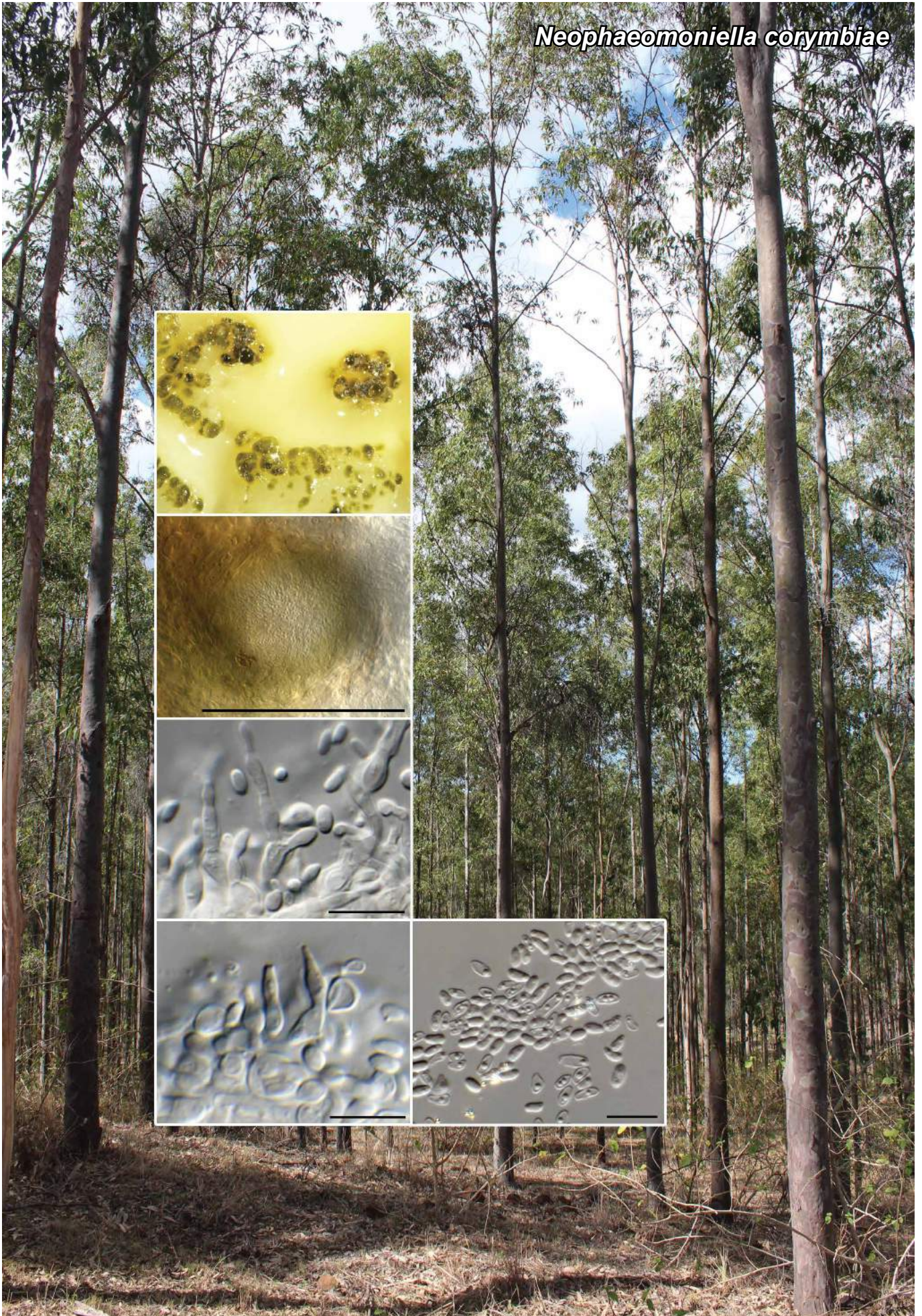


*Neophaeomoniella corymbiae*



Fungal Planet 819 – 14 December 2018

## *Neophaeomoniella corymbiae* Crous, sp. nov.

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

*Classification* — *Phaeomoniellaceae*, *Phaeomoniellales*, *Eurotiomycetes*.

Coelomycetous morph: *Conidiomata* pycnidial, olivaceous brown, globose, 100–200 µm diam with central ostiole. *Conidiophores* lining inner cavity, hyaline, smooth, branched, 0–1-septate, subcylindrical, 5–10 × 1.5–2 µm. *Conidiogenous cells* similar to those on hyphae. Hyphomycetous morph: *Mycelium* consisting of hyaline, smooth, 2–3 µm diam hyphae, branched, septate, encased in mucoid sheath. *Conidiophores* solitary, erect, subcylindrical, 1–2-septate, branched or not, 5–15 × 2–2.5 µm. *Conidiogenous cells* hyaline, smooth, subcylindrical to cymbiform, 5–7 × 2–2.5 µm, phialidic. *Conidia* aseptate, hyaline, smooth, subcylindrical to ellipsoid, apex obtuse, tapering at basal region to a truncate hilum, 0.5 µm diam, (3–)3.5–4(–5) × 1.5–2(–2.5) µm.

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

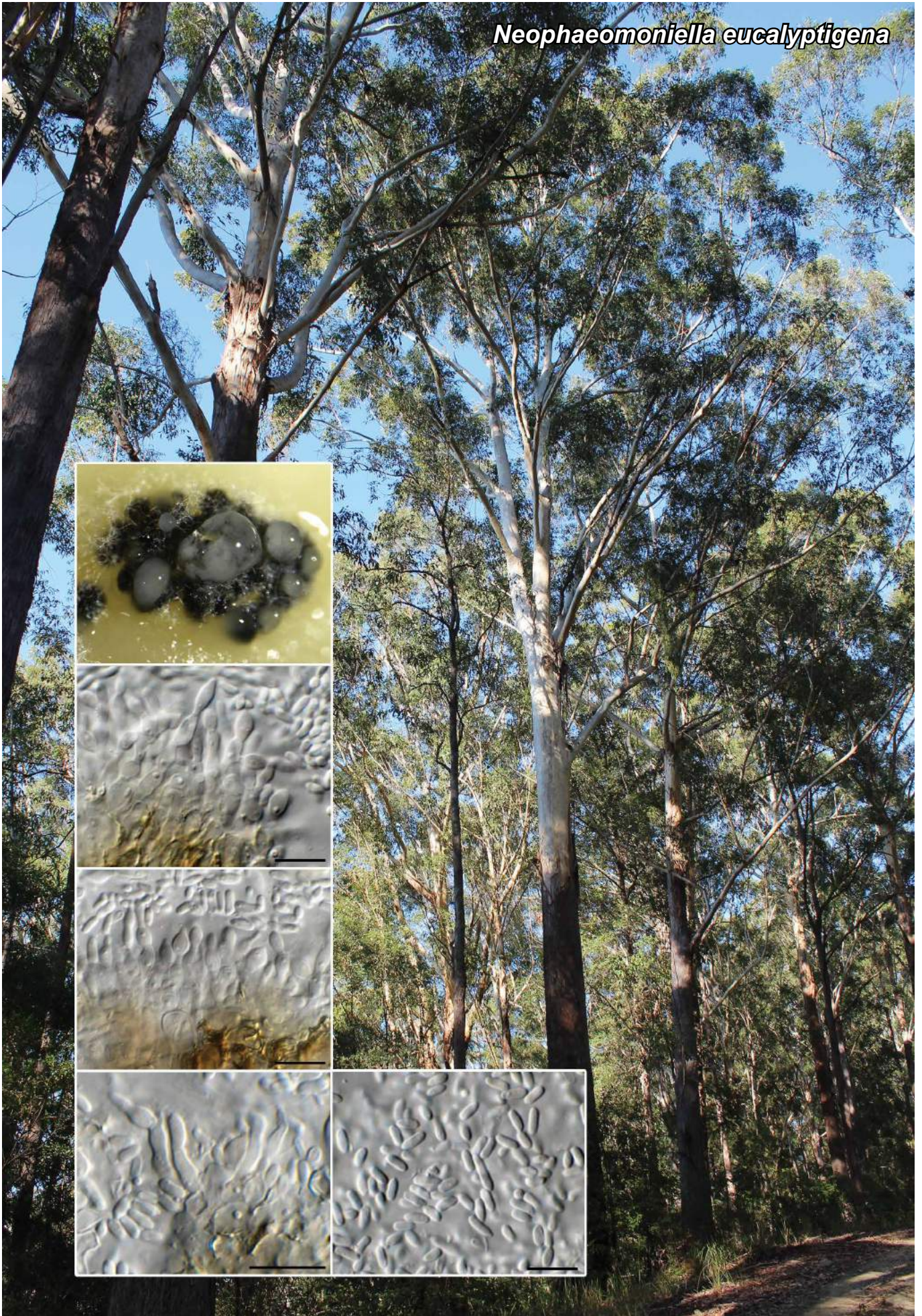
*Typus.* AUSTRALIA, New South Wales, Dyraba, Dyraba plantation, on leaves of *Corymbia citriodora* (*Myrtaceae*), 14 Mar. 2015, A.J. Carnegie, HPC 2027 (holotype CBS H-23784, culture ex-type CPC 33273 = CBS 145092, ITS and LSU sequences GenBank MK047457.1 and MK047507.1, MycoBank MB828213).

*Notes* — The *Phaeomoniella* generic complex is commonly associated with brown wood streaking (Crous & Gams 2000, Halleen et al. 2007). Taxa in this complex have a hyphomycetous and yeast morph, with a coelomycetous synasexual morph. *Neophaeomoniella* (based on *N. eucalypti*) is a genus closely related to *Phaeomoniella* (Crous et al. 2015b), which has three species, isolated as endophytes from leaves and pine needles. *Neophaeomoniella corymbiae* was isolated from thyrothelial ascromata on leaves, although the sexual link is unconfirmed.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Neophaeomoniella eucalypti* (GenBank NR\_138001.1; Identities = 581/607 (96 %), 9 gaps (1 %)), *Neophaeomoniella niveniae* (as *Phaeomoniella niveniae*, GenBank JQ044435.1; Identities = 550/579 (95 %), 10 gaps (1 %)) and *Neophaeomoniella zymoides* (GenBank KR909194.1; Identities = 568/601 (95 %), 9 gaps (1 %)). Closest hits using the LSU sequence are *Neophaeomoniella niveniae* (as *Phaeomoniella niveniae*, GenBank JQ044454.1; Identities = 838/851 (98 %), no gaps), *Neophaeomoniella eucalypti* (GenBank NG\_058174.1; Identities = 804/818 (98 %), 1 gap (0 %)) and *Neophaeomoniella zymoides* (GenBank MH874535.1; Identities = 832/851 (98 %), 3 gaps (0 %)).

*Colour illustrations.* *Corymbia citriodora*, Dyraba plantation, Australia; colony sporulating on oatmeal agar, conidioma, conidiogenous cells and conidia. Scale bars: conidioma = 200 µm, all others = 10 µm.

*Neophaeomoniella eucalyptigena*



Fungal Planet 820 – 14 December 2018

## *Neophaeomoniella eucalyptigena* Crous, sp. nov.

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

*Classification* — *Phaeomoniellaceae*, *Phaeomoniellales*, *Eurotiomycetes*.

*Conidiomata* pycnidial, globose, brown, erumpent, 150–300 µm diam, exuding a creamy conidial mass. *Conidiophores* lining the inner cavity, hyaline, smooth, subcylindrical, 0–1-septate, branched or not, 5–10 × 2–2.5 µm. *Conidiogenous cells* terminal and intercalary, subcylindrical to ampulliform, hyaline, smooth, phialidic, 4–6 × 2–2.5 µm. *Conidia* solitary, hyaline, smooth, aseptate, subcylindrical, apex obtuse, tapering in lower region to truncate hilum, 0.5 µm diam, (3.5–)4–4.5(–5) × 1.5–2 µm.

*Culture characteristics* — Colonies flat, spreading, lacking aerial mycelium, surface folded, with smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface and reverse pale luteous. On PDA surface and reverse grey olivaceous in centre, cream in outer region. On OA surface cream to dirty white.

*Typus.* AUSTRALIA, New South Wales, Coffs Harbour, Pine Creek State Forest, on leaf litter of *Eucalyptus pilularis* (*Myrtaceae*), Jan. 2015, A.J. Carnegie, HPC 2036 (holotype CBS H-23785, culture ex-type CPC 33358 = CBS 145093, ITS, LSU, *tef1* and *tub2* sequences GenBank MK047458.1, MK047508.1, MK047569.1 and MK047584.1, MycoBank MB828214).

*Notes* — *Neophaeomoniella eucalyptigena* is closely related to *N. corymbiae*, with both species being isolated from eucalypt leaves. Morphologically, they are very similar, and best distinguished based on their DNA data (579/607 (95 %) similar, including 10 gaps).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neophaeomoniella niveniae* (as *Phaeomoniella niveniae*, GenBank JQ044435.1; Identities = 554/580 (96 %), 10 gaps (1 %)), *Neophaeomoniella eucalypti* (GenBank NR\_138001.1; Identities = 577/607 (95 %), 9 gaps (1 %)) and *Neophaeomoniella zymoides* (GenBank KR909194.1; Identities = 574/604 (95 %), 13 gaps (2 %)). Closest hits using the **LSU** sequence are *Neophaeomoniella niveniae* (as *Phaeomoniella niveniae*, GenBank JQ044454.1; Identities = 852/863 (99 %), 1 gap (0 %)), *Neophaeomoniella eucalypti* (GenBank NG\_058174.1; Identities = 807/818 (99 %), no gaps) and *Neophaeomoniella zymoides* (GenBank MH874535.1; Identities = 847/863 (98 %), 4 gaps (0 %)). Closest hits using the **tef1** sequence had highest similarity to *Phaeomoniella chlamydozoa* (GenBank KP213113.1; Identities = 197/209 (94 %), no gaps) and *Pseudophaeomoniella oleae* (GenBank KP635968.1; Identities = 191/205 (93 %), no gaps). No significant hits were obtained when the **tub2** sequence was used in blastn and megablast searches.

*Colour illustrations.* *Eucalyptus pilularis*, Pine Creek State Forest, Australia; colony sporulating on oatmeal agar, conidiogenous cells and conidia. Scale bars = 10 µm.

*Absidia terrestris*



Fungal Planet 821 – 14 December 2018

***Absidia terrestris*** Rosas de Paz, Dania García, Guarro, Cano & Stchigel, *sp. nov.*

**Etymology.** Referring to the substrate from which the fungus was recovered (soil).

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

**Hyphae** hyaline to brownish, coenocytic, smooth- and thick-walled, 5–12.5 mm wide, with a septum at the branching site, usually filled with orange oil droplets and presenting more or less abundant solitary or catenulate ovoid swellings, 7.5–12.5 mm wide. **Stolons** hyaline to brownish, 5–14 mm wide. **Rhizoids** well developed, hyaline, originating along the stolon but never in the same place where sporangiophores arise. **Sporangiophores** hyaline to brownish, erect to slightly curved, smooth- and thick-walled, 25–215 × 2.5–5 mm, with a single septum below the sporangium and occasionally with an extra septum at the base when sporangiophores are short, arising along and terminally on the stolons and never grouped in whorls, swellings occasionally seen. **Sporangia** hyaline to brownish due to the mass of sporangiospores, pyriform, multi-spored, smooth-walled, apophysate, 17.5–27.5 × 17.5–22.5 mm. **Apophysis** funnel-shaped, smooth-walled, 12.5–17.5 × 7.5–12.5 mm. **Columellae** globose, smooth-walled, showing a short collarete, sometimes with a wall projection, 5–7.5 mm diam. **Sporangiospores** hyaline when solitary, brownish in mass when mature, smooth-walled, cylindrical, 4–5 × 2–4 mm. **Chlamydospores** absent. **Zygosporangia** not observed.

**Culture characteristics** — Colonies on MEA initially white, soon becoming greyish brown (M.6E3; Kornerup & Wanscher 1978), covering the diameter of the Petri dish (90 mm) in 7 d at 25 °C, reaching 10 mm height in some points; initially white, then becoming brownish grey (M.8F3). Minimum and maximum temperature of growth 15 and 27 °C, respectively.

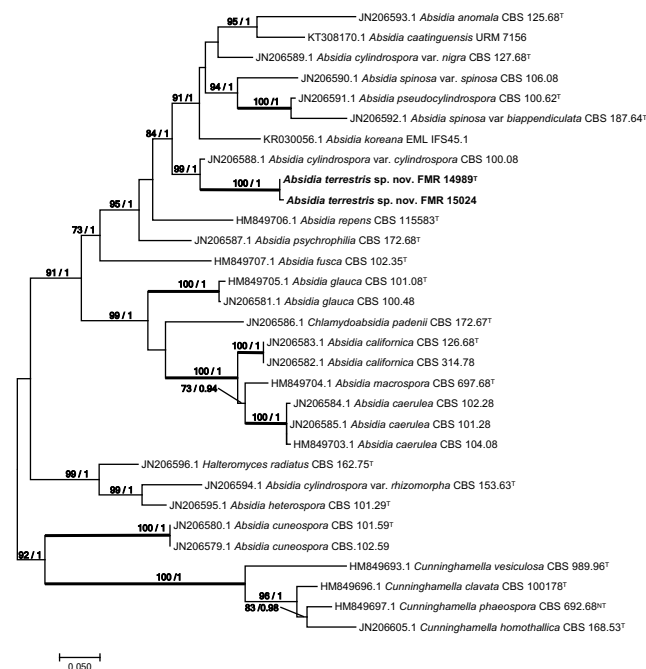
**Typus.** MEXICO, Mexico DF, Delegación Gustavo A. Madero, 'Corpus Christi' Public Park (19.467385–99.120635), from soil sample, 26 Aug. 2015, *E. Rosas de Paz* (holotype CBS H-23789, ex-type living culture FMR 14989, ITS and LSU sequences GenBank LT795003 and LT795005, MycoBank MB828081).

**Additional material examined.** MEXICO, Mexico DF, Delegación Gustavo A. Madero, 'Los Cocodrilos' Public Park (19.475391–99.116705), from soil sample, 26 Aug. 2015, *E. Rosas de Paz*, living culture FMR 15024, ITS and LSU sequences GenBank LT795004 and LT795006).

**Notes** — This fungus was isolated from a soil sample collected in Mexico DF. Morphologically, *Absidia terrestris* resembles the species of *Absidia* s.str. with cylindrical sporangiospores (Hoffmann et al. 2007), i.e., *Absidia anomala*, *A. cylindrospora* var. *cylindrospora*, *A. pseudocylindrospora*, *A. psychrophilia*, *A. repens* and *A. spinosa*. Based on a megablast search of NCBI's GenBank nucleotide database using the ITS sequence of the isolate FMR 14989 (the ex-type strain), the closest hits are *A. cylindrospora* (GenBank AY944889.1; Identities 505/579 (87 %), 21 gaps (3 %)) and *A. spinosa* (GenBank AY944887.1; Identi-

**Colour illustrations.** 'Corpus Christi' Public Park; colony on PDA, sporangiophore, columellae, sporangiospores. Scale bars = 15 µm, with the exception of the sporangiospores (= 5 µm).

ties 379/463 (82 %), 34 gaps (7 %)). The closest hits using the LSU sequence was *A. cylindrospora* var. *cylindrospora* (GenBank JN206588.1; Identities 620/657 (94 %), 5 gaps (0 %)). In a similar search using the CBS database (Crous et al. 2004), the closest hits using the LSU sequence of the isolate FMR 14989 were *A. spinosa* var. *spinosa* (CBS 106.08, Identities 308/406 (75.68 %), 9 gaps (2.2 %)), and *A. repens* (FSU 939, Identities 543/575 (94.43 %), 1 gap (0 %)). While using the ITS sequence the closest hits were *A. cylindrospora* var. *cylindrospora* (CBS 100.08, Identities 470/548 (86 %), 18 gaps (3 %)), and *A. pseudocylindrospora* (CBS 100.62, Identities 236/262 (90 %), 10 gaps (3 %)). Our phylogenetic tree, built using the LSU sequences, corroborated that our fungus represents a new species of the genus *Absidia*, *A. cylindrospora* var. *cylindrospora* being phylogenetically the most closely related species. *Absidia terrestris* differs from *A. cylindrospora* var. *cylindrospora* in its lower growth rate on MEA at 25 °C and in the absence of growth at 30 °C (*A. cylindrospora* var. *cylindrospora* grows up to 34 °C), the sporangiophores not arranged in whorls, the absence of chlamydospores and the presence of both apical and basal septa in the shorter sporangiophores.



Maximum likelihood (ML) tree obtained from the LSU sequence dataset of our isolates and sequences retrieved from GenBank. Fully supported branches (100 % ML bootstrap / 1.0 Bayesian posterior probability) are thickened. The novel species is indicated in bold face. The alignment was performed by using MEGA v. 6.06 (Tamura et al. 2013), and the tree was built by using MEGA v. 6.06 and MrBayes v. 3.2.4 (Huelsenbeck & Ronquist 2001). Ex-type strains of the different species are indicated with <sup>T</sup> or <sup>NT</sup>.

