maximum growth temperature is 42–44 °C.

Typus. Russia, Moscow, Park Tsaritsyno, from *Exomias pellucidus* (*Curculionidae*), Oct. 2018, *A.M. Glushakova*, Ins19-23 (holotype KBP Y-6457 preserved in a metabolically inactive state, ex-type culture VKM Y-3050 = DSM 110120 = CBS 16171; SSU, ITS-D1/D2 domains of LSU nrDNA, *TEF1* and *RPB1* sequences GenBank MN908677, MN908679, LR745525 and LR745526, MycoBank MB834513).

Additional materials examined. Russia, Moscow, Park Tsaritsyno, from *E. pellucidus*, Oct. 2018, *A.M. Glushakova*, KBP Y-6456, KBP Y-6465 and KBP Y-6466; ITS-D1/D2 domains of LSU nrDNA sequences GenBank MN908680, MN908681 and MN908682; Moscow, as endophyte from almond seeds bought on local market, Oct. 2019, *A.M. Glushakova*, KBP Y-6679; ITS-D1/D2 domains of LSU nrDNA sequence GenBank MT013027.

Colour illustrations. Russia, Moscow, Park Tsaritsyno, meadows with herbaceous flowering plants (the habitat of *Exomias pellucidus*). *Candida pellucida* KBP Y-6457: growth of yeast colonies on MEA, yeast cells on MEA (after 7 d at 25 °C). Scale bar = 10 µm.

Notes — Analysis of the ITS-D1/D2 regions of the surveyed yeasts suggested that they were conspecific and represented a hitherto undescribed species of the *Candida/Lodderomyces* clade. Based on the NCBI GenBank nucleotide database, the best hits using the **ITS** sequence are *Candida viswanathii* CBS 7889 (GenBank KY102513; 90.24 % similar, 18 subst. and 23 gaps) and *Candida viswanathii* ATCC 22981T (GenBank NR_138345; 88.07 % similar, 24 subst. and 36 gaps), using **LSU** it is *Candida viswanathii* CBS 4024T (GenBank KY106885; 98.20 % similar, 9 subst.), using **SSU** it is *Candida labiduridarum* NRRL Y-27940T (GenBank NG_063271; 99.88 % similar, 2 subst.), using ***TEF1*** it is *Candida dubliniensis* CD36T (GenBank XM_002417390; 95.67 % similar, 19 subst.) and using ***RPB1*** it is *Candida viswanathii* CBS 4024T (GenBank AY497714; 88.83 % similar, 66 subst.). In compliance with a recent phylogenetic analysis of the genus (Zhai et al. 2019), the placement of the new species is demonstrated using the combined ITS and LSU rDNA phylogeny. *Candida pellucida* can be differentiated from the phylogenetically most close species *C. viswanathii* based on its ability to grow on vitamin-free medium, good growth at the temperature 42 °C, and negative growth on soluble starch.



Maximum likelihood (ML) tree obtained from the combined analysis of ITS and LSU sequence data. Bootstrap support values above 50 % are shown at the nodes. The alignment included 965 bp and was performed with MAFFT v. 7 (Katoh et al. 2019). The General Time Reversible model (GTR) with Gamma distribution and invariant sites (G+I) was used as the best nucleotide substitution model. The phylogenetic analysis was conducted in MEGA v. 6 (Tamura et al. 2013). *Saccharomyces cerevisiae* (AB018043/JQ689017) was used as outgroup (hidden).

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Cladophialophora cabanerensis

Fungal Planet 1069 – 29 June 2020

Cladophialophora cabanerensis Maciá-Vicente, *sp. nov.*

Etymology. Named after the Cabañeros National Park in central Spain, where the soil sample was collected.

Classification — *Herpotrichiellaceae*, *Chaetothyriales*, *Eurotiomycetes.*

Mycelium consisting of hyaline, branched, septate hyphae, (0.5–) 0.7–1.3(–1.6) µm diam, forming hyphal strands. *Conidiophores* mostly single, sympodial, erect, subcylindrical, hyaline, smooth, bearing one phialide, often reduced to a conidiogenous cell. *Conidiogenous cells* phialidic, hyaline, smooth, fusiform with one locus at the apex that leaves a scar, (2.8–)3.6–6.2(–7.6) × (1.3–)1.7–2.6(–2.9) µm. *Conidia* aseptate, produced in mass, hyaline, smooth, globose with a scar, (1.7–)1.9–2.3(–2.4) µm diam (n = 40). *Chlamydospores* absent. *Sexual morph* unknown.

Culture characteristics — *Colonies* slow-growing, reaching 11–14 mm diam on malt extract agar (MEA), 13–17 mm diam on potato-dextrose agar (PDA), and 9–12 mm diam on cornmeal agar (CMA) after 7 d at 25 °C. Colonies velvety, white, becoming light earthy after 3–4 wk, with a compact and suede-like surface; reverse white-cream.

