

Geosmithia xerotolerans



Fungal Planet 845 – 14 December 2018

***Geosmithia xerotolerans* Rodr.-Andrade, Cano & Stchigel, sp. nov.**

Etymology. From Greek ξερός-, dry, and Latin *-tolerans*, tolerance, due to the ability of this fungus to grow on culture media with a low water activity.

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

Mycelium composed of hyaline, septate, funiculose hyphae, 2–3 µm wide. *Conidiophores* borne on vegetative mycelium, determinate, erect, septate, penicillate, bi- to terverticillate, mostly solitary, sometimes funiculose; stipes hyaline, 25–155 × 2–3 µm, septate, smooth-walled to verrucose, asymmetrically branched; primary branch (= rami) cylindrical, 20–40 × 2–3 µm, mostly septate, smooth-walled to verrucose; terminal branch (= metulae) cylindrical, 7–15 × 2 µm, rarely 1-septate, with smooth to verrucose walls, in whorls of 2–3; phialides cylindrical, 8–10 × 1.5–2 µm, abruptly tapering at the apex, with smooth to verrucose walls, in whorls of 2–5. *Conidia* hyaline, aseptate, ellipsoid to ovoid, 3–4 × 1.5–2 µm, rounded at both ends, smooth-walled, disposed in chains of up to 20 conidia. *Sexual morph* not observed.

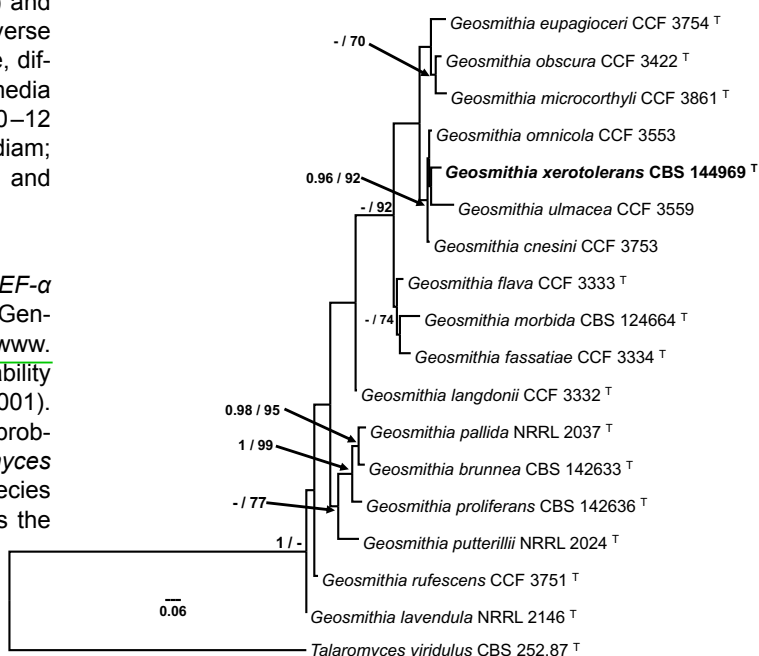
Culture characteristics — *Colonies* on MEA reaching 38–39 mm diam after 2 wk at 25 °C, slightly elevated, powdery, margins irregular, orange white (5A2; Kornerup & Wanscher 1978) at centre and white (5A1) at edge, exudates absent, sporulation abundant; reverse orange (6A6), diffusible pigment absent. Colonies on CYA reaching 49–51 mm diam after 2 wk at 25 °C, slightly elevated, powdery, margins regular, white (4A1) at centre and pale yellow (4A3) at edge, exudates absent, sporulation abundant; reverse reddish orange (7B7) at centre and pale orange (6A5) at edge, diffusible pigment absent. Colonies on CZD 62–63 mm diam after 2 wk at 25 °C, cottony, margins irregular, white (3A1), exudates absent, sporulation abundant; reverse yellowish white (3A2), diffusible pigment absent. Colonies on YES reaching 62–63 mm diam after 2 wk at 25 °C, slightly elevated with radial waves, reddish grey (12B2) and white (4A1), exudates absent, sporulation abundant; reverse reddish brown (9E7) at centre and orange (6A6) at edge, diffusible pigment absent. This fungus grows on culture media with a low water activity (on DG18 after 2 wk at 25 °C, 10–12 mm diam; on G25N in the same conditions, 27–29 mm diam; on MY70S, 39–40 mm diam; and on MEA with 30, 40 and

50 % (glucose 50 % / fructose 50 %), 23–24 mm diam, 18–19 mm diam and 12–13 mm diam, respectively). In these culture media the fungal sporulation is abundant. Minimum, optimal and maximum temperature of growth: 15 °C, 25 °C and 35 °C, respectively.

Typus. SPAIN, Tarragona province, Els Pallaresos, isolated from a darkened wall of a house, 19 Apr. 2018, J. Cano & A.M. Stchigel (holotype CBS H-23734, cultures ex-type FMR 17085 = CBS 144969; *BenA*, *EF1-α*, ITS and LSU sequences GenBank LS998791, LS998792, LS998789 and LS998790; MycoBank MB827825).

Notes — *Geosmithia xerotolerans* was recovered from the surface of a darkened house wall taken in Els Pallaresos, Tarragona province, Spain. The genus *Geosmithia* was erected to accommodate species previously placed in *Penicillium*, with the following differentiable combination of characters: colonies in colours other than greyish blue or greyish green, penicillate and roughened conidiophores, with both phialides and conidia cylindrical (Pitt 1979). Based on a megablast search of NCBI's GenBank nucleotide database, the closest hit using the ITS sequence is the ex-type strain of *Geosmithia cnesini* MK 1820 (GenBank AM947671; Identities = 965/978 (99 %), 1 gap (0 %)); using the LSU sequence it was *Geosmithia microcorthyli* CCF3861 (GenBank MG954241; Identities = 809/815 (99 %), no gaps); using the *EF1-α* sequence, it was *Geosmithia omnnicola* CNR8 (GenBank KR135476; Identities = 238/280 (85 %), 13 gaps (4 %)); and using the *BenA* sequence it matched with *Geosmithia omnnicola* CNR43 (GenBank KP990575; Identities = 429/460 (93 %), 9 gaps (1 %)). Our ITS-*BenA*-*EF1-α* phylogenetic tree corroborated the placement of our isolate as a new species of *Geosmithia*, being phylogenetically close to *Geosmithia omnnicola*.

Maximum likelihood tree obtained from the ITS-*BenA*-*EF1-α* alignment of our isolate and sequences retrieved from GenBank. The tree was built by using RAXML CIPRES (http://www.phylo.org/sub_sections/portal/) and the analysis of probability was run in MrBayes v. 3.2.1 (Huelsenbeck & Ronquist 2001). Bootstrap support values ≥ 70 % and Bayesian posterior probability values ≥ 0.95 are presented at the nodes. *Talaromyces viridulus* CBS 252.87 was used as outgroup. The new species proposed in this study is indicated in **bold**. † represents the ex-type strain of the novel species.



Colour illustrations. Darkened wall in Els Pallaresos, Tarragona province, Spain; colonies growing on different culture media (MEA, CYA, CZD and YES at 25 °C) and conidiophores. Scale bars = 10 µm.

Henningsia resupinata



Fungal Planet 846 – 14 December 2018

***Henningsia resupinata* A.M.S. Soares & Ryvarden, sp. nov.**

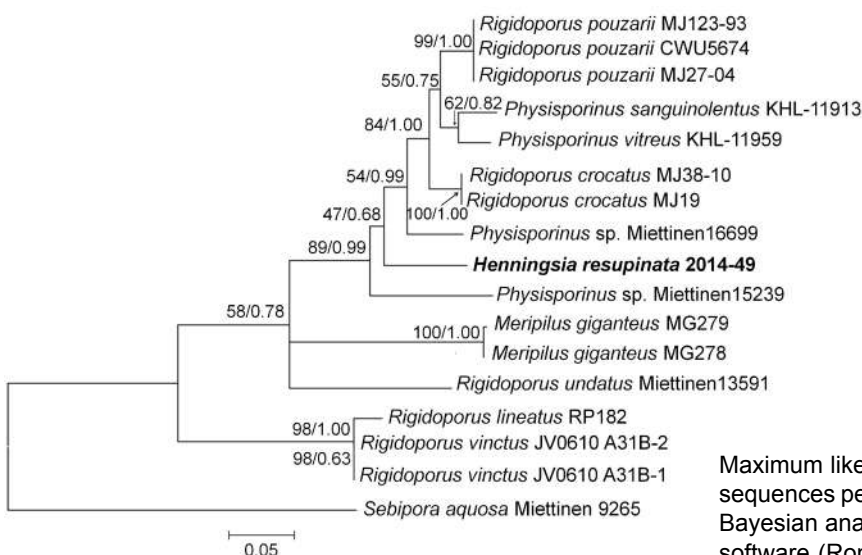
Etymology. (L.) *resupinata*, bent, referring to the shape of the basidiomata.

Classification — *Meripilaceae*, *Polyporales*, *Agaricomycetes*.

Basidiomata annual, resupinate, 2–4 cm wide and long and 1 mm thick, adnate, fleshy and white when fresh (2B) becoming distinct rusty red when bruised after collecting, hard and fragile and black when dry (black 37) (Watling 1969), pores irregular, about 1–2 mm in the sloping substrate, in other parts of the holotype more regular and 4–5 pores per mm, tubes concolorous with the pore surface. Context almost absent, dense and black when dry (37). **Hyphal system** monomitic; generative hyphae with simple septa, hyaline to pale yellow, thin-walled, 3–6 µm wide. **Gloeoplerous hyphae** and **cystidia** absent. **Basidia** not seen. **Basidiospores** 4–5 µm diam, globose to subglobose, smooth, thin-walled, IKI–.

Typus. BRAZIL, Amapá, Porto Grande, Serra da Capivara, on dead wood, 2014, A. Soares 2014-49 (holotype URM, isotype O, ITS and LSU sequences GenBank MG255826, MycoBank MB823555).

Notes — The black basidiomata when dry, the simple septate hyphae and the globose to subglobose basidiospores clearly place this species in *Henningsia* where all species share the same colour and simple septate generative hyphae. *Henningsia resupinata* can be separated from the other species of the genus by the resupinate basidiomata. *Henningsia macrospora* is another species also found in Brazil and also has a black basidioma when dry, but it is separated by the pileate basidiomata with numerous gloeoplerous hyphae in the context and the larger, subglobose to ellipsoid basidiospores (6–7 × 4.5–5 µm) (Gibertoni & Ryvarden 2014). In the phylogenetic tree, *H. resupinata* clustered with low support with *Physisporinus* sp. (47 %/0.68) collected in Indonesia and it is distantly related to *P. sanguinolentus* (KHL_11913) collected in Norway. *Physisporinus sanguinolentus* is similar by the white basidiomata when fresh and becoming bright rusty red when bruised or greyish to blackish on drying. However, the pores in *P. sanguinolentus* are smaller (8–10 per mm) and the basidiospores are larger and ovoid to subglobose (6–7 × 5–6 µm). Besides, *P. sanguinolentus* has fusoid cystidioles (15–27 × 5–6 µm) which are lacking in the new species (Ryvarden & Gilbertson 1994). There is no molecular data regarding *Henningsia*, and, for the time being, the new species will be kept in this genus due its morphological characters. Moreover, *Henningsia* is a Neotropical genus and the type species is from Brazil, while *Physisporinus* occurs mostly in Europe.



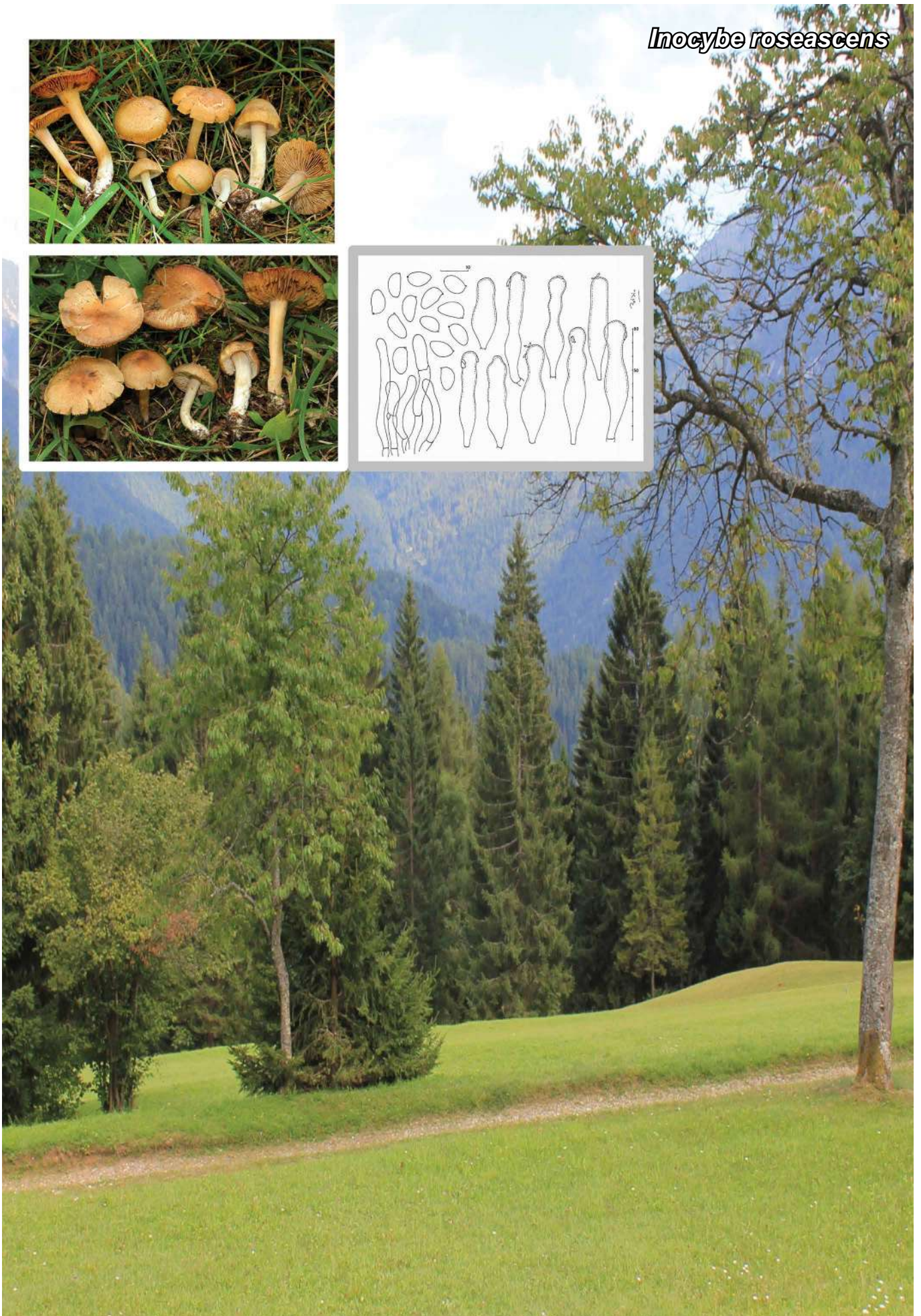
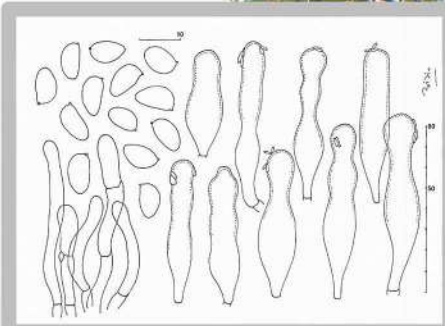
Maximum likelihood phylogenetic tree inferred from ITS+LSU sequences performed with RAxML v. 7.0.4 (Stamatakis 2006). Bayesian analysis (BY) was performed with MrBayes v. 3.2.1 software (Ronquist et al. 2012) for 5 M generations with four Markov chains, and trees sampled every 1000 generations, similar topology was obtained (not shown). Bootstrap support values (1000 replicates) and posterior probabilities (PP) from Bayesian analysis to each node are shown from left to right. The new species described in this study is in **bold face**. *Sebipora aquosa* represents the outgroup. The alignment is deposited in TreeBASE (ID 22819).

Colour illustrations. Environment where the type specimen was collected in Porto Grande, Serra da Capivara, Amapá, Brazil; *Henningsia resupinata* fresh basidiomata (top), dried basidioma, generative hyphae and basidiospores (bottom). Scale bars = 2 cm (basidiomata), 20 µm (generative hyphae), 10 µm (basidiospores).

Adriene M. Soares & Tatiana B. Gibertoni, Departamento de Micologia, Universidade Federal de Pernambuco, Avenida da Engenharia, S/N - Cidade Universitária, Recife, PE, Brazil; e-mail: adriene_soares@yahoo.com.br & tbgibertoni@hotmail.com

Leif Ryvarden, University of Oslo, Department of Botany, P.O. Box 1045, Blindern, N-0316, Oslo, Norway; e-mail: leif.ryvarden@bio.uio.no

Inocybe roseascens



Fungal Planet 847 – 14 December 2018

Inocybe roseascens* Bizio, Bahram, Tedersoo, Orzes & Saitta, sp. nov.Etymology.* Refers to the colour of the pileus and stipe.Classification — *Inocybaceae*, *Agaricales*, *Agaricomycetes*.