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*Amanita paludosa*



Fungal Planet 822 – 14 December 2018

***Amanita paludosa* Bulyonk., Filippova & O.V. Morozova, sp. nov.**

**Etymology.** The epithet *paludosa* (boggy) refers to the preferred habitat of the species.

**Classification** — *Amanitaceae*, *Agaricales*, *Agaricomycetes*.

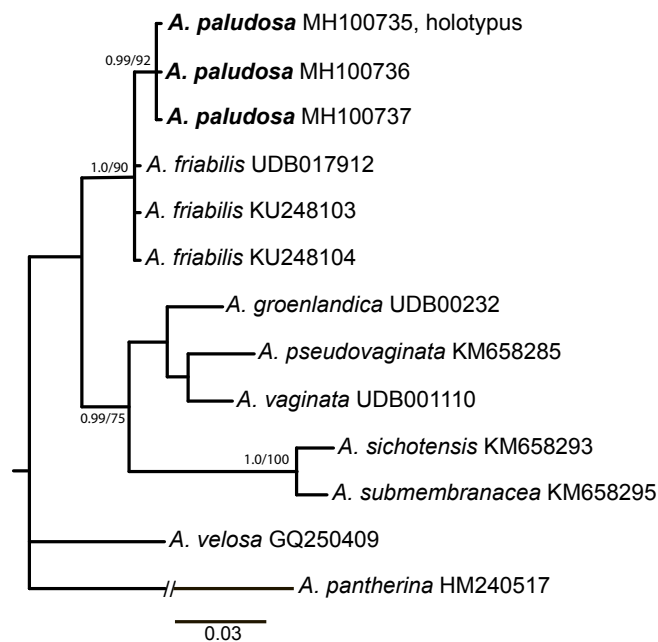
**Cap** 40–65 mm diam, planoconvex, obtusely umbonate, light brownish grey; surface glabrous, almost dry, ingrown-fibrillose under lens; margin very distinctly sulcate up to 5 mm with paler context showing between ribs. **Lamellae** subcrowded, off-white with light yellow-brown fimbriate edge concolorous with stipe apex, ventricose up to  $\pm 7$  mm, free. Universal veil fragments absent or present as a few small scattered greyish patches and warts. **Stipe** 70–90  $\times$  10–17 mm, tapering upwards, with a broad rounded base but not bulbous; context white, firm, fistulose; surface light grey-brown and pruinose near apex, with paler zebroid fibrils below, in the lower third bearing fragments of volval material. **Volva** friable, up to 2 mm thick, brownish grey, appearing as wart-like floccules appressed to the stipe surface or partially or completely remaining bound to the substrate. **Pileipellis: suprapellis** an ixocutis of thin, filamentous hyaline hyphae in a gelatinous matrix; **subpellis** hyphae with yellow-grey intracellular pigment, some slightly constricted at septa, some forked, (2.9–)3.2–7.2(–8)  $\mu\text{m}$  (av. 5.4  $\mu\text{m}$ ) thick; vascular hyphae not plentiful, irregular, aseptate, present in all layers, 2–12  $\mu\text{m}$  thick. **Lamella trama** bilateral. **Mediostratum** of well-inflated elements, filamentous hyphae scarce. **Lateral stratum** of inflated intercalary elements, appearing pseudoparenchymatous near lamellar base, closer to margin becoming mostly broadly ellipsoid and broadly fusiform, some branched and irregular-shaped, solitary and in chains of 2 or 3. **Subhymenium** near lamellar base virtually pseudoparenchymatous, of thin-walled, well-inflated elements, transitioning into the similarly well-inflated mediostratum; closer to the edge more structured, appearing as 2 or 3 layers of inflated, subglobose, angular or irregular ('jigsaw-puzzle'-like) elements. **Vascular hyphae** in lamella trama overall very rare, but common in the subhymenial layer of the lamella margin, where they sometimes form tangled masses of branching filamentous hyphae 2.5–3.2(–3.5)  $\mu\text{m}$  wide. **Inflated elements on the lamella margin** sphaeropedunculate, some utriform to broadly clavate, some slightly thick-walled, with pale greyish yellow intracellular pigment, 21.2–54.3  $\times$  14.1–32.5  $\mu\text{m}$  (av. L = 31.6, W = 22.0). **Universal veil** differentiated; outer layer dominated by sphaerocysts, some slightly collapsed, often in chains of 3 or 4, and often with pale yellowish grey intracellular pigment, linked by very thin, thin-walled, often collapsed, branching and forked filamentous hyphae; filamentous hyphae more abundant in the inner layer.

**Colour illustrations.** Top: treed transitional fen in Kondinskiye Ozera nature park in Yugra; bottom: bogged forest hollow in deciduous forest near Akademgorodok; inset: fruitbodies *ex situ* and *in situ*; detail of stipe base with veil and lamella margins; spores, veil with inflated elements; (all from holotype). Scale bars = 1 cm (basidiomata), 10  $\mu\text{m}$  (spores, veil).

**Typus.** RUSSIA, Novosibirsk district, vicinity of Novosibirsk Akademgorodok, bogged hollow in mixed deciduous forest (*Betula pendula*, *Populus tremula*, *Salix* spp.), N54°50'55.38" E83°07'52.90", 9 Sept. 2011, T. Bulyonkova (holotype LE211974, ITS and LSU sequences GenBank MH100735 and MH100732, MycoBank MB825171).

**Additional materials examined.** RUSSIA, KhMAO-Yugra, Kondinskiy district, Kondinskiye Ozera nature park, treed fen (*Betula* spp.), 1 Aug. 2008, T. Bulyonkova, LE311975; same location, 14 Aug. 2008, T. Bulyonkova, LE311976.

**Notes** — *Amanita paludosa* is a rare ringless *Amanita* so far known only from three collections along the Ob river basin, spanning across several hundred kilometres. The closest and most similar species is the European *A. friabilis*, mycorrhizal with *Alnus* in wetland habitats (Tulloss 2018). *Amanita paludosa* differs from *A. friabilis* by sparser and less fragmented velar remnants on pileus surface and stipe base due to its more differentiated veil structure with more abundant filamentous elements; markedly rounder, subglobose spores; mycorrhizal association with *Betula*; and a known distribution limited to West Siberia. Despite the proximity of the two taxa on molecular level, the significant differences in morphology, ecology, and distribution validate separating *A. paludosa* as a new species.



Phylogenetic tree derived from Bayesian analysis based on nrITS1-5.8S-ITS2 data. Analysis was performed under GTR model, for 5 M generations, using MrBayes v. 3.2.1 (Ronquist et al. 2012). The ML analysis was run in the RAxML server (Stamatakis et al. 2008). Posterior probability (PP > 0.95) values from the Bayesian analysis followed by bootstrap support values from the Maximum Likelihood (BS > 50 %) analysis are added to the left of a node (PP/BS).

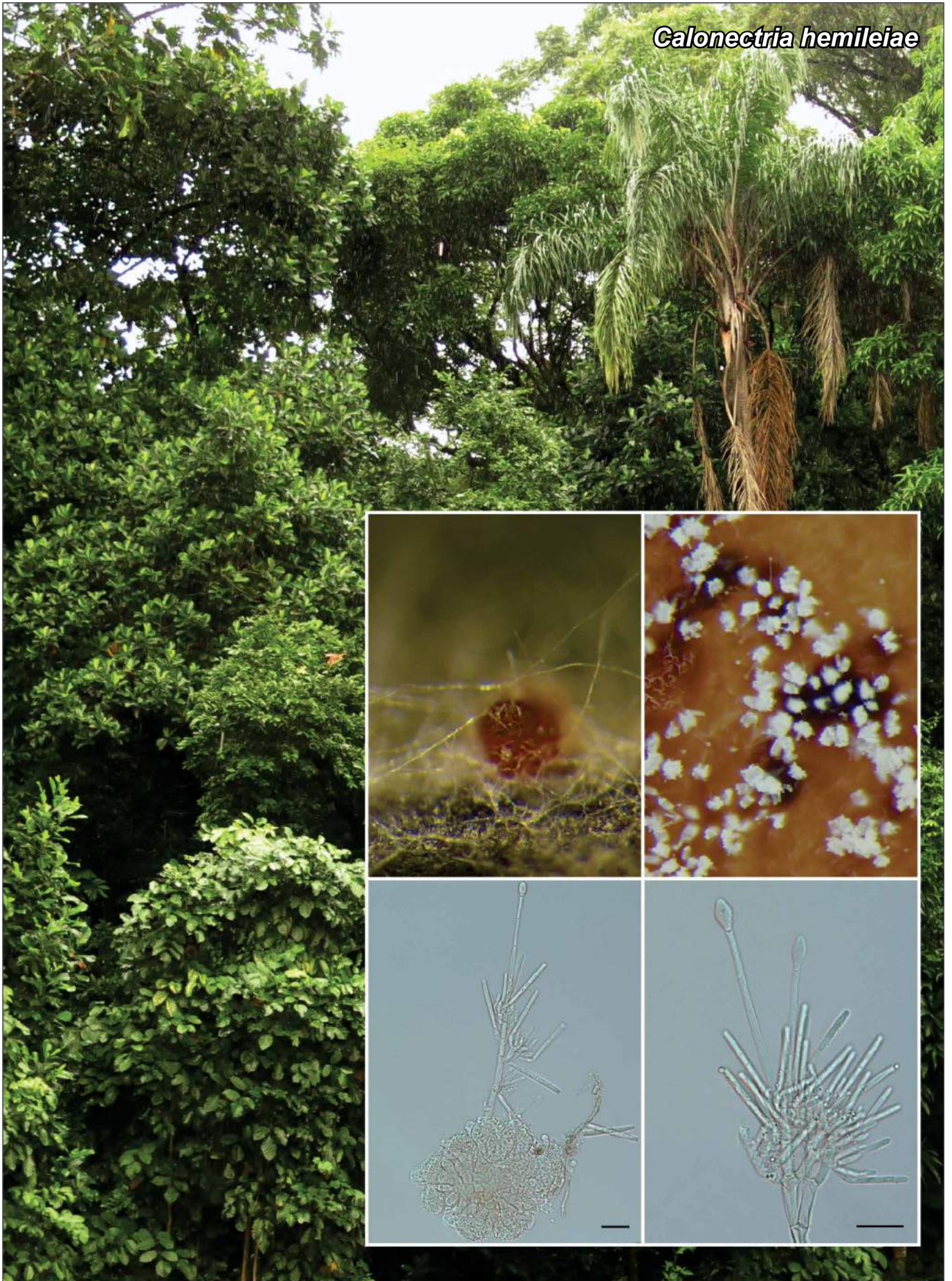
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*Calonectria hemileiae*



Fungal Planet 823 – 14 December 2018

***Calonectria hemileiae*** S.S. Salcedo, A.A. Colmán, H.C. Evans & R.W. Barreto, *sp. nov.*

*Etymology.* Named after its host, *Hemileia vastatrix*, the coffee leaf rust fungus.

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

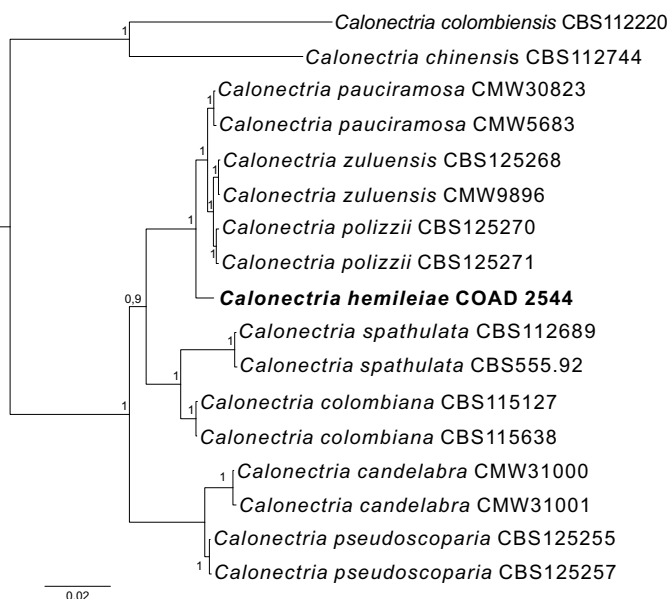
*Conidiophores* erect, stipe bearing a penicillate arrangement of fertile branches followed by an extension with a terminal vesicle, smooth, hyaline. *Stipe* cylindrical, 120–220 × 3–8 µm; stipe extension cylindrical, straight to flexuous, 109–209 µm long, 2–4 µm wide at the apical septum, terminating in an obpyriform to fusoid vesicle, 5–10 µm diam. *Conidiogenous apparatus* penicillate, 45–75 µm long × 45–100 µm wide; primary branches, 8–27 × 3–6 µm, 0–1-septate; secondary branches, 8–18 × 3–7 µm, aseptate; tertiary branches, 6–14 × 3–5 µm, aseptate. *Conidiogenous cells* phialidic formed in groups of 2–6 at apex of terminal branches, elongate-doliiform to reniform, 5–13 × 2–4 µm, aseptate, apex with minute periclinal thickening and inconspicuous collarette. *Macroconidia* cylindrical, straight, (35–)40–45(–48) × 3–5 µm (av. = 42 × 4 µm), rounded at both ends, 1-septate, lacking a visible abscission scar, held in parallel cylindrical clusters by colourless slime. *Sexual morph* absent – only sterile perithecial-like structures formed in culture. *Mega-* and *microconidia* not seen. *Chlamydospores* catenulate, thick-walled, hyaline.

*Culture characteristics* — Fast growing (42–60 mm diam on malt extract agar (MEA), synthetic nutrient poor agar (SNA) and oatmeal agar (OA), after 7 d); low convex, margins entire, aerial mycelium cottony, white, bay or salmon, blood or bay reverse; sporulation sparse on MEA and OA and abundant in SNA; infertile perithecia and chlamydospores arranged in chains, produced throughout the medium and aggregating to form microsclerotia in SNA.

*Typus.* BRAZIL, state of Rio de Janeiro, Rio de Janeiro, on pustules of *Hemileia vastatrix* formed on leaves of *Coffea arabica*, 1 Sept. 2015, R.W. Barreto (holotype VIC 47145, ex-type culture COAD 2544, *tef1* sequences GenBank MK006026, *tub2* sequences GenBank MK037391, *his3* sequences GenBank MK006027 and *cal* sequences GenBank MK037392, MycoBank

MB828262).

*Notes* — *Calonectria hemileiae* is a new member of the *C. candelabra* species complex (Alfenas et al. 2015, Lombard et al. 2015a, Lopes et al. 2018) based both on morphological characteristics and phylogenetic inference. The morphology of *C. hemileiae* is similar to that of *C. zuluensis* and *C. polizzii*. Nevertheless, it is clearly distinct from those taxa both in terms of ecological niche (the sole species of *Calonectria* recorded as a mycoparasite) and phylogenetically. Species of the *C. candelabra* complex are found worldwide, occurring on a range of plant hosts. Morphologically, they are characterised by having ellipsoidal to obpyriform vesicles, and 1-septate macroconidia (Schoch et al. 1999, Crous 2002, Lombard et al. 2010).



Consensus tree obtained by Bayesian Inference using the combined sequences of  $\beta$ -tubulin, translation elongation factor 1 $\alpha$ , histone H3, and calmodulin gene regions of *Calonectria* spp. The tree was rooted to *C. chinensis* (CBS 112744) and *C. colombiensis* (CBS 112220). Bayesian posterior probabilities are given at the nodes and the accession numbers are presented together with the species names. Ex-type strain is indicated in **bold**.

*Colour illustrations.* Secondary Atlantic rainforest overgrowing old coffee plantation in Rio de Janeiro (Brazil); *Calonectria hemileiae* (ex-type COAD 2544); infertile perithecium, sporulating conidiophores giving rise to 1-septate macroconidia, *Hemileia vastatrix* urediniospore fascicle colonised by *Calonectria hemileiae*. Conidiogenous apparatus with variation in vesicle shape. Scale bars = 20 µm.

*Calvatia caatinguensis*



Fungal Planet 824 – 14 December 2018

***Calvatia caatinguensis*** R.L. Oliveira, R.J. Ferreira, B.D.B. Silva, M.P. Martín & Baseia, *sp. nov.**Etymology.* Referring to the biome in which it was collected.Classification — *Agaricaceae*, *Agaricales*, *Agaricomycetes*.

*Basidiomata* growing solitary, 35–40 mm wide × 45–58 mm high, pyriform to turbinate. *Exoperidium* slightly tomentose, evanescent, greyish brown (7E3, Kornerup & Wanscher 1978), at the base with sand encrusted at maturity. *Mesoperidium* membranaceous, smooth, greyish yellow to brown (4B4 to 5F5) at maturity. *Endoperidium* papyraceous externally, persistent in the basal portion, olive brown to brown (4E3 to 5E4). *Gleba* initially compact and white to yellowish white (4A1 to 4A2), becoming lanose and powdery, brownish grey to dark brown (5D2 to 9F4) at maturity. *Subgleba* well-developed, occupying two thirds of the basidioma, when mature pale yellow at base to dark brown going up (4A3 to 6F8), and presenting a different colour band, yellowish white (4A2) at the apex of subgleba. *Rhizomorphs* densely encrusted with sand, 2.5–6.2 µm diam, regular walls ≤ 1.3 µm thick, curved, branched, septate, hyaline in 5% KOH, and dextrinoid. *Exoperidium* composed for hyphae, 2.7–4.5 µm diam, with regular walls ≤ 0.7 µm thick, straight, rarely branched and septate, hyaline in 5% KOH and not dextrinoid. *Endoperidium* with hyphae 2.8–5.1 µm diam, with regular walls ≤ 1.16 µm thick, straight, branched, frequently septate, pale brown in 5% KOH, and dextrinoid; presence of mycosclereids globose, subglobose, pyriform, triangular, ovoid, ellipsoid or rectangular shape, present in the apical portion, 14.4–29.5 × 7.6–17.8 µm, with regular walls ≤ 1.35 thick, and straight. *Subgleba* with hyphae measuring 2.3–4.2 µm diam, with regular walls ≤ 1.2 µm thick, curved, branched, septate, hyaline in 5% KOH, and dextrinoid. *Paracapillitium* absent. *Capillitium* *Calvatia*-type, hyphae 2.7–4.5 µm diam with regular walls ≤ 0.88 µm thick, straight, frequently branched, septate, with small and numerous circular pits, hyaline in 5% KOH, dextrinoid. *Basidiospores* subglobose, equinulated, 5.4–7.4 × 5.1–6.7 µm [ $\chi = 5.9 \pm 0.5 \times 5.6 \pm 0.4$ ;  $Q_m = 1.06$ ;  $n = 20$ ], pedicels present in some spores, ≤ 1.09 µm, hyaline in 5% KOH, dextrinoid and acyanophilic.

*Habit & Habitat* — Growing solitary or two basidiomata on decaying leaves.

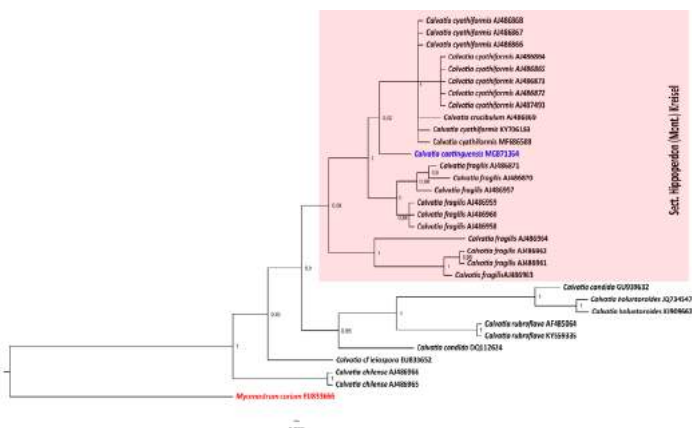
*Typus.* BRAZIL, Rio Grande do Norte, João Câmara, Serra do Torreão, near trail, soil, Feb. 2017, R.L. Oliveira (holotype UFRN fungos 2945, ITS and LSU sequences GenBank MG871364 and MH988750, MycoBank MB824127).

*Notes* — *Calvatia caatinguensis* is a typical species in section *Hippoperdon*. Based on morphological and molecular

*Colour illustrations.* Brazil, Rio Grande do Norte, João Câmara, Serra do Torreão, where the specimens were collected; immature basidiome *in situ* (UFRN-Fungi 2946); longitudinal section through mature basidiome (UFRN-Fungi 2945); mature basidiome *in situ* (UFRN-Fungi 2945); capillitium under SEM (UFRN-Fungi 2266); basidiospores under SEM (UFRN-Fungi 2266). Scale bars = 10 mm (basidiomata), 1 µm (basidiospores and capillitium).

characters, it is closely related to some other *Calvatia* species, such as *C. crucibulum*, *C. cyathiformis*, *C. fragilis* and *C. lilacina*.

*Calvatia fragilis* has a lycoperdon-type capillitium with numerous small circular pits; however, *C. fragilis* does not have a subgleba or it is reduced, and basidiospores are smaller and finely equinulated (Morgan 1890, Silveira 1943). *Calvatia crucibulum*, a species reported only by Kreisel (1992, 1994), has similar morphological characteristics, such as a capillitium with small and numerous pits, woolly gleba, and fine exoperidium. However, in those publications the author does not describe some macroscopic (subgleba) and microscopic structures (basidiospores), which makes a comparison difficult. In the present study these two species are well separated by their ITS nrDNA barcode sequences. *Calvatia lilacina* is another morphologically similar species to *C. caatinguensis*, mainly based on the distinct colour band at the apex of the subgleba; however, *C. lilacina* has smaller basidiospores (3–5 µm), which are verrucose to spinulose (Bottomley 1948). In recent decades, *C. fragilis* and *C. lilacina* have been considered by some researchers as synonyms of *C. cyathiformis* (Bottomley 1948, Zeller & Smith 1964, Liu 1984, Moyersoen & Demoulin 1996, Poumarat 2003, Wartchow & Silva 2007), while others have considered *C. lilacina* as a synonym of *C. fragilis* (Kreisel 1992, 1994). *Calvatia cyathiformis* is recognised by the violaceous gleba, pulverulent, verrucose to echinate basidiospores, subgleba cellular and well developed, capillitium long, branched and with numerous circular pits (Dissing & Lange 1962, Zeller & Smith 1964). This species has been reported in several parts of the world (Morgan 1890, Dissing & Lange 1962, Zeller & Smith 1964, Liu 1984, Moyersoen & Demoulin 1996, Poumarat 2003), including Brazil (Silveira 1943, Viégas 1945, Wartchow & Silva 2007). *Calvatia cyathiformis* is characterised by a marked morphological variation in basidiospores and capillitium. However, *C. caatinguensis* has a distinct colour band at the apex of the subgleba, in addition to a marked encrustation at the basal exoperidium when mature, not observed in *C. cyathiformis*. Morphological and molecular data (ITS nrDNA) provide strong support for *C. caatinguensis* as a distinct species of *Calvatia*.