Typus. Spain, Ciudad Real, Cabañeros National Park, from rhizospheric soil from a wet heathland ('trampal'), N39.35 W4.36, 725 m asl, isolated from surface-sterilised, asymptomatic roots of an *Arabidopsis thaliana* plant inoculated with soil and grown under controlled conditions, 19 Apr. 2018, coll. *J.G. Maciá-Vicente*, isol. 20 June 2018, *J.G. Maciá-Vicente* (holotype FR 0214084, ex-type culture CBS 146718 = P6481; ITS and LSU sequences GenBank MN310213 and MN308512, MycoBank MB834845).

Additional materials examined. Spain, Ciudad Real, Cabañeros National Park, from rhizospheric soil from a wet heathland ('trampal'), N39.35 W4.36, 725 m asl, isolated from surface-sterilised, asymptomatic roots of an *A. thaliana* plant inoculated with soil and grown under controlled conditions, 19 Apr. 2018, coll. *J.G. Maciá-Vicente*, isol. 20 June 2018, *J.G. Maciá-Vicente*, culture P6476; ITS and LSU sequences GenBank MT179621 and MN308507; Ciudad Real, Cabañeros National Park, from rhizospheric soil from a wet heathland ('trampal'), N39.35 W4.36, 725 m asl, isolated from surface-sterilised, asymptomatic roots of an *A. thaliana* plant inoculated with soil and grown under controlled conditions, coll. 19 Apr. 2018, *J.G. Maciá-Vicente*, isol. 20 June 2018, *J.G. Maciá-Vicente*, culture P6479; ITS and LSU sequences GenBank MN310212 and MN308510.

Notes — The three isolates examined have identical morphologies and partial ITS and LSU sequences. Since they originate from the same soil sample, they likely represent clonal isolates. Based on a megablast search of NCBIs GenBank nucleotide database, the **ITS** sequence has low similarity with several unidentified *Chaetothyriales* strains (e.g., GenBank KX822488.1, identities 566/690 (82 %), 43 gaps (6 %); GenBank KF614863.1, identities 566/690 (82 %), 43 gaps (6 %); GenBank KF614863.1, identities 566/690 (82 %), 43 gaps (6 %)) and with *Cladophialophora immunda* (GenBank MH864254.1, identities 580/715 (81 %), 57 gaps (7 %)). However, the low identity values result from a long insert at the 3' end of the 18S rDNA gene, similarly to what has been found in other fungi (e.g., Tedersoo et al. 2015, Cross et al. 2017), but that is not present in most GenBank records. When analysing only the partial ITS1 region (nt 551–679) that is homologous to other sequences in GenBank, the megablast search yields highest similarity with 15 environmental sequences originating from a single study (e.g., GenBank MF793689.1, identities 129/129 (100 %), no gaps), and to two unidentified fungi (GenBank MG592689.1, identities 129/129 (100 %), no gaps; GenBank GQ996076.1, identities 127/129 (98 %), 1 gap (0 %)) and two *Cladophialophora* sp. isolates (GenBank LC189029.1, identities 129/129 (100 %), no gaps; and GenBank LC229675.1, identities 127/129 (98 %), 1 gap (0 %)). The closest hits using the **LSU** sequence are an unidentified fungus (GenBank GU552546.1, identities 675/676 (99 %), 1 gap (0 %)), *Cladophialophora* sp. (GenBank MF588895.1, identities 669/676 (99 %), 1 gap (0 %)), unidentified *Chaetothyriales* (GenBank KF614869.1, identities 666/676 (99 %), 1 gap (0 %)), and *Cladophialophora carrionii* (GenBank AF050262.1, identities 665/676 (98 %), 1 gap (0 %)).

The genus *Cladophialophora* is polyphyletic, including species that are commonly isolated from soil and living plants, but also found as causal agents of human infections. *Cladophialophora cabanerensis* is phylogenetically placed outside the *Carrionii* and *Bantiana* clades defined by Badali et al. (2008) that contain most species pathogenic to humans. All the closest hits in the megablast search using the insert-free ITS1 sequence originate from fungi associated with plant roots, like the type specimen of *C. cabanerensis*, suggesting a preference of the species toward this habitat

Colour illustrations. Wet heathland ('trampal') located in the Cabañeros National Park, Ciudad Real, Spain. Seven-day-old colonies growing at 25 °C on PDA; from top to bottom, overview of mycelium bearing conidiophores under phase-contrast microscopy; conidiophores under light microscopy; loose conidia under light microscopy. Scale bars = 10 µm (mycelium) and 5 µm (conidiophores and conidia).

Supplementary material

FP1069 Maximum likelihood phylogenetic tree inferred from concatenated ITS and LSU rDNA sequences using RAxML v. 8.2.12 (Stamatakis 2014) with the GTR+I+G model.