Pileus up to 40 mm, widely campanulate, then convex to plane, with central umbo, obtuse and irregular profile, with sulcated-cracked margin. *Cuticle* fibrillose-rimose, slightly chapped-squamulose, more cracked at the centre; colour yellowish to bread crust (Munsell 7.5YR: 8/6, 7/8; 10YR: 7/8; 2.5Y: 7/8), then pinkish, old-pink to orange-fulvous and reddish bronze all over the basidioma (Munsell 2.5YR: 6/8; 5YR: 7/8; 7.5YR: 7/8; 10YR: 7/8). *Cortina* white, observed in early stages. *Lamellae* close, thick, colour very light (Munsell 2.5Y: 8/3-4), then ochraceous, olivaceous (Munsell 2.5Y: 7/6) to rust-concolorous (Munsell 2.5Y: 7/8), white floccose edge, crenulated. *Stipe* 40–50 × 3–7 mm cylindrical, pruinose on the upper part, first whitish to straw coloured (Munsell 2.5Y: 8/3-4), then grey to grey-rose pale, concolorous with pileus; covered with coarse, long, and whitish fibrils. *Flesh* white, firm, red staining absent, *smell* absent. *Basidiospores* (7.5–)8.2–10(–10.7) × (5–)5.3–6.2(–6.6) µm, Q = (1.2–)1.3–1.5(–1.7), smooth, subamygdaliformis, with small soprapicular depression and variable apex, obtuse to subconic and rarely conic-papillate; germinative pore sometimes visible. *Basidia* 35–40 × 9–12 µm, tetrasporic. *Paracystidia* not observed. *Hymenial cystidia* 50–85 × 10–15 µm cylindrical or slightly clavate, clavate-subutriformis, sinuose, subcapitate to capitate, not lageniforme; wall 0.5–1(–2) µm thick, without oxalate crystals calcium or rarely present; NH₃⁻. *Caulocystidia* only in the upper part of the stipe, (1/4), 100 × 10 µm, flexuose, subcylindrical, catenulate.

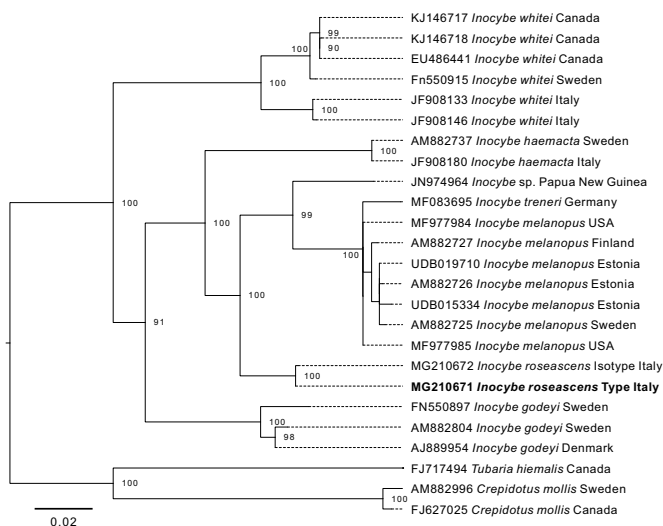
Typus. ITALY, Veneto, Agordo, loc. Campon, N46.30010 E12.05280, 1300 m asl, mixed forest of *Picea abies* and *Corylus avellana*, 2015, *R. Orzes* (holotype MCVE29329, ITS-LSU sequence GenBank MG210671; *ibid.*, 2015, *E. Bizio*, paratype TU124466, ITS-LSU sequence GenBank MG210672, MycoBank MB823058).

Notes — Only two *Inocybe* species with smooth spores, *I. whitei* and *I. godeyi*, have both metuloid cystidia and a reddening surface, as in the new species proposed here. The basidiomata of *I. roseascens* are at first yellow-ochre, which gradually turn reddish, but this is not the case in its odourless flesh. Based on a morpho-chromatic point of view, *I. roseascens* is close to the group of *I. withei*, because of its partially cystidiate stipe and the absence of basal bulb. *Inocybe godeyi* has ochre to orange-fulvous-red, brick-pink or rarely red carmine sporocarps, and it belongs to the supersection *Marginatae* because of its fully cystidiate stipe and marginate basal bulb. Our phylogenetic analysis showed that *I. godeyi* is closer to *I. roseascens* than *I. whitei*. The flesh of *I. godeyi* is white when cut and it quickly

Colour illustrations. Campon, Agordo, Italy, mixed forest of *Picea abies* and *Corylus avellana*; *Inocybe roseascens*, basidiomata in habitat, basidiospores, hymenial cystidia caulocystidioid.

turns to orange-red, concolorous to the external surface (Alessio & Rebaudengo 1980). Because the flesh of *I. roseascens* does not change colour when damaged, and the absence of smell, it cannot be placed in the section *Lactiferae*, and it most likely belongs to the supersection *Cortinatae* (Boursier & Kühner 1928). Species in *Cortinatae* have a cortina at young states, and a stipe that is slightly pruinose at the apex only, or not at all.

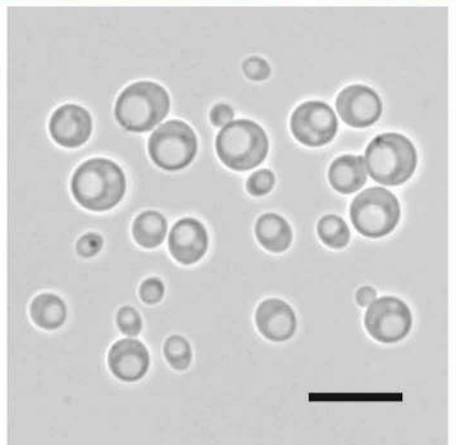
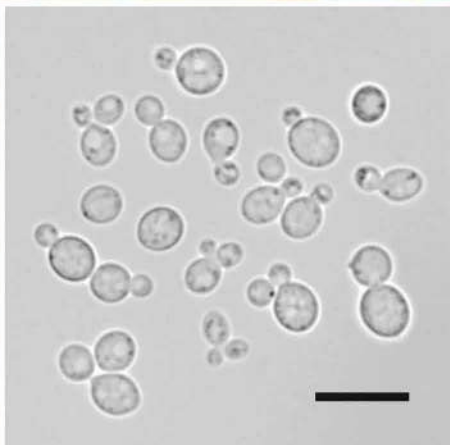
Based on our molecular analysis, the closest species to *I. roseascens* is *I. melanopus*, a species described from Northern America and well known in Europe (Kuyper 1986, Stangl 1989, Bon 1997, Alpago Novello 2006, Bizio 2012). *Inocybe melanopus* was first described by Stuntz as *I. melanopoda* (Stuntz 1954), as cited in Index Fungorum. However, it is universally accepted with the orthographic variant *I. melanopus*. *Inocybe melanopus* is not a reddening species, with stipe dark brown to blackish, pileic surface lanose feltrate, ochraceous to beige with infrequent cystidia, cylindrical-fusiform, caulocystidia absent. In *I. roseascens*, the stipe is never blackish.



The data matrix was aligned in MAFFT v. 7 (Katoh & Standley 2013). A phylogeny was constructed under maximum likelihood (ML), and ML bootstrap support values (100 replicates) were obtained as implemented in RAXML Blackbox (<http://embnet.vital-it.ch/raxml-bb/>) with the default settings. The alignment and tree are deposited in TreeBASE (Submission ID 22854).

Enrico Bizio, Società Veneziana di Micologia, S. Croce 1730, 30135, Venezia, Italy; e-mail: enrico.bizio@gmail.com
 Mohammad Bahram, Department of Botany, Institute of Ecology and Earth Sciences, University of Tartu, 40 Lai St., 51005 Tartu, Estonia;
 Department of Organismal Biology, Evolutionary Biology Centre, Uppsala University, Norbyvägen 18D, 75236 Uppsala, Sweden;
 e-mail: bahram@ut.ee
 Leho Tedersoo, Department of Botany, Institute of Ecology and Earth Sciences, University of Tartu, 40 Lai St., 51005 Tartu, Estonia;
 e-mail: leho.tedersoo@ut.ee
 Renata Orzes, Gruppo Micologico Bresadola di Belluno, Via Bries 25, Agordo, 32021, Italy; e-mail: renataluigi@alice.it
 Alessandro Saitta, Department of Agricultural, Food and Forest Sciences, University of Palermo, Viale delle Scienze, Palermo, 90128, Italy;
 e-mail: alessandro.saitta@unipa.it

Kwoniella endophytica



Fungal Planet 848 – 14 December 2018

***Kwoniella endophytica* A.M. Glushakova & Kachalkin, sp. nov**

Etymology. Name refers to the original endophytic isolations from different fruit tissues.

Classification — *Cryptococcaceae*, *Tremellales*, *Tremellomycetes*.

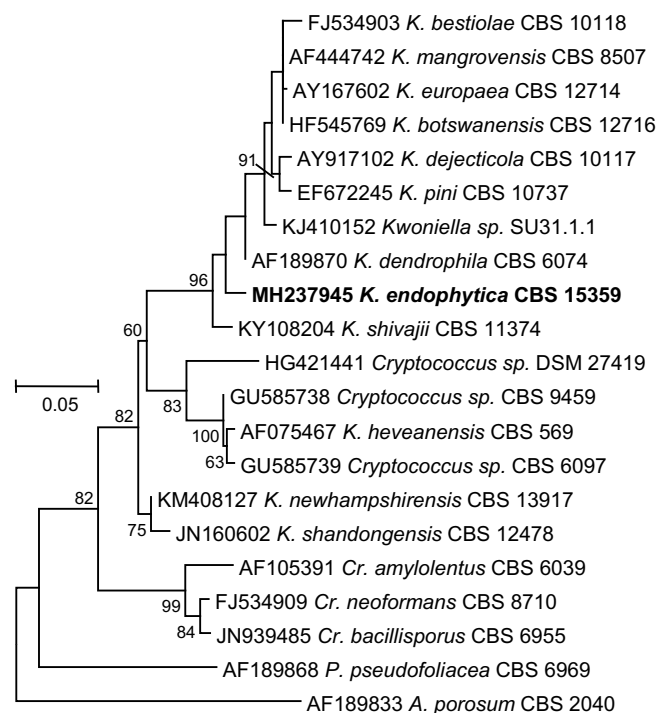
On potato dextrose agar (PDA) and 2 % glucose yeast nitrogen base agar (YNB), after 7 d at 22 °C, streak is white, butyrous, smooth surface and an entire straight margin. Cells are subglobose to globose, 5–6 × 4–5 µm, occur singly, in pairs and in clusters, divide by multilateral budding, cells with one or two buds. On glucose peptone yeast extract agar (GPYA), after 7 d at 22 °C, streak colonies are cream, cells are mostly globose, 5–7 × 5–6 µm, occur singly and in pairs, *divide by multilateral budding*, budding is single. Pseudohyphae, ballistoconidia and sexual structures have not been observed during 1–2 wk in culture (pure cultures and in mating test) grown on YNB agar, GPYA, PDA and commmeal agar. Glucose is not fermented. Glucose, galactose, D-ribose, D-xylose, L-arabinose, D-arabinose, L-rhamnose, sucrose, maltose, trehalose, cellobiose, lactose, raffinose, melezitose, inulin (variable), soluble starch (variable), glycerol, ribitol, D-glucitol, D-mannitol, galactitol, *myo*-inositol, ethanol, 2-keto-D-gluconate, 5-keto-D-gluconate, D-gluconate, D-glucuronate, DL-lactic acid (weak) and succinic acid are assimilated; no growth occurs on L-sorbose, D-glucosamine, methyl alpha-D-glucoside, salicin, arbutin, melibiose, erythritol, methanol, citric acid, propane-1,2-diol, butane-2,3-diol and hexadecane. Nitrogen compounds: ammonium sulfate, potassium nitrate (variable), L-lysine are assimilated. Growth on vitamin-free medium, on 50 % w/w glucose / yeast extract (0.5 %) agar is positive. Growth is absent with 0.01 % cycloheximide, on YM agar with 10 % NaCl. Positive result for the Diazonium blue B reaction and for urease activity. Starch-like compounds are produced. Maximum growth temperature is 31–32 °C.

Typus. RUSSIA, Moscow, Kuskovo from the hypanthium of pear fruit (*Pyrus communis*), Aug. 2015, A.M. Glushakova (holotype OK21, ex-type cultures KBP Y-5323 = VKM Y-3035 = DSM 106749 = CBS 15359, SSU, ITS-D1/D2 domains of LSU nrDNA, *TEF1* and *RPB1* sequences GenBank MH237944, MH237945, LS992196 and LS992197, MycoBank MB825499).

Additional specimens examined. RUSSIA, Moscow region, Lobnya, from the hypanthium of apple (*Malus communis*), Aug. 2015, A.M. Glushakova, KBP Y-5326; Moscow, Rublevo, from the hypanthium of pear fruit (*Pyrus communis*), Aug. 2015 and Sept. 2015, A.M. Glushakova, KBP Y-5327 and KBP Y-5328; Moscow, Rublevo, from the hypanthium of cherry (*Cerasus* sp.), Sept. 2015, A.M. Glushakova, KBP Y-5329; Moscow, Kuskovo, from the hypanthium of pear fruit (*Pyrus communis*), Sept. 2015, A.M. Glushakova, KBP Y-5330 and KBP Y-5331; Moscow, Karacharovo, from the hypanthium of apple (*Malus communis*), June 2015, A.M. Glushakova, KBP Y-5332, ITS sequences GenBank MH337639–MH337645.

Colour illustrations. Russia, Moscow, pear fruits on tree; growth of yeast colonies on YNB agar, morphology of cells on YNB agar and GPYA (after 7 d at 22 °C). Scale bars = 10 µm.

Notes — Analysis of the ITS region of the surveyed yeasts suggested that they were conspecific and represented a hitherto undescribed species of *Kwoniella*. Based on NCBI's GenBank database, the best hit using the ITS sequence is *K. botswanensis* CBS 12716, GenBank NR_119822 (96 %, 10 subst. and 7 gaps), using LSU it is *K. dendrophila* CBS 6074, GenBank NG_058326 (98 %, 12 subst.), using SSU it is *K. mangrovensis* CBS 8507, GenBank KF036681 (99 %, 10 subst.), *K. shivajii* CBS 11374, GenBank KF036652 (99 %, 9 subst. and 1 gap), using *TEF1* it is *K. dendrophila* CBS 6074, GenBank FJ534856 (95 %, 15 subst.), and using *RPB1* it is *K. dendrophila* CBS 6074, GenBank KF036320 (82 %, 147 subst.). In compliance with a recent revision of the genus (Liu et al. 2015), the phylogenetic placement of the new species is demonstrated using the LSU rDNA phylogeny. No growth on L-sorbose, methyl alpha-D-glucoside, salicin, citric acid, methanol, YM agar with 10 % NaCl and growth on DL-lactic acid, 50 % w/w glucose / yeast extract (0.5 %) agar are good physiological tests for the distinction of the new species from the phylogenetically closely related species of the genus.



Maximum likelihood (ML) tree obtained from the analysis of LSU sequence data. Bootstrap support values above 55 % are shown at the nodes. The alignment included 455 bp and was performed with MAFFT v. 7. The General Time Reversible model (GTR) with Gamma distribution and invariant sites (G+I) was used as the best nucleotide substitution model. Phylogenetic analysis was conducted in MEGA v. 6.

Lareunionomyces loeiensis



Fungal Planet 849 – 14 December 2018

Lareunionomyces loeiensis Pinruan, Nuankaew & P. Khamsuntorn, *sp. nov.*

Etymology. Refers to the location where the fungus was collected, Loei province, Thailand.

Classification — *Neolauriomycetaceae*, *Helotiales*, *Leotiomyces*.

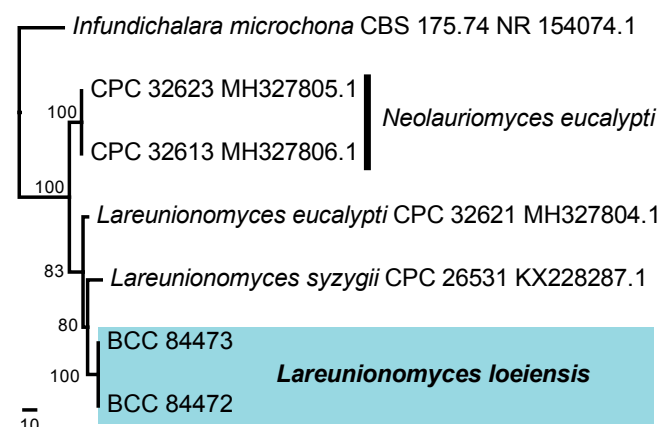
Conidiophores solitary, erect, dark brown, thick-walled, smooth, straight, subcylindrical, unbranched, 2–3-septate, 90–150(–165) × 5–6.5 µm, base lacking rhizoids. *Penicillate conidiogenous apparatus* brown to pale brown, smooth; primary branches brown, smooth, aseptate, subcylindrical to clavate, 6–8 × 3–6.5 µm, giving rise to 6–8 secondary branches; secondary branches pale brown, subcylindrical to clavate, 6–7.5 × 3–4 µm; tertiary branches pale brown, 4–5 × 2–3 µm, giving rise to several conidiogenous cells. *Conidiogenous cells* subcylindrical, pale brown, 12–14 × 1.5–2 µm. *Conidia* aggregating in mucoid mass, hyaline, smooth, guttulate, subcylindrical, aseptate, apex and base truncate, 4.5–5.5 × 1.5–2.5 µm, in long chains.

Culture characteristics — Colonies on PDA reaching up to 5 cm diam after 4 wk at 25 °C, with spreading, smooth surface; margins smooth, sparse aerial mycelium, surface pale brown to cream, reverse pale brown. Sporulation on PDA after incubation at 25 °C for 30 d.

Typus. THAILAND, Loei, on leaves of unknown tree, 12 Feb. 2017, *P. Khamsuntorn* (holotype BBH 43483, culture ex-holotype BCC 84473 ITS and LSU sequences GenBank MK047459.1 and MK047509.1, culture ex-isotype BCC 84472, ITS and LSU sequences GenBank MK047460.1 and MK047510.1, MycoBank MB827980).

Colour illustrations. Leaf litter in Thailand (background photo); fungus growing on the substrate (scale bar = 100 µm), conidiophores (50 and 25 µm), conidiogenous head with phialides (10 µm), conidia (10 µm), colonies on PDA after 3 wk; (left) above (right) and below, conidiophores in culture from sporulating colony (50 µm).