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*Carolinigaster bonitoi*



Fungal Planet 825 – 14 December 2018

***Carolinigaster* M.E. Sm. & S. Cruz, gen. nov.**

*Etymology.* The genus name *Carolinigaster* refers to North Carolina, the region where this truffle was collected, and 'gaster' (Greek for 'stomach') in reference to the fact that the spores of this truffle species are enclosed inside of the fruiting body.

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

Distinguished from other *Boletaceae* by a combination of the following characters: *Basidiomata* hypogeous to partially emergent,

***Carolinigaster bonitoi* M.E. Sm. & S. Cruz, sp. nov.**

*Etymology.* The epithet *bonitoi* is given in reference to mycologist Gregory Bonito – a truffle expert, North Carolina native, and co-collector of the type specimen.

*Basidiomata* hypogeous, globose to subglobose, 0.5–2 cm diam, attached to the substrate by fine white rhizomorphs. *Peridium* bright white to pinkish white, completely enclosing the gleba when young but thinning and wearing away with age, not changing colour when handled or bruised. *Gleba* loculate, locules up to 0.5 mm diam but mostly 0.25 mm or smaller, light pink when young but becoming pinkish brown to light brown in mature specimens, rubbery when fresh. Lacking a columella or sterile base. *Odour* indistinct, *taste* not recorded. *Peridium* 50–210 µm thick, hyaline, comprised of loosely interwoven gelatinised hyphae mostly 5 µm diam, notably softer in 3 % KOH than in water or Melzer's, with occasional incorporated rhizomorphs up to 10 µm diam and slightly dextrinoid. *Basidia* 40–55 × 10–15 µm but narrowing to 5 µm at the base, four-spored, clavate to subcapitate and scattered. Sterigmata mostly 5–6.5 µm long and 0.5–1 µm diam. *Trama* tissues appearing gelatinised, especially when mounted in KOH. *Basidioles* numerous, hyaline, clavate or occasionally subcapitate, 30–45 × 8–13 µm wide, narrowing to 3.5–4.5 µm at the base. *Clamp connections* not observed. *Cystidia* not observed. *Basidiospores* statismosporic, 8.8–11 × 5.9–8.4 µm (av. 9.7 × 7.3 µm), Q = 1.2–1.8 (mean Q = 1.35), globose to subglobose, pink in water, inamyloid and strongly dextrinoid in Melzer's reagent, bleaching to almost hyaline in KOH, spore wall mostly 1 µm, ornamented with triangular to rounded warts that are 0.5–1.5 µm tall × 1–2 µm wide at the base, with a hyaline perispore that is always visible in young spores but is more difficult to see in mature spores, often with a visible hilar appendage that is approximately 0.5 µm diam and 1–2 µm long.

*Habitat & Distribution* — Fruiting in the soil beneath the leaf litter in mixed forests dominated primarily by *Quercus*, *Fagus* and *Pinus* on silty-clay soil. Known only from Durham County but likely present at appropriate sites across North Carolina's Piedmont region.

*Typus.* USA, North Carolina, Durham County, Durham, Duke University Campus, c. 150 m a.s.l., in mixed pine and hardwood forest, hypogeous in

*Colour illustrations.* Mixed *Fagaceae*-dominated forest near in Durham, North Carolina where *Carolinigaster bonitoi* was collected; section of hyaline trama viewed in Melzer's reagent (scale bar = 25 µm), basidiospores showing strong dextrinoid responses when viewed in Melzer's reagent (scale bar = 10 µm), fresh basidiomata (scale bar = 1 cm). All photos are of the holotype MES331 (FLAS-F-62017).

sequestrate, globose to subglobose. *Peridium* not changing colour when handled. *Gleba* loculate. Lacking a stipe or columella. *Basidiospores* statismosporic, globose to subglobose, ornamented with short irregular warts at maturity, pink in water and inamyloid but strongly dextrinoid, bleaching to almost hyaline in KOH. *Clamp connections* and *hymenial cystidia* absent.

*Type species.* *Carolinigaster bonitoi* M.E. Sm. & S. Cruz. MycoBank MB827451.

soil below the leaf litter, 21 Oct. 2009, G. Bonito & J. Trappe MES331 (holotype FLAS-F-62017, ITS, LSU and *tef1* sequences GenBank MH747178, MH747179 and MH753704, MycoBank MB827455).

*Additional specimen examined.* USA, North Carolina, Durham County, Durham, Eno River State Park, c. 200 m a.s.l., in mixed pine and hardwood forest, hypogeous in soil below the leaf litter, 16 Oct. 2009, M.E. Smith, MES330, FLAS-F-62018.

*Notes* — *Carolinigaster bonitoi* is unique in having a hypogeous sequestrate fruiting habit, a bright white peridium that does not stain when handled or bruised, and a loculate gleba without a columella or sterile base that is light pink when young but becomes pinkish brown to brown at maturity. It has lightly ornamented spores covered by a perispore. The spores are pinkish in water and strongly dextrinoid in Melzer's reagent but bleach almost completely hyaline in 3 % KOH.

*Carolinigaster bonitoi* is related to species of *Austroboletus*, *Fistulinella*, *Veloporphyrellus* and *Mucilopilus* in the *Austroboletoidae*. *Mucilopilus castaneiceps* forms a sister clade to *C. bonitoi* but without support. *Mucilopilus castaneiceps* is a Japanese epigeous bolete that is superficially quite different from *C. bonitoi* but it actually shares some important features. Both taxa have dextrinoid spores, both have hymenial surfaces that are light when young but become dark pink or pinkish brown at maturity, and both fruit in association with trees in the *Fagaceae* (Takahashi 1988). The only other known truffle in the *Austroboletoidae* is *Soliococcus polychromus* (Trappe et al. 2013, Wu et al. 2016). *Soliococcus polychromus* is a brightly coloured tropical associate of *Myrtaceae* and *Fabaceae* that has smooth ellipsoid spores and is known only from Australasia.

No other bolete truffle has all of the same morphological features as *C. bonitoi* but the most similar taxon is *Jimtrappea guyanensis* (Smith et al. 2015). However, *J. guyanensis* is phylogenetically distant and has large, amyloid hymenial cystidia and smooth fusoid spores that are not dextrinoid, and is restricted to *Dicymbe*-dominated forests in Guyana.

*Carolinigaster bonitoi* is thus far known only from two collections from mixed, *Fagaceae*-dominated forests in North Carolina, USA. It is interesting that this species has not been found previously, particularly since Coker & Couch (1928) extensively studied the gasteromycetes (including hypogeous sequestrate species) of North Carolina. Coker & Couch (1928) recognized 26 species of 'Hymenogasteraceae' in their book but none of the species they studied are similar to *C. bonitoi*.

For supplementary information see MycoBank.

*Cercospora solani-betacei*



Fungal Planet 826 – 14 December 2018

***Cercospora solani-betacei* B.W. Ferreira & R.W. Barreto, sp. nov.**

*Etymology.* Referring to the host, *Solanum betaceum*, from which it was described.

*Classification* — *Mycosphaerellaceae*, *Capnodiales*, *Dothiomyces*.

*Lesion* on living leaves, starting as small necrotic dots, becoming sub-circular, to irregular, 5–15 mm diam, brown, with dark brown margins, coalescing and leading to extensive blight. *Internal mycelium* indistinct. *Stromata* reduced to few angular cells, 12–25 × 35–55 µm. *Conidiophores* predominantly hypophyllous, rarely epiphyllous, in fascicles of 5–22 conidiophores, sub-cylindrical, geniculate, 100–172 × 4–5 µm, 3–7-septate, unbranched, pale olivaceous brown, smooth. *Conidiogenous cells* terminal, subcylindrical, sympodial, sub-hyaline, 15–65 × 3–5 µm. *Conidiogenous loci* conspicuous, 2–3 µm diam, strongly thickened, darkened. *Conidia* obclavate to subcylindrical, straight to slightly curved, 47–130 × 3–5 µm, apex rounded to subacute, base truncate, 3–12-septate, guttulate, hyaline, smooth.

*Culture characteristics* — Slow-growing (45 mm in PDA and 35 mm in PCA, after 15 d) at 25 °C. Colony sub-umbonate, edge entire, aerial mycelium dense and felty, white; in PDA radially sulcate. Reverse rosy buff with concentric haloes olivaceous. Sporulation absent.

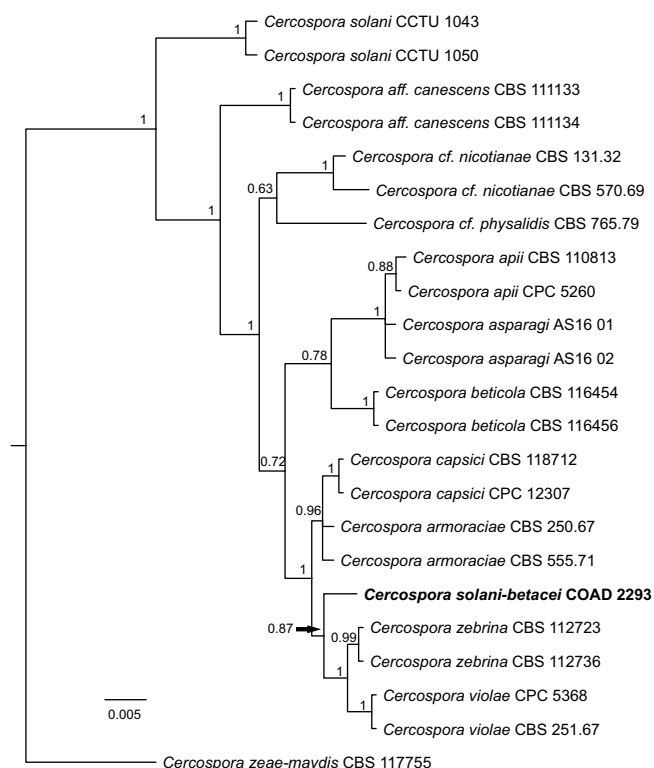
*Typus.* BRAZIL, Minas Gerais, Antônio Carlos, Dr. Sá Fortes, on living leaves of *Solanum betaceum* (tree tomato), 10 June 2017, B.W. Ferreira (holotype VIC 44319, ex-type culture COAD 2293, ITS, LSU, *cmdA* and *actA* sequences GenBank MH223464, MH700245, MH428037 and MH445457, MycoBank MB826812).

Phylogenetic tree inferred from Bayesian analysis based on concatenated sequences (ITS, *cmdA* and *actA*). The analysis was performed with 10 million generations in MrBayes v. 3.1.1. The Bayesian posterior probability values are indicated at the nodes. The tree was rooted to *Cercospora zea-maydis*. The new species is highlighted in **bold face**.

*Colour illustrations.* *Solanum betaceum* in subsistence orchard; leaf spots on *S. betaceum*, *Cercospora solani-betacei* conidiophore fascicle and conidia. Scale bars = 40 µm (conidiophores) and 10 µm (conidia).

*Notes* — A *Cercospora* sp. has been reported on *Cyphomandra betacea* (= *S. betaceum*) in Malawi (Peregrine & Siddiqi 1972) and Zimbabwe (Whiteside 1966). Other records of *Cercospora* spp. on members of *Solanum* spp. are: *Cercospora apii*, *C. canescens*, *C. cyperacearum*, *C. lanugiflori*, *C. physalidis*, *C. puyana*, *C. solanacea*, *C. solani*, *C. solanicola*, *C. solanigena* (Farr & Rossman 2018). The morphology of the *Cercospora* on tree tomato was similar to that of species belonging to the *C. apii* complex (Groenewald et al. 2013). A BLASTn search on GenBank indicated a considerable similarity of *C. solani-betacei* to other species belonging to *Cercospora*. A concatenated phylogenetic tree was constructed with ITS, *cmdA* and *actA* and, the combined result clearly supported *S. betaceum* as a distinct species.

Koch's postulates were performed and the pathogenicity of the fungus to *S. betaceum* was demonstrated.





*Acaulium pannemaniae*



Fungal Planet 827 – 14 December 2018

***Acaulium pannemaniae*** Sandoval-Denis, *sp. nov.*

*Etymology.* Named after Amina Panneman, who collected the sample. This species was discovered during a Citizen Science project in the Netherlands, 'Wereldfaam, een schimmel met je eigen naam', describing novel fungal species isolated from Dutch soils.

*Classification* — *Microasceae*, *Microascales*, *Sordariomycetes*.

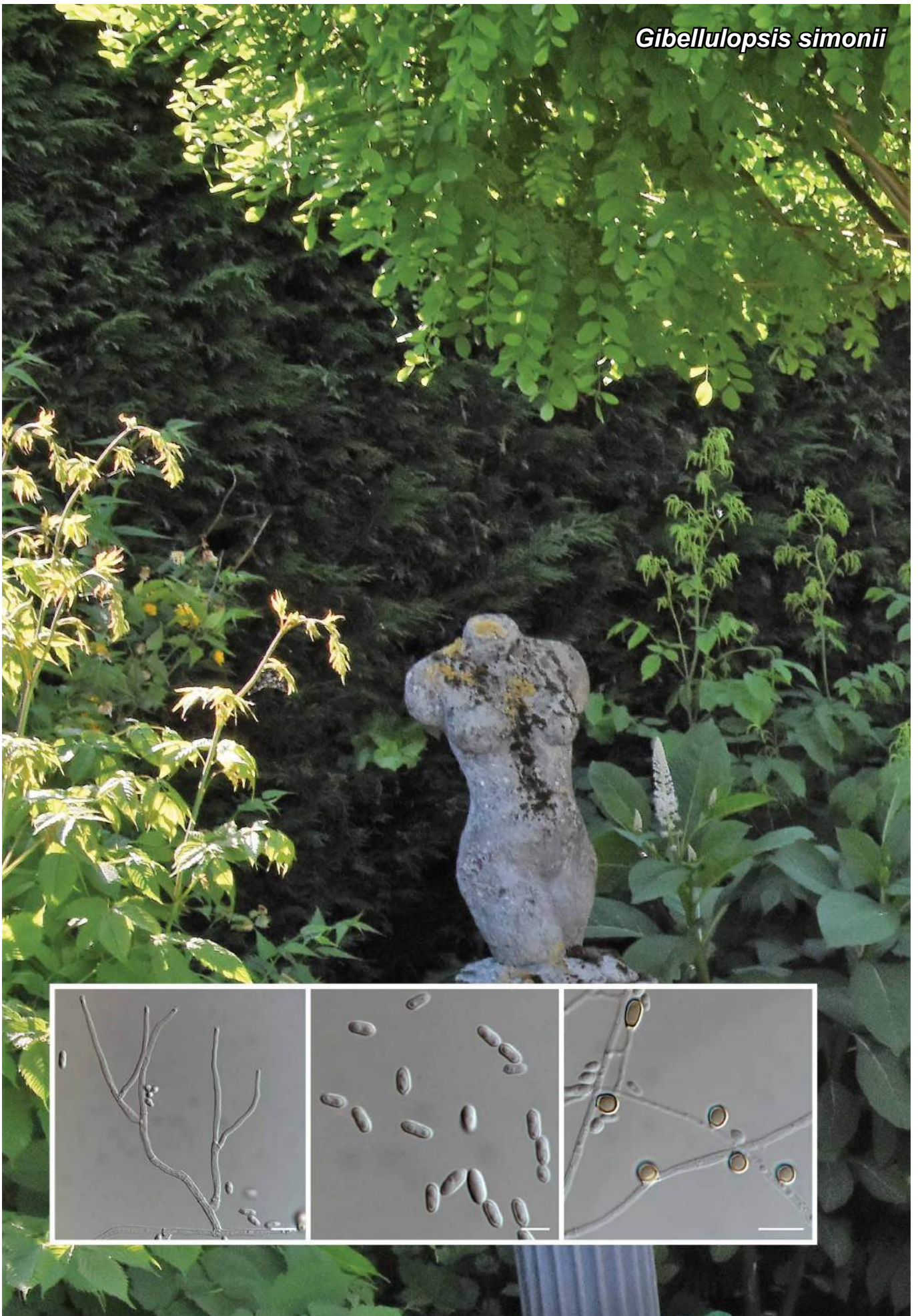
*Colonies* on OA at 25 °C attaining 18–24 mm in 14 d, ochreous to buff coloured, flat, membranous with regular margins. On PDA at 25 °C attaining 13–15 mm in 14 d, white to light buff, flat, fluffy to dusty with membranous periphery and regular margins. *Vegetative hyphae* septate, hyaline, smooth- and thin-walled. *Conidiophores* mononematous, penicillate branched; irregularly bi- to terverticillate, bearing groups of 2–4 conidiogenous cells, rarely reduced to single conidiogenous cells borne laterally on the aerial hyphae, hyaline to subhyaline, smooth-walled. *Conidiogenous cells* percurrent, lageniform to ampulliform, (11–)13.5–29(–44) × 3–4.5 µm, 21.4 ± 7.5 × 3.9 ± 0.3 µm long, broad at the widest part, tapering to a long cylindrical, annellated zone, 1.5–2.5 µm wide, up to 23 µm long, annellations inconspicuous. *Conidia* bullet-shaped or broadly clavate, (5.5–)6.5–10.5(–13) × (2.5–)3–4(–5), 8.6 ± 1.7 × 3.5 ± 0.4 µm, with a distinctive truncate base and rounded or slightly pointed apex, subhyaline to pale brown in mass, smooth- or finely roughened, thick-walled, arranged in long chains.

*Typus.* THE NETHERLANDS, Gelderland, Kapel-Avezaath, from soil under wooden chippings, 2017, *A. Panneman* (holotype CBS H-23741, culture ex-type CBS 145025 = JW79009; ITS, LSU, *tef1* and *tub* sequences GenBank LS999990, LS999991, LS999992 and LS999993, MycoBank MB827981).

*Notes* — The genus *Acaulium* was recently reinstated and segregated from *Scopulariopsis* (Sandoval-Denis et al. 2016). Four species are currently accepted (Woudenberg et al. 2017). *Acaulium pannemaniae* closely resembles *Acaulium album*. However, the new species differ by producing mononematous conidiophores only in contrast to the synnematous conidiophores of *A. album*. *Acaulium pannemaniae* also exhibits much larger conidiogenous cells, often with exceptionally long annellated necks which also contrast with all other known species of the genus.

*Colour illustrations.* Background, collection site; branched conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

*Gibellulopsis simonii*



Fungal Planet 828 – 14 December 2018

***Gibellulopsis simonii*** Giraldo López, *sp. nov.*

*Etymology.* *simonii*, refers to the name of the collector of the ex-type strain, Simon van Stuijvenberg. This species was discovered during a Citizen Science project in the Netherlands, 'Wereldfaam, een schimmel met je eigen naam', describing novel fungal species isolated from Dutch soils.

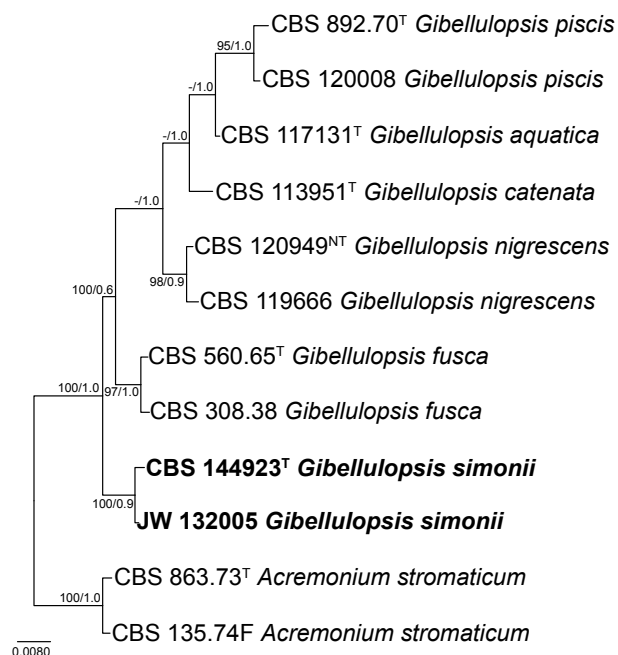
*Classification* — *Plectosphaerellaceae*, *Glomerellales*, *Sordariomycetes*.

*Mycelium* consisting of branched, septate, smooth, hyaline and thin-walled hyphae, up to 2 µm wide. *Conidiophores* simple or poorly branched, hyaline, smooth-walled, up to 83 µm long. *Phialides* lateral or terminal, subcylindrical to subulate, hyaline, smooth, 17–46 × 1.5–2 µm, with minute cylindrical collarette and periclinal thickening at the conidiogenous locus. *Conidia* cylindrical or ellipsoidal, sometimes with a slightly truncate base, 1-celled, hyaline, thin- and smooth-walled, 3.5–6 × 1.5–2 µm, arranged in slimy heads. *Chlamydospores* lateral or intercalary, single, with or without intermittent hyaline cells, subglobose or clavate, brown, smooth- and thick-walled, 4–7 × 3.5–5.5 µm.

*Culture characteristics* — Colonies on OA and PDA after 10 d at c. 25 °C, reaching 25–27 and 28–29 mm diam, respectively, flat, surface and reverse dark mouse grey to fuscous black, with a pale mouse grey mycelium forming concentric rings.