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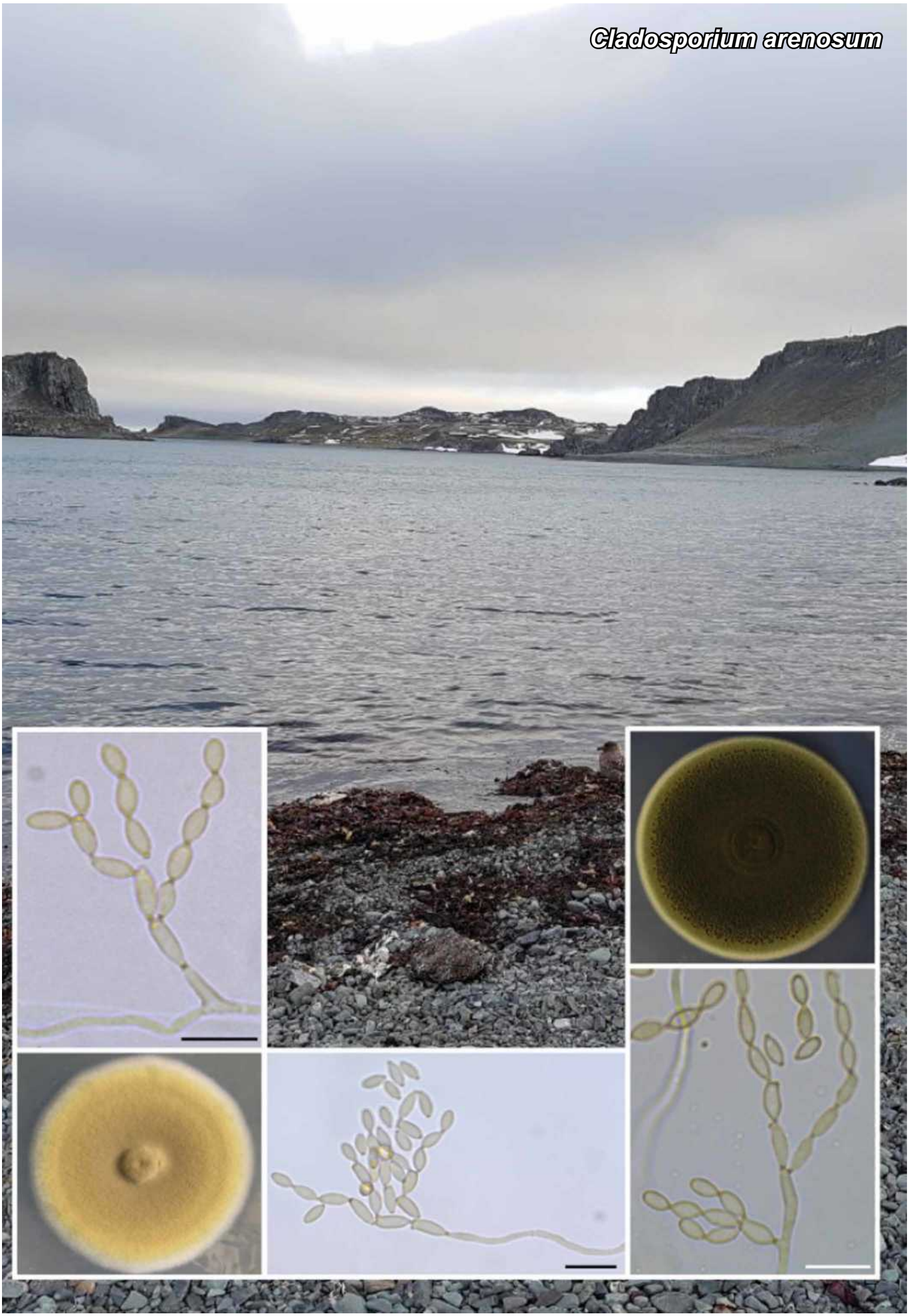

Cladosporium arenosum

Fungal Planet 1070 – 29 June 2020

Cladosporium arenosum C. Gil-Durán & L. Sanhueza, *sp. nov.*

Etymology. *arenosum* means sandy, referring to substrate (sea sand) from which the fungus was isolated.

Classification — *Cladosporiaceae*, *Cladosporiales*, *Dothideomycetes*.