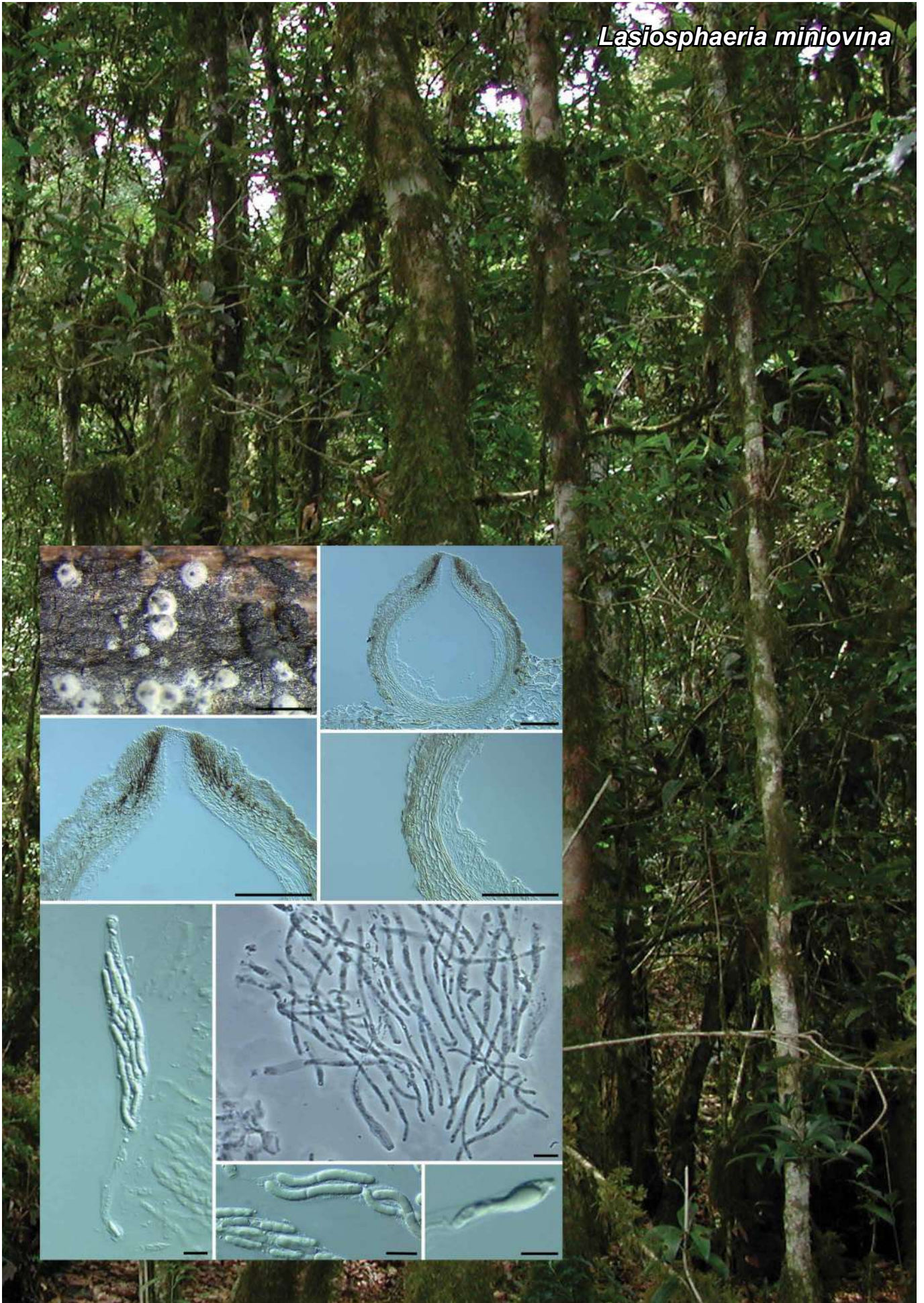
Notes — The genus *Lareunionomyces* was established by Crous et al. (2016b), with *L. syzygii* as the type species. *Lareunionomyces loeiensis* is designated as a new species based on both morphological characteristics and phylogenetic analyses. *Lareunionomyces loeiensis* is similar to *L. syzygii* and *L. eucalypti*, but distinct from them in that it has conidia aggregating in longer chains that form a mucoid spore mass. Conidiophores are longer than those of *L. syzygii* (50–100 × 5–8 µm) and similar to those of *L. eucalypti* (60–160 × 5–6 µm) but up to 3-septate only while other are 2–7-septate. Conidia of *L. loeiensis* are slightly wider than those species, the apex and base are truncate, and occur in long chains.



Single most parsimonious tree obtained from the ITS alignment using PAUP v. 4.0b10 (Swofford 2003; seven sequences including the outgroup, 518 included characters of which 28 were parsimony-informative). The tree was rooted with *Infundichalara microchona* (GenBank NR_154074.1). The novel species described here is indicated in **bold italic** text. The scale bar represents the number of changes and parsimony bootstrap support values > 50 % from 1000 replicates are indicated at the nodes.

Umpawa Pinruan & Phongswat Khamsuntorn, Microbe Interaction and Ecology Laboratory, National Center for Genetic Engineering and Biotechnology (BIOTEC), 113 Thailand Science Park, Phahonyothin Rd., Khlong Nueng, Khlong Luang, Pathum Thani 12120, Thailand; e-mail: umpawa.pin@biotec.or.th & phongswat.kha@ncr.nstda.or.th
Salilaporn Nuankaew, Fungal Biodiversity Laboratory, National Center for Genetic Engineering and Biotechnology (BIOTEC), 113 Thailand Science Park, Phahonyothin Rd., Khlong Nueng, Khlong Luang, Pathum Thani 12120, Thailand; e-mail: salilaporn.nua@biotec.or.th
Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: e.groenewald@westerdijkinstitute.nl

Lasiosphaeria miniovina



Fungal Planet 850 – 14 December 2018

***Lasiosphaeria miniovina* A.N. Mill. & Huhndorf, sp. nov.**

Etymology. The specific epithet refers to this species resembling a smaller version of *L. ovina*.

Classification — *Lasiosphaeriaceae*, *Sordariales*, *Sordariomycetes*.

Ascomata ampulliform to ovoid, papillate, 200–250 µm diam, 200–350 µm high, numerous, scattered to gregarious, superficial; young ascomata tomentose, white, tomentum becoming tightly appressed, crust-like and cream to waxy and brownish grey with age, areolate, finally tomentum wearing away and ascomata becoming black and glabrous; neck conical, glabrous, black. *Ascomatal wall* of *textura angularis* in surface view, in longitudinal section 3-layered, 20–40 µm thick, inner layer pseudoparenchymatous, 5–8 µm thick, composed of 3–5 layers of elongate, flattened, pale brown cells, middle layer pseudoparenchymatous, 10–16 µm thick, composed of 3–5 layers of polygonal to angular, pale brown cells, outer layer prosenchymatous, 5–16 µm thick, composed of several to few layers of hyphae depending on age of ascomata, hyphae 1–2.5 µm wide, hyaline to pale brown, septate, thin-walled. *Ascomatal apex* with periphyses. *Centrum* with yellow pigments that quickly diffuse in water. *Paraphyses* filiform, 2–5 µm wide, longer than asci, hyaline, numerous, septate, unbranched, persistent. *Asci* cylindrical, 85–130 × 8–14 µm, stipitate, stipe 24–46 × 2.5–4.5 µm, numerous, unitunicate, thin-walled, apex truncate; ring narrow, shallow, refractive; subapical globule smooth, 2–4 µm wide; with 8 bi- to triseriate ascospores. *Ascospores* cylindrical, ends rounded, 22–33 × 2.5–4.5 µm (av. 28 ± 2.5 × 3.5 ± 0.5), straight when first produced, hyaline, aseptate, without appendages; becoming sigmoid to geniculate, 1-septate, after liberation from the ascus head slightly swelling up to 5.5 µm wide, remaining hyaline, rarely becoming up to 7-septate with age, hyaline to yellowish, occasionally producing phialides directly from the ascospores.

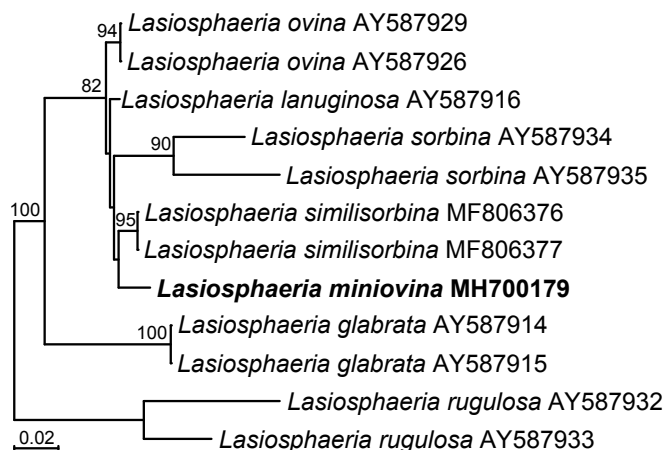
Habitat — Decayed wood in a tropical forest.

Distribution — Known only from Costa Rica.

Typus. COSTA RICA, San Jose, San Gerardo de Dota, Albergue de Montage, Savergre, Sendero la Quebrada, on 10 cm branch with loose bark, N9.33 W83.48, 701 m elev., 12 May 1996, S.M. Huhndorf & F.A. Fernandez (holotype SMH 2392 (F), isotype at ILLS, ITS-LSU sequence GenBank MH700179, MycoBank MB827965).

Colour illustrations. Background photo of typical tropical forest in Costa Rica; ascomata, longitudinal section through ascoma, longitudinal section through ascomal neck, longitudinal section through ascomal wall, ascus, paraphyses, ascospores and ascospore with swollen head. Scale bars = 500 µm (ascomata), 100 µm (ascomal sections), 10 µm (all others). Photos: Andrew N. Miller, Sabine M. Huhndorf, Gregory M. Mueller.

Notes — *Lasiosphaeria miniovina* possesses the typical characters known for the genus: tomentose ascomata containing yellow centrum pigments (Miller & Huhndorf 2004a, b). This species can be distinguished by its small whitish ascomata, presence of a distinct ascal subapical globule, and short cylindrical ascospores that lack appendages and produce swollen heads with age. It has ascomata, asci and ascospores resembling *L. ovina*, but all characters are about half the size as those found in *L. ovina*. *Lasiosphaeria ovina* has ascospores with appendages but the ascospores never form a swollen head, whereas *L. miniovina* has ascospores that lack appendages and that form a swollen head with age. *Lasiosphaeria miniovina* is only known from Costa Rica, whereas *L. ovina* occurs widespread throughout north temperate regions, although it has been reported once from Costa Rica (as *Lasiosphaeria chrysentera*; Miller & Huhndorf 2004b). *Lasiosphaeria lanuginosa* occurs in Costa Rica and was collected at the same time (GenBank AY587916) as *L. miniovina*, but it differs in having longer ascospores (33–60 vs 22–33 µm) and ascospores with long, lash-like appendages.



Maximum likelihood tree generated using PhyML in Seaview v. 4.5.4 (Gouy et al. 2010). *Lasiosphaeria miniovina* is in **bold**. Numbers above branches refer to bootstrap support values. GenBank accession numbers for the ITS region are given after taxon names.

Neocochlearomyces chromolaenae



Fungal Planet 851 – 14 December 2018

Neocochlearomyces* Pinruan, Sommai, Suetrong, J.Z. Groenew. & Crous, *gen. nov.

Etymology. Refers to its morphological similarity to *Cochlearomyces*.

Classification — *Muyocoproneae*, *Muyocoproneales*, *Dothiomyces*.

Mycelium partly superficial and partly immersed, pale brown, smooth. *Conidiophores* solitary, macronematous, mononematous, subcylindrical, septate, erect, straight, brown, smooth, thick-walled, with basal rhizoids; stalk forming an apical fan-like conidiogenous region consisting of radiating brown, warty, septate, tightly aggregated cylindrical arms, with acute terminal cells. *Conidiogenous cells* terminal and intercalary on the one

side of the swollen fan-like structure; loci inconspicuous, phialidic. *Conidia* falcate, aseptate, equilateral, with convex and flat plane, both ends obtuse to subobtusely rounded, hyaline, smooth-walled, guttulate, with a single, filiform, unbranched setula at each end on the inner straight plane, forming a slimy spore mass.

Type species. *Neocochlearomyces chromolaenae* Pinruan, Sommai, Suetrong, J.Z. Groenew. & Crous.
Mycobank MB828085.

Neocochlearomyces chromolaenae* Pinruan, Sommai, Suetrong, J.Z. Groenew. & Crous, *sp. nov.

Etymology. Name reflects the genus from which it was isolated, *Chromolaena*.

Conidiophores solitary, macronematous, mononematous, subcylindrical, unbranched, with 6–8 thickened transverse septa, erect, straight, brown, smooth, thick-walled, tapering slightly towards the apex, 7.5–12.5 µm diam at base, (90–)100–170 (–226) µm long, 3.5–5 µm diam at the apex, with basal rhizoids; stalk forming an apical fan-like conidiogenous region, 37.5–62.5 × 20–42.5 µm, consisting of radiating brown, warty, 3–5-septate, tightly aggregated cylindrical arms, with acute terminal cells. *Conidiogenous cells* terminal and intercalary on the one side of the swollen fan-like structure; loci inconspicuous, phialidic. *Conidia* 1.5–2.5 × 8.5–12.5 µm, falcate, aseptate, equilateral, with convex and flat plane, both ends obtuse to subobtusely rounded, hyaline, smooth-walled, guttulate, with a single, filiform, unbranched setula at each end, 3.8–5 µm long, on the inner straight plane, aggregating in mucoid droplet. *Sexual morph* unknown.

Culture characteristics — Colonies on PDA reaching 1.5 cm diam after 3 wk at 25 °C, effuse or punctiform, margins feathery, surface dark brown to black, reverse black. Fertile on PDA after incubation at 25 °C for 27 d.

Typus. THAILAND, Nakhon Ratchasima, on leaves of *Chromolaena odorata*, 25 Sept. 2013, U. Pinruan (holotype BBH 41327, isotypes BBH 41328, 41329, culture ex-holotype BCC 68250, cultures ex-isotypes BCC 68251, 68252, ITS, LSU, SSU and *tef1* sequences GenBank MK047464.1–MK047466.1, MK047514.1–MK047516.1, MK047552.1–MK047554.1 and MK047573.1–MK047575.1, MycoBank MB828926).

Colour illustrations. *Chromolaena odorata* in Nakhon Ratchasima province; fungus growing on host substrate; erect conidiophores, conidia, germinating conidium, colonies on PDA after 3 wk surface (left), and reverse (right). Scale bars morphological structures = 20 µm, Petri dishes = 1 mm.

Notes — Morphologically *Neocochlearomyces* differs from other known genera of hyphomycetes, being morphologically closest to *Cochlearomyces* (Crous et al. 2017b). It can easily be distinguished from the latter, however, as *Cochlearomyces* has synnemata with the swollen spoon-shaped conidiogenous region situated a third below the apex, and has conidia that are cylindrical, lacking setulae.

Umpawa Pinruan, Phongswat Khamsuntorn & Sujinda Sommai, Microbe Interaction and Ecology Laboratory, National Center for Genetic Engineering and Biotechnology (BIOTEC), 113 Thailand Science Park, Phahonyothin Rd., Khlong Nueng, Khlong Luang, Pathum Thani 12120, Thailand; e-mail: umpawa.pin@biotec.or.th, phongswat.kha@ncr.nstda.or.th & sujinda.som@biotec.or.th
Salilaporn Nuankaew & Satinee Suetrong, Fungal Biodiversity Laboratory, National Center for Genetic Engineering and Biotechnology (BIOTEC), 113 Thailand Science Park, Phahonyothin Rd., Khlong Nueng, Khlong Luang, Pathum Thani 12120, Thailand; e-mail: salilaporn.nua@biotec.or.th & satinee.sue@biotec.or.th

Ophiocordyceps houaynhangensis



Fungal Planet 852 – 14 December 2018

Ophiocordyceps houaynhangensis Keochanpheng, Thanakitp., Mongkols. & Luangsa-ard, *sp. nov.*

Etymology. Named after the place where the species was found – Houay Nhang Conservation Forest, Vientiane Province, Laos.

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

Stroma solitary, up to 11 cm long and 1.5–2.5 mm in width, cylindrical, cream; stipe simple. *Rhizoids* flexuous, arising from the head of *Coleoptera* larva, c. 2–6 cm long buried under the ground. Fertile part distinctly subterminal with asexual state at apex. *Ascomata* subterminal, cylindrical, pale yellow-brown with dark brown ostioles, 10–30 mm long, 2–3 mm in width. *Perithecia* completely immersed, obclavate, (300–)443–360(–450) × (80–)94–140(–170) µm. *Asci* cylindrical, (100–)115–207(–250) × 4–5(–7.5) µm. *Ascospores* hyaline, cylindrical, breaking into 32 small truncate part-spores, (4–)5(–7) × 1–2 µm. *Asexual morph* terminal, whitish to pale yellow, up to 10 mm long, 0.5–1 mm in width. *Conidiogenous cells* monophialidic, phialides flask-shaped with long necks, up to 30 µm long and 2–4 µm in width; phialide necks up to 18 µm long and 0.5 µm in width. *Conidia* hyaline, smooth, spherical, 2–3 µm.

Culture characteristics — Colonies developed from germinating ascospores. The ascospores germinated within 24 h on PDA. Colonies on PDA moderately growing, c. 1 cm diam in 21 d at 25 °C. Colonies white, reverse pale brown. *Asexual morph* hirsutella-like, observed in some strains. Conidiogenous cells monophialidic, phialides (15–)18–26(–34) × 3–5 µm, necks present, (7–)9–16(–21) × 0.5 µm. Conidia, hyaline, smooth, spherical, 3–5 µm.