*Typus.* THE NETHERLANDS, Gelderland, Meteren, isolated from soil, 2017, coll. *S. van Stuijvenberg*, isol. *A. Giraldo* (holotype CBS H-23735, cultures ex-type CBS 144923 = JW132008, ITS and LSU sequences GenBank MK047467.1 and MK047517.1, MycoBank MB828025).

*Notes* — *Gibellulopsis* species are commonly soil-borne fungi, morphologically characterised by sparse branched conidiophores, ellipsoidal to cylindrical conidia and olive-brown chlamydospores (Domsch et al. 2007). Batista & Maia (1959) introduced the genus based on *G. piscis*, which was subsequently synonymised with *Verticillium nigrescens* (Zare et al. 2007). The genus was recently revised, and five species were accepted. *Gibellulopsis chrysanthemy* (Hirooka et al. 2014) was segregated from *Gibellulopsis* and accommodated elsewhere (Giraldo & Crous 2019). Morphologically, *G. simonii* resembles *G. nigrescens* in having lateral or intercalary subglobose chlamydospores. *Gibellulopsis simonii*, however, produces shorter and less branched conidiophores than those of *G. nigrescens* (up to 100 µm long), and is phylogenetically different from the ex-type strain of that species.



*Colour illustrations.* Garden where the soil sample was collected; conidiophores, conidia and chlamydospores. Scale bars: = 10 µm (conidiophores and conidia) and 5 µm (chlamydospores).

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*Fusicolla septimanifiniscientiae*



Fungal Planet 829 – 14 December 2018

***Fusicolla septimanifiniscientiae*** L. Lombard & Hern.-Restr., *sp. nov.*

*Etymology.* From Latin *septimana*- meaning week, *fini*- meaning the end of, and *scientiae*- meaning science. Named after the 'Weekend of Science'.

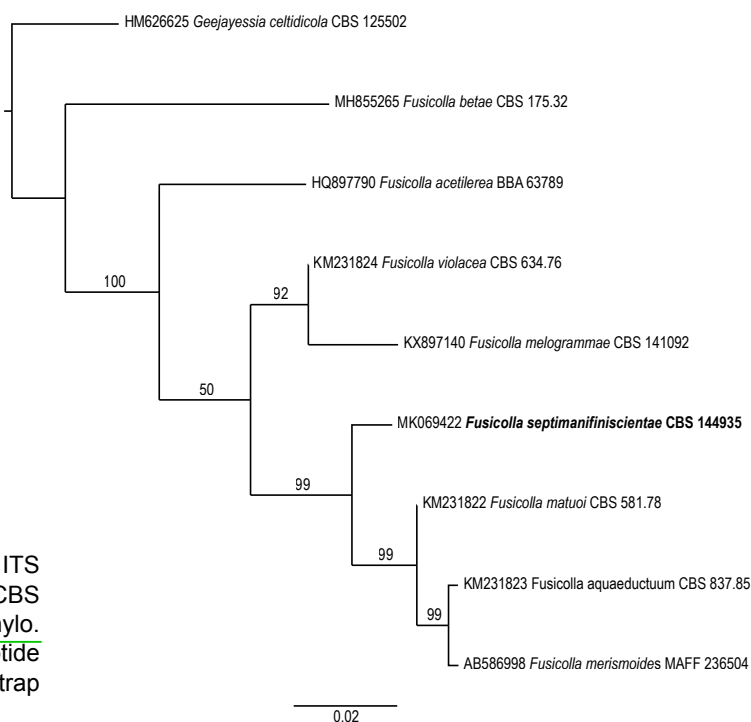
*Classification* — *Nectriaceae*, *Hypocreales*, *Sordariomycetes*.

*Conidiophores* initially as lateral phialides arising directly from somatic hyphae, simple or rarely branched, monochasial or verticillate, straight, hyaline, smooth-walled, aseptate or with basal septum, up to 32 µm long. *Conidiogenous cells* monophaialidic or rarely polyphialidic, arising laterally from hyphae or in terminal pairs, or verticils of three, cylindrical to subulate, 6–16 × 3–4 µm, thin- and smooth-walled, hyaline with inconspicuous collarettes and periclinal thickening. *Macroconidia* falcate, more or less straight, slightly narrowing towards the ends, apical cell often hooked with a more or less pointed tip, basal cell slightly pedicellate, (1–)3-septate, (19–)25–29(–34) × 3–4 µm (av. 27 × 3 µm), hyaline, thin- and smooth-walled. *Microconidia* absent. *Chlamydospores* single or in pairs, intercalary or terminal, globose to obovoid, thick-walled and verruculose. *Sexual morph* unknown.

*Culture characteristics* — Colonies on OA, MEA and PDA at 25 °C attaining 25–30 mm in 7 d. On OA aerial mycelium absent with slimy appearance due to abundant sporulation on medium surface, buff to primrose, margin entire. On MEA aerial mycelium absent with slimy appearance due to abundant sporulation on medium surface, rosy buff to buff, reverse buff, margin entire. On PDA aerial mycelium absent with slimy appearance due to abundant sporulation on medium surface, pale luteous to buff, reverse pale luteous, margin entire.

*Typus.* THE NETHERLANDS, Utrecht Science Park, Westerdijk Fungal Biodiversity Institute, from soil in front of the bronze statue of Johanna Westerdijk, Mar. 2017, *M. Hernandez-Restrepo* (holotype CBS H-23749, culture ex-type CBS 144935); ITS, LSU, *tef1* and *tub2* sequences GenBank MK069422, MK069418, MK077808 and MK069408, MycoBank MB828215).

*Notes* — *Fusarium* s.lat. has recently been segregated into several fusarium-like genera, one of which is *Fusicolla* (Lombard et al. 2015b, Guarnaccia et al. 2018). *Fusicolla septimanifiniscientiae* can be distinguished from other species in the genus *Fusicolla* by the formation of polyphialidic conidiogenous cells on the somatic hyphae (Gräfenhan et al. 2011). Based on phylogenetic inference of the ITS sequences, *F. septimanifiniscientiae* is closely related to *F. aquaeductuum*, *F. matuoi* and *F. merismoides*. However, *F. septimanifiniscientiae* mostly produced 3-septate macroconidia ((19–)25–29(–34) × 3–4 µm (av. 27 × 3 µm)), rarely 1-septate, which are smaller than the 3-septate macroconidia of *F. aquaeductuum* (30–55 × 2.5–3.5 µm; Gerlach & Nirenberg 1982), *F. matuoi* ((25–)33–56 × (1.5–)2–3 µm; Hosoya & Tubaki 2004) and *F. merismoides* (26–48 × 3–4.3 µm; Gerlach & Nirenberg 1982).

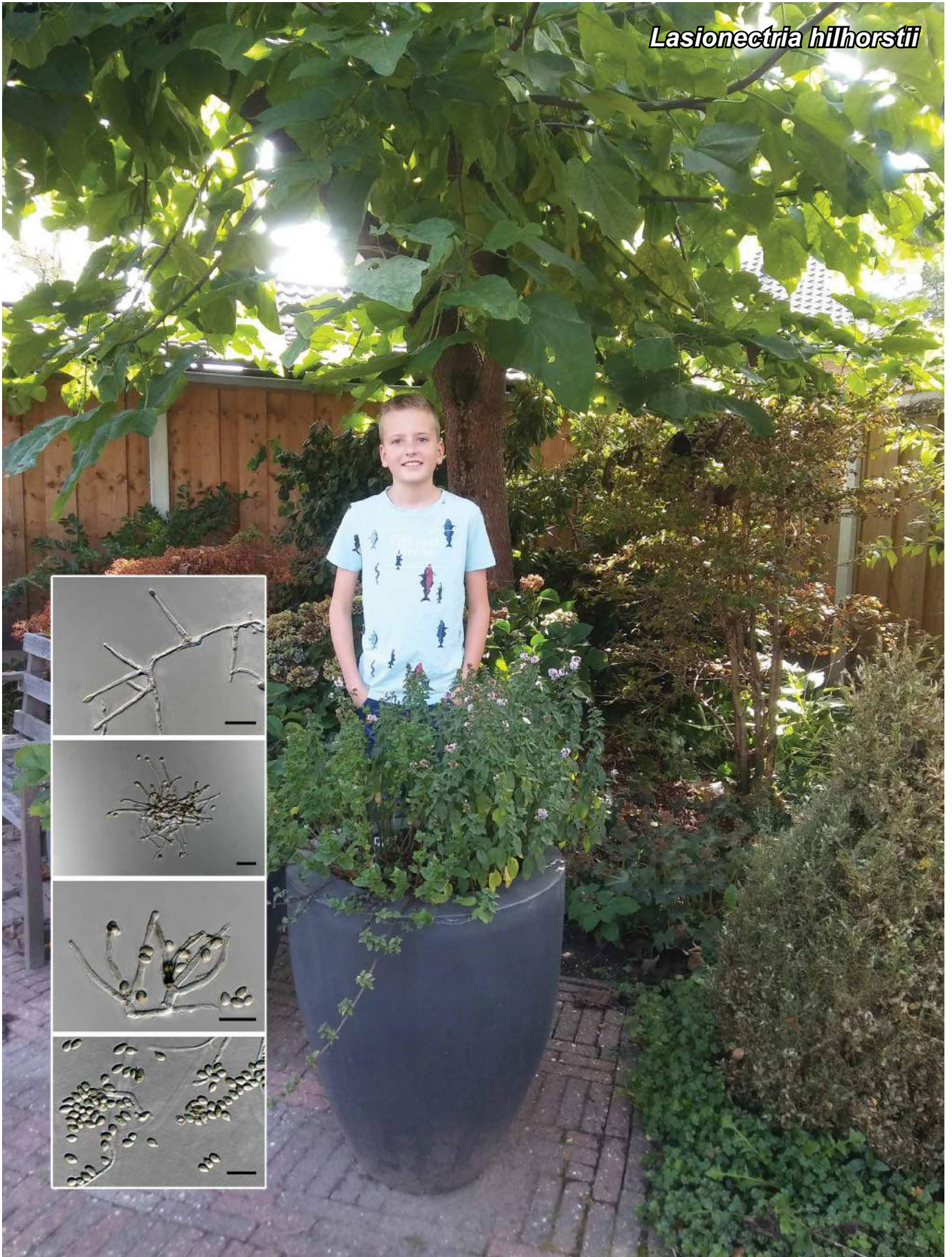


Maximum likelihood phylogeny of *Fusicolla* inferred from ITS sequences. The tree is rooted to *Geejayessia celtidicola* (CBS 125502). Analysis performed online in CIPRES ([www.phylo.org](http://www.phylo.org)) using RAxML BlackBox using the GTR+I+G nucleotide substitution model. Branch support assessed using bootstrap with replicates determined by the software.

*Colour illustrations.* Background, collection site (grounds of the Westerdijk Fungal Biodiversity Institute); conidiophores, mono- and polyphialidic conidiogenous cells, macroconidia and chlamydospores. Scale bars = 10 µm

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*Lasionectria hilhorstii*



Fungal Planet 830 – 14 December 2018

***Lasionectria hilhorstii* L. Lombard, sp. nov.**

**Etymology.** Named for Tjebbe Hilhorst, who collected the sample. This species was discovered during a Citizen Science project in the Netherlands, 'Wereldfaam, een schimmel met je eigen naam', describing novel fungal species isolated from Dutch soils.

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

Colonies on OA at 25 °C attaining 12–20 mm in 7 d, aerial mycelium collapsed with abundant sporulation on the medium surface forming vinaceous green to vinaceous black droplets of conidial masses, margin undulate surrounded by a vinaceous to greyish rose halo, surface vinaceous black, reverse isabelline in the centre becoming vinaceous towards the margins. On MEA at 25 °C attaining 20–25 mm in 7 d, with moderate aerial mycelium, felty with string folds into the medium, margin undulate, surface olivaceous black in the centre due to abundant sporulation becoming brick to rosy vinaceous towards the margin, surrounded by a vinaceous halo, reverse vinaceous to rosy buff. *Sexual morph* not seen. *Vegetative hyphae* septate, hyaline, smooth- and thin-walled, becoming slightly verrucose with age, 1–2.5 µm wide. *Conidiophores* erect, arising directly from vegetative hyphae, simple or branched, straight, hyaline and smooth-walled becoming slightly verrucose and subhyaline with age, aseptate or with basal septum, up to 56 µm long. *Conidiogenous cells* phialidic, arising laterally from hyphae or in terminal pairs, or verticils of three, or small monopodially branched tufts of up to four from conidiophores, monopodialic, aseptate, elongate-ampulliform to subcylindrical, 13–24 µm long, 1–3 µm wide at the base, thin- and smooth-walled to slightly verrucose, hyaline to subhyaline with inconspicuous collarettes and periclinal thickening. *Conidia* unicellular, ovoid to broadly ellipsoidal, 3–5 × 2–3 µm (av. 4 × 2 µm), subhyaline to olivaceous green, thick- and smooth-walled, forming slimy heads on the phialides. *Chlamydospores* not seen.

**Typus.** THE NETHERLANDS, Gelderland, Eibergen, from soil, Mar. 2017, *T. Hilhorst* (holotype CBS H-23747, culture ex-type CBS 144938 = JW85024; ITS, LSU, *act* and *tef1* sequences GenBank MK069421, MK0269417, MK069414 and MK069411, MycoBank MB828216).

**Notes** — *Lasionectria hilhorstii* is morphologically reminiscent of *Acremonium cereale* (Gams 1971), but can be distinguished by the lack of flared collarettes and basal swelling of the phialides. Additionally, megablast searches of NCBI's GenBank nucleotide database using LSU sequences indicated that the closest species were *L. oenanthicola* (GenBank KY607557.1; Identities = 839/839 (100 %), no gaps), *A. cereale* (GenBank MH877716.1; 839/840 (99 %), 1 gap) and *L. mantuana* (GenBank GQ505994.1; Identities = 838/839 (99 %), no gaps). The closest hits using ITS sequences were *L. oenanthicola* (GenBank KY607542.1; 864/898 (96 %), 14 gaps (1 %)), *A. persicinum* (GenBank KM030294.1; 782/851 (92 %), 25 gaps (2 %)) and *Ljuhya dentifera* (GenBank KY607540.1; 793/869 (91 %), 21 gaps (2 %)). The closest hits using *act* sequences were *Gliocladium* sp. (GenBank KY608883.1; 606/650 (93 %), 7 gaps (1 %)), *Clonostachys rosea* (GenBank KP274072.1; 605/652 (93 %), 7 gaps (1 %)) and *Alternaria hyacinthi* (GenBank JQ671603.1; 604/653 (92 %), 7 gaps (1 %)). The closest hits using *rpb2* sequences were *Septofusidium berlinense* (GenBank KM232417.1; 699/856 (82 %), 11 gaps (1 %)), *Heleococcum aurantiacum* (GenBank JX158463.1; 701/861 (81 %), 11 gaps (1 %)) and *Stromatonectria caraganae* (GenBank HQ112290.1; 688/857 (80 %), 10 gaps (1 %)). The closest hits using *tef1* sequences were *L. mantuana* (GenBank HM484844.1; 376/398 (94 %), 2 gaps (0 %)), *Neocosmospora* sp. (GenBank LT746219.1; 229/263 (87 %), 11 gaps (4 %)) and *Hydropisphaera* sp. (GenBank HM484845.1; 232/268 (87 %), 13 gaps (4 %)).

**Colour illustrations.** Background, collection site (backyard); conidiophores and conidia. Scale bars = 10 µm.



*Leptodiscella rintellii*



Fungal Planet 831 – 14 December 2018

## *Leptodiscella rintelii* Hern.-Restr., *sp. nov.*

**Etymology.** *rintelii*, refers to the name of the collector of the ex-type strain, Marinus Rintel. This species was discovered during a Citizen Science project in the Netherlands, 'Wereldfaam, een schimmel met je eigen naam', describing novel fungal species isolated from Dutch soils.

**Classification** — *Muyocoproneae*, *Muyocoprionales*, *Dothi-deomycetes*.

**Mycelium** hyaline to pale brown composed of smooth-walled, septate, 1–2 µm wide hyphae. **Conidiophores** micro- to semi-micronematous composed of one to many globose to irregular cells, thin-walled, hyaline, smooth. **Conidiogenous cells** mono- or polyblastic, lateral or terminal, subcylindrical, globose or irregular, non-denticulate, hyaline, smooth, 3.5–6.5 × 3.5–5 µm. **Conidia** solitary, cylindrical, rounded at both ends or truncate base, hyaline, 1-septate, smooth, multi-guttulate, 8–14.5 × 3–4 µm, with a simple, filamentous subterminal appendage at each end, 2.5–6 µm long. **Chlamydospores** not observed.

**Culture characteristics** — Colonies on OA and CMA after 1 wk at 25 °C, aerial mycelium lacking except in the centre, where occasionally white tufts are observed, pale ochreous to cinnamon with age, reverse concolourous.

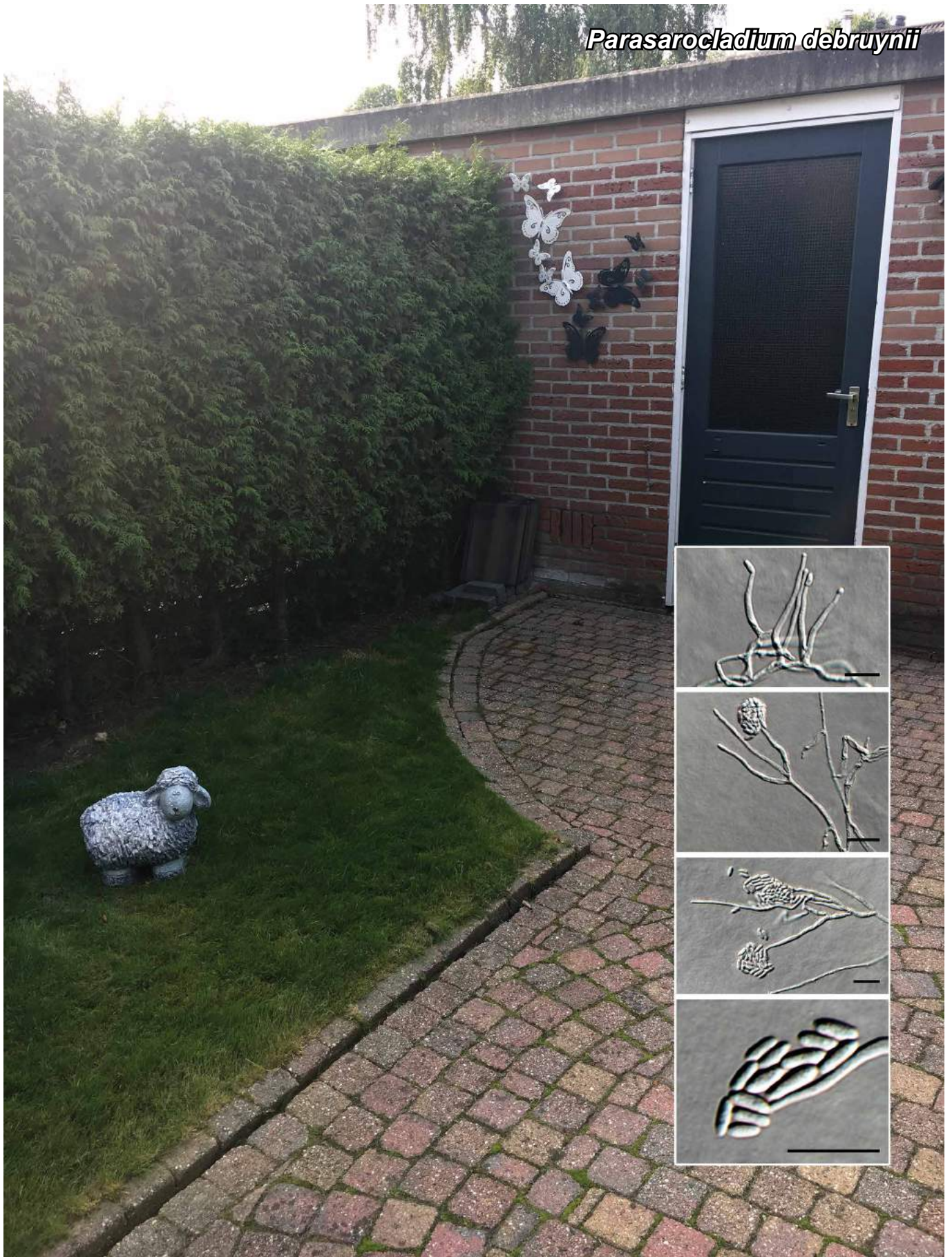
**Typus.** THE NETHERLANDS, Noord-Holland, Langedijk, Zuid-Scharwoude, isolated from soil, 2017, *M. Rintel* (holotype CBS H-23742, cultures ex-type CBS 144927 = JW174006, ITS and LSU sequences GenBank LR025180 and LR025181, MycoBank MB828022).

**Notes** — *Leptodiscella* is an uncommon genus known mainly from soil (Papendorf 1967, Matsushima 1975, Madrid et al. 2012) and dust (Udagawa & Toyazaki 1985). *Leptodiscella rintelii* is more similar to *L. africana* in having hyaline, 1-septate conidia and lacking chlamydospores (Papendorf 1967). However, *L. rintelii* can be distinguished from *L. africana* by having shorter and wider conidia with shorter appendages (11–17.5 × 2–3 µm, 6.5–13 µm long, in *L. africana*, Papendorf 1975).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *L. brevicatenata* (GenBank FR821312.1; Identities = 485/455 (96 %), 7 gaps (1 %)), *L. chlamydospora* (GenBank FR745398.1; Identities = 449/489 (92 %), 12 gaps (2 %)) and *L. africana* (GenBank NR\_145359.1; Identities = 457/509 (90 %), 14 gaps (2 %)).