Mycelium scarcely submerged and superficial; hyphae sinuous, unbranched, smooth, 1.8–3 µm wide, septate, not constricted at septa, subhyaline to olive brown. *Conidiophores* smooth, occasionally geniculate, multiseptate, erect to slightly flexuous, oblong, proliferating sympodially; macronematous conidiophores arising terminally or laterally from hyphae, up to 80 µm long, 3.1–4 µm wide; semimacronematous conidiophores arising terminally or laterally from hyphae, 1.3–1.6 µm wide, pale olive brown, with a single apical scar; micronematous conidiophore arising laterally from hyphae, 3.1–3.5 µm wide. *Ramoconidia* straight, smooth, concolourous, subcylindrical, 7.0–13.2 × 2.9–4.3 µm, 1-septate. *Secondary ramoconidia* ellipsoid to subcylindrical, smooth, 7.2–12 × 3.1–4.2 µm, 0–1-septate in the middle, with 2–3 distal hila, proliferating sympodially. *Conidia* numerous, catenated, dichotomously branched in all directions, straight, smooth, with up to 7 conidia; small terminal conidia obovoid, 2.5–5.8 × 1.4–2.8 µm; intercalary conidia ovoid or limoniform, 6–8.2 × 2.3–4.1 µm; microcyclic conidiogenesis not observed.

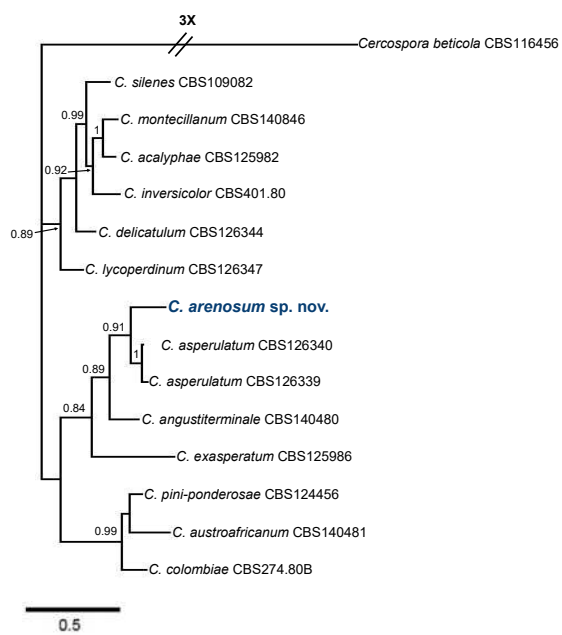
Culture characteristics — (after 2 wk at 20 °C in the dark): On potato dextrose agar (PDA), colonies reach 44–47 mm diam, round shape, flat, dark olive green, dusty, aerial mycelium absent, profuse sporulation, margin white and glabrous, exudates (blackish droplets) produced mainly on the outermost colony surface; reverse olive green to olive black. On malt extract agar (MEA), colonies reach 40–43 mm diam, irregular flat growth, elevated centre, dusty, olive green to yellowish green, aerial mycelium absent, exudates absent, white filiform margin; reverse, irregular olive-black. On synthetic nutrient-poor agar (SNA), colonies reach a 28–30 mm diam, irregular flat growth, dusty, olive-green, profuse sporulation mainly in the centre of the colony, exudates absent; reverse olive grey with white filiform margin. On oatmeal agar (OA), colonies reach 40–45 mm diam, round shape, flat, olive-green, abundant velvety aerial mycelium, absent on the outermost colony surface, profuse sporulation, exudates absent, margin grey-green, narrow and glabrous.

Cardinal temperature for growth — Optimum 20 °C, maximum 25 °C, minimum 5 °C.

Typus. Antarctica, South Shetland archipelago, King George Island, Fildes Bay, from marine sediment sand, 24 Feb. 2018, *L. Sanhueza* LS-2 (holotype CHFC-EA 566 stored in a metabolically inactive state in Chilean Fungal Collection; ITS, LSU, *actA* and *tef1* sequences GenBank MN879328, MT015967, MN890008 and MN890011, MycoBank MB834383).