Typus. LAOS, Vientiane Prov., Ban Danxang district, N18°05'28" E102°40'34", on *Coleoptera* larva, buried in soil, 31 Aug. 2016, P. Nupason, K. Keochanpheng, J.J. Luangsa-ard, S. Mongkolsamrit, W. Noisripoom & D. Thanakitpipattana (holotype BBH43166, culture ex-type TBRC8428, ITS, LSU and *tef1* sequences GenBank MH092891, MH092902 and MH092894, MycoBank MB825000).

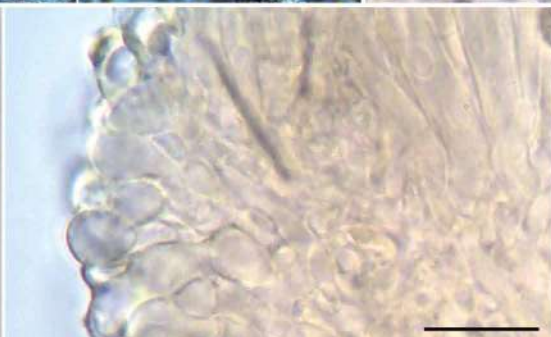
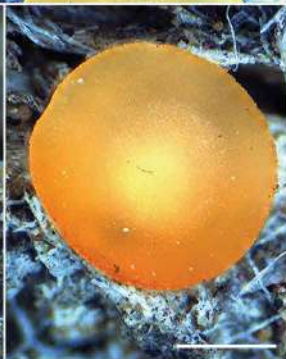
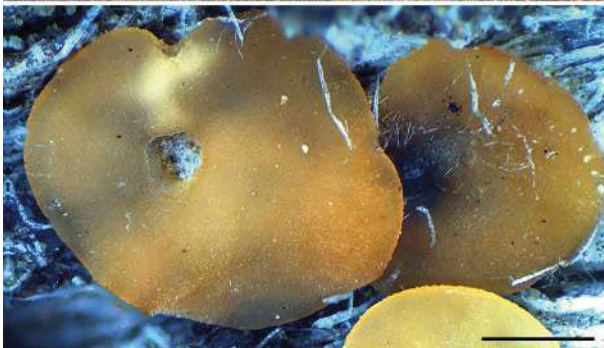
Additional materials examined. THAILAND, Saraburi Prov., Mueang Saraburi district, N14°31'33" E100°54'36", on *Coleoptera* larvae, buried in soil, 21 Sept. 2016, J.J. Luangsa-ard, S. Mongkolsamrit & K. Keochanpheng, BBH41960, BBC82809, ITS, LSU and *tef1* sequences GenBank MH092892, MH092908 and MH092899, BBH41961, BCC82810, ITS, LSU and *tef1* sequences GenBank MH092893, MH092909 and MH092900; Chiang Mai Prov., Ban Hua Thung district, N19°25'12" E98°58'15", on *Coleoptera* larvae, buried in soil, 5 Aug. 2015, U. Pinruan, S. Preedanon, S. Sommai, P. Srikitkulchai, K. Tasanathai & S. Wongkanoun, BBH41184, BCC78421, LSU and *tef1* sequences GenBank MH092904 and MH092897, BBH40264, BCC78167, LSU and *tef1* sequences GenBank MH092905 and MH092898.

Colour illustrations. Type locality – a trail in Houay Nhang Conservation Forest (photo by P. Nupason); stromata, fertile part with ascomata and asexual morph (arrow), perithecia, asci, ascus tip, part-spores, phialides, conidia, culture on PDA, asexual morph on PDA. Scale bars = 10 mm (stromata), 100 µm (perithecia), 25 µm (asci), 10 µm (ascus tip and part-spores), 5 µm (phialides and conidia), 8 mm (plate culture), 5 µm (hirsutella-like morph on PDA).

Notes — *Ophiocordyceps houaynhangensis* produces ascomata on the subterminal part of the stroma, while the asexual morph is on the apex of the stroma, a feature reminiscent of *O. brunneipunctata* and *O. stylophora*. Their hosts are coleopteran larvae that can be found buried in soil. *Ophiocordyceps brunneipunctata* can be found throughout Thailand (Luangsa-ard et al. 2008) and Laos (our surveys and observation) while *Ophiocordyceps stylophora* is a rare species that was reported from North America (South Carolina; Minnesota) and China (Chachula et al. 2011). Our phylogenetic analyses and morphological assessment support the placement of *O. houaynhangensis* in *Ophiocordycipitaceae* (Sung et al. 2007). Based on its micro-morphological characters, *O. houaynhangensis* more closely resembles *O. brunneipunctata* in the size of its part-spores that range from 4–6 × 1–1.5 µm (Hywel-Jones 1995, Evans et al. 2018), while *O. stylophora* produces whole ascospores, 102–164 × 2–3 µm (Mains 1958). However, *O. houaynhangensis* differs significantly from *O. brunneipunctata* in the size of perithecia and colour of its stroma as well as in the length of the phialides. In *O. houaynhangensis* the perithecia are longer than those reported for *O. brunneipunctata* (270–335 µm long) by Hywel-Jones (1995), and the stromata are pale yellow-brown with brown ostioles. In *O. brunneipunctata* they are cinnamon coloured, and the phialides are longer (up to 30 µm long) while they are shorter in *O. brunneipunctata* (up to 23 µm long). The results of our phylogenetic study using LSU and *tef1* sequences clearly separates *O. houaynhangensis* from *O. brunneipunctata*.

For supplementary information see MycoBank.

Orbilia amarilla



Fungal Planet 853 – 14 December 2018

***Orbilia amarilla* Quijada & Baral, sp. nov.**

Etymology. Spanish: amarilla = yellow, after the yellow-orange apothecial colour, which coincides with the locality name Llanos de Amarilla.

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

Apothecia rehydrated (0.5–)0.8–1.8 mm diam, to 0.2 mm high (receptacle 0.17 mm), bright orange-yellow to vivid orange, non-translucent, round to slightly undulating, scattered to subgregarious; disc slightly concave to slightly convex, margin smooth, 0–8 µm protruding; broadly sessile, superficial. **Asci** *(49.5–)53–58(–61) × 4.5–5.5 µm, †(36.5–)39–46(–52) × 3.4–4.3 µm, cylindrical-clavate, 8-spored, spores (obliquely) *2-seriate, 2–4(–6) lower spores inverted (usually mixed), pars sporifera *20–26 µm long; apex (†) strongly truncate (with a slight dent, laterally hardly inflated), hemispherical in profile view, thin-walled; base with medium to long, thin, flexuous stalk, L- to Y-shaped. **Ascospores** *(5.8–)6.4–7.3(–8) × (1.9–)2–2.2(–2.4) µm, †4.3–6.8 × 1.6–2 µm, fusoid to fusiform-clavate, straight, apex obtuse to subacute, base with a straight to slightly curved tail of *0.7–1.8 × 0.5–0.9 µm, sometimes slightly to distinctly bulbous at base; **SBs** *1.7–2.1 × 0.6–0.8(–1) µm, plug- to rod-shaped with a slightly bulbous base, straight to slightly, rarely medium bent, apically slightly widened and broadly attached at spore apex, often obliquely oriented. **Paraphyses** apically slightly to very strongly spatulate to mammiform, terminal cell *(10–)14–19(–22) × 2.5–4.5 µm, apical beak 1.3–1.7 × 1.7–2.2 µm (including exudate), exceeding the living asci by up to 3–7 µm, lower cells *(9–)10–13.3(–14.7) × 1.5–2.3(–3) µm, unbranched at upper septum, hymenium pale orange. **Medullary excipulum** very pale orange, 120 µm thick in centre, of loose to dense *textura intricata(-globulosa)*, at flanks sharply delimited from ectal excipulum (partly by an indistinct ~5–10 µm thick layer of *textura porrecta*). **Ectal excipulum** from base to mid flanks of thin-walled, *textura globosa*, at flanks and margin light yellow-orange, 50 µm thick at base, cells *(8–)11–20(–23) × (7–)10–15(–17) µm, 25–35 µm thick at flanks, of vertically oriented *textura globulosa-angularis-prismatica*, cells *3.5–8.5 × 3.5–7 µm, at margin of 17 µm thick *textura prismatica-globulosa* oriented at 80°, marginal cortical cells *4–9 × 3–5 µm. Anchoring hyphae 2.5–5 µm wide, thin-walled, forming a rather dense *t. intricata-globulosa*. **VBs** often abundant in terminal cells of paraphyses, ± globose, medium refractive, hyaline. **SCBs** line- or ring-shaped, in lower cells of paraphyses and in ectal excipulum at lower flanks. **Exudate** over paraphyses 0.5–1 µm thick, cloddy to cap-like, individually firmly attached on beak and also sublaterally (beak seemingly thick-walled), pale yellow, at margin and flanks 1–1.5 µm thick, yellow-brownish. **Asexual morph**: unknown.

* = living state, † = dead state, VBs = vacuolar bodies, SCBs = KOH-soluble cytoplasmic bodies

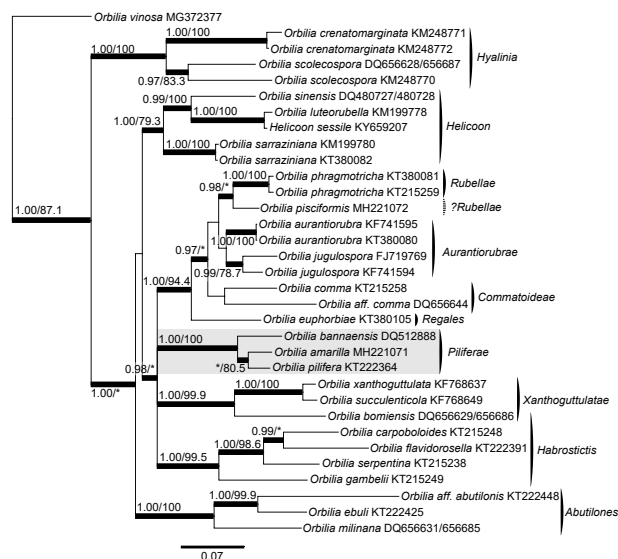
Colour illustrations. *Euphorbia* scrubs in Llanos de Amarilla; morphological features of *Orbilia amarilla*, from holotype, (top left to bottom right) fresh apothecia, living asci, living paraphyses (terminal cell with subglobose vacuolar bodies = VBs, lower cells with line-shaped KOH-sensitive cytoplasmic bodies = SCBs), living ascospores (with spore bodies = SBs), living excipular tissues in section, section at margin and section at base (cells with ring-shaped SCBs). Scale bars = 500 µm (apothecia), 10 µm (all others). All material mounted in H₂O.

Habitat — On superficially decayed, greyed wood of detached, branch of *Euphorbia canariensis* lying on the ground. **Association**: *Orbilia asomatica*, *O. beltraniae*, *O. pisciformis*. **Desiccation tolerance**: examined a few days after collecting in dry state, but certainly tolerant for several months.

Typus. SPAIN, Canary Islands, Tenerife, San Miguel de Abona, NE of Costa del Silencio, NNE of Monumento Natural de la Montaña Amarilla, N28°00'59" W16°38'03", 35 m alt., on detached branch of *Euphorbia canariensis* (*Euphorbiaceae*), 16 Dec. 2012, L. Quijada & R. Castro (holotype TFC Mic. 23767, ITS-LSU sequence GenBank MH221071, MycoBank MB825108).

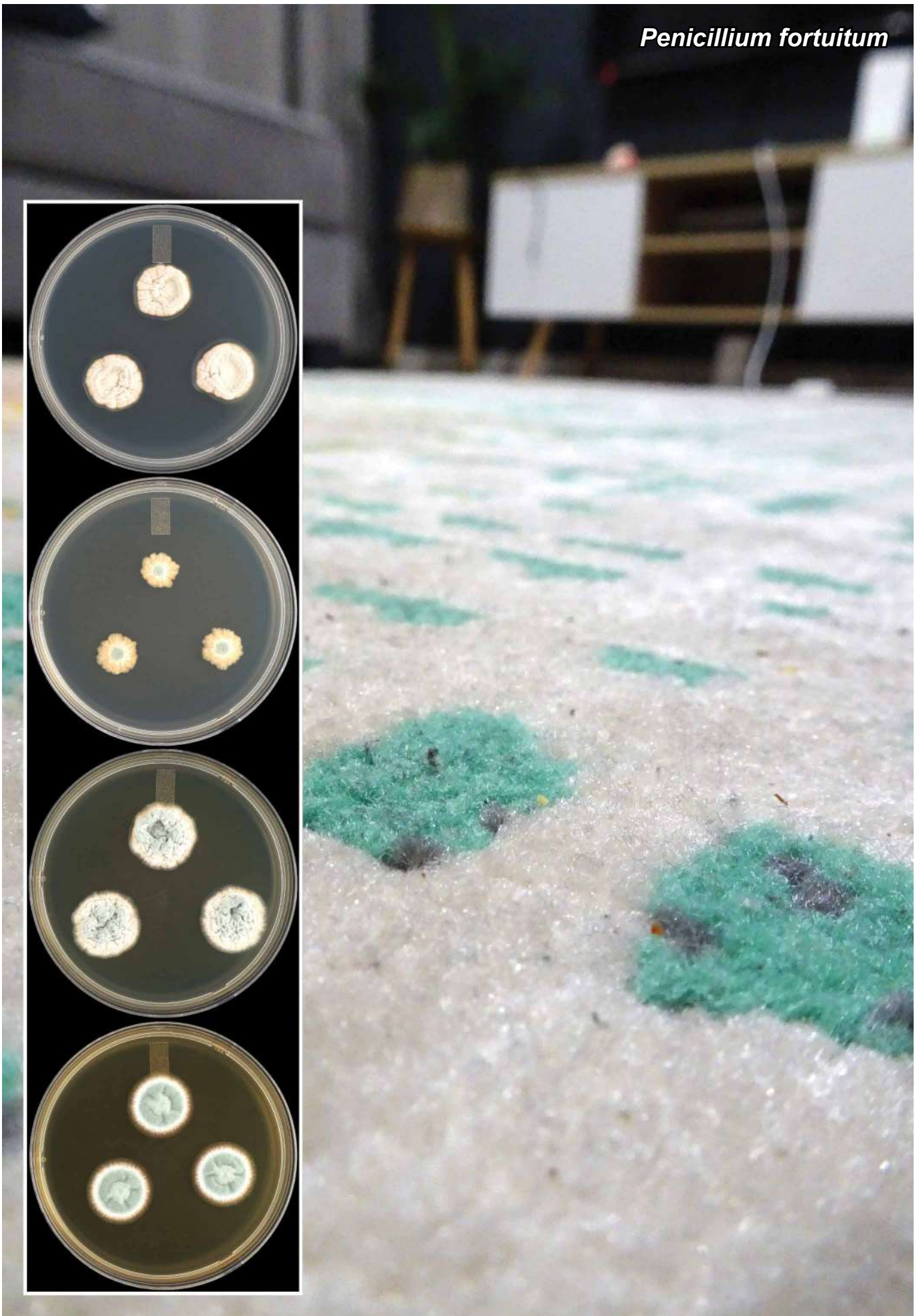
Notes — *Orbilia amarilla* was collected on rotten wood of a detached, xeric branch of *Euphorbia canariensis* in the hyper-arid *Euphorbia* scrubs in the south of Tenerife. In ascospore shape it resembles *O. pisciformis* (series *Commatoideae* or *Rubellae* ined.), which occurs in the same habitat, and *O. caudata* (series *Piliferae* ined.). These two species sharply differ, however, in having capitate paraphyses and partly glassy processes. Also, it resembles *O. pilifera* (series *Piliferae*), but this latter and *O. pisciformis* differ in having tear-shaped, narrowly attached spore bodies. A sequence of *O. amarilla* comprising SSU, ITS and LSU (S1506 intron absent) was obtained by Guy Marson (pers. comm.) from apothecia of the holotype. *Orbilia amarilla* shows an ITS distance of 7.5 % and LSU (D1–D2) distance of 3 % to *O. pilifera*, but 20 % (ITS) and 5.5 % (LSU) to *O. pisciformis*.

Our phylogenetical analyses supported the relationships between *O. amarilla* and *O. pilifera* in the clade of series *Piliferae* within sect. *Aurantiorubrae* of subg. *Habrostictis* (1.00 BIPP, 100 % ML-BS), see Baral et al. (2017).



Bayesian majority-rule consensus tree based on the ITS1-5.8S-ITS2 region of nrDNA. Thickened branches are those which were well supported by ML/BI methods (for Methods see Quijada et al. 2014). The eight different series of sect. *Aurantiorubrae* are indicated in the phylogenetic tree: here and also in the combined analysis in Baral et al. (2017), this section did not form a monophyletic clade with regard to sections *Helicoon* and *Habrostictis*. Asterisks (*) indicate a branch supported by only one of the two phylogenetic methods.

Penicillium fortuitum



Fungal Planet 854 – 14 December 2018

***Penicillium fortuitum* Visagie & Seifert, sp. nov.**

Etymology. Latin, *fortuitum*, meaning fortuitous, named in reference to the new species having only one representative strain amongst ~2000 *Penicillium* strains isolated during this project.