**Colour illustrations.** Garden where the soil sample was collected; conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

*Parasarocladium debruynii*



Fungal Planet 832 – 14 December 2018

**Sarocladiaceae** L. Lombard, *fam. nov.*

Classification — *Sarocladiaceae*, *Hypocreales*, *Sordariomycetes*.

*Vegetative hyphae* septate, hyaline, smooth- and thin-walled. *Conidiophores* erect, arising directly from vegetative hyphae, simple or branched, straight, hyaline, smooth-walled, aseptate or with basal septum. *Conidiogenous cells* phialidic, arising laterally from hyphae or in terminal pairs, or verticils of three, or small monopodially branched tufts of up to four from conidiophores, monophialidic, aseptate, elongate-ampulliform to subcylindrical, thin- and smooth-walled, hyaline with incon-

spicuous collarettes and periclinal thickening; adelophialides and schizophialides present or absent. *Conidia* unicellular, ellipsoidal, bacilliform to fusiform, sometimes slightly curved, hyaline to subhyaline, thin- and smooth-walled, forming slimy heads on the phialides or produced in chains.

*Type genus.* *Sarocladium* W. Gams & D. Hawksw.  
Mycobank MB828245

*Notes* — The family *Sarocladiaceae* presently includes *Parasarocladium* and *Sarocladium*.

**Parasarocladium debruynii** L. Lombard, *sp. nov.*

*Etymology.* Named for Remco de Bruyn, who collected the sample. This species was discovered during a Citizen Science project in the Netherlands, 'Wereldfaam, een schimmel met je eigen naam', describing novel fungal species isolated from Dutch soils.

Colonies on OA at 25 °C attaining 45–55 mm in 7 d, salmon due to abundant sporulation on medium surface giving a wet and slimy appearance, effuse, with edge entire surrounded by a light cyan blue halo; reverse salmon. On MEA at 25 °C attaining 38–50 mm in 7 d, rosy buff, effuse, with strong folds into the medium with edge entire; reverse rosy buff. *Vegetative hyphae* septate, hyaline, smooth- and thin-walled, 1–2.5 µm wide. *Conidiophores* erect, arising directly from vegetative hyphae, simple or rarely branched, straight, hyaline, smooth-walled, aseptate or with basal septum, up to 75 µm long. *Conidiogenous cells* phialidic, arising laterally from hyphae or in terminal pairs, or verticils of three, or small monopodially branched tufts of up to four from conidiophores, monophialidic, aseptate, elongate-ampulliform to subcylindrical, 13–27 µm long, 1–3 µm wide at the base, thin- and smooth-walled, hyaline with inconspicuous collarettes and periclinal thickening. *Conidia* unicellular, ellipsoidal, bacilliform to fusiform, sometimes slightly curved, 3–5 × 1–2 µm (av. 4 × 2 µm), hyaline, thin- and smooth-walled, forming slimy heads on the phialides. *Chlamydospores* not seen.

*Typus.* THE NETHERLANDS, Utrecht, IJsselstein, from soil, Mar. 2017, *R. de Bruyn* (holotype CBS H-23746, culture ex-type CBS 144942 = JW180016; ITS, LSU, *tef1* and *tub2* sequences GenBank MK069420, MK069416, MK069410 and MK069407, MycoBank MB828217).

*Notes* — The genus *Parasarocladium* was recently introduced by Summerbell et al. (2018) and included three species, *P. breve*, *P. gamsii* and *P. radiatum*. Conidia of *P. debruynii* (3–5 × 1–2 µm) are smooth-walled compared to the chromophilic roughened conidia of *P. breve* (Gams 1971) and smaller than those of *P. gamsii* ((4–)5–7(–12) × 0.5–1 µm; Tichelaar 1972). Furthermore, the phialides of *P. debruynii* lack any septation, distinguishing it from *P. radiatum* (Gams 1971). Additionally, ribosomal DNA sequences resolved *P. debruynii* as a distinct lineage within the genus *Parasarocladium*.

*Colour illustrations.* Background, collection site (backyard); conidiophores and conidia. Scale bars = 10 µm.

*Conioscypha boutwelliae*



Fungal Planet 833 – 14 December 2018

## *Conioscypha boutwelliae* Hern.-Restr., *sp. nov.*

*Etymology.* *boutwelliae*, refers to the name of the collector of the ex-type strain, Katrina Boutwell. This species was discovered during a Citizen Science project in the Netherlands, 'Wereldfaam, een schimmel met je eigen naam', describing novel fungal species isolated from Dutch soils.

*Classification* — *Conioscyphaceae*, *Conioscyphales*, *Sordariomycetes*.

*Description on OA.* *Mycelium* composed of septate, hyaline, smooth, 1–2.5(–4)  $\mu\text{m}$  wide hyphae. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* monoblastic, cupulate, endogenous, multilayer cup-like collarete after several percurrent enteroblastic tiny elongations, hyaline, smooth, 11.5–20.5  $\times$  8–15  $\mu\text{m}$ . *Conidia* solitary, unicellular, ellipsoidal, obovoid or subglobose, base truncate with a central pore of 1–1.5  $\mu\text{m}$  diam, brown, pitted-wall, 10.5–21  $\times$  8–13.5  $\mu\text{m}$ .

*Culture characteristics* — Colonies on OA after 1 wk at 25 °C, flat, spreading with scarce aerial mycelium, powdery, shiny, black, margin effuse.

*Typus.* THE NETHERLANDS, Zuid-Holland, Alphen aan den Rijn, isolated from soil, 2017, *K. Boutwell* (holotype CBS H-23743, cultures ex-type CBS 144928 = JW203008, ITS and LSU sequences GenBank LR025182 and LR025183, MycoBank MB828023).

*Notes* — *Conioscypha* includes 13 species mainly isolated as saprobes from submerged dead wood and leaves (Matsushima 1975, 1993, 1996, Shearer 1973, Crous et al. 2014a, Zelski et al. 2015, Chuaseeharonnachai et al. 2017, Hernández-Restrepo et al. 2017). *Conioscypha boutwelliae* is the first species described from soil, besides *C. varia* that has been reported from agricultural soil according to the CBS database. *Conioscypha boutwelliae* is similar to *C. japonica*, *C. lignicola* and *C. pleiomorpha* in having dark brown pitted conidia. However, they differ in shape and size, while in *C. boutwelliae* conidia are wider (8–13.5  $\mu\text{m}$ ) than in *C. japonica* (4.5–10  $\mu\text{m}$ ) and *C. pleiomorpha* (6–9  $\mu\text{m}$ ), they are narrower than in *C. lignicola* (11–12  $\mu\text{m}$ ).

*Colour illustrations.* Garden where the soil sample was collected; conidiogenous cells and conidia. Scale bars = 10  $\mu\text{m}$ .

*Sarocladium dejongiae*



Fungal Planet 834 – 14 December 2018

## *Sarocladium dejongiae* L. Lombard, *sp. nov.*

*Etymology.* Named for Astrid de Jong, who collected the sample. This species was discovered during a Citizen Science project in the Netherlands, 'Wereldfaam, een schimmel met je eigen naam', describing novel fungal species isolated from Dutch soils.

*Classification* — *Sarocladiaceae*, *Hypocreales*, *Sordariomycetes*.

Colonies on OA at 25 °C attaining 27–32 mm in 14 d, pale saffron to rosy buff, effuse, glabrous with undulate to lobate margin. On PDA at 25 °C attaining 38–43 mm in 14 d, saffron to salmon, effuse, glabrous, with edge entire. *Vegetative hyphae* septate, hyaline, smooth- and thin-walled, 1–2.5 µm wide. *Conidiophores* erect, arising directly from vegetative hyphae or from ropes of hyphae, simple or rarely branched, straight, hyaline, smooth-walled, up to 35 µm long. *Phialides* subcylindrical, 17–24 µm long, 1–2 µm wide at the base, thin- and smooth-walled, hyaline with inconspicuous periclinal thickening; adelophialides and schizophialides not observed. *Conidia* unicellular, cylindrical, ellipsoidal, ovoid to irregular, 3–5 × 1–2 µm (av. 3 × 1.5 µm), hyaline, thin- and smooth-walled, arranged in slimy heads. *Chlamydospores* rare, intercalarily, smooth-walled, 5 µm diam.

*Typus.* THE NETHERLANDS, Friesland, Jowert, from soil, Mar. 2017, A. de Jong (holotype CBS H-23744, culture ex-type CBS 144929 = JW244007; ITS, LSU, *tef1* and *tub2* sequences GenBank MK069419, MK069415, MK069409 and MK069406, MycoBank MB828218).

*Notes* — *Sarocladium dejongii* is morphologically similar to several species characterised by producing conidia in slimy heads (Giraldo et al. 2015). However, this species is distinguished from all these species by the multiple conidial shapes produced and the formation of intercalary chlamydospores. Additionally, ribosomal DNA sequences resolved *S. dejongiae* as a distinct lineage within the genus *Sarocladium*.

*Colour illustrations.* Background, collection site (backyard); colonies on OA and PDA, conidiophores with slimy heads, conidia and chlamydospores. Scale bars = 10 µm.



*Lectera nordwiniana*



Fungal Planet 835 – 14 December 2018

***Lectera nordwiniana*** Giraldo López, *sp. nov.*

*Etymology.* *nordwiniana*, refers to the school named 'Nordwin College' where the soil sample was collected by the students Dylan van der Pol, Rémon Verf, Joost Wilks and Mathis de Ruiter. This species was discovered during a Citizen Science project in the Netherlands, 'Wereldfaam, een schimmel met je eigen naam', describing novel fungal species isolated from Dutch soils.

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

*Mycelium* consisting of branched, septate, smooth, hyaline and thin-walled hyphae, up to 2 µm wide. *Conidiomata* sporodochial, punctiform, dark brown, solitary or gregarious, surrounded by abundant setae. *Setae* dark brown, 3–8-septate, flexuous, tapering to acutely rounded apices, thick- and smooth-walled, intermingled among the conidiogenous cells, 78–193 × 3–5 µm. *Phialides* subcylindrical, hyaline, smooth-walled, 13–24.5 µm long, 1.5–2.5 µm wide at the base, with conspicuous periclinal thickening at the conidiogenous locus. *Conidia* broadly fusiform, acute ends, inequilateral, with inner plane flat, and outer plane convex, 1-celled, hyaline, becoming orange in mass, thick- and smooth-walled, 6–8 × 2–3 µm.

*Culture characteristics* — Colonies on PDA after 14 d at c. 25 °C, reaching 22–23 mm diam, elevated, slightly folded, salmon, with brown punctiform sporodochia on the top.

*Typus.* THE NETHERLANDS, Friesland, Leeuwarden, Nordwin College, from soil, 2017, coll. *D. van der Pol, R. Verf, J. Wilks & M. de Ruiter*, isol. *A. Giraldo* (holotype CBS H-23736, cultures ex-type CBS 144921 = JW231009, ITS, LSU, *tef1-α* and *rpb2* sequences GenBank MK047461.1, MK047511.1, MK047549.1 and MK047570.1, MycoBank MB828024).

*Additional materials examined.* THE NETHERLANDS, Friesland, Leeuwarden, Nordwin College, from soil, 2017, coll. *D. van der Pol, R. Verf, J. Wilks & M. de Ruiter*, isol. *A. Giraldo*, JW231013, ITS, LSU, *tef1-α* and *rpb2* sequences GenBank MK047462.1, MK047512.1, MK047550.1 and MK047571.1; Gelderland, Arnhem, from soil, 2017, coll. *J. & L. Visser*, isol. *A. Giraldo*, CBS 144922 = JW 46012, ITS, LSU, *tef1-α* and *rpb2* sequences GenBank MK047463.1, MK047513.1, MK047551.1 and MK047572.1.

*Colour illustrations.* Netherlands, Nordwin College where the soil sample was collected; sporodochium, setae, conidiogenous cell and conidia. Scale bars = 10 µm.

*Notes* — *Lectera* was introduced based on the plant pathogen *Lectera colletotrichoides* as the type species, along with *L. longa* (Cannon et al. 2012). Recently, three more species have been added to the genus, i.e., *Lectera capsica* from *Capsicum annum*, *L. phaseola* from *Phaseolus vulgaris* and *L. humicola* from soil (Crous et al. 2017a, Giraldo & Crous, in prep.). Morphologically, *L. nordwiniana* resembles *L. longa* and *L. phaseola* in the profuse production of flexuous setae in artificial media. However, in *L. nordwiniana* these structures are longer (up to 193 µm long) than those produced by the other species (*L. longa* up to 111 µm long, *L. phaseola* up to 38 µm long).

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*Clathrus natalensis*



Fungal Planet 836 – 14 December 2018

***Clathrus natalensis*** G.S. Medeiros, Melanda, T.S. Cabral, B.D.B Silva & Baseia, *sp. nov.*

*Etymology.* Named in reference to the type locality, Natal City.

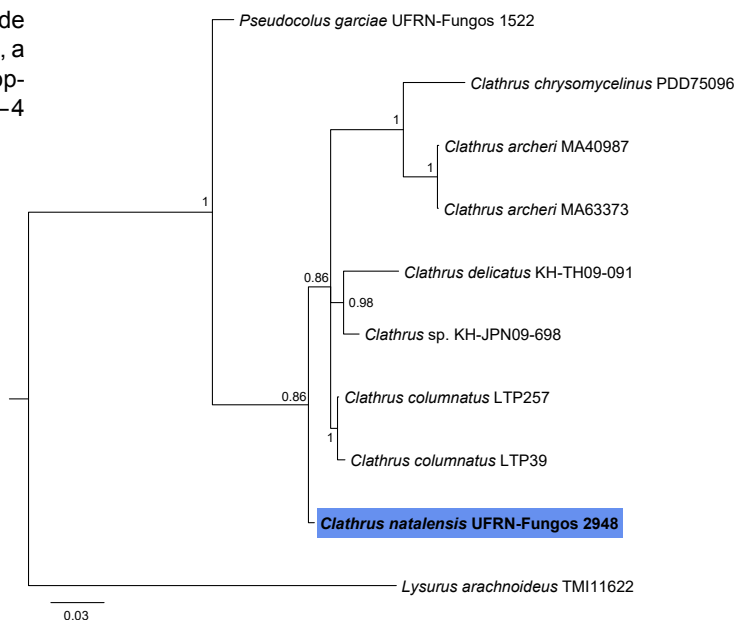
*Classification* — *Clathraceae*, *Phallales*, *Phallomycetidae*.

Immature *basidiomata* subglobose, 13–18 × 16–22 mm, greyish white (12A1–12B1 KW) with a single and thick rhizomorph greyish white (12A1–12B1 KW). Expanded *basidiomata* obovate to subglobose 46–95 × 24–71 mm. *Arm meshes* pentagonal to hexagonal, rugose at the beginning of development, becoming smooth afterwards, 32–90 × 20–70 mm, dull red to pinkish white (8B3–8A2), transverse section of an arm shows 3–4 tubes subglobose, elongated to piriform. *Pseudostipe* absent. *Gleba* mucilaginous, in all inner part of arms, olive brown (KW 4F4), with an unpleasant smell. *Volva* 50–140 × 10–40 mm, greyish white (12A1–12B1 KW), with thick rhizomorph, greyish white (12A1–12B1 KW). *Basidiospores* cylindrical, 4.6–5.6 × 1.9–2.7 μm (5.2 ± 0.4 × 2.3 ± 0.3 μm; Qm = 2.29; n = 30 spores), wall ≤ 0.7 μm, smooth, hyaline in KOH. Arms exhibiting subglobose to globose and pyriform cells, 19.5–45.6 × 13–33.5 μm, wall ≤ 2.2 μm diam, hyaline. *Volva* composed of filamentous hyphae, 2.7–5.2 μm diam, wall ≤ 1.1 μm diam. *Rhizomorph* composed of filamentous hyphae, 3.2–4.7 μm diam, wall ≤ 0.9 μm diam.

*Typus.* BRAZIL, Rio Grande do Norte, Natal, Centro de Biociências, on soil with litter, 5 Apr. 2017, G.S. Medeiros (holotype UFRN-Fungos 2948, isotype UFRN-Fungos 2947, paratype UFRN-Fungos 2946, ITS and LSU sequences GenBank MH107232 and MH107235, MycoBank MB824737).

*Notes* — *Clathrus natalensis* was found in a remnant of Atlantic rainforest at the Universidade Federal do Rio Grande do Norte (UFRN) and is characterised by robust *basidiomata*, a pale red colouration, rugose arms at the beginning of development, becoming smooth afterwards, with the presence of 3–4

tubes in transverse section. This species presents similarities with *Clathrus cristatus* with the colour of the arms and mesh arrangement, but that presents *basidiomata* with crests along the arm edges (Fazolino et al. 2010), a characteristic absent in *C. natalensis*. In a BLASTn search, the ITS sequence obtained in this study has 94 % similarity to *Clathrus ruber* (GenBank GQ981501). However, *C. ruber* can easily be distinguished by the bright red colour, smaller meshes, and the immature *basidiome* marked by reticulations (Dring 1980). In the phylogenetic analysis, *C. natalensis* does not group with any species available on GenBank; in fact, they are clearly morphologically different. *Clathrus columnatus* and *C. archeri* show distinct receptacle arrangements, columnar in the first, and united arms below with pointed tips initially attached in the latter (Bosc 1811, Dring 1980); *C. crysomycelinus* and *C. delicatus* have white *basidiomata*, the first differs by a *glebifer* attached at the junction of the arms, and the second by a smaller receptacle (up to 25 mm high × 15 mm wide) and deep grooves in the outer face of the arms (Möller 1895, Dring 1980) – characteristics absent in *C. natalensis*. Thus, both morphological characters and the phylogenetic analysis separate *C. natalensis* from the already known species.



*Colour illustrations.* Brazil, Universidade Federal do Rio Grande do Norte, Centro de Biociências, locality where the type species was collected; *basidiomata*, transverse section of an arm showing the tubes, subglobose to globose and pyriform cells on arm, smooth spores, and filamentous hyphae in the rhizomorph. Scale bars = 20 mm (*basidiomata*), 2 mm (tubes), 10 μm (cells on arm, spores and rhizomorph hyphae). All morphology photos from the holotype UFRN-Fungos 2948.

Phylogenetic tree obtained with MrBayes v. 3.1.2. (Huelsenbeck & Ronquist 2001) using ITS, nuc-LSU and *atp6* (MK035869), under GTR+G (ITS/nucLSU) and HKY+G models (*atp6*), for 20 M generations. The type specimen is marked with a rectangle. Posterior probability values are indicated on the branches. TreeBASE submission ID 22520.

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*Colletotrichum arboricola*



Fungal Planet 837 – 14 December 2018

***Colletotrichum arboricola* M. Zapata, M.A. Palma & Piont., sp. nov.**

*Etymology.* The epithet refers to being a tree inhabitant.

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

*Sexual morph on Anthriscus stem* (microscopic preparations in 60 % lactic acid, with 50 measurements per structure). *Ascomata* globose to pyriforme, glabrous to slightly pilose, medium brown to uniformly darker. *Peridium* 8–13 µm thick, composed of brown flattened angular cells, 6–14 µm diam. *Ascogenous hyphae* hyaline, smooth-walled, delicate. *Interascal tissue* composed of fine paraphyses with scarce septa, more apparent in immature perithecia, arranged in irregular masses of hyaline filament with round tips, 35–85 × 1–2 µm. *Asci* cylindrical, unitunicate, 8-spored, 67–86 × 8–13 µm. *Ascospores* uni- to biserial, aseptate, hyaline, smooth-walled, with both ends round, sometime slightly curved, (12–)13–16(–17) × (3.5–)4–5.3(–6) µm, mean ± SD 14.3 ± 1.1 × 4.4 ± 0.5, L/W ratio 3.2.

*Asexual morph on SNA. Vegetative hyphae* 1.5–7 µm diam, hyaline to pale brown, smooth-walled, septate, branched. *Clamydospores* not observed. *Setae* not observed or rare. *Conidiomata* absent, conidiophores formed directly from vegetative hyphae, simple or septate and frequently branched, 14–41 µm long. *Conidiogenous cells* hyaline, smooth-walled cylindrical to ampulliform, sometimes integrated (not separated from fertile hyphae by a septum), polyphialides rarely observed, phialides measuring 10–22 × 1.8–3.3 µm, opening 1–1.5 µm diam, collarette not visible or ≤ 0.3 µm long, periclinal thickening not observed or rare. *Conidia* hyaline, smooth-walled, aseptate, mainly straight, sometimes slightly constricted in the middle, cylindrical, with one end rounded and the other slightly acute to truncate with cytoplasm little granular, (16.2–)17.1–20(–23.3) × (4.8–)5–5.6(–5.9) µm, mean ± SD 18.6 ± 1.4 × 5.4 ± 0.2 µm, L/W ratio = 3.5. *Appressoria* single, solitary, brown, smooth-walled, clavate to elliptical, the edge entirely or slightly undulated, (6.9–)7.6–12.4(–16.9) × (3–)4.1–6.3(–6.9) µm, mean ± SD 9.6 ± 2.1 × 5.1 ± 0.9 µm, L/W ratio = 2 (more abundant in oat meal agar).

*Asexual morph on Anthriscus stem. Conidiomata* absent. *Setae* not observed. *Conidiophores* formed directly on hyphae, abundant, hyaline, smooth-walled, sometimes septate, branched, to 35 µm long. *Conidiogenous cell* hyaline, smooth-walled, cylindrical to clavate 9–16.5 × 2–4 µm, opening 1–1.5 µm, collarette ≤ 0.5 µm long or not visible, periclinal thickening not observed or rare. *Conidia* hyaline, smooth-walled, aseptate (sometimes with a septum before germination), straight to slightly curved, cylindrical, with one end round and other end sometimes slightly acute, (15.7–)16.7–19.2(–20.3) × (4.4–)4.9–5.3(–5.6) µm, mean ± SD 17.9 ± 1 × 5.1 ± 0.2 µm, L/W ratio = 3.5.