Notes — Based on the combined analysis of ITS, *actA* and *tef1* markers, *Cladosporium arenosum* belongs to the *C. cladosporioides* complex (Bensch et al. 2015) and is phylogenetically related to *Cladosporium asperulatum*. However, *C. asperulatum* exhibits asperulate surface ornamentation of its conidia, conidiophores and mycelium (Bensch et al. 2010), characters not found in *C. arenosum*. In addition, *C. asperulatum* has longer conidiophores ((15–)45–210(–360) × (2–)3–4(–5) µm) and ramoconidia (15–50 × 3–4 µm)) (Bensch et al. 2010). Finally, *C. arenosum* produces exudates on PDA, limoniform conidia, and its colonies have a characteristic yellowish green colour after 2 wk at 20 °C on MEA, characters not found in *C. asperulatum* (Bensch et al. 2010).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence are *Cladosporium perangustum* ID58 (GenBank MN511354.1; Identities 551/551 (100 %), no gaps), *Cladosporium globisporum* DTO 220-D4 (GenBank KP701967.1; Identities 551/551 (100 %), no gaps), and *Cladosporium asperulatum* UTHSC DI-13-216 (GenBank LN834357.1; Identities 551/551 (100 %, no gaps). The closest hits using the **LSU** sequence are *Cladosporium cladosporioides* CBS 129108 (GenBank MH876646.1; Identities 608/608 (100 %), no gaps), *Cladosporium herbarum* CBS 129088 (GenBank MH876640.1; Identities 608/608 (100 %), no gaps), and *Cladosporium tenuissimum* CBS 125995 (GenBank MH876286.1; Identities 608/608 (100 %), no gaps). The closest hits using the *actA* sequence are *Cladosporium asperulatum* UTHSC DI-13-216 (GenBank LN834541.1; Identities 218/227 (96 %), 1 gap (0 %)), *Cladosporium myrtacearum* CBS 126350 (GenBank HM148606.1; Identities 204/227 (90 %), 4 gaps (1 %)), and *Cladosporium longicatenatum* CPC 17189 (GenBank KT600598.1; Identities 202/224 (90 %), 5 gaps (2 %)). The closest hits with *tef1* sequence are *Cladosporium asperulatum* BP3I2 (GenBank KU605784.1; Identities 242/242 (100 %), no gaps), *Cladosporium angustiterminale* CPC 15564 (GenBank KT600476.1; Identities 222/243 (91 %), 5 gaps (2 %)), and *Cladosporium lycoperdinum* CBS 126347 (GenBank HM148356.1; Identities 213/245 (87 %), 3 gaps (1 %)).



Phylogram obtained by combined analysis of ITS, *actA* and *tef1* sequences of *C. arenosum* and related species from the *C. cladosporoides* complex (Bensch et al. 2018). Analyses were done in MrBayes v. 3.2.6 (Huelsenbeck & Ronquist 2001) under GTR + G model for 5 M generations. Posterior probabilities values > 0.84 are shown at the nodes. *Cercospora beticola* CBS 116456 was used as outgroup.

Colour illustrations. Sea shore of Fildes Bay, Antarctica, where the sample was taken. *Cladosporium arenosum* growing on PDA and MEA; conidiophores and conidium on SNA after 14 d at 20 °C. Scale bars = 10 µm.

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Cortinarius balteatoindicus

Fungal Planet 1071 – 29 June 2020

Cortinarius balteatoindicus Dima, Semwal, V. Papp, Brandrud & V.K. Bhatt, *sp. nov*.

Etymology. The first part of the epithet ('*balteato*') refers to the relationship with *C. balteatocumatilis*, the second part ('*indicus*') refers to India where the species occurs.

Classification — *Cortinariaceae*, *Agaricales*, *Agaricomycetes*.

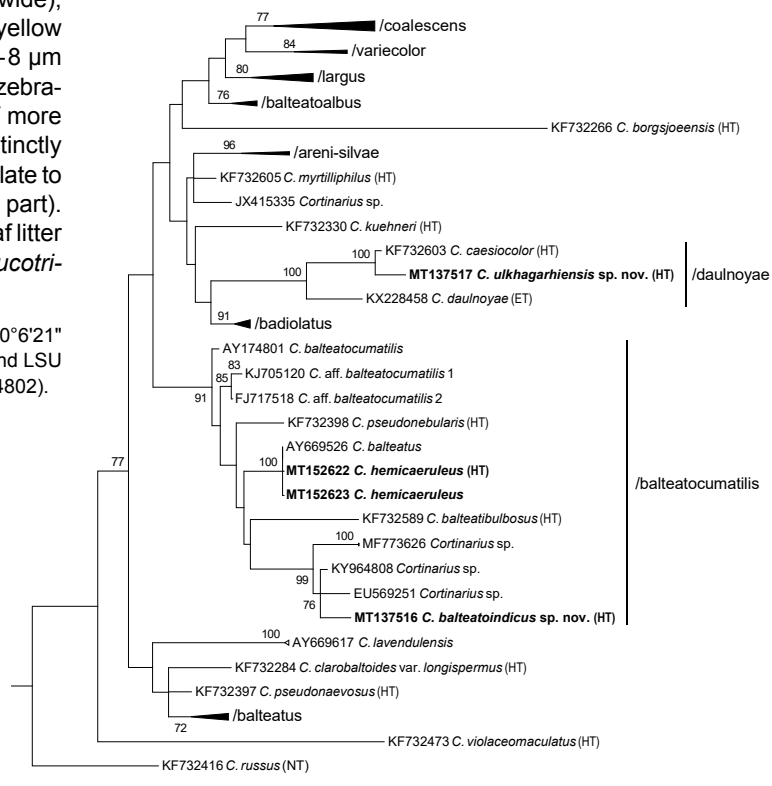
Pileus up to 75 mm diam, plano-convex to applanate, slightly glutinous when young, reddish golden to greyish orange (6B7–6B5); margin smooth or slightly innately fibrillose, incurved. *Lamellae* emarginate, moderately crowded, up to 6 mm broad, greyish when young, later greyish orange (6B4–6B6), lamellulae present, of various lengths. *Stipe* 65 × 17 mm, cylindrical, with slightly clavate base, up to 25 mm broad, greyish orange to brownish orange (6B5–6B6). *Context* dull lilac (15C3) to purplish in pileus and in stipe base. *Odour* distinct, earth-like. *Taste* indistinct. *Spore print* light brown (6D8). *Basidiospores* (9.4–)9.7–10.3(–10.7) × (5.4–)5.6–5.9(–6.1) µm, av. = 10.07 × 5.7 µm, Q = (1.65–)1.73–1.80(–1.85), Qav = 1.77, n = 50, amygdaloid, verrucose. *Basidia* 4-spored, 26–32 × 6–8 µm, clavate. *Pileipellis* more or less simplex (1-layered); strongly coloured in KOH. *Epicutis* at surface of narrow (2–4 µm wide), loosely erect-entangled, gelatinous, distinctly brownish yellow hyphae (many more or less collapsed); below wider (4–8 µm wide), parallel hyphae, with yellow thick walls or distinctly zebra-striped, encrusted pigment; the basal part of epicutis of more or less cemented hyphae up to ± 15 µm wide, with distinctly thickened, yellow walls, some filled with dark brown granulate to oleiferous pigment (most pigment in the basal, cemented part).