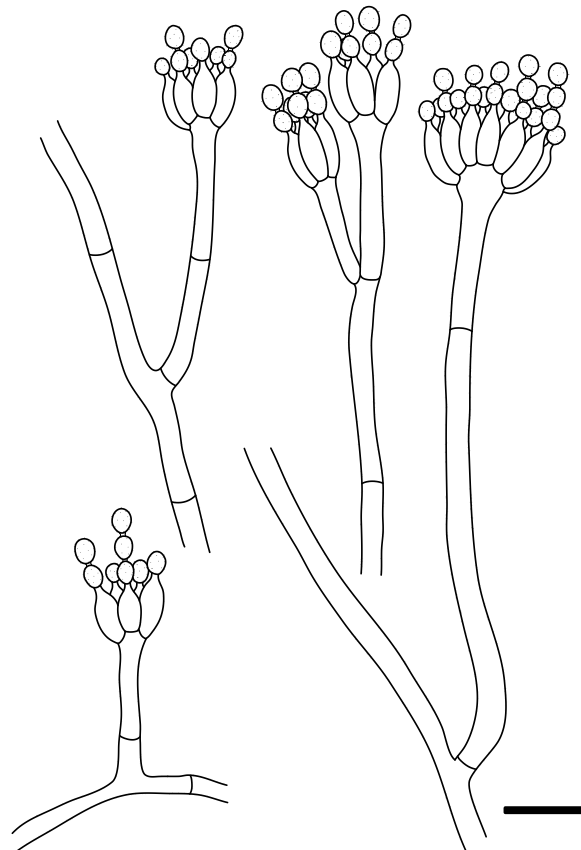
Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetes*.

Conidiophores monoverticillate, minor proportion divaricate. **Stipes** smooth, (35–)50–130 × 2.5–3.5 µm. **Vesicle** 4–6(–7) µm. **Branches** two when present, 16–30 µm. **Phialides** ampulliform, 6–8 (rarely up to 16) per stipe/branch, 7.5–10 × 2.5–3.5 µm (av. 8.8 ± 0.8 × 3.1 ± 0.2). **Conidia** finely roughened, globose to subglobose, 3–4 × 2.5–3.5 µm (av. 3.3 ± 0.3 × 3.1 ± 0.2), average width/length = 0.94, n = 71.

Culture characteristics (25 °C, 7 d) — **CYA:** Colonies moderately deep, randomly sulcate, sunken in at centre; margins moderately deep, somewhat irregular; mycelia white; texture floccose; sporulation dense, conidia *en masse* dull green (25D4–26D4), greenish grey (25B2); soluble pigments absent, sometimes brown; exudates absent; reverse brownish orange to light brown (6C7–7D8). **MEA:** Colonies low, raised centrally, sulcate; margins low, irregular; mycelia white; texture floccose; sporulation moderate, conidia *en masse* greyish green (25C5–D5); soluble pigments absent; exudates absent; reverse orange to light brown (6B8–7D8). **DG18:** Colonies similar colours to MEA, but faster growth and better sporulation. **YES:** Colonies similar to those on CYA, larger growth, reverse a deeper yellow (4A8) at centre. **CREA:** Growth moderate, no acid produced. Colony diam, after 7 d, in mm – CYA 15–19; CYA 37 °C no growth; CYA20S 19–20; MEA 14–15; MEA20S 22–26; DG18 14–18; YES 24–28; OA 17–18; MY1012 no growth; MY50G no growth; CREA 10–11.

Typus. USA, California, from house dust, 2009, coll. A. Amend, isol. E. Whitfield & K. Mwangi, AA01US-904 = SLOAN 7240 (holotype DAOM 745786, cultures ex-type DAOMC 251497 = DTO 313-A3, ITS, *BenA* and *CaM* sequences GenBank MF803942, MF803836 and MF803932; MycoBank MB827860).

Notes — A BLAST search against an ex-type reference sequence dataset (Visagie et al. 2014b), placed the new species in *Penicillium* sect. *Aspergilloides*. A multigene phylogeny resolves *P. fortuitum* as sister to a clade containing *P. infra-aurantiacum*, *P. malmesburiense* and *P. sublectaticum*. Morphologically, it is easily distinguished from these based on its restricted growth on MEA, a character typical of *P. brunneoconidiatum*, *P. tsitsikammaense* and *P. turcoconidiatum*. However, conidia of *P. brunneoconidiatum* have thick rough walls and are brown, colonies of *P. tsitsikammaense* typically produce sclerotia, while conidiophores of *P. turcoconidiatum* have very short stipes (Houbraken et al. 2014).



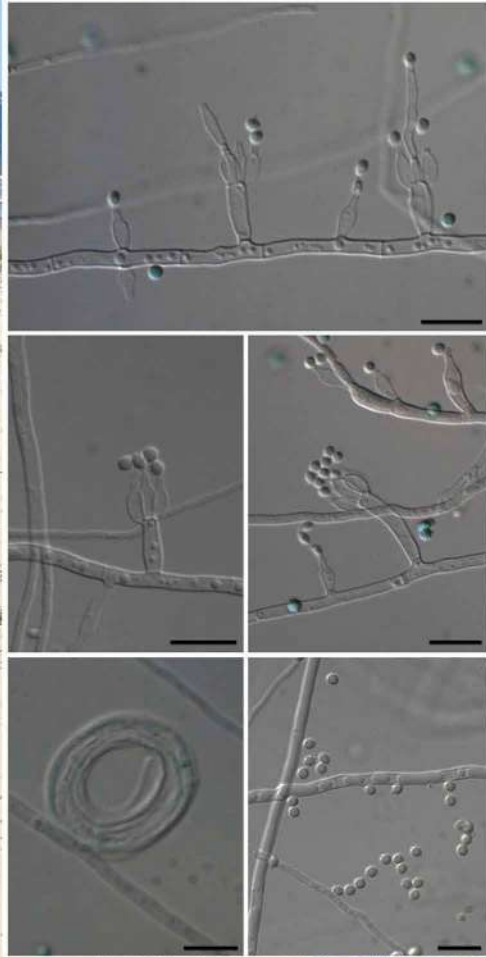
Left: Combined phylogeny of sect. *Aspergilloides* based on ITS, *BenA* and *CaM*. Aligned datasets were analysed in IQ-tree v. 1.4 (Nguyen et al. 2015) and MrBayes v. 3.2.6 (Ronquist et al. 2012), with the tree obtained from the former shown. Bayesian posterior probabilities (≥ 0.95) and bootstrap support values ($\geq 80\%$) are given above the branches. The new species is indicated by **bold red text**, ^T = ex-type strain. The tree is rooted to *P. thiersii*. Alignments and trees can be accessed at TreeBASE (Submission ID 23322).

Above: Line drawing of *P. fortuitum* (DAOMC 251497^T). Scale bar = 10 µm.



Colour illustrations. Carpet inside home; colonies on CYA, MEA, YES and DG18.

Penicillium guabinense



Fungal Planet 855 – 14 December 2018

Penicillium guaibinense J.P. Andrade, C.N. Figueiredo, R.P. Nascimento,
P.A.S. Marbach, & J.T. De Souza, *sp. nov.*

Etymology. *guaibinense*, refers to Guaibim, an environmental protection area located in Bahia, Brazil, from where this species was collected.

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

Conidiophores short and monoverticillate (83 % of the cases) and frequently occurring as side branches of the divaricate type of conidiophores, occasionally biverticillate (17 %). Isolated phialides born directly on hyphae occur frequently and mycelial coilings were sometimes observed. *Stipes* smooth to finely rough walled; monoverticillate stipes (6–)7–120(–170) × (1–)2–3(–4) μm. *Metulae* 1–2 per stipe of biverticillate conidiophores, (7–)8–14 × 2–3(–4) μm (av. 10.5 ± 2.3 × 2.6 ± 0.65). *Phialides* ampulliform, 1–6 per stipe, 4–8(–9) × (1–)2–3 μm (av. 5.9 ± 1.1 × 2 ± 0.26). Secondary elongated phialides resulting from percurrent proliferations were observed on approximately 10 % of the conidiophores (average of one secondary elongated phialide per conidiophore) on 7-d-old cultures grown on Blakeslee's Malt extract agar (MEAbI); these elongated phialides measured (6–)11–24 × 1.5–2 (av. 14.8 ± 6 × 1.8 ± 0.26). *Conidia* finely rough, broadly subglobose, 2–3 × 2–3 μm (av. 2.3 ± 0.37 × 2.2 ± 0.32), average width/length = 0.98 ± 0.03, n = 78.

Culture characteristics — Colony diam, 7 d, in mm: Czapek Yeast Autolysate agar (CYA) 27–31; CYA 30 °C (20–)36–38; CYA 37 °C 26–28(–36); CYA 5 °C no growth; MEAbI 25–28; Yeast extract sucrose agar (YES) 21–25; Dichloran 18 % Glycerol agar (DG18) 18–20; Czapek Yeast Autolysate agar with 5 % NaCl (CYAS) 16–17; Oatmeal agar (OA) 34–40; Czapek's agar (CZ) (21–)27–32; Creatine sucrose agar (CREA) 20–23, acid production absent.

CYA, 25 °C: Colonies moderately deep, radially and concentrically sulcate; margins low, narrow, entire; mycelia white; texture floccose; sporulation sparse to moderate; conidia *en masse* pale yellow, grey to greenish grey (1A3–B1–1C2–D2); exudate clear and soluble pigment bright yellow sometimes present; reverse dull yellow, greyish yellow to greyish orange (3B3–B4–4B6–5B5) at centre and dull yellow to greyish green (3B3–28B3) at margin. MEAbI, 25 °C: Colonies raised in the centre and sometimes radially and concentrically sulcate; margins low, narrow, entire; mycelia white; texture floccose; sporulation sparse to moderate, conidia *en masse* pastel yellow to grey (1A4–2C1); exudate clear, sometimes present, soluble pigment absent; reverse olive yellow, greyish orange to brownish orange (3C6–D6–5B5–6C7), light yellow (4A5) at centre and greyish yellow (4B3–B4) at margin. YES, 25 °C: Colonies moderately deep, radially, concentrically and randomly sulcate, margins low, narrow, entire; mycelia white; texture floccose; sporulation sparse to moderate, conidia *en masse* grey (2C1–D1); exudate absent, soluble pigment absent; reverse greyish yellow (4B6) at centre and greyish yellow (4A4–B4–B3–C3) at margin. DG18,

Colour illustrations. Guaibim environmental protection area located in Bahia, Brazil; 7-d-old colonies growing at 25 °C, top row left to right, obverse CYA, MEAbI, YES and OA; bottom row left to right, reverse CYA, MEAbI, YES and obverse CREA, conidiophores with elongated secondary phialides, phialides born directly on hyphae, conidiophores, coiling of mycelia and conidia. Scale bars = 10 μm.

25 °C: Colonies moderately deep, radially sulcate; margins low, narrow, entire; mycelia white; texture floccose; sporulation sparse to dense, conidia *en masse* greyish yellow, greenish grey to greyish green (1B4–1C2–1D3); exudate absent, soluble pigment yellow, sometimes present; reverse greenish yellow to greyish yellow (1A7–1B6) at centre and pale yellow (1A3) at margin. CYAS, 25 °C: Colonies moderately deep, randomly sulcate; margins low, narrow, entire; mycelia white; texture floccose; sporulation sparse to moderate; conidia *en masse* pale yellow to grey (2A3–B1–C1); exudate absent, soluble pigment bright yellow; reverse greyish yellow (2B4–4C6) at centre and yellowish white (2A2) at margin. OA, 25 °C: Colonies low, plane; margins low, narrow, entire; mycelia white; texture floccose; sporulation sparse to moderate, conidia *en masse* brownish grey (5C2); exudate clear, sometimes present, soluble pigment yellow; reverse greyish yellow (3C5–4C7) at centre and dull yellow to greyish yellow (3B4–C3–C4) at margin. CZ, 25 °C: Colonies low, plane; margins low, narrow, irregular to entire; mycelia white; texture floccose; sporulation absent to sparse, conidia *en masse* yellowish white to greenish grey (1A2–1B2); exudate absent, soluble pigment absent; reverse white to yellowish white (1A1–A2).

Typus. BRAZIL, Bahia, in soil from the Guaibim sandbank, S13°18' W38°57', 5 Nov. 2011, J.P. Andrade (holotype HURB 18573 (dried culture on MEA); culture ex-type CCDCA 11512 = 23EM8, ITS, *BenA* and *CaM* sequences GenBank MH674389, MH674391 and MH674393, MycoBank MB827182).

Additional materials examined. BRAZIL, Bahia, in soil from the Guaibim sandbank, CCDCA 11510 = 23EM7, 30 Oct. 2011, J.P. Andrade, ITS, *BenA* and *CaM* sequences GenBank MH674390, MH674392 and MH674394; *ibid.*, 2 Dec. 2011, J.P. Andrade, 67M4 and 67EM8.

Notes — *Penicillium guaibinense* morphologically resembles *P. curticaule* (Visagie et al. 2015) and is phylogenetically more related to *P. singorense* (Visagie et al. 2014a), both included in sect. *Lanata-Divaricata*. However, comparisons of ITS, *BenA* and *CaM* revealed that it differs from *P. singorense* by six transitions in *BenA* and nine in *CaM*, three transversions in *BenA* and six in *CaM*, one indel in each of these genes, and by one transition in ITS (TreeBASE submission ID 23052). The differences between *P. guaibinense* and its closest related species, *P. singorense*, are larger than the differences between other described species in sect. *Lanata-Divaricata*, such as *P. coeruleum* and *P. levitum* (Visagie et al. 2014a). *Penicillium guaibinense* grows slower than *P. singorense* on all media and temperatures tested, but it grows faster than *P. curticaule* on CYA 37 °C, CYAS and OA. *Penicillium guaibinense* may produce a soluble bright yellow pigment in CYA and secondary elongated phialides in ± 10 % of the conidiophores, both of these characteristics were not reported for *P. singorense* and *P. curticaule*. *Penicillium guaibinense* has shorter stipes than *P. singorense* and longer stipes than *P. curticaule*. *Penicillium guaibinense* produces mycelial coils similar to *P. curticaule*, but these structures were not reported for *P. singorense*. All macroscopic and microscopic measurements were done twice, independently, for isolates CCDCA 11512 and CCDCA 11510.

For supplementary information see MycoBank.

Jackeline Pereira Andrade, Universidade Estadual de Feira de Santana, Bahia, Brazil; e-mail: jackelineandrade@hotmail.com
Phellippe Arthur Santos Marbach & Cristiane Nascimento Figueiredo, Recôncavo da Bahia Federal University, Bahia, Brazil;
e-mail: phmarbach@ufrb.edu.br & cristianefigueiredoo@gmail.com

Rodrigo Pires Nascimento, Rio de Janeiro Federal University, Rio de Janeiro, Brazil; e-mail: rpn1978@gmail.com
Jorge Teodoro De Souza, Federal University of Lavras, Minas Gerais, Brazil; e-mail: jorge.souza@dfp.ufla.br

Periconia caespitosa



Fungal Planet 856 – 14 December 2018

***Periconia caespitosa* Cantillo, Gusmão & Madrid, sp. nov.**

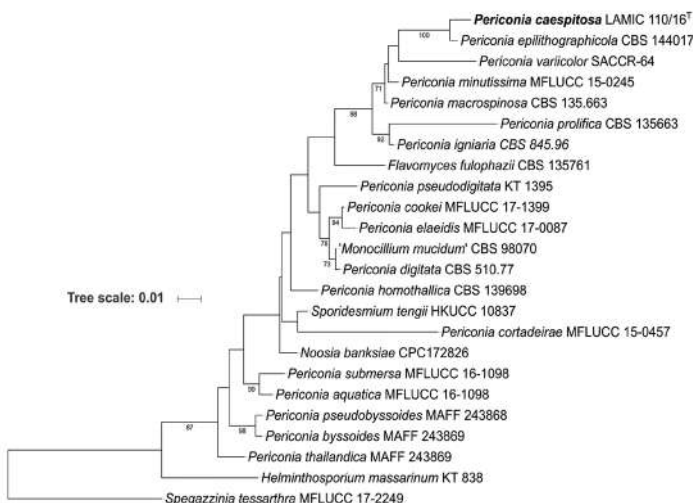
Etymology. Named after its conidiophores that developed in tufts or dense patches.

Classification — *Periconiaceae*, *Pleosporales*, *Dothideomycetes*.

On natural substrate. *Colonies* on decaying leaves dark brown to black, producing a reddish pigment. *Mycelium* immersed in the substrate, composed of septate, pale brown to subhyaline, smooth, 3.5–4 µm wide hyphae. *Conidiophores* macronematous, mononematous, septate, unbranched or rarely branched, caespitose, straight to flexuous, setiform and sometimes uncinated at the tip, pale brown at the base, brown towards the apex, minutely roughened at the base and at the apex, as well as in the areas nearest of conidiogenous cells, otherwise smooth, up to 500 µm long, 5–6 µm wide at the base, fertile at the lower-median part and sometimes also at the apex. *Conidiogenous cells* polyblastic, pale brown, finely roughened, intercalary and terminal, globose, subglobose or obpyriform (6–)7.5–9 × 6.5–7.5 µm. *Conidia* globose, aseptate, reddish brown, thick walled, dry, solitary or in short basipetal chains of 2–4 conidia, (6–)6.5–9 µm diam, strongly echinulate, spines 1–1.5 µm long, maturation basipetal. *Secession* schizolytic. *Sexual morph* not observed.

Culture characteristics — *Colonies* cottony, fast growing, with regular edges, attaining 90 mm diam after 6 d on PDA and CMA at 25 °C, hyaline hyphae on vegetative mycelium, aerial mycelium rosaceous white with white reverse on PDA, dark green to olivaceous green with blackish green reverse on CMA; diffusible pigments absent in both culture media. Conidiophores same as in natural substrate but more frequently branched and fertile at tips.

Typus. BRAZIL, Ceará, Missão Velha Waterfall Geosite, on decaying leaves of unidentified dicotyledonous plant, 30 Apr. 2016, *T. Cantillo* (holotype HUEFS 239357, culture ex-type LAMIC 110/16, ITS and LSU sequences GenBank MH051906 and MH051907, MycoBank MB827635).



Colour illustrations. Missão Velha Waterfall Geosite, Ceará state (photo by M.O. Marques); conidia, conidiogenous cells and conidiophores from type, colonies on PDA (top) and CMA (bottom) and colonies on natural substrate with a reddish pigment. Scale bars = 50 µm (conidiophores), 10 µm (conidiogenous cells and conidia).