*Culture characteristics* — (near UV light with a 12 h photoperiod, 20 °C after 10 d): Colonies on SNA flat with entire margin, hyaline to pale olivaceous grey, with low white aerial

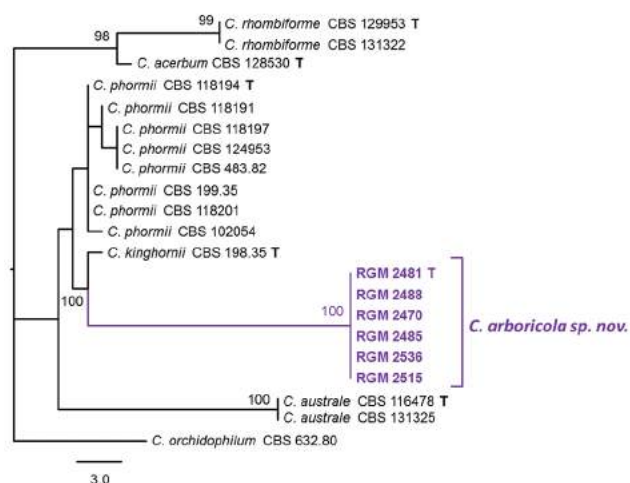
*Colour illustrations.* *Fuchsia magellanica* growing in natural habitats of Chile (courtesy Fernan Silva 2017); asci, ascospores and conidiophores on *Anthriscus* stem (in lactophenol-cotton-blue), appressoria and conidia. Scale bars = 10 µm.

mycelium, filter paper and *Anthriscus* stem partly covered with grey fruiting bodies (ascmata), reaching 58.8 ± 1.4 mm diam. Colonies on OA flat with entire margin, with felty or short floccose olivaceous grey aerial mycelium, reaching 65.6 ± 1 mm diam. *Conidia* in mass salmon.

*Typus.* CHILE, Los Ángeles, on leaves of *Fuchsia magellanica* (*Onagraceae*), 11 July 2012, J. Jure (holotype RGM 2481, culture ex-type SAG 53350-12 = CBS 144795; ITS, LSU, *GAPDH*, *ACT* and *TUB2* sequences GenBank MH817944, MK014743, MH817950, MH817956 and MH817962, MycoBank MB827627, TreeBASE Submission ID 23265).

For additional material examined, see MycoBank.

*Notes* — *Colletotrichum arboricola* was isolated for the first time on leaves of *Fuchsia magellanica*, but its presence has since been observed in different arboreal hosts in the central area of Chile. A phylogenetic analysis based on sequence data from four loci (ITS, *GAPDH*, *ACT* and *TUB2*) places the fungus in clade 5 of the *Colletotrichum acutatum* complex (Damm et al. 2012). *Colletotrichum arboricola* is separated from other species by *GAPDH* and *ACT*, with *GAPDH* performing best as a diagnostic sequence. The closest matches in a BLASTn searches with the *GAPDH* sequence were *C. phormii* CBS 118194 (GenBank JQ948777; Identities = 245/252 (97 %), no gaps), *C. acerbum* CBS 128530 (GenBank JQ948790; Identities = 242/252 (96 %), no gaps) and *C. johnstonii* CBS 128532 (GenBank JQ948775; Identities = 241/252 (96 %), no gaps). Due to size and shape overlapping of conidia, appressoria and ascospores with others members of the complex, *C. arboricola* is not reliably distinguishable using morphological characteristics.



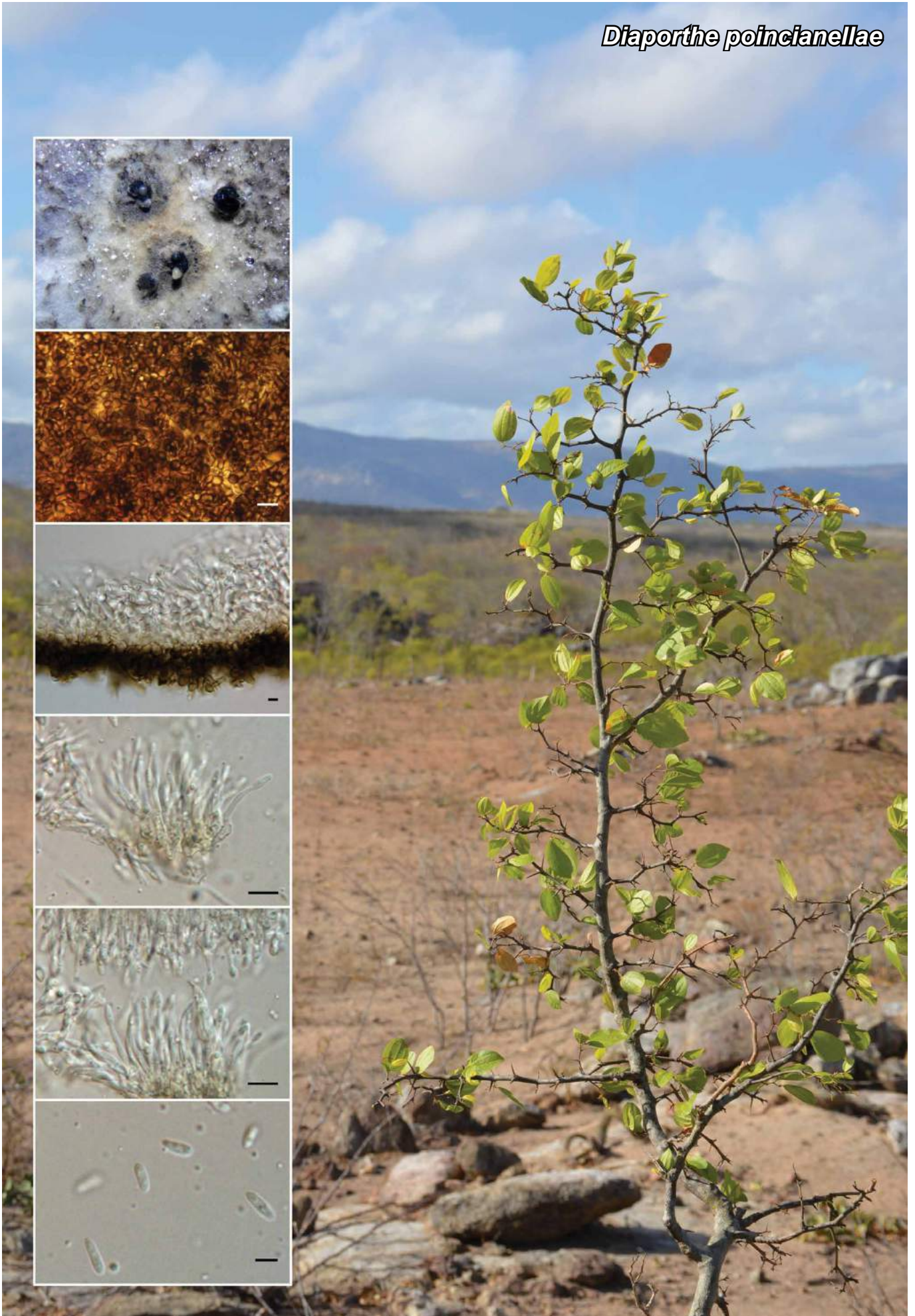
One of the two equally most parsimonious trees (67 steps, CI = 0.896, HI = 0.104, RI = 0.957) obtained from the multilocus phylogenetic analysis (ITS-*GAPDH*-*ACT*-*TUB2*) for selected *Colletotrichum* species belonging to the *C. acutatum* complex. The analysis was conducted with PAUP v. 4.0b10 (Swofford 2003). DNA sequences were aligned using MAFFT v. 7.0 employing the E-INS-i strategy. Bootstrap support values ≥ 75 % are shown above nodes (1 000 replicates). The tree was rooted with *Colletotrichum orchidophilum*. T = ex-type.

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*Diaporthe poincianellae*



Fungal Planet 838 – 14 December 2018

***Diaporthe poincianellae*** T.G.L. Oliveira, O.M.C. Magalhães & J.D.P. Bezerra, *sp. nov.*

*Etymology.* Name refers to *Poincianella*, the host plant genus from which it was isolated.

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

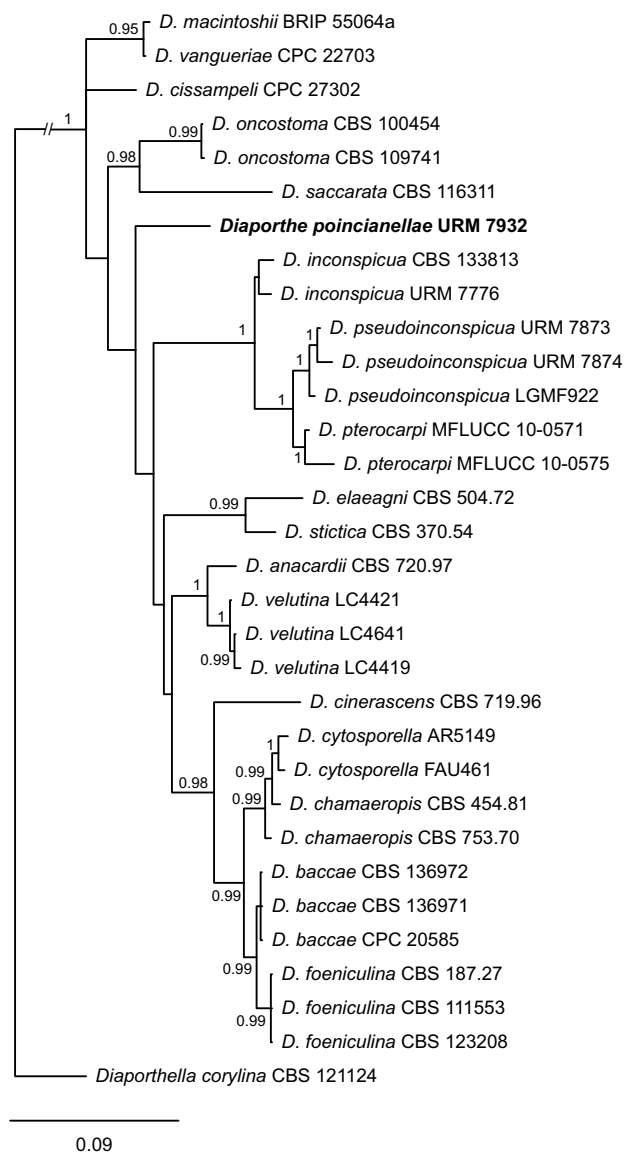
*Conidiomata* pycnidial in culture, globose to subglobose with thin wall, solitary or aggregated, dark brown to black, (212–)265–350 × (180–)265–318 µm, with cream to yellowish conidial drops exuding from the ostioles. *Conidiogenous cells* phialidic, hyaline, occasionally branched, straight to sinuous, slightly tapering towards the apex and slightly curved, 10.5–12.5 × 2–2.2 µm. *Alpha conidia* aseptate, hyaline, smooth, guttulate, fusoid to ellipsoidal, slightly tapered towards the rounded end, truncated base, 5.5–7.5(–8.5) × 3–3.5 µm. *Beta conidia* not observed. *Sexual morph* not observed.

*Culture characteristics* — On PDA at 25 °C in darkness, 8 cm diam after 15 d, colony initially white greyish, becoming yellowish, fluffy and whitish aerial mycelium. Reverse dark brown to black. Pycnidia forming after 15 d. On MEA at 25 °C in darkness, colony initially white to greyish, becoming yellowish, fluffy and whitish aerial mycelium, with slow growth reaching 5.5 cm diam after 15 d. Reverse dark brown to black with small whitish parts. Pycnidia forming after 15 d.

*Typus.* BRAZIL, Paraíba state, Santa Teresinha, Tamanduá farm (S07°1.524 W037°23.518), as endophyte from branches of *Poincianella pyramidalis* (*Fabaceae*), May 2013, J.D.P. Bezerra (holotype URM 91976, culture ex-type URM 7932, ITS, LSU, *CaM*, *his3*, *tef1-α* and *tub2* sequences GenBank MH989509, MH989513, MH989540, MH989539, MH989538 and MH989537, MycoBank MB827977).

*Notes* — The genus *Diaporthe* has been extensively reviewed and several new species have been included in it (Marin-Felix et al. 2019). BLASTn searches using ITS sequence of *Diaporthe poincianellae* demonstrated 99 % similarity to *D. velutina* (GenBank NR\_152470.1), amongst others. The LSU sequence is 99 % similar to *D. phragmitis* (GenBank MH878644.1), amongst others. The *CaM* sequence has 93 % similarity to *D. anacardii* (GenBank KC343266.1). The *his3* sequence is 94 % similarity to *D. inconspicua* and *D. pseudoinconspicua* (e.g., GenBank KC343607.1 and MH122517.1). Based on the *tef1* sequence *D. poincianellae* is 88 % similarity to *D. velutina* (GenBank KX999178.1), and based on *tub2* sequence it is 95 % similar to *D. cissampeli* (GenBank KX228384.1). Morphologically, *D. poincianellae* differs from *D. velutina* based on the size of pycnidia (69–428 µm diam), conidiophores (10–23 × 1–2.5 µm), alpha conidia sometimes clavate (5.5–10 × 2–2.5 µm) and by the presence of beta conidia (Gao et al. 2017). Furthermore, *D. poincianellae* also differs from *D. cissampeli* by the size of its pycnidia (up to 200 µm diam), conidiogenous cells phialidic (10–15 × 1–2 µm) and alpha conidia subcylindrical (7.5–12 × 2–3 µm) (Crous et al. 2016b).

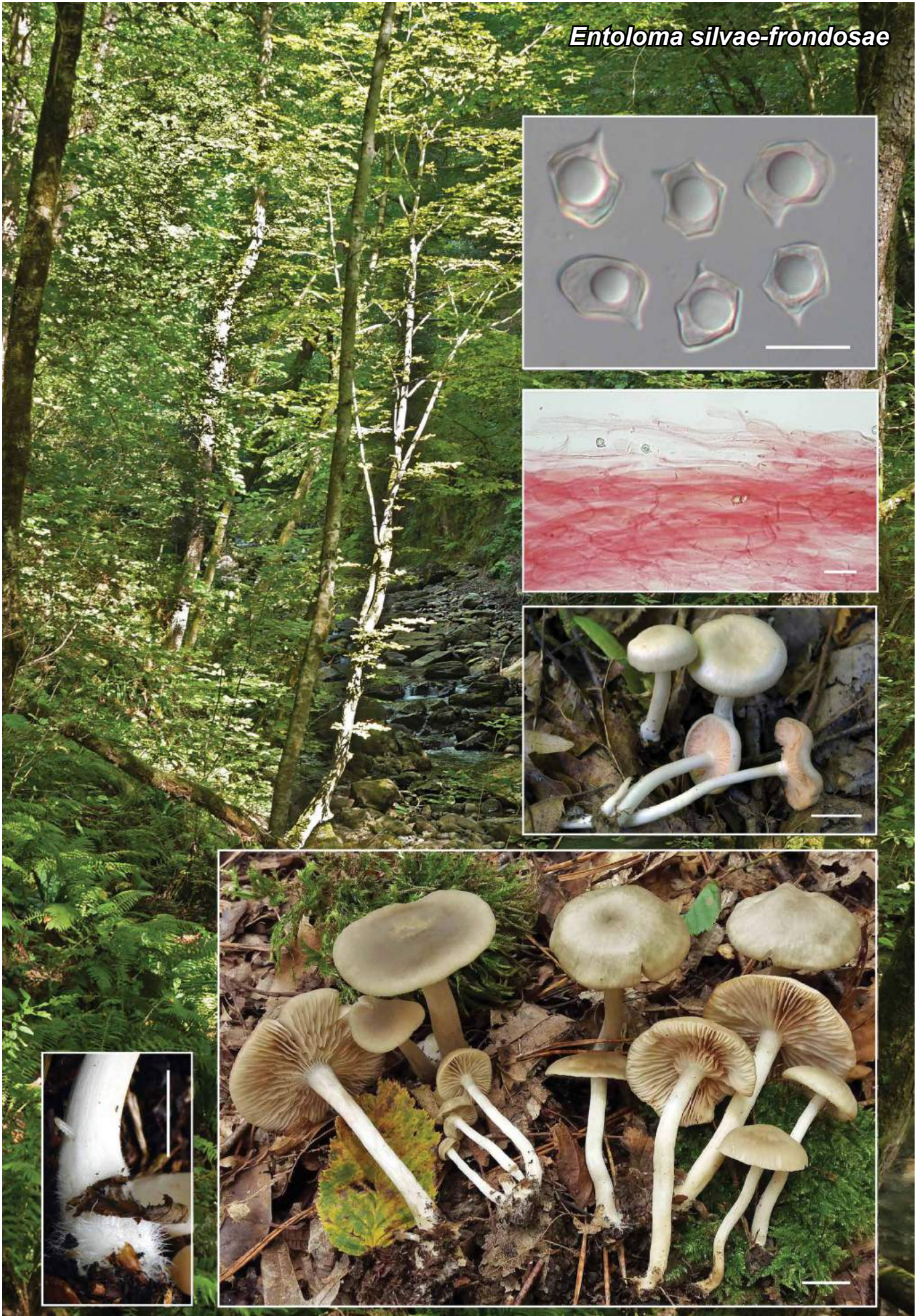
*Colour illustrations.* Brazilian tropical dry forest; conidiomata pycnidial; alpha conidiophores and conidia. Scale bars = 10 µm.



Bayesian inference tree obtained by a phylogenetic analysis of the combined ITS rDNA, *tef1-α* and *tub2* sequences conducted in MrBayes on XSEDE in the CIPRES science gateway (Miller et al. 2010). The substitution model K80+I+G was used for ITS and HKY+G for *tef1-α* and *tub2* alignments. Bayesian posterior probability values are indicated at the nodes. The new species is indicated in bold face. *Diaporthella corylina* (CBS 121124) was used as outgroup.



*Entoloma silvae-frondosae*



Fungal Planet 839 – 14 December 2018

***Entoloma silvae-frondosae*** Dima, O.V. Morozova, Noordel., Brandrud & Krisai, *sp. nov.*

*Etymology.* The epithet refers to the habitat of the species in broad-leaved forests.

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

*Basidiomata* medium-sized, collybioid to tricholomatoid. *Pileus* 11–50 mm diam, initially hemispherical to convex with or without a small acute umbo, becoming applanate with central depression, with involute then straight margin, hygrophanous, translucently striate at margin when expanded, quickly pallescent on drying, when moist initially pale brownish grey to ochraceous grey, becoming paler, whitish grey (3B3–4, 4B3–4, 4C3–4, 5B3–4, 6D5–6, Kornerup & Wanscher 1978), often almost white when dry (4A2), surface dry, smooth, glabrous, sometimes with a few scattered, white hairs at margin (when young and fresh). *Lamellae* moderately distant ( $L = 30–40$ ,  $l = 1–3$ ), adnexed, adnate-emarginate or adnate with small tooth, arcuate-segmentiform, narrow, whitish, pale grey, becoming pinkish or orange-white (5A2, 6A2), with entire, concolorous edge. *Stipe* 30–80 × 3–7 mm, cylindrical or fusiform, base rarely broadened, sometimes tapering towards base, white, greyish pale to watery grey, longitudinally fibrillose striate, base distinctly hairy. *Context* greyish beige, hygrophanous, solid then hollow. *Smell* nitrous or somewhat soap-like, or with a sweetish, perfume-component, somewhat farinaceous. *Spores* (7–)8–9.5(–12) × (5.5–)6–8(–9) µm,  $Q = (1–)1.2–1.3(–1.5)$ , subisodiametrical, with 5–7 angles in side-view. *Basidia* 28–45 × 8–11 µm, 4-spored, narrowly clavate to clavate. *Cheilocystidia* absent. *Hymenophoral trama* regular, made up of inflated elements, 55–130 × 6–13 µm. *Pileipellis* a cutis of parallel, cylindrical hyphae, 3–7 µm wide, with slender clavate terminal elements up to 12 µm wide, these a bit uplifted; subpellis well-differentiated, made up of inflated elements, 40–100 × 8–28 µm. *Pileitrampa* regular, made up of inflated elements, 45–120 × 20–35 µm. *Pigment* intracellular and sometimes with additionally incrustated thin hyphae of pileipellis. *Clamp-connections* abundant in all structures.

*Habit, Habitat & Distribution* — In groups on soil in broad-leaved forests, mainly under *Carpinus*, *Quercus*, *Fagus* or *Tilia*. Known from Austria, Estonia, Hungary, Norway, Russian Caucasus, and Iran (from root samples).

*Typus.* HUNGARY, Vas, Apátistvánfalva, N46.888488° E16.261684°, in *Carpinus betulus*-*Pinus sylvestris* mixed forest, 30 Sept. 2017, B. Dima & L. Albert, DB6568 (holotype L, isotypes BP, O, ITS and LSU sequences GenBank MH790432 and MH792065, MycoBank MB827526).

For additional material examined, see MycoBank.