Habitat & Distribution — Solitary, occurring among leaf litter in temperate forests dominated mainly by *Quercus leucotrichophora* and *Pinus roxburghii*.

Typus. India, Uttarakhand, Pauri Garhwal, Teka, 1 965 m asl, N30°6'21" E78°45'12", 4 Sept. 2015, *K.C. Semwal* (holotype KCS 2509; ITS and LSU sequences GenBank MT137516 and MT241837, MycoBank MB834802).

Colour illustrations. India, Uttarakhand, Pauri Garhwal, Teka, type locality. Spores and basidiomata (from KCS 2509, holotype). Scale bar = 10 µm (spores).

Notes — *Cortinarius balteatoindicus* is a member of sect. *Phlegmacioides* based on morphological and molecular (nrDNA ITS and LSU regions) data, belonging to the /balteatocumatilis clade. It forms a well-supported (BS = 99 %) lineage with three sequences known from the Americas: USA, Tennessee (GenBank MF773626), USA, Minnesota (GenBank KY964808) and Mexico (GenBank EU569251). The closest sequence is the one from Minnesota; they differ by 5 nucleotide and indel positions, but only in the ITS1 region. Further studies are needed to unveil whether this sequence belongs to *C. balteatoindicus* with such a disjunct distribution. The other North American sequence from Tennessee differs by 8 nucleotide and indel positions, so it might well represent a separate species. The phylogenetically more distant European species of this clade have more robust basidiomata too, e.g., *C. balteatocumatilis*, *C. balteatobulbosus*, *C. pseudonebularis*, and the recently described *C. hemicaeruleus* (Brotzu et al. 2019; ITS sequence GenBank MT152622) and have slightly larger spores. The special ecology and the unique ITS sequence are, however, the best delimiting characters for the time being.



Phylogenetic tree derived from Maximum Likelihood analysis based on nrITS1-5.8S-ITS2 and binary data from indel coding with FastGap v. 1.2 (Borchsenius 2009). Analysis was performed in raxmlGUI v. 1.5.2 (Silvestro & Michalak 2012) using the GTRGAMMA substitution model for the partitioned (ITS1-5.8S-ITS2) nucleotide data and the default setting for binary (indel) data. ML bootstrap support (BS) values shown at the nodes (BS > 70 %). Sequences generated for this study are highlighted in **bold** face. HT and NT abbreviations refer to holotype and neotype sequences, respectively.

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Cortinarius ulkhagarhiensis

Fungal Planet 1072 – 29 June 2020

Cortinarius ulkhagarhiensis Dima, Semwal, V. Papp, Brandrud & V.K. Bhatt, *sp. nov*.

Etymology. The epithet refers to the type locality at Ulkhagarhi which is named after the temple of the goddess Ulkheshwari in Uttarakhand, India.

Classification — *Cortinariaceae*, *Agaricales*, *Agaricomycetes*.