Notes — BLAST searches indicated that the closest relative of *Periconia caespitosa* represented in GenBank is *P. epilithographicola* CBS 144017 (ITS GenBank MF422162, Identities = 578/590 (98 %), 4 gaps (0 %)). Both species have finely roughened conidiogenous cells, produce reddish pigment, and have a similar conidial size; but, on PDA, *P. epilithographicola* has creeping hyphae and greyish to black conidiophores forming small agglutinated, black, sticky drop-like structures instead of caespitose, brown and setiform conidiophores with dry conidia in short chains, as occurs with *P. caespitosa*. These species clustered together with a maximum-likelihood bootstrap support value of 100 % but no LSU sequences of *P. epilithographicola* are available for comparison and therefore a phylogenetic analysis could not be performed. Given the morphological and cultural differences and also the low clustering quality values produced by both genetic markers at the generic level, we consider *P. caespitosa* as a new species. In addition, *P. caespitosa* is morphologically different from all currently accepted *Periconia* species (Subramanian 1955, Rao & Rao 1964, Ellis 1971, 1976, Cantrell et al. 2007, Markovskaja & Kačergius 2014, Tanaka et al. 2015, Wu et al. 2015, Liu et al. 2017, Coronado-Ruiz et al. 2018, Crous et al. 2018b, Vu et al. 2019). Among all the species of *Periconia* with clustered conidiophores the most similar to *P. caespitosa* are *P. clitoriae*, *P. tirupatiensis*, *P. saraswatipurensis* and *P. atropurpurea*, but these can be differentiated from *P. caespitosa* by the combination of features such as the aggragation of conidiophores and the position of conidiogenous cells in them, conidial size and ornamentation, and pigment production on natural substrates and/or in culture. The most similar species to *P. caespitosa* is *P. clitoriae*, whose conidiophores arise in dense clusters and conidiogenous cells are located laterally at the upper three cells or at apex. Also, conidia of *P. clitoriae* are slightly bigger (8.5–9.5 µm diam) and also distinctly verrucose (Subramanian 1955) whereas in *P. caespitosa* conidia are echinulate; in addition, lateral conidiogenous cells in *P. caespitosa* are located in the lower portion of the conidiophore and sometimes terminally. Unfortunately, no DNA sequence data of *P. clitoriae* is available in GenBank for comparison.

Maximum Likelihood (ML) tree inferred from ITS-LSU nrDNA sequences. Phylogenetic analyses were performed with MEGA v. 7 (Kumar et al. 2016), with the best DNA substitution model determined by the same software. Statistical support was determined by bootstrap analysis of 1 000 replicates. Bootstrap support values ≥ 70 % are depicted at the internodes. *Periconia caespitosa* is marked in bold face.



Fungal Planet 857 – 14 December 2018

Phaeothecaceae* B.A. Darveaux, *fam. nov.

Classification — *Phaeothecaceae*, *Capnodiales*, *Dothideomycetes*.

Mycobank MB828184.

Mycelium consisting of hyaline to brown, smooth-walled, septate, branched hyphae, that swell up in terminal or intercalary cells, and develop numerous endoconidia. Endoconidia brown,

smooth to verruculose, thin- to thick-walled, globose to obovoid, aseptate to muriformly septate.

Type genus. Phaeotheca Sigler et al.
Mycobank MB9323.

Note — The family *Phaeothecaceae* presently only includes *Phaeotheca*, based on *P. fissurella*.

Phaeotheca shathenatiana* B.A. Darveaux, *sp. nov.

Etymology. From the first three letters of my children's names, Shawn, Theresa and Natalie.

Microscopic characteristics on 2 % malt extract agar: *Hyphae* brown, smooth, thin-walled, 10–20 × 3–4 µm. *Conidiophores* absent. *Conidiogenous cells* integrated, vegetative hyphae cells become conidiogenous, brown, 15–25 × 3–5 µm, expanding to 20–30 × 15–30 µm as endoconidia develop, enlarging as the cytoplasm compartmentalizes, one endoconidium forms from each compartment, successive enlarged cells resemble sausages, often one large cell that has ruptured or is near rupturing, bracketed by 3–5 lesser enlarged cells on both sides, mature conidiogenous cell finally ruptures and releases mature endoconidia. *Conidia* endogenous, unicellular, brown when seen *en masse*, pale brown when viewed individually, thin-walled, smooth, irregularly angular, especially when recently released, due to being pressed together in the conidiogenous cell, later becoming globose to subglobose, becoming less angular as they get older after release, 4–6(–7) µm diam, 5–30 per conidiogenous cell. *Secondary conidia* none.

Culture characteristics (2 % malt extract agar) — Very slow growth, colony diameter increase is 2–4 mm/wk (27 °C) eventually stopping, not covering plate. Mycelium dense, growing edge sharp, aerial hyphae developing just behind slowly advancing submerged hyphae, aerial hyphae on older areas, exudate droplets on surface containing conidia, centre of colony becoming raised. Colour dark brown to black, reverse black.

Typus. USA, Alaska, Anchorage, from twig and cone litter, 30 Sept. 1997, coll. D. Duffy, isol. B.A. Darveaux, on 2 Oct. 1997, MSX102094 (holotype SYRF0012523, permanently preserved on microscope slide), isotypes NY03304532, BPI 910718, DAOM836219, DUKE0351831, permanently preserved on microscope slides; ITS sequences GenBank MH745097 and MH745098, LSU sequence GenBank MH745096, Mycobank MB826890.

Colour illustrations. Twig and cone litter; MSX102094 colony sporulating on 2 % malt extract agar showing integrated conidiogenous cells swelling, compartmentalising, and rupturing to release endospores (inset), sausage-like appearance of conidiogenous cell development and rupture (bottom photo). Scale bars = 10 µm. Photos: Blaise A. Darveaux.

Notes — The current fungus shares generic diagnostic features of *Phaeotheca* such as predominant endogenous conidiogenesis, slow restricted growth at room temperature, and angular brown conidia (Sigler et al. 1981.) However, *P. shathenatiana* differs from the other four species of the genus by: *P. fissurella* usually has 1–3 (rarely more) endoconidia per conidiogenous cell (Sigler et al. 1981); *P. dimorphospora* forms hyaline, cylindrical secondary conidia from primary endoconidia (DesRochers & Ouellette 1994); *P. triangularis* and *P. salicorniae* both produce septate endoconidia (De Hoog et al. 1997, Crous et al. 2016b). Our phylogenetic analysis using partial LSU sequence data along with described species of *Phaeotheca* including members of asexual *Capnodiales* from an alignment published by Bose et al. (2014), shows strain *P. shathenatiana* clusters with the type species *P. fissurella* as a strongly supported clade (91 % RAxML bootstrap support). Our analysis also shows that *Phaeotheca* is a polyphyletic genus consistent with conclusions drawn in previous studies (Crous et al. 2016b). *Phaeotheca* represents an undescribed, monotypic family in *Capnodiales*, for which *Phaeothecaceae* is herewith introduced.

There are many other genera that produce endoconidia, usually to a minor extent, but relatively few rely on this mode as their main form of conidiogenesis. Several genera of the latter type are *Coccidioides*, *Phaeothecoidea*, *Endoconidioma* and *Hyphospora* (Seifert et al. 2011.)

Endospores of *Coccidioides* come from sphaerules rather than intercalary hyphal cells and it has alternate-arthric conidia which *P. shathenatiana* does not have (Seifert et al. 2011).

Phaeothecoidea differs in that the endoconidia are verruculose, 1–2-septate, and give rise to additional endoconidia. However, the photomicrographs of *Phaeothecoidea melaleuca* look very similar to the current fungus (Crous et al. 2010).

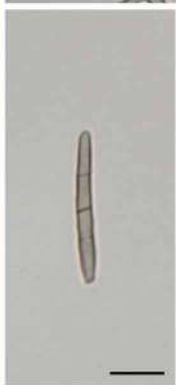
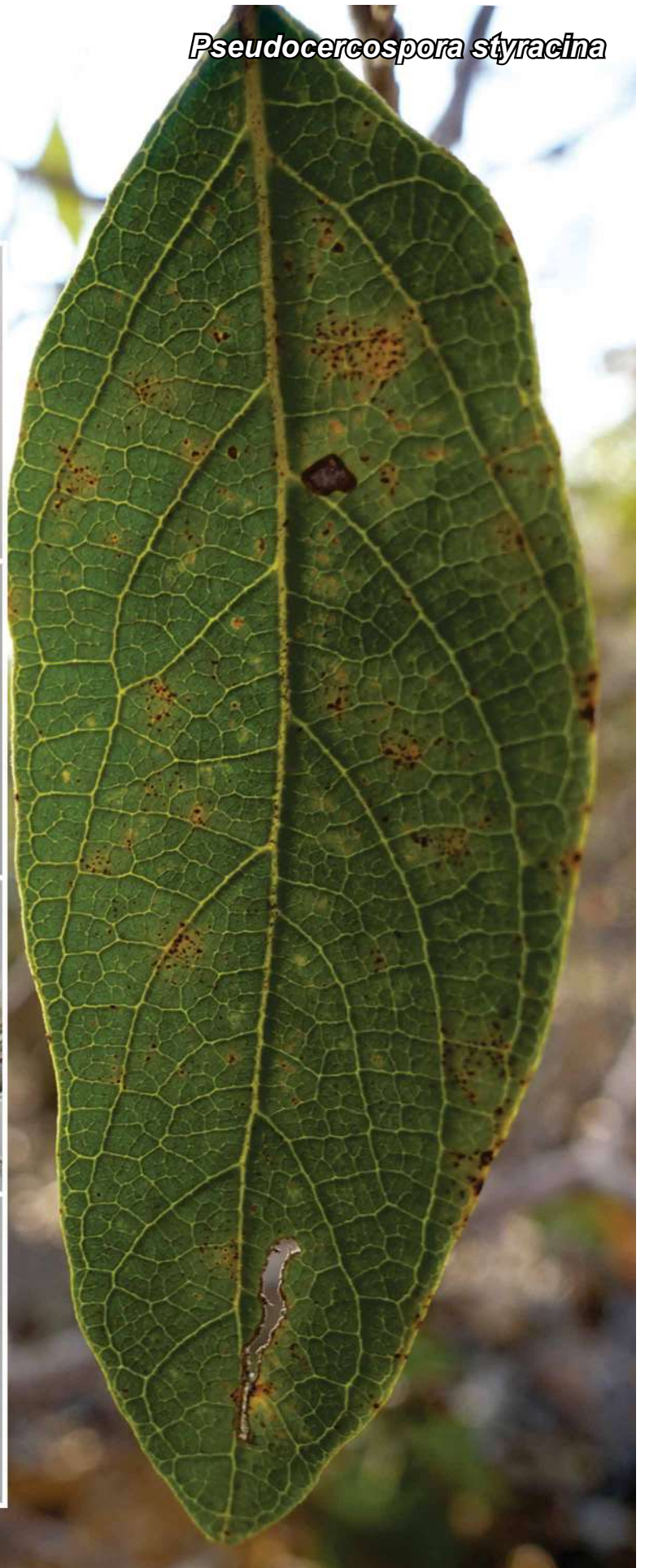
Endoconidioma differs in that it has a pycnidium-like conidiomata and solitary blastoconidia. Seifert et al. (2011) considers *Endoconidioma* a coelomycete.

Hyphospora differs in that it has hyaline mycelium and conidia and a depressed hemispheric central part of the colony surrounded by a halo of hyaline hyphae in the agar (Ramaley 1996).

Blaise A. Darveaux & Cedric J. Pearce, Mycosynthetix, Inc., 505 Meadowlands Dr., Suite 103, Hillsborough, North Carolina, USA 27278; e-mail: bdarveaux@mysynthetix.com & cpearce@mysynthetix.com

Huzefa A. Raja, Department of Chemistry and Biochemistry, University of North Carolina at Greensboro, 435 Sullivan Science Building, P.O. Box 26170, Greensboro, NC 27402-6170, USA; e-mail: haraja@uncg.edu

Pseudocercospora styracina



Fungal Planet 858 – 14 December 2018

***Pseudocercospora styracina* V.P. Abreu & O.L. Pereira, sp. nov.**

Etymology. Name derived from its host genus, *Styrax*.

Classification — *Mycosphaerellaceae*, *Capnodiales*, *Dothi-deomycetes*.

Leaf spots amphigenous, circular to irregular, initially chlorotic, becoming brown with age, 4–10 mm diam. *Internal mycelium* indistinct. *External mycelium* brown, septate, branched, smooth, 1.5–2.5 µm diam, colonising the trichomes. *Stromata* absent. *Conidiophores* hypophyllous, cylindrical, branched, solitary, 19–57 × 2–4.5 µm, 1–7-septate, straight or geniculate, brown, smooth, sometimes restricted to conidiogenous cells. *Conidiogenous cells* terminal, 7–13.5 × 2.5–4.5 µm, or conidiophores reduced to conidiogenous cells, 3.5–12.5 × 2–4 µm, subcylindrical, brown, smooth, proliferating sympodially. *Conidiogenous loci* inconspicuous, unthickened, not darkened. *Conidia* solitary, guttulate, pale brown to brown, smooth, subcylindrical, straight to slightly curved, 22.5–47.5 × 2–3 µm, base truncate, 1–3-septate, hila neither unthickened nor darkened, 1–1.5 µm diam.

Culture characteristics — Colonies on PDA 34 mm diam after 20 d at 25 °C with a photoperiod of 12 h; with aerial mycelium sparse, grey, reverse iron-grey, sterile.

Typus. BRAZIL, Minas Gerais, Paraopeba, Floresta Nacional de Paraopeba (FLONA-Paraopeba), on leaves of *Styrax* sp. (*Styracaceae*), 1 July 2015, O.L. Pereira (holotype VIC 44382, culture ex-type COAD 2369; ITS, LSU, *tef1* and *actA* sequences GenBank MH397664, MH480643, MH480642 and MH480641, MycoBank MB824660).

Notes — Cercosporoid fungi include several genera of micro-fungi with cosmopolitan distribution and are highly diverse especially in tropical and subtropical countries (Crous et al. 2013, Bakhshi et al. 2014, Silva et al. 2016). *Pseudocercospora* species can be found as saprobes, endophytes, hyperparasites, being very common as plant pathogens – causing mainly leaf spots (Crous et al. 2013, Braun et al. 2016, Guatimosim et al. 2016). Cercosporoid fungi have been reported as host-specific (Guatimosim et al. 2016, Silva et al. 2016). Four cercosporoid fungi have been described from *Styrax* spp.: *Passalora styracis*, *Cercospora apii* s.lat. (= *Cercospora styracicola*), *Pseudocercospora fukuokaensis* and *Cercoramularia koreana* (Crous & Braun 2003, Videira et al. 2017). Morphologically, *P. styracina* clearly differs from *P. fukuokaensis* and *P. brackenicola* by having external mycelium colonising the trichomes and stromata absent. Additionally, the conidia length of *P. styracina* (22.5–47.5 µm) are shorter than *P. fukuokaensis* (30–70 µm) and *P. brackenicola* (20–77 µm) (Chupp 1954, Guatimosim et al. 2016). *Pseudocercospora styracina* does not correspond to any sequence available in GenBank at present. Hence, it is described here as a new species.

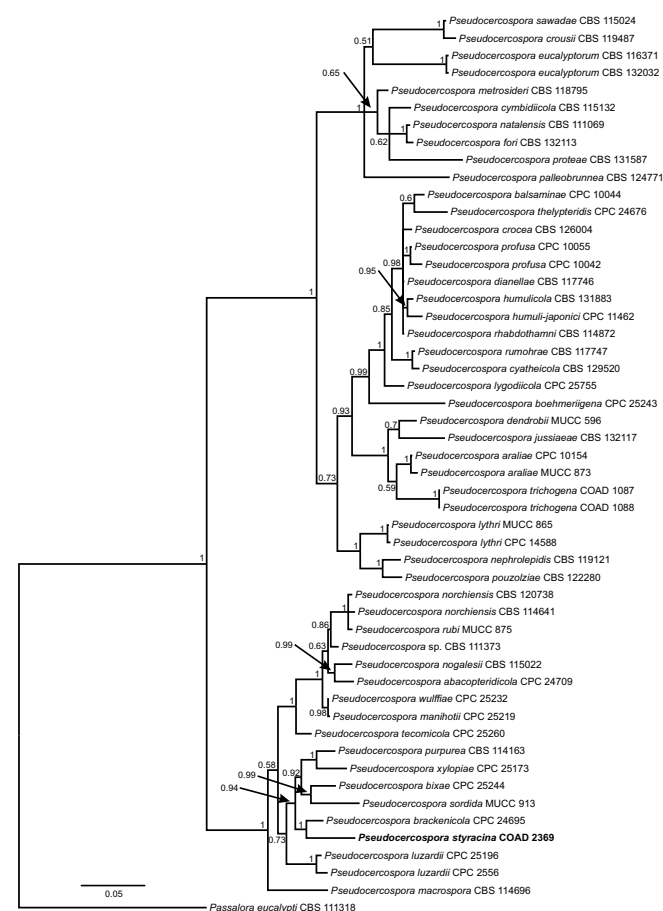
Based on a megablast search of NCBI's GenBank nucleotide database, the ITS sequence is identical to *P. norchiensis* (GenBank MF663573), *P. brackenicola* (GenBank NR_147290) and *P. abacopteridicola* (GenBank KT037518).

Colour illustrations. Chlorotic leaf spots symptoms on *Styrax* sp. (*Styracaceae*) in Floresta Nacional de Paraopeba, state of Minas Gerais, Brazil; external mycelium with conidiophores and conidiogenous cells colonising the trichomes and pigmented conidia with inconspicuous, unthickened, not darkened conidiogenous loci. Scale bars = 20 µm.