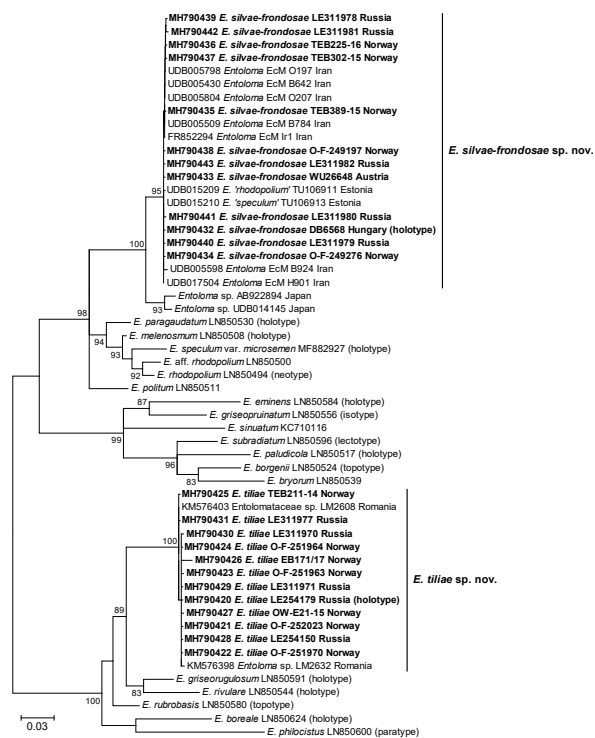
*Notes* — *Entoloma silvae-frondosae* is nested within the *E. rhodopolium* s.str. group, which is characterised by rather pale basidiomata, often developing a slightly clitocyboid habit with depressed pileus centre, with a hygrophanous, often trans-

*Colour illustrations.* Russia, Krasnodar Territory, Adler District, Aibga forestry, valley of the Bezymyannaya River, flood-plain forest; spores, pileipellis (all from holotype DB6568), basidiomata *in situ* (LE311980), hairs at stipe base of the basidiomata from LE311981, basidiomata *in situ* (holotype DB6568). Scale bars = 1 cm (basidiomata), 10 µm (microstructures).

lucently striate pileus, a relatively fragile white stipe, isodiametrical or subisodiametrical spores, and a nitrous (to soap-like) smell. The smell of the species in the *E. rhodopolium*-*E. nidorosum* group is rather variable, and perceived differently by different mycologist, but it is definitely different from the pure and often strong farinaceous smell and taste found in other rhodopolioid *Entoloma* species.

Diagnostic features of *E. silvae-frondosae* are pale basidiomata with distinctly hairy stipe base, and occurrence in temperate broad-leaved forests with *Carpinus*, *Fagus* and *Tilia*. Similar species within the *E. rhodopolium* clade, such as *E. melanosmum* (= *E. nidorosum*, Kokkonen 2015), *E. nidorosum* and *E. politum*, have another ecology, preferring moist to swampy *Betula* and *Salix* forests. In addition, they usually have darker basidiomata. However, *E. rhodopolium* s.str. often grows in similar habitat as *E. silvae-frondosae* like *Corylus* and *Fagus* forests in boreonemoral-temperate regions (Kokkonen 2015, Brandrud et al. 2018). Although *E. rhodopolium* s.str. has on average somewhat darker, larger basidiomata with less distinct hairy stipe base, it might sometimes be difficult to distinguish it morphologically from *E. silvae-frondosae*.

For supplementary information see MycoBank



Phylogenetic tree derived from Maximum Likelihood analysis based on nrITS1-5.8S-ITS2 data. Analysis performed in PhyML v. 3.0 (Guindon et al. 2010) using the non-parametric Shimodaira-Hasegawa version of the approximate likelihood-ratio test (SH-aLRT) and the GTR+I+Γ model of evolution. ML bootstrap support values shown at the nodes (BS > 80 %). Sequences of the new species generated for this study in **bold face**.

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*Entoloma tiliae*



Fungal Planet 840 – 14 December 2018

***Entoloma tiliae* Brandrud, O.V. Morozova, Dima, Bendiksen & Noordel., sp. nov.**

*Etymology.* The epithet refers to the occurrence of the species with *Tilia* spp., in calcareous *Tilia* forests and parks with *Tilia*.

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

*Basidiomata* medium-sized, tricholomatoid. *Pileus* 20–60 mm diam, initially hemispherical-campanulate to convex-umbonate, becoming applanate with or without a low and broad central umbo, with slightly involute then straight margin, typically strongly hygrophanous, in exposed habitats often only seen in dried up state, and then rather pale brownish grey, in shadow rich places in water-soaked state starting off rather dark greyish brown to greyish brown (6F4–6, 7F3–6, Kornerup & Wanscher 1978), sometimes almost black at centre or the entire pileus when young, pallescent when drying up to pale brownish but small or expanded, thin-fleshed basidiomata can be much paler when dry grey (5D4–6, 5E4–6 up to 5C3–4); surface dry, glabrous, smooth or slightly rugose in the centre, initially sometimes finely white-silvery fibrillose-pruinose at centre, not striate when young, only weakly striate at margin when mature. *Lamellae* moderately distant (L = 30–40, I = 3–5), adnexed, adnate-emarginate or adnate with small decurrent tooth, whitish to pale greyish, becoming pinkish or greyish pink (7A2–3), with entire, concolorous edge. *Stipe* 30–70 × 3–11 mm, cylindrical or slightly fusiform, base sometimes tapered, sometimes distinctly clavate-bulbous (up to 1 cm broad) longitudinally fibrillose striate due to whitish fibrils on more or less greyish background, with age or when dry whitish; basal mycelium sparse, white, cottony, sometimes with white rhizomorphs; sometimes with reddish spots at the stipe base (also in context). *Context* greyish in the stipe and under the pileus surface, usually whitish in the inner part of the pileus, when dry whitish in most of context. *Smell* and *taste* farinaceous. *Spores* (8–)9–9.5(–11.5) × (6.5–)7–7.5(–9) µm, Q = (1–)1.2–1.3(–1.4), subspherical, with 6–7 angles in side-view. *Basidia* 38–48 × 11–12.5 µm, 4-spored, narrowly clavate to clavate, clamped. *Cheilocystidia* absent. *Hymenophoral trama* regular, made up of inflated elements, 70–150 × 5–10 µm. *Pileipellis* a cutis with a transition to a trichoderm in the centre made up of cylindrical hyphae, 3–6 µm wide, with cylindrical to irregular terminal elements, sometimes differentiated as clavate to sphaeropedunculate cystidia-like elements up to 15 µm wide and 53 µm long; with brown intracellular pigment, often also with encrusted pigment in some narrow hyphae of pileipellis and subpellis. *Clamp-connections* abundant in all structures.

*Habit, Habitat & Distribution* — In groups on soil in calcareous *Tilia cordata* forests and parks with *Tilia × europaea* (= *T. ×*

*Colour illustrations.* Russia, Saint Petersburg, Botanical Garden of the Komarov Botanical Institute RAS, park with planted *Tilia × europaea*, type locality; spores, hymenium, pileipellis near the pileus margin, pileipellis in the centre with pileocystidia (all from holotype), basidiomata in situ (LE254150), basidiomata in situ (holotype), longitudinal section of the basidioma from holotype. Scale bars = 1 cm (basidiomata), 10 µm (microstructures).

*vulgaris*) and *T. cordata*. Known from SE Norway (Oslofjord area), Romania (environmental/soil sample) and European Russia (Saint Petersburg).

*Typus.* RUSSIA, Saint Petersburg, Botanical Garden of the Komarov Botanical Institute RAS, N59.968889° E30.320833°, under *Tilia × europaea*, 19 Aug. 2011, O. Morozova (holotype LE254179, ITS and LSU sequences GenBank MH790420 and MH792063, MycoBank MB827527), as *E. gerriae* in Morozova et al. (2014).

For additional material examined, see MycoBank.

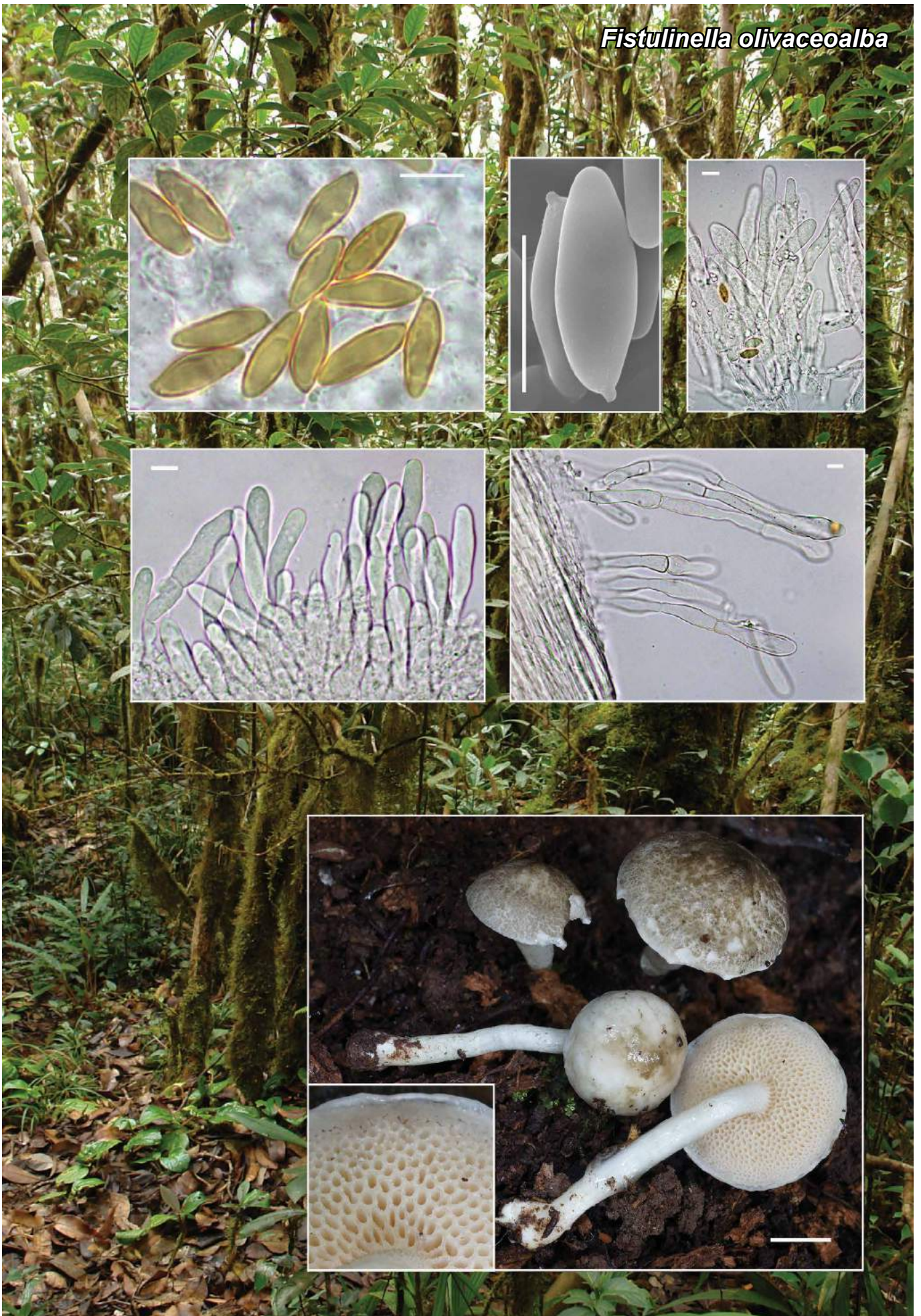
*Notes* — *Entoloma tiliae* is characterised by an usually uniformly dark-coloured pileus, longitudinally fibrillose striate rather rigid greyish stipe, isodiametrical or subisodiametrical spores, intracellular and additionally minutely incrusting pigments and a farinaceous smell. The majority of collections also exhibit some reddish spots/stains at bulb base on a few specimens. According to our phylogeny, the species belongs to a well-supported clade including, e.g., *E. rubrobasis* and *E. griseorugulosum* (Brandrud et al. 2018). In our phylogram, the species comes out as a sister to *E. griseorugulosum* and *E. rivulare*. *Entoloma griseorugulosum* has a resembling morphology and ecology, but it is distinguished on the rugulose pileus surface and habitat in the *Quercus* and *Castanea* forests. Furthermore, reddish stains at the base of the stipe is never noted on *E. griseorugulosum*. The recently described *E. rivulare* (Kokkonen 2015) is a small, boreal species, associated with wet habitats with *Alnus* or *Populus*. *Entoloma rubrobasis* (also demonstrating reddish tinge in the stipe base) and *E. boreale* are so far found only in Fennoscandian boreal coniferous forests, probably associated mainly with *Betula* and *Picea*, respectively (Kokkonen 2015, Brandrud et al. 2018).

*Entoloma griseoluridum* is another deciduous forest species described with somewhat similar features, but we have not been able to sequence the type of this species. According to the protologue (Kühner in Kühner & Romagnesi 1954), *E. griseoluridum*, however, lacks incrusting pigment on the narrow hyphae of pileipellis, it is more robust species with purplish red tinge in pileus, has dark lamellae, and it grows in *Quercus*, *Fagus*, *Carpinus* forests. Ludwig (2007) considered *E. griseopruinatum* and *E. griseoluridum* synonymous. *Entoloma gerriae*, also a very dark species from a similar habitat, differs by the more slender and tender basidiomata, coarsely incrusting and very dark intracellular pigment, and its holotype sequence nests in a distinct, rather distant clade. Some specimens of *Entoloma tiliae* previously were erroneously interpreted as *Entoloma griseoluridum* (e.g., in Zhukova et al. 2017), another deciduous forest species described with somewhat similar features. Unfortunately, we have not been able to sequence the type of this species.

See tree on Fungal Planet 839.

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*Fistulinella olivaceoalba*



Fungal Planet 841 – 14 December 2018

***Fistulinella olivaceoalba*** T.H.G. Pham, Y.C. Li & O.V. Morozova, *sp. nov.*

*Etymology.* The epithet refers to the white and olivaceous colours of the basidiomata.

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

*Basidiomata* small to medium sized, boletoid. *Pileus* 15–50 mm diam, hemispherical to convex or subapplanate; with dark olivaceous grey (4D3–4, 4E3–5, 5D3–5E3, Kornerup & Wanscher 1978), greyish beige (4C3–4) to dark green, greyish green or olive green (28E8, 28C3–5, 30E7–8) scales and flakes over white background, becoming when mature grass green to yellowish green (30E7, 29B5–6), embedded in the gelatinous matter, more closely spaced in centre; slimy to viscid, in wet condition; margin almost lacking scales, white, overhanging the hymenophore, entire, slightly inrolled when young. *Hymenophore* tubular, adnate-emarginate to shortly decurrent with tooth to the stipe, 3–8 mm thick, whitish to creme (4A1–3), unchanging in colour when bruised, pinkish from spores in maturity; pores rounded to angular, 1–2/mm, with fringed edge; tubes concolorous with the hymenophore surface. *Spore print* brownish pink. *Stipe* 40–90 × 3–7 mm, cylindrical or slightly broader in the basal part, white, sparsely covered with dotted or granular scales (especially in the upper part) on white background, sometimes yellowish near the base, slimy to viscid. *Context* white, unchanging. *Smell* spicy, *taste* mild or sometimes bitter. *Basidiospores* (11–)13.5–14(–16.5) × (4–)4.5–5(–5.5) µm, Q = (2.5–)2.8(–3.3), fusoid, subfusoid and inequilateral in side view with weak suprahilar depression, narrowly oblong to subfusoid in ventral view, yellowish to brownish yellow in KOH, weakly dextrinoid, smooth. *Basidia* 22–37 × 8–11 µm, 4-spored, sometimes 2-spored, clavate. *Cheilocystidia* 55–130 × 8–18 µm, forming a sterile edge, septate, consist of 2–3 cells, cylindrical with broadened and sometimes rostrate terminal cells 25–41 × 5–9 µm, thin-walled. *Pleurocystidia* 35–75 × 5–10 µm, cylindrical, fusiform, subfusoid to narrowly lageniform, or subfusoid-mucronate to ventricose-mucronate, thin-walled, sparse. *Hymenophoral trama* divergent. *Pileipellis* an ixotrichoderm, made up of yellowish to brownish, cylindrical gelatinous interwoven hyphae 2.5–4 µm wide with narrowly clavate or fusiform terminal cells, 26–80 × 5–10 µm, pigment incrusting and additionally pale intracellular. *Pileal trama* composed of interwoven hyphae 3.5–5.5 µm wide. *Stipitipellis* a cutis of hyaline parallel hyphae, 2–5 µm wide. *Caulocystidia* 68–130 × 11–16 µm, as cylindrical, septate hairs with clavate or sometimes rostrate terminal cells. *Clamp connections* absent.

*Habit, Habitat & Distribution* — In groups on soil in tropical lowland and montane evergreen broadleaf forest. Known from Vietnam, China and Japan.

*Colour illustrations.* Vietnam, Lam Dong Prov., Lac Duong Dist., Bidoup-Nui Ba National Park, Hon Giao Mt, upper montane mossy evergreen broadleaf forest, type locality; spores, SEM photos of spores, cheilocystidia, elements of pileipellis, caulocystidia, basidiomata in situ. Scale bars = 1 cm (basidiomata), 10 µm (microstructures).

*Typus.* VIETNAM, Lam Dong Prov., Lac Duong Dist., Bidoup-Nui Ba National Park, Hon Giao Ranger Station, path to Hon Giao Mt, N12.192222° E108.711111°, 1850 m alt., upper montane mossy evergreen broadleaf forest, on soil and on the base of tree, 26 May 2014, O. Morozova (holotype, LE312004, *tef1α*, ITS and LSU sequences GenBank MH733592, MH718344 and MH718396, MycoBank MB827509).

*Additional specimens examined.* CHINA, Fujian Prov., Sanming City, Sanming Nature Reserve of *Castanopsis kawakamii*, 260 m alt., 26 Aug. 2007, Y.C. Li 1022, HKAS 53367, *tef1α* sequence GenBank KF112304; Hunan Prov., Yizhang County, Mangshan, 4 Sept. 2007, 880 m alt., Y.C. Li 1087, HKAS 53432, *tef1α* and LSU sequences GenBank MH746438 and MH745969; Hainan Prov. Wuzhishan City, Wuzhushan National Nature Reserve, 2 Aug. 2009, 950 m, N.K. Zeng 416, FHMU 202, *tef1α* sequence GenBank MH746439.

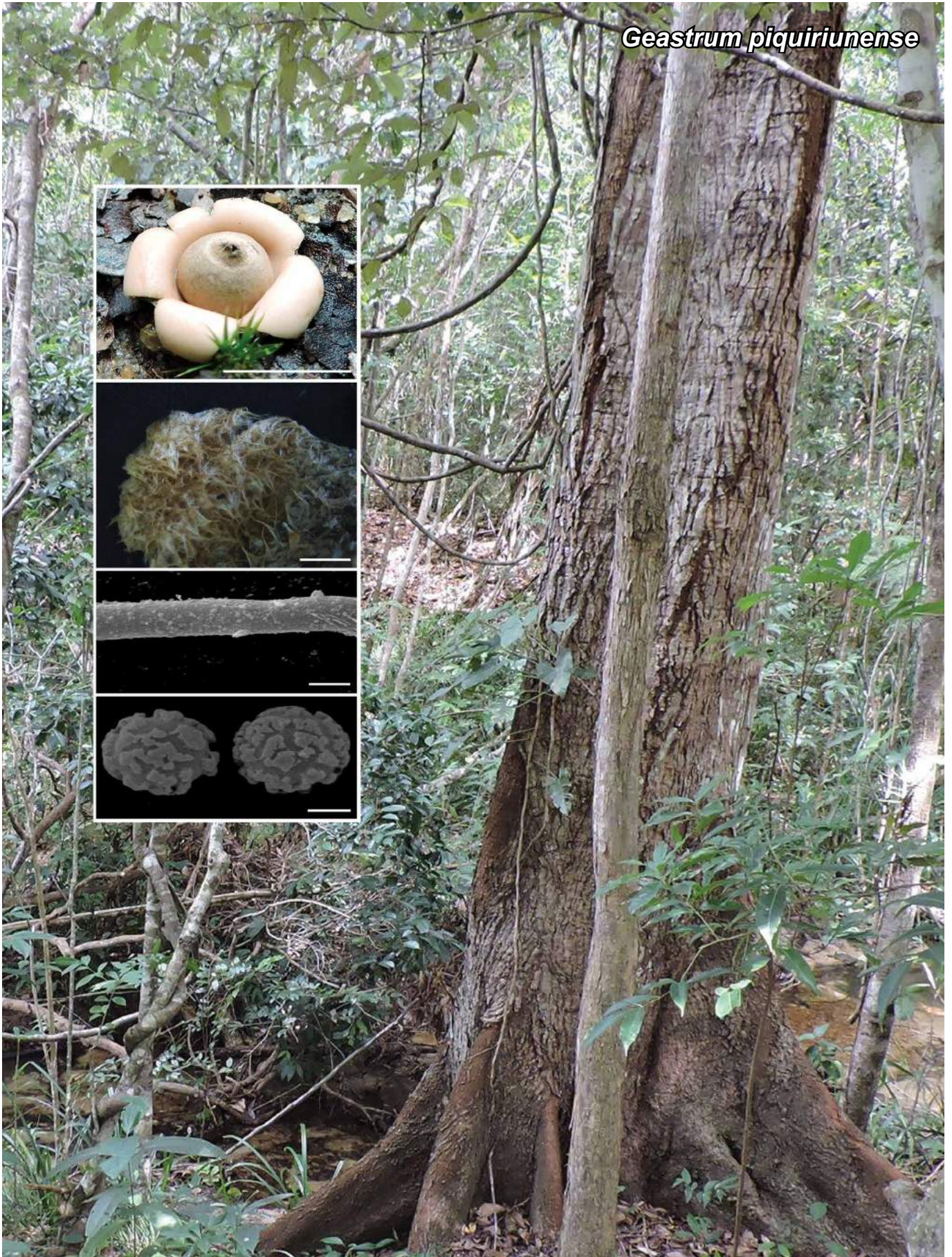
*Notes* — The genus *Fistulinella* was originally described based on a species from Cameroon (Hennings 1901). It is characterised by the whitish to pink tubular hymenophore, the pinkish to brownish pink spore print, the smooth, elongate to fusiform, more or less dextrinoid basidiospores, and the presence of gelatinised structures in the pilei- and stipitipellis (Wu et al. 2014). *Fistulinella olivaceoalba* fits these characteristics rather well. It is recognised by the small slimy basidiomata with distinct greenish or olivaceous colours in the pileus and pinkish hymenophore. Microscopically long cylindrical septate cheilo- and caulocystidia, as well as fusiform pleurocystidia are also characteristic. Based on these features it is close to *F. cinereoalba* (Fulgenzi et al. 2010), which, however, lacks greenish colours in basidiomata and grows in South America. In GenBank this species is represented by the ITS sequence, which is significantly different from that of *F. olivaceoalba*.