Pileus up to 110 mm diam, plano-convex to applanate, slightly inflated at centre, surface glabrous, slimy when young, slightly bluish greyish when young, but soon becoming reddish golden to light brown (6C8–6D8); margin smooth, fairly undulate. *Lamellae* emarginate, crowded, greyish when young, later greyish orange (6B4), brownish orange (6C5) when mature, lamellulae present, of various lengths. *Stipe* 60–90 × 10–22 mm, prominently clavate at the base, bulb up to 30 mm wide, pale brown, becoming brownish orange to reddish orange (6D5, 6B7–7B7) with greyish lilac (15B4-3) tinge throughout the stipe, especially at apex. *Context* greyish to bluish lilac. *Odour* and *taste* not recorded. *Spore print* brown (8E8). *Basidiospores* (10.2–)10.6–11.3(–11.7) × (5.7–)5.9–6.6(–6.8) µm, av. = 10.97 × 6.2 µm, Q = (1.63–)1.71–1.83(–1.94), Qav = 1.77, n = 50, amygdaloid, verrucose. *Basidia* 4-spored, 25–30 × 5–7 µm, clavate. *Pileipellis* more or less simplex (1-layered); rather weakly coloured in KOH. *Epicutis* at surface of narrow, 2–5 µm diam, loosely erect-entangled, gelatinous, pale yellow hyphae; below a few layers of slightly wider, 3–8 µm diam hyphae with slightly thickened yellow walls, a few with pale, weakly encrusted wall pigment; the basal part of epicutis of hyphae up to approx. 10 µm diam, with distinctly thickened, yellow walls, forming tightly cemented bundles which in surface view forms a zig-pattern.

Habitat & Distribution — Caespitose, occurring among leaf litter of *Quercus leucotrichophora*, on humicolous soil, in temperate broadleaved forests dominated by mainly *Q. leucotrichophora*, *Rhododendron arboreum*, and *Myrica esculenta*.

Typus. India, Uttarakhand, Pauri Garhwal, Ulkhagarhi, 2025 m asl, N30°09'36" E78°50'53", 31 Aug. 2015, *K.C. Semwal* (holotype, KCS 2490; ITS and LSU sequences GenBank MT137517 and MT241838, MycoBank MB834804).

Notes — *Cortinarius ulkhagarhiensis* belongs to sect. *Phlegmacioides* based on both morphological and molecular (nrDNA ITS and LSU regions) data. Within the section it belongs to the /daulnoyae clade, where it forms a close sister species of the European *C. caesiocolor*. They differ by 5 nucleotide and indel positions, and in morphological characters. The spores of *C. ulkhagarhiensis* are significantly larger than those of *C. caesiocolor* (av. 10.97 × 6.2 µm vs 9.85 × 5.8 µm, respectively), and they are also longer (Qav = 1.77 vs 1.70). Macromorphologically they are rather similar, with e.g., bluish context. Another closely related species is the European *C. daulnoyae* (syn.: *C. chromataphilus* and *C. sabuletorum*) which has a strong earth-like smell, yellowing, never bluish context, and phylogenetically is more distant. Morphologically, other species in sect. *Phlegmacioides* might also resemble *C. ulkhagarhiensis*, but the ecology and ITS sequence data will be helpful in identification.

Colour illustrations. India, Uttarakhand, Pauri Garhwal, Ulkhagarhi, type locality. Spores and basidiomata (from KCS 2490, holotype). Scale bar = 10 µm (spores).

For phylogenetic tree see FP1071.

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Cortinarius paezii

Fungal Planet 1073 – 29 June 2020

Cortinarius paezii Garrido-Benavent, Ballarà, Liimat. & Mahiques, *sp. nov.*

Etymology. The species is named after the Spanish Jesuit missionary Pedro Páez (1564–1622), who was the first European that visited the Blue Nile source in Ethiopia and described the natural history of this country.

Classification — *Cortinariaceae*, *Agaricales*, *Agaricomycetes.*

Basidiomata rather small. *Pileus* 10–25(–35) mm diam, at first hemispheric, later convex with a persistent, obtuse, rounded and low umbo; margin first very incurved and highly lobulated and later extended and slightly serrate, retaining whitish veil remnants; surface hygrophanous, smooth to fibrous, dark grey, dark grey-brown (Caill. T31, T30; Cailleux 1981) to ochraceous, pale ochraceous or reddish brown (Caill. M49, M35, M25) when dry; mature pilei with necropigments. *Lamellae* moderately dense, uncinated, pale ochraceous to beige ochraceous (Caill. M29, N30); lamellae edges slightly paler, and slightly mustard brown with age; lamellulae present. *Stipe* (15–)20–35(–45) mm long and 3–6(–8) mm wide, cylindrical to clavate or subglobose at the base; surface white, later pale beige, with universal veil copious towards the base, partial veil fugacious, not forming an annular area. *Context* generally fibrous, pale ochraceous, and brownish in the stipe cortex. *Taste* mild and *smell* indistinguishable. *Macrochemical reactions*: negative to KOH, guaiac tincture, Ph.A. and methol. *Basidiospores* broadly ellipsoid in front and side view, (10–)11–*11.8*–12.5(–13) × (6.25–)7–*7.3*–7.5(–8) µm in size, with a Q (length/width ratio) = (1.5–)1.55–*1.61*–1.73(–1.8), and with a marked apical depression; spore surface densely ornamented with projecting warts of moderate size. *Basidia* 36–45 × 9–12 µm, 4-spored; lamellar edge with basidia and some claviform cells, 26–34 × 9–11 µm. *Pileipellis* a cutis formed by a layer of 4–8 µm wide, clamped, more or less cylindrical hyphae, with scattered pale ochraceous incrusted wall pigments; *subcutis* composed of short and irregularly-arranged, septate hyphae, 30–75 × 20–32 µm; hyphae of the veil remnants 2–3 µm diam.