Based on a megablast search of NCBI's GenBank nucleotide database, the LSU sequence is identical to *P. brackenicola* (GenBank KT037565), *P. tecomicola* (GenBank KT290183) and *P. bixae* (GenBank KT290180).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the *tef1* sequence are *P. brackenicola* (GenBank KT037484; Identities = 470/504 (93 %), 7 gaps (1 %)), *P. bixae* (GenBank KT290207; Identities = 457/501 (91 %), 2 gaps (0 %)) and *P. luzardii* (GenBank KT290194; Identities = 462/511 (90 %), 10 gaps (1 %)).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the *actA* sequence are *P. macrospora* (GenBank GU320447; Identities = 154/163 (94 %), no gaps), *P. luzardii* (GenBank GU320440; Identities = 154/164 (94 %), 1 gap (0 %)) and *P. purpurea* (GenBank GU320486; Identities = 153/164 (93 %), no gaps).



Bayesian inference tree obtained by phylogenetic analyses of the combined ITS, *actA* and *tef1* sequences conducted in MrBayes on XSEDE at the CIPRES Science Gateway (Miller et al. 2010). Bayesian posterior probability values are indicated at the nodes. The new species is indicated in bold face. *Passalora eucalypti* (CBS 111318) was used as outgroup.

Vanessa P. Abreu, Departamento de Microbiologia, Universidade Federal de Viçosa, 36570-000, Viçosa, Minas Gerais, Brazil; e-mail: vanessa.abreu@ufv.br
 Olinto L. Pereira, Departamento de Fitopatologia, Universidade Federal de Viçosa, 36570-000, Viçosa, Minas Gerais, Brazil; e-mail: oliparini@ufv.br

Pseudopenidiella gallaica



Fungal Planet 859 – 14 December 2018

Pseudopenidiella gallaica Iturrieta-González, Dania García, Gené, *sp. nov.*

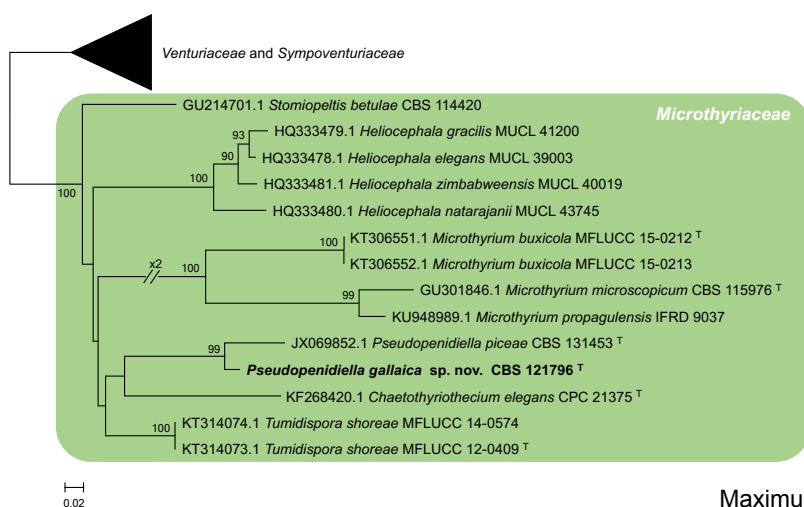
Etymology. Name refers to the Spanish region where the species was collected.

Classification — *Microthyriaceae*, *Microthyriales*, *Dothideomycetes*.

Mycelium consisting of branched, septate, pale brown, smooth-walled to verruculose hyphae of 1–1.5 µm diam. *Conidiophores* mononematous, dimorphic: microconidiophores reduced to conidiogenous cells on hyphae, 13–19 µm high, apex truncate 2 µm wide, pale brown; macroconidiophores unbranched, erect, subcylindrical, with up to 3-septate, pale brown to brown, often verruculose towards the apex, smooth- and thick-walled towards an often swollen base, up to 55 µm long (up to 120 µm long on the natural substratum), 2–3 µm wide. *Conidiogenous cells* terminal or subterminal, mono- or polyblastic, with up to 4 inconspicuous conidiogenous loci, verruculose, pale brown, 11–21.5 × 1.5–3 µm. *Ramoconidia* subcylindrical, aseptate, pale brown, smooth to verruculose, 7.5–11 × 2–3 µm, forming conidia in acropetal branched chains. *Conidia* cylindrical to ellipsoidal, aseptate, pale brown, smooth-walled to verruculose, 6–12 × 1–3 µm. *Sexual morph* not observed.

Culture characteristics — Colonies on PDA reaching 8–9 mm diam after 30 d at 25 °C, golden grey to black, velvety, erumpent, aerial mycelium scarce, feathery margin; reverse dark brown to black. On OA reaching 5–6 mm diam after 30 d at 25 °C, olive brown to black, slightly dusty, flat, aerial mycelium scarce; reverse dark brown to black.

Typus. SPAIN, Galicia, Pontevedra, Natural Park of Monte Aloia, on unidentified dead leaves, Feb. 2006, *J. Mena* & *C. Silvera* (holotype FMR H-9234, cultures ex-type CBS 121796 = FMR 9234; ITS and LSU sequences GenBank LT984842 and LT984843, MycoBank MB828082).



Colour illustrations. Natural Park of Monte Aloia, Pontevedra, Galicia, Spain; colony sporulating on PDA after 30 d at 25 °C and conidia after 10 d at 25 °C. Scale bars = 10 mm (colony) and = 10 µm (microscopic structures).

Notes — *Pseudopenidiella* was introduced to accommodate *P. piceae* (Crous et al. 2012b), a hyphomycetous fungus morphologically similar to *Cladosporium*, but phylogenetically distant to the family *Cladosporiaceae* (*Capnodiales*, *Dothideomycetes*). The genus was characterised by the formation of dimorphic conidiophores with terminal aseptate ramoconidia producing branched conidial chains, and by the absence of coronate-type scars on conidia or conidiogenous cells. In addition to the type, *P. pini* (formerly *Polyscytalum pini*; Kirk 1983) is currently included in *Pseudopenidiella* (Kirk 2014). However, the phylogeny of this latter species is obscure since only herbarium material (holotype IMI 242163) is available for comparison. *Pseudopenidiella pini* is characterised by the production of short and broad denticulate conidiogenous cells, a feature not described in *Pseudopenidiella*. *Pseudopenidiella gallaica* differs from *P. piceae* in its shorter conidiophores (up to 55 µm long in culture – up to 120 µm on the natural substratum – vs 150 µm long in *P. piceae*) and slightly longer conidia (up to 12 µm in *P. gallaica* vs up to 10 µm in *P. piceae*).

Based on a megablast search of NCBI's GenBank nucleotide, LSU sequence of *P. gallaica* showed a similarity of 95 % (742/785) with that of *P. piceae* (CBS 131453, GenBank NG_042681); while ITS sequence did not reveal any close hits. Our phylogenetic reconstruction shows that *Pseudopenidiella* is related to the members of the family *Microthyriaceae* (Abarca et al. 2011, Singtripop et al. 2016).

Maximum likelihood tree obtained from the analysis of LSU sequences of *Pseudopenidiella* and related genera of the family *Microthyriaceae*. Bootstrap support values above 70 % are indicated on the nodes. The alignment included 555 bp and was performed with ClustalW. Tamura Nei with Gamma distribution (G) was used as the best nucleotide substitution model. Both the alignment and tree were constructed with MEGA v. 6 software (Tamura et al. 2013). The new species proposed in this study is indicated in **bold face**. A superscript^T denotes ex-type cultures.

Pseudopyricularia persiana



Fungal Planet 860 – 14 December 2018

***Pseudopyricularia persiana* G. Ghorbani, Pordel & Jav.-Nikkh., sp. nov.**

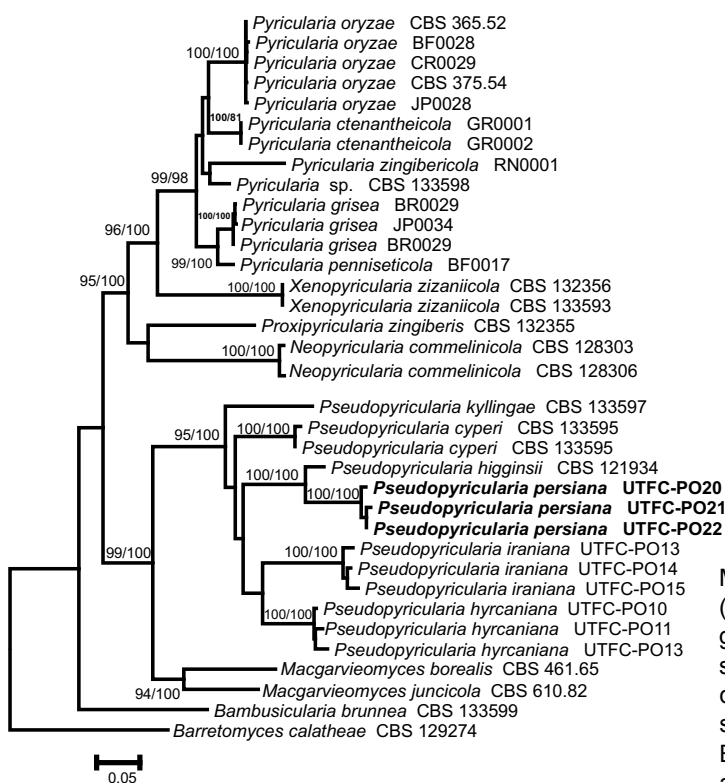
Etymology. Name refers to the old name of Iran, Persia.

Classification — *Pyriculariaceae*, *Magnaporthales*, *Sordariomycetes*.

Mycelium on SNA, and OA, consisting of smooth, hyaline, branched, septate hyphae. *Conidiophores* scattered, solitary, erect, pale brown, swollen at the base, macronematous, mononematous, typically unbranched, rarely branched, straight, aseptate, some conidiophores consisting of 1–6 cells, 137–332(–380) × 5–7 μm. *Conidiogenous cells* integrated, terminal, intercalary, sympodial, cylindrical, geniculate, denticulate; denticles cylindrical, thin-walled, pale brown. *Conidia* solitary, dry, obclavate, hyaline, (30–)36–52(–65) × 10–13 μm, 2(–3)-septate, hilum often protuberant, conidia produce secondary conidiophore. *Sexual morph* unknown.

Culture characteristics — Colonies on OA transparent, buff, reaching 42 mm diam after 1 wk at 23–25 °C; on PDA transparent, white, and straw reverse, reaching 26 mm diam after 1 wk at 23–25 °C.

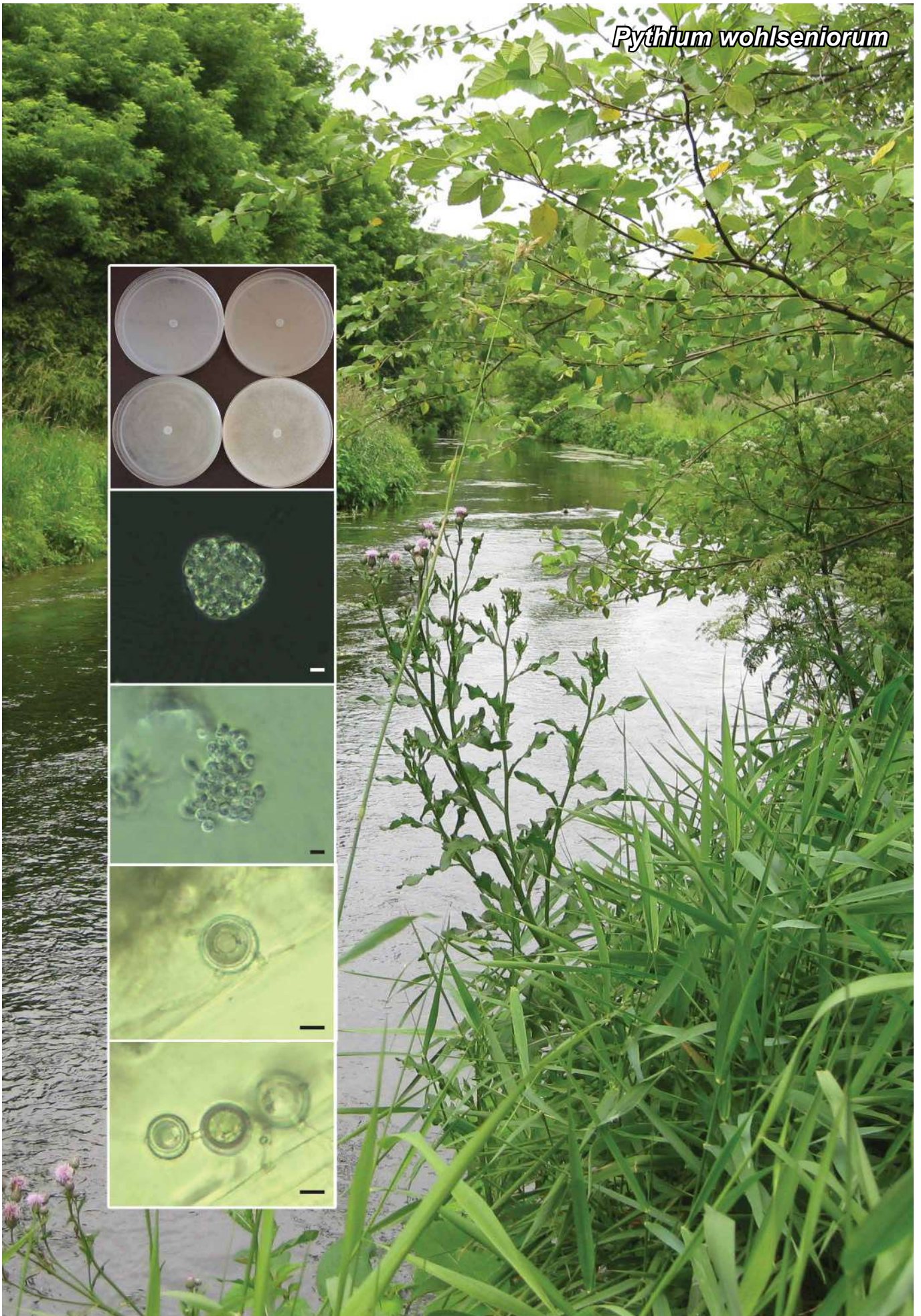
Typus. IRAN, Guilan province, Lasht-e Nesha city, on infected leaves of *Cyperus* sp., 19 Oct. 2017, G. Ghorbani (holotype UTF-C-PO20, culture ex-type UTF-C-PO21, ITS, LSU, *RPB1* and *CAL* sequences GenBank MH780926, MH780974, MH699975 and MH699978, MycoBank MB826968).



Notes — This species is similar to *Ps. higginsii*, *Ps. cyperi*, *Ps. iraniana*, *Ps. kyllingae* and *Ps. haghagae* in having 2-septate conidia (Klaubauf et al. 2014, Pordel et al. 2017). However, the conidia and conidiophores of *Ps. persiana* are larger than those of *Ps. higginsii*, *Ps. cyperi*, *Ps. kyllingae* and *Ps. haghagae*. It differs from *Ps. iraniana* in conidial shape and size. To clarify the identification of *Ps. persiana* within *Pseudopyricularia*, *CAL*/*ITS*/*RPB1* sequences were combined in a phylogenetic analysis. The phylogenetic tree suggested phylogenetic relatedness of the taxa from Iran to *Pseudopyricularia* with high statistical support (Bayesian Posterior Probability = 100 %, Maximum Likelihood bootstrap support = 100 %). Our and previous data identified seven species in *Pseudopyricularia*, which is sister to *Macgarvieomyces*. *Macgarvieomyces* is morphologically well-separated from *Pseudopyricularia* because the former produces chlamydospores, has conidiophores that are mostly unbranched and conidia that are narrowly obclavate, granular and 1-septate. Isolates of *Ps. persiana* clustered sister to *Ps. higginsii*. However, conidia and conidiophores sizes of *Ps. persiana* are distinct from those of *Ps. higginsii*. Maximum likelihood and Bayesian Inference analyses of the combined *CAL*, *ITS* and *RPB1* sequences support the classification of the new species in *Pseudopyricularia*, a genus that is distantly related to *Pyricularia*. Morphological characteristics combined with analyses of DNA sequences allowed us to identify and illustrate *Ps. persiana* as a novel species from Iran.

Colour illustrations. Leaves of *Cyperus* sp.; solitary, erect, unbranched and branched conidiophores, obclavate conidia. Scale bars = 10 μm.

Pythium wohlseniorum



Fungal Planet 861 – 14 December 2018

***Pythium wohlseniorum* J.E. Blair, sp. nov.**

Etymology. Named in honour of Carolyn W. and Robert S. Wohlsten, who founded Millport Conservancy in Lititz, Pennsylvania, USA in 1969.

Classification — *Pythiaceae*, *Pythiales*, *Oomycetes*.

Main *hyphae* up to 5 µm diam. *Sporangia* filamentous non-inflated, giving rise to vesicles containing abundant zoospores at room temperature on 0.2 % water agar with sterile grass blades. *Encysted zoospores* 7–10 µm (av. 8.5 µm) diam, form large grape-like clusters. *Oogonia* produced in single culture after several weeks, globose, smooth-walled, mostly intercalary, occasionally catenulate, 20–23 µm (av. 21.6 µm) diam. *Antheridia* monoclinal, one per oogonium. *Oospores* single, aplerotic or nearly plerotic, globose, 16–19 µm (av. 17.9 µm) diam, wall 1.1–1.6 µm (av. 1.3 µm) thick.