There are no sequences of the type species, *Fistulinella staudtii*, available. But according to a 3-gene (*tef1α*, *rpb2*, LSU) phylogeny (Wu et al. 2014), a specimen from China (HKAS 53367) is grouping together with *Fistulinella prunicolor*, and belongs to the subfamily *Austroboletoidae*. However, they are rather distant – p-distance = 12.6 % difference of *tef1α* sequences. The genus *Fistulinella* appears to be polyphyletic and needs additional examination.

A BLASTn search of the ITS sequence of LE312004 in GenBank shows 99–100 % similarity with sequences obtained in the course of environment studies in Japan (e.g., GenBank LC315825 – ectomycorrhiza of *Pinus amamiana*, GenBank AB807905 – ectomycorrhiza of *Quercus*, and also GenBank AB973727 and AB509575).

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*Geastrum piquiriunense*



Fungal Planet 842 – 14 December 2018

***Geastrum piquiriunense*** Accioly, A.A. Lima, J.O. Sousa, M.P. Martín & Baseia, *sp. nov.*

*Etymology.* Name refers to 'Piquiri-Una' environmental preservation area in Rio Grande do Norte State, Brazil, where the type specimen was collected, around a community at the margins of Catu River. In Tupi-Guarani indigenous language, *piquiri* means 'river with little fishes'; *una* means black, dark.

Classification — *Geastraceae*, *Geastrales*, *Agaricomycetes*.

*Immature basidiomata* epigeous, orange-yellow ( $N_{10}Y_{80}M_{30}$ ; Küppers 2002), subglobose, 3 mm high  $\times$  3 mm wide, rounded apex, surface not encrusted, hirsute, short hairs (< 0.5 mm high), presence of subicular base with rhizomorphs (up to 15 mm long), encrusted with debris. *Expanded basidiomata* saccate, 3.5–6 mm high (including peristome)  $\times$  10–18 mm wide. *Rhizomorphs* composed of up to 1  $\mu$ m wide hyaline hyphae, covered by bipyramidal prism crystals (3.7–6.3  $\times$  1.3–1.5  $\mu$ m), not grouped to grouped, or in rose-shaped aggregates 3.8–11.4  $\times$  3.6–11.4  $\mu$ m. *Exoperidium* splitting into 5–6 revolute, and non-hygroscopic rays. *Mycelial layer* orange yellow ( $N_{10}Y_{80}M_{40}$ ), persistent, surface not encrusted, hirsute, composed by small mycelial tufts (0.3–0.4 mm), densely organized, orange yellow ( $N_{10}Y_{80}M_{40}$ ), formed by yellowish hyphae in 5 % KOH, not branched, 1.8–3.7  $\mu$ m wide, lumen evident, with sinuous and thin walls (< 1  $\mu$ m thick), surface not encrusted. *Fibrous layer* white to yellowish ( $N_{00}Y_{00}M_{00}$  to  $N_{00}Y_{10}M_{00}$ ), papery, composed of hyaline hyphae, 1.5–2.8  $\mu$ m wide, with sinuous and thin walls (< 1  $\mu$ m), not encrusted, lumen non-evident. *Pseudoparenchymatous layer* greyish brown ( $N_{40}Y_{50}M_{40}$ ), persistent, formed by hyaline, subglobose, oval to elongated sphaerocysts, 21.3–60.8  $\mu$ m high  $\times$  15.8–29.7  $\mu$ m wide, thin-walled (< 1  $\mu$ m thick). *Endoperidium* greyish brown ( $N_{60}Y_{60}M_{40}$ ), globose to subglobose, 2–5 mm high (including peristome)  $\times$  3–7 mm wide, sessile, glabrous. *Peristome* finely fibrillose, delimited by a yellowish pale brown ( $N_{10}Y_{20}M_{10}$ ) annulum, lighter than endoperidium, mammiform (< 1 mm high), 1.9–2.3 mm wide. *Gleba* powdery, darkened grey ( $N_{99}Y_{00}M_{00}$ ). *Eucapillitium* brownish, 2.9–5.6  $\mu$ m wide, not branched, surface encrusted, verrucose, lumen non-evident, tapering towards the end, thin walls (< 1  $\mu$ m thick). *Basidiospores* subglobose, 4.7–6.3  $\mu$ m diam (av. = 5.5  $\pm$  0.4  $\times$  5.3  $\pm$  0.4  $\mu$ m,  $Q_m = 1.03$ ,  $n = 30$ ), brownish in 5 % KOH, slightly flattened, conspicuous ornamentation at light microscopy, composed of confluent warts (0.2–0.5  $\mu$ m high) with truncate apex, and irregularly distributed under SEM.

*Habitat, Habit & Distribution* — Specimens exhibited solitary to gregarious habit, on soil covered by leaf litter, in a clearing area. The type location presents Ombrophilous Dense Forest phytophysiology.

*Colour illustrations.* Brazil, Rio Grande do Norte, Área de Preservação Ambiental Piquiri-Una, where the specimens were collected; mature basidioma *in situ*, mycelial layer, capillitium under SEM, basidiospores under. Scale bars = 5 mm (basidioma), 1 mm (mycelial layer), 2  $\mu$ m (capillitium and basidiospores). All photos from UFRN-Fungos 2892.

*Typus.* BRAZIL, Rio Grande do Norte, Goianinha, Área de Preservação Ambiental Piquiri-Una, Catú trail, alt. 64 m, S06°21'22.52" W35°12'57.86", on soil covered by leaf litter, 6 June 2016, A.A. Lima & D.O. Andrade (holotype UFRN-Fungos 2892, ITS and LSU sequences GenBank MH260269 and MH260270, MycoBank MB825194).

*Additional species examined.* ***Geastrum pusillipilosum***, BRAZIL, Paraíba, Mamanguape, REBIO Guaribas, SEMA II, 26 June 2014, J.O. Sousa JM100 (holotype UFRN-Fungos 2315, ITS and LSU sequences GenBank KX761175 and KX761176).

*Notes* — *Geastrum piquiriunense* is mainly characterised by its small basidiomata (up to 18 mm wide), hirsute mycelial layer, presence of a subicular base with rhizomorphs, delimited peristome, and subglobose basidiospores 4.7–6.3  $\mu$ m, slightly flattened, with irregular confluent warts with truncate apex. This species is morphologically similar to *G. pusillipilosum* regarding its small size, hirsute mycelial layer, and delimited fibrillose peristome. *Geastrum pusillipilosum* can be recognised by its slightly larger, globose basidiospores (5–6.8  $\mu$ m,  $Q_m = 1.0$ ), covered by longer columnar warts (0.6–2  $\mu$ m high; Crous et al. 2016a), and also by rhizomorphs covered by irregular oblique prism crystals, 2.5–2.8  $\times$  4.8–8.6  $\mu$ m. *Geastrum schweinitzii* and *G. pleosporum* also have small size basidiomata (up to 20 mm wide) and delimited peristome; however, *G. schweinitzii* has well-developed subiculum, caespitose growth, and smaller basidiospores (up to 5  $\mu$ m diam) (Sousa et al. 2014), while *G. pleosporum* is characterised by smooth to subsmooth irregular shaped basidiospores up to 5  $\mu$ m diam (Douanla-Meli et al. 2005). *Geastrum piquiriunense* could be also confused with *G. hirsutum*, but the latter can be distinguished by having longer and strigose mycelial tufts (up to 3 mm long) at its mycelial layer, and quite smaller basidiospores (2.5–3  $\mu$ m wide) (Baseia & Calonge 2006, Silva et al. 2015). In our phylogenetic analysis *G. piquiriunense* grouped tightly with GenBank JN845120 (TENN:061141, MLbs = 99 %, PP = 1, MPbs = 100 %); nonetheless, this sequence is identified as *G. saccatum* both at the online database of University of Tennessee (TENN Herbarium) and the GenBank database, while in Kasuya et al. (2012), the same code (JN845120–TENN:061141) is identified as *G. sessile* (= *G. fimbriatum*, according to Index Fungorum). The hirsute mycelial layer clearly distinguishes *G. piquiriunense* from *G. saccatum* or *G. sessile* (= *fimbriatum*); moreover, these two species have predominantly smooth, sometimes felted or wrinkled mycelial layers (Sunhede 1989). In addition, *G. sessile* has an endoperidium with protruding hyphae and smaller basidiospores (2.7–5.2  $\mu$ m diam) (Leite & Baseia 2007, Alfredo et al. 2016); also *G. saccatum* has smaller basidiospores (3.6–4.5  $\mu$ m diam) (Leite et al. 2011). Thus, our analysis confirms a misidentification of collection TENN:061141, since it is not included in the clades of the sections *Corollina* nor *Fimbriata*; this collection needs to be morphologically reassessed in order to determine if it belongs to *G. piquiriunense*, or even if it is a new species awaiting description.

For supplementary information see MycoBank

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*Ganoderma chocoense*



Fungal Planet 843 – 14 December 2018

***Ganoderma chocoense* J.A. Flores, C.W. Barnes, & Ordoñez, sp. nov.**

*Etymology.* Name refers to the locality where the species was collected.

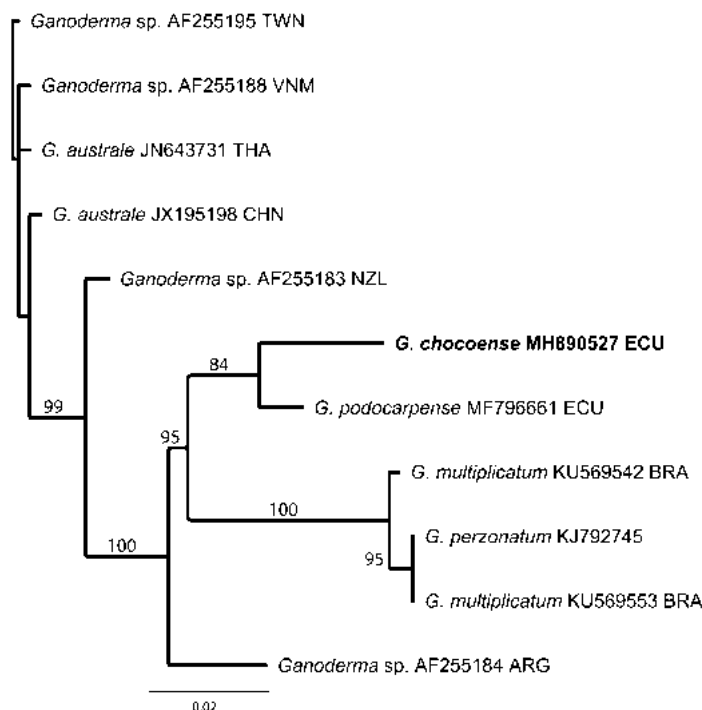
*Classification* — *Polyporaceae*, *Polyporales*, *Agaricomycetes*.

*Basidiomata* perennial, flattened, 5.5 × 3.8 cm, dimidiate with thicker base, woody, hard consistency when dry, pileus glabrous, sulcate, opaque, dark brown, covered with cinnamon coloured basidiospores, distinct cuticle in section of uniform width throughout the basidiomata, margin of light cream colour, context woody, 1.4 cm in width, no resin bands. *Hymenial surface* creamy white when fresh, ochre as it dries, turns darker upon contact, pores round, 6 per mm, thick wall, tubes dark brown, 0.4 cm wide, slightly stratified with white mycelium in the interior of old tubes. *Cutis* trichoderm. *Hyphal system* trimitic, generative hyphae yellowish, 1.5–3 µm wide, thin-walled, clamp connections present, skeletal hyphae brown, abundant, thick-walled to solid, up to 7 µm wide, connective hyphae very thin, hyaline, branched, 1.2 µm wide. *Basidia* not observed. *Basidiospores* double-walled, truncate, yellowish 8.9–11 × 4.7–6.4 µm, Q = 1.7.

*Habit & Habitat* — Solitary, on decomposing tree trunk.

*Typus.* ECUADOR, Esmeraldas province, Chocó Tropical Rainforest, alt. 357 m, July 2012, A. Salazar (holotype QCAM 3123, Fungarium QCAM, ITS-LSU sequence GenBank MH890527, MycoBank MB827824, TreeBASE Submission ID 23292).

*Notes* — Morphologically, the sample belongs to the *G. applanatum* complex (Gottlieb & Wright 1999). The Neotropical Polypores key (Ryvarden 2004) indicates *G. australe* as the closest species. However, there are some morphological discrepancies, such as the shape and uniform thickness of the cuticle across the basidiocarp, the thickness of the tubes, the homogeneous context, lack of resin deposits, and the trimitic hyphal system in *G. chocoense*. Phylogenetically, *G. chocoense* is distinct from all taxa presently known to occur in the genus, with the closest species from the megablast search using the full ITS sequence being *G. podocarpense* (GenBank MF796661; 100 % Query Coverage, Identities = 544/568 (96 %), 11 gaps (1 %)). *Ganoderma podocarpense* was first described as a new species from Ecuador in 2017 (Crous et al. 2017b). Subsequent megablast hits are of *Ganoderma* species from Argentina and Brazil. The ITS phylogenetic tree of the top 10 megablast hits for the *G. chocoense* holotype sequence substantiates that it is a new species.



The phylogenetic tree was constructed using the Maximum Likelihood plugin PHYML in Geneious R9 (<http://www.geneious.com>; Kearse et al. 2012), and the substitution model determined by jModelTest 2.1.10 (Guindon & Gascuel 2003, Darriba et al. 2012) according to the Corrected Akaike Information Criterion (AICc). *Ganoderma* sp. (GenBank AF255195) represents the outgroup. Bootstrap support values > 80 % are given above branches. The phylogenetic position of *G. chocoense* is indicated in **bold**. The species name is followed by the GenBank accession number, and when the country of origin was indicated, the three letter United Nations country code, in order of appearance, is used, namely TWN: Taiwan, VNM: Vietnam, THA: Thailand, CHN: China, NZL: New Zealand, ECU: Ecuador, BRA: Brazil, and ARG: Argentina.

*Colour illustrations.* Ecuador, Chocó Tropical Rainforest; basidiocarps, basidiospores and skeletal hyphae. Scale bars = 10 µm.

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*Geosmithia carolliae*



Fungal Planet 844 – 14 December 2018

***Geosmithia carolliae*** A.O.B. Cunha, A.R. Machado & Souza-Motta, *sp. nov.*

*Etymology.* The name refers to the host from which it was isolated, *Carollia perspicillata*.

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

On MEA, 25 °C, 7 d: *Hyphae* hyaline, smooth, septate, 2–7.5 µm wide. *Conidiophores* hyaline, tall, septate, erect, solitary, often branched, mono- to quaterverticillate, verrucose, borne on hyphae, (23.5–)65–80(–104) × 1–1.5 µm. *Stipe* verrucose, (10.5–)26–49.5(–65) × 1–1.5 µm; branch (rami) verrucose, (10.5–)13–20.5(–26) × 1–1.5 µm. *Metulae* verrucose, (9.5–)10.5–11.5(–12.5) × 2–2.5 µm. *Phialides* verrucose, cylindrical to ellipsoidal, (4–)6.5–8.5 × 1.5–2 µm. *Conidia* hyaline, cylindrical to ellipsoid, smooth-walled, rounded at both ends, 4–5.5 × 2–2.5 µm; conidial chains up to 53 µm long, not persistent.

*Culture characteristics* — Colonies at 25 °C for 7 d. On MEA, the colonies are plane, dense, velutinous, opaque, ranging from rose vinaceous to rose greyish; reverse umber to pale brown; irregular margins, narrow and diffuse, ranging from salmon to white colours; pigmentation and exudate are absent, growing up to 50 mm. On CYA, the colonies are similar to MEA, but are pale vinaceous and the reverse vinaceous brown to dark brown, growing fast up to 70 mm. On CDA, the colonies are irregular, centrally filamentous, yeast-like aspect at the borders, umber to dark brown and margins salmon to white; reverse pale brown to yellowish; slight yellowish pigmentation around the colony, exudate absent, growing up to 20 mm. Colonies at 37 °C for 7 d. On MEA and CYA are similar, planes, dense, velutinous to floccose, opaque, ranging from pale brown to greyish, reverse umber to dark brown; margins, narrow and diffuse, ranging from pale vinaceous to buff, pale brown to pale yellow; pigment and exudate absent, growing up to 0.5 mm. On CDA, the colonies are similar to CDA at 25 °C, but are white to pale cream and the reverse umber to dark brown, growing up to 0.6 mm.

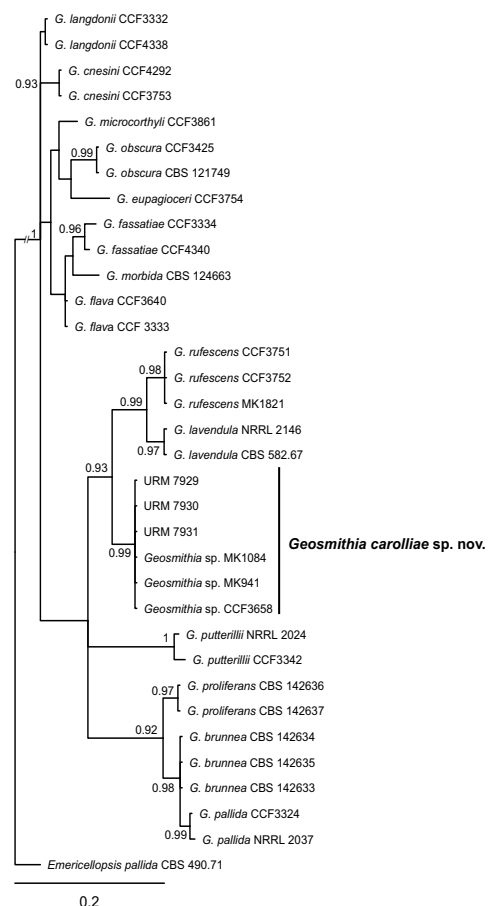
*Typus.* BRAZIL, Pernambuco state, Tupanatinga, Catimbau National Park, Bat cave 'Meu Rei', S08°29'14.1" W37°16'48.8", isolated from the bat wing of *Carollia perspicillata*, 20 Sept. 2017, A.O.B. Cunha & E. Barbier (holotype URM 91977, culture ex-type URM 7929, ITS, LSU and *tub2* sequences GenBank MH989506, MH989510 and MH989534, MycoBank MB827978).

*Additional material examined.* BRAZIL, Pernambuco state, Tupanatinga, Catimbau National Park, Bat cave 'Meu Rei', S08°29'14.1" W37°16'48.8", isolated from the bat wing of *Carollia perspicillata*, 20 Sept. 2017, A.O.B. Cunha & E. Barbier, URM 7930 and URM 7931. URM 7930: ITS, LSU and *tub2* sequences GenBank MH989507, MH989511 and MH989535; URM 7931: ITS, LSU and *tub2* sequences GenBank MH989508, MH989512 and MH989536.

*Notes* — The genus *Geosmithia* was proposed by Pitt (1979) to accommodate *Penicillium lavendulum* and related species. Since its description, 20 species were included in it according to Index Fungorum and MycoBank databases (25 Sept. 2018). BLASTn searches using ITS sequences of *G. carolliae* demonstrated that they are identical to sequences deposited as *Geo-*

*Colour illustrations.* *Carollia perspicillata* during collection in the Catimbau National Park; colony on MEA after 7 d at 25 °C, conidiophores and conidia. Scale bars = 10 µm.

*smithia* sp. living in association with bark beetles in the Mediterranean area (Kolařík et al. 2007). These sequences grouped together with our sequences in the phylogenetic tree, and here they are named as *G. carolliae*. The LSU sequences have high identities (99 %) to sequences from *G. lavendula* (e.g., GenBank MH867927.1, Vu et al. 2019), amongst other. The *tub2* sequences have *G. morbida* (GenBank KF853911.1) as the closest identity (89 %). *Geosmithia carolliae* is phylogenetic related and morphologically similar to *G. lavendula*, but differ from it by culture characteristics (growth on MEA and CYA at 25 °C up to 35 mm and on CYA at 37 °C up to 12 mm), and by the size and ramification of conidiophores (200–400 × 3–3.5 µm), rami (15–25 × 3–3.5 µm), metulae (12–15 × 3–3.5 µm), phialides (10–12 × 2.2–2.5 µm) and conidia (4–5.5 × 2–2.5 µm) (Pitt 1979). Also, *G. carolliae* differs from *G. rufescens* by culture characteristics (growth on MEA at 25 °C up to 30 mm and on CYA up to 22 mm; no growth at 37 °C), and by the size and ramification of conidiophores (30–70 µm), rami (15–30 µm × 2–3 µm), metulae (9–11 × 2–2 µm), phialides (8.5–11.5 × 2–2.5 µm) and conidia (3–5 × 1.5–2.5 µm) (Kolařík & Kirkendall 2010).



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