Habitat & Distribution — Restricted to the alpine belt (> 2000 m asl) in association with *Dryas octopetala*. So far found in the Pre-Pyrenees (north-eastern Iberian Peninsula). The existence of an ITS sequence in GenBank (FR852009) identical to the ones obtained in the present study indicates the presence of *C. paezii* in the Hyrcanian forests of Iran.

Typus. Spain, Catalonia, Barcelona province, Berguedà, Saldes, Serra d'Encija, Creu de Ferro, N42°18'28" E1°76'69", 2250 m asl, associated with *Dryas octopetala* on calcareous soil, 26 Aug. 2018, *J. Ballarà* JB-9511-18 (holotype MA-90461; ITS sequence GenBank MT184898, MycoBank MB833243).

Colour illustrations. Spain, Catalonia, Serra d'Encija, prairie with *Dryas octopetala* in the alpine belt, > 2000 m asl, where the holotype of *Cortinarius paezii* was collected (MA-90461). Basidiomata in upper photos correspond with the holotype; bottom left photo corresponds with MA-90460; holotype basidiospores. Scale bar = 10 µm.

Notes — *Cortinarius paezii* is a rather small telamonioid species with relatively large spores that we initially considered to conform to the morphological variability of *C. casimiri* due to the general size, habitat and pigmentation. However, basidiomata of the latter species are in general slenderer than those of *C. paezii*, and show reddish and somewhat lilaceous tinges, their smell is more or less raphanoid, and the spores are smaller, 10–11.5 × 6–7 µm (Brandrud et al. 1998). *Cortinarius paezii* produces hygrophanous pilei that are very dark when hydrated, without lilaceous traces, and instead shows pale ochraceous to reddish brown tinges with time. Furthermore, *C. casimiri* distributes preferentially in altimontane-subalpine habitats, and more rarely forms mycorrhizal associations with *Salix* spp. in the alpine belt. Considering other species growing in the alpine belt, *C. cavipes* would share two additional characters with *C. paezii*: the evident change in colour of pilei after drying and the clavate stipe (Favre 1955). As indicated by its epithet, however, *C. cavipes* has a hollow stipe; additionally, it shows lilaceous traces in the stipe apex and context (as in *C. casimiri*), and produces smaller, less ornamented spores.

Two additional alpine species described by Favre (1955) were *C. levipileus* and *C. rusticellus*. The former differs from *C. paezii* in producing smaller basidiomata, with a finely granulose pileus cuticle, with the surface dark to reddish brown, and by the less abundant veil remnants and the slightly smaller, more ovoid spores (lower Q value). Lamoure (1978) obtained similar values for spore size in *C. levipileus* and provided further evidence of its habitat on calcareous soils in the alpine belt. *Cortinarius rusticellus* produces spores more similar in size to those of the new species but has smaller basidiomata, pilei are more umbonate and fibrous to felty, lamellae are darker, and there is an abundant and persistent veil forming an evident annulus on the stipe.

The two ITS sequences obtained for the new species were 19 bp (plus four indels), 16 bp (plus eight indels), and 19 bp (plus six indels) different from those of *C. casimiri*/*subsertipes*, *C. levipileus* and *C. rusticellus*, respectively. The phylogenetic tree revealed *C. tatrensis* as a close relative of *C. paezii*. This species was described from *Salix* and *Dryas* communities in the alpine belt of the Belaer Tatras, in northern Slovakia (Fellner & Landa 1993). Apart from the similar habitat, *C. paezii* and *C. tatrensis* share the general habitat of basidiomata, the hygrophaneity of pilei and their pigmentation, and the spores, which the authors described as broadly ovoid, (10–)10.5–12.5 × (6.5–)7–8.5 µm. However, lilaceous to vinaceous tinges were originally noticed in the surface of the stipe base and in the stipe context of *C. tatrensis* while these characters are absent in *C. paezii*. Additionally, the stipe in *C. tatrensis* is described as 'cylindrical, slightly narrowing towards the base', whereas in the new species it is markedly clavate. The ITS sequence of *C. tatrensis* is provided for the first time in the present work, and shows five different nucleotides from *C. paezii* at the ITS1 region.

Supplementary material

FP1073-1 Additional materials examined.

FP1073-2 Phylogram depicting the evolutionary relationships of *Cortinarius paezii* and their relatives based on ITS sequence data.

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Cylindrium magnoliae