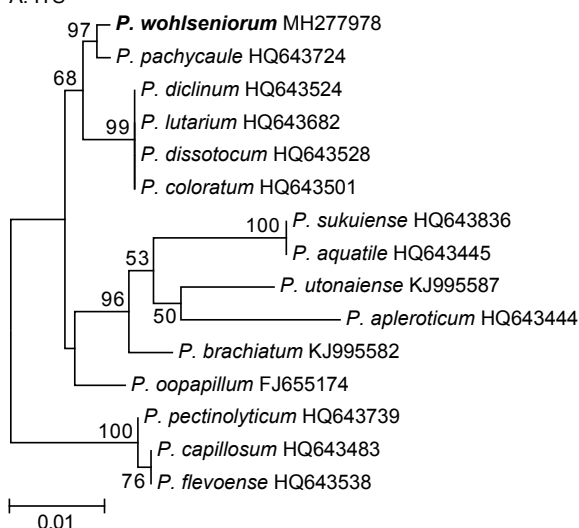
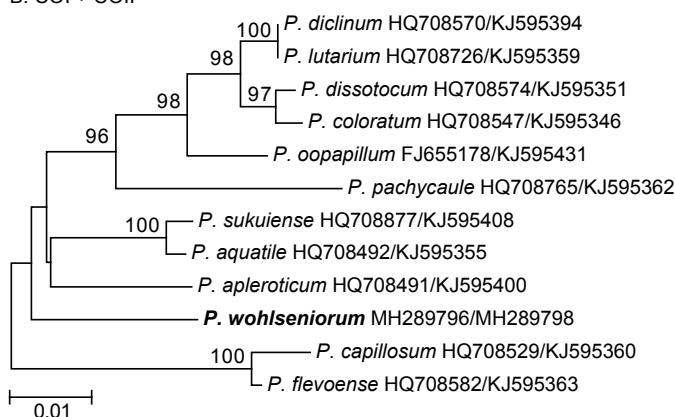
Culture characteristics — Produces dense, aerial hyphae on potato-dextrose agar (PDA), thin aerial hyphae with no special pattern on potato-carrot (PCA) and clarified V8 agars (V8A), and a chrysanthemum pattern with light aerial hyphae on cornmeal agar (CMA). Colony diam. after 24 h at 25 °C on PDA 26 mm, PCA 28 mm, V8A 25 mm, CMA 23 mm. Optimal growth at 28 °C.

Typus. USA, Pennsylvania, Warwick Township, Millport Conservancy, from stream water, 12 May 2015, J.E. Blair & S. Lobdell W15-2 (holotype CBS 144501, preserved as metabolically inactive culture, ITS, *COI*, *COII*, beta-tubulin and LSU sequences GenBank MH277978, MH289796, MH289798, MH289799 and MH289800; MycoBank MB826753).

Additional material examined. USA, Pennsylvania, Warwick Township, Millport Conservancy, from stream water, 20 June 2017, J.E. Blair & A.M. Bauer (CBS 144502 = W17-58; *COI* sequence GenBank MH289797).

Notes — Isolates were first collected in 2013 and subsequently in 2015 and 2017; this species is commonly baited from stream water with hemp seed, or in association with various submerged pondweeds. Despite extensive stream sampling in the area, *Pythium wohlseniorum* has only been recovered to date from Lititz Run at Millport Conservancy. Phylogenetic analysis of both mitochondrial and nuclear loci place *P. wohlseniorum* in *Pythium* Clade B2 sensu Levesque & De Cock (2004), closely related to *P. pachycaule*. Sequences from 11 isolates were identical for *COII*, ITS, LSU and beta-tubulin loci; a single nucleotide polymorphism was present in *COI* sequences. *Pythium wohlseniorum* has a higher optimal temperature compared to *P. pachycaule*, and a faster growth rate at 25 °C than *P. pachycaule*, *P. coloratum*, *P. diclinum*, *P. dissotocum* and *P. lutarium*. Other morphological features overlap with other Clade B2 species.

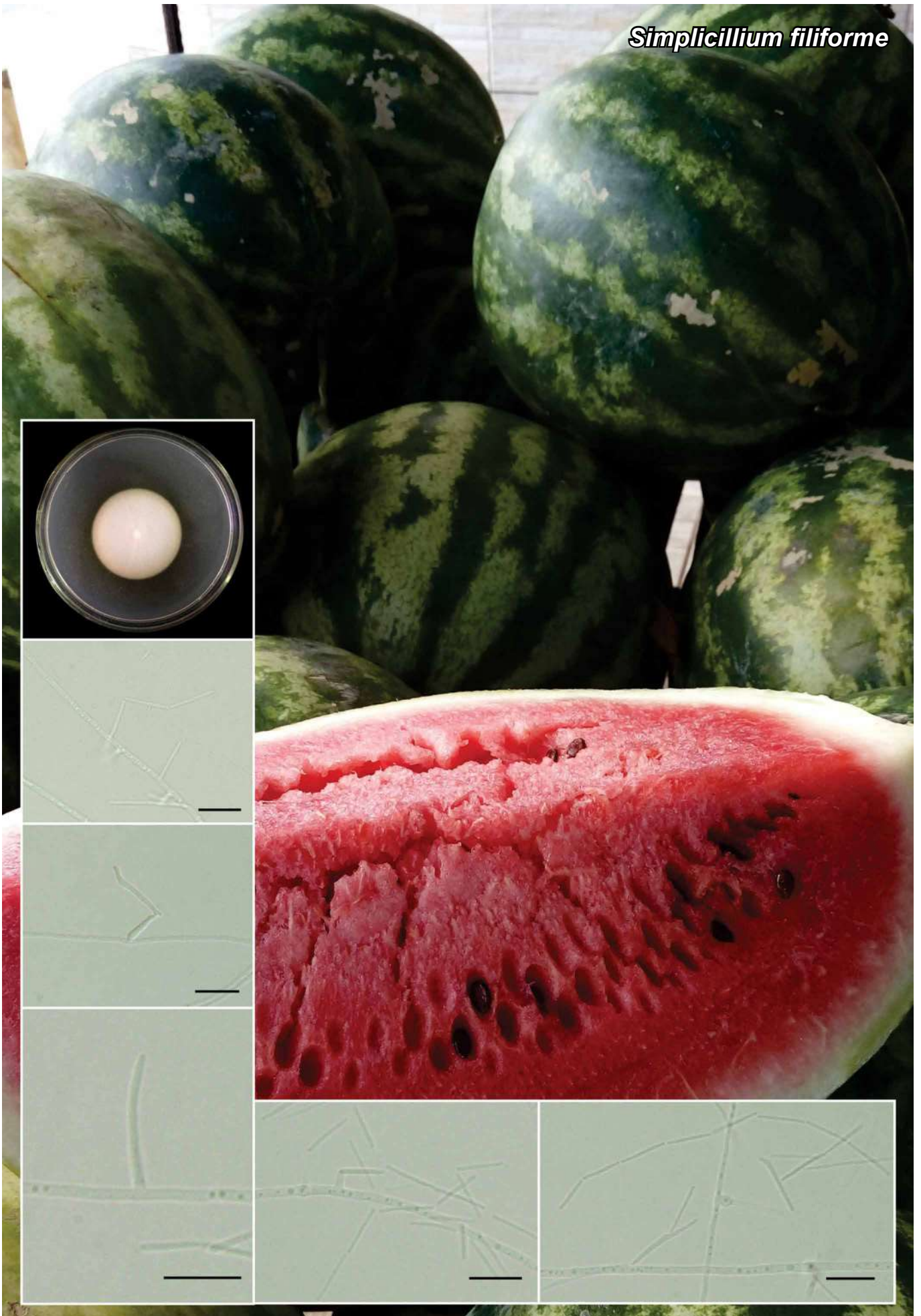
A. ITS

B. *COI* + *COII*

Pythium Clade B2 neighbour-joining phylogenies (Kimura-2-parameter model) for ITS (A) and *COI* + *COII* (B) alignments, indicating the position of *P. wohlseniorum*. Phylogenies were reconstructed using MEGA6 (Tamura et al. 2013). Bootstrap support values ≥ 50 % (2000 replicates) are shown on each node; NCBI accession numbers are given after each species name.

Colour illustrations. Lititz Run at Millport Conservancy; culture morphology (clockwise from top-left) on V8A, PCA, CMA and PDA, vesicle containing zoospores, cluster of encysted zoospores, intercalary oogonium with single oospore, catenulate oogonia. Scale bars = 10 µm.

Simplicillium filiforme



Fungal Planet 862 – 14 December 2018

Simplicillium filiforme R.M.F. Silva, R.J.V. Oliveira, Souza-Motta, J.L. Bezerra & G.A. Silva, *sp. nov.*

Etymology. The name refers to the filiform shape of its conidia.

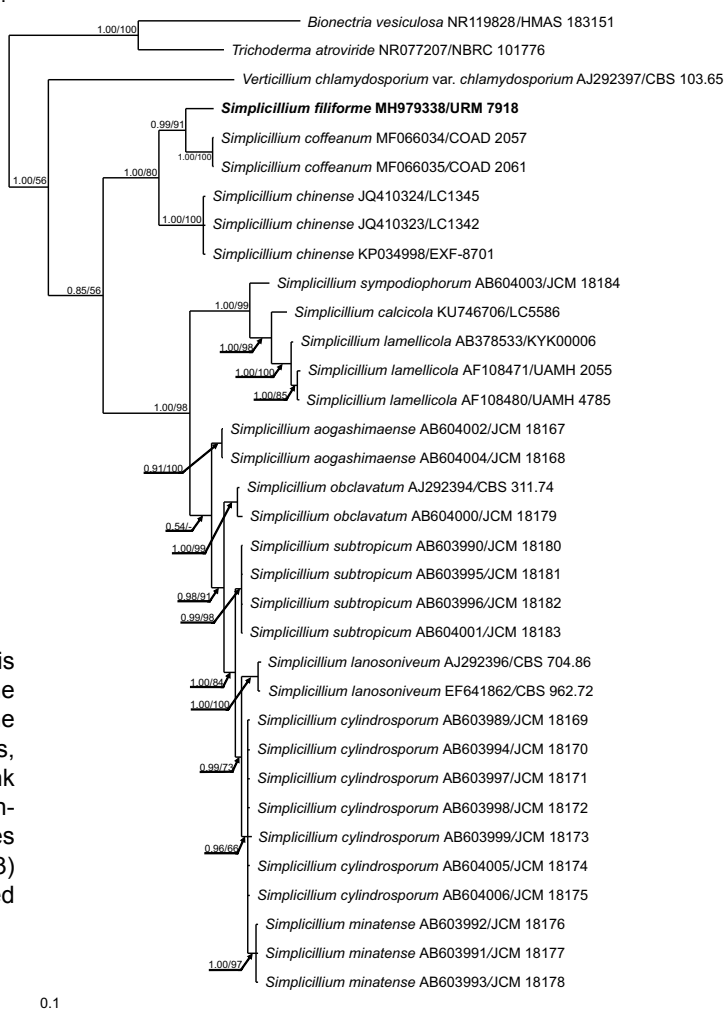
Classification — *Cordycipitaceae*, *Hypocreales*, *Sordariomycetes*.

Mycelial hyphae thin, hyaline, septate, branched, smooth-walled, 1.8–2.7 µm diam. *Phialides* hyaline, produced on aerial hyphae, solitary, elongate, slightly tapering towards the apex, 9–18 × 1 µm. *Conidia* long, fusoid to filiform, hyaline, smooth-walled, catenulate, straight to curved, sometimes forming zigzag chains, 7.2–12.5 × 1 µm.

Culture characteristics — Colonies on PDA reaching 44 mm diam after 10 d at 25 °C, white, slow growth, moderate aerial mycelium, cottony surface, compact. Reverse white to yellowish cream. Colonies on MEA reaching 40 mm diam after 10 d at 25 °C, white, slow growth, cottony surface, moderate aerial mycelium. Reverse dark yellow.

Typus. BRAZIL, Pernambuco state, Petrolândia municipality, isolated as endophyte from leaves of *Citrullus lanatus* (*Cucurbitaceae*), 25 July 2016, R.M.F. Silva (holotype URM 91886, culture ex-type URM 7918, ITS and LSU sequences GenBank MH979338 and MH979399, MycoBank MB827982).

Notes — The genus *Simplicillium* was introduced by Zare & Gams (2001). Members of this genus include endophytic species, parasites and saprobes isolated from different environments such as soil, freshwater, plants and other parasitic fungi (Liu & Cai 2012, Nonaka et al. 2013, Gomes et al. 2018). Morphologically, *S. filiforme* is similar to *S. obclavatum* and *S. chinense* which also form conidial chains. However, *S. filiforme* is different from *S. obclavatum* and *S. chinense* based on the size and shape of its conidia. *Simplicillium filiforme* produces conidia that are long, fusoid to filiform, catenulate, straight to curved (7.2–12.5 × 1 µm) while *S. obclavatum* produces conidia obclavate to ellipsoidal (2.5–3.5 × 1–2 µm) and *S. chinense* produces conidia that are mostly ovoid, ellipsoidal or cylindrical (3.5–5 × 1–1.5 µm). Based on ITS rDNA, the new species *S. filiforme* is phylogenetically close to *S. coffeanum*, though *S. coffeanum* form macroconidia and microconidia with subglobose to ellipsoidal heads at the apex of the phialides (Gomes et al. 2018).



Bayesian inference (BI) tree obtained by phylogenetic analysis of ITS rDNA sequences from members of *Simplicillium*. The new species is in **bold** face. Support values, shown at the nodes, are from BI and Maximum Likelihood (ML) analyses, respectively. *Bionectria vesiculosa* (HMAS 183151, GenBank NR119828) and *Trichoderma atroviride* (NBRC 101776, GenBank NR077207) were used as outgroup. BI and ML analyses were performed in MrBayes (Ronquist & Huelsenbeck 2003) and PhyML (Guindon & Gascuel 2003), respectively, launched from TOPALI v. 2.5 (Milne et al. 2004).

Colour illustrations. Watermelons for sale, Pernambuco, Brazil; colony on PDA, phialides and conidia, conidial chain. Scale bars = 10 µm.

Superstratomyces tardicrescens



Fungal Planet 863 – 14 December 2018

Superstratomyces tardicrescens Valenz.-Lopez, Rodr.-Andrade, Cano, Guarro & Stchigel, *sp. nov.*

Etymology. From Latin *tarde*-, slowly, and *-crescens*, growing, due to the slow growing rates of the colonies on culture media.

Classification — *Superstratomycetaceae*, *Superstratomyceales*, *Dothideomycetes*.

Hyphae hyaline to brown, smooth- and thin- to thick-walled, septate, 2–3.5 µm wide. *Conidiomata* pycnidial, superficial, solitary or confluent, brown to black, glabrous, globose, 110–125 µm diam, filled by a white mass of slimy conidia; *pycnidial wall* 25–45 µm broad, pseudoparenchymatous, of *textura angularis*, composed of 3–5 layers of pale brown to brown, flattened polygonal cells of 2.5–5 µm diam. *Setae* erect to recurved, hyaline to subhyaline at apex and turning brown towards the base, 1–2-septate, 10–70 µm in length, 3–5 µm wide at the base, strongly verrucose to tuberculate. *Conidiophores* branched, hyaline, smooth-walled, up to 30–40 µm long, bearing lateral conidiogenous cells. *Conidiogenous cells* phialidic, hyaline, cylindrical to barrel-shaped or ampulliform, 5–8.5 × 1.5–2 µm, smooth-walled, solitary or laterally disposed on the conidiophores. *Conidia* hyaline, aseptate, smooth- and thin-walled, guttulate, cylindrical to navicular, 4–5 × 1.5–2 µm.

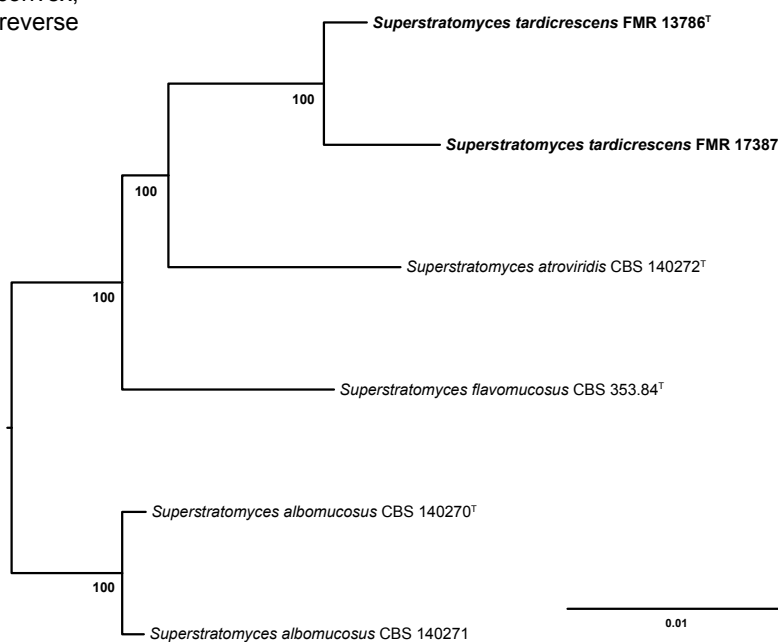
Culture characteristics — Colonies on OA reaching 7 mm diam after 14 d at 25 ± 1 °C, margins lobate, flattened, both surface and reverse black (M. 2F1). Colonies on MEA reaching 7 mm diam after 14 d at 25 ± 1 °C, margins lobate, convex, felted, surface white (M. 2A1) to olive grey (M. 2E2); reverse black (M. 2F1).

Colour illustrations. USA, South Carolina; colony on OA and MEA after 14 d at 25 ± 1 °C; conidiomata under the stereomicroscope; pycnidia, conidiophores, conidiogenous cells and conidia. Scale bars: 50 µm (pycnidia), 10 µm (conidiophores, conidiogenous cells and conidia).

Typus. USA, South Carolina, from a human eye specimen, 2010, D.A. Sutton (holotype FMR H-13786, culture ex-type FMR 13786, ITS, LSU and *tef-1α* sequences GenBank LR025130 and LR025141, MycoBank MB828061).

Additional material examined. SPAIN, Tarragona, Els Pallaresos, from the darkened surface of a wall house, 19 Apr. 2018, E. Rodríguez-Andrade, FMR 17387, ITS, LSU and *tef-1α* sequences GenBank LR025131 and LR025142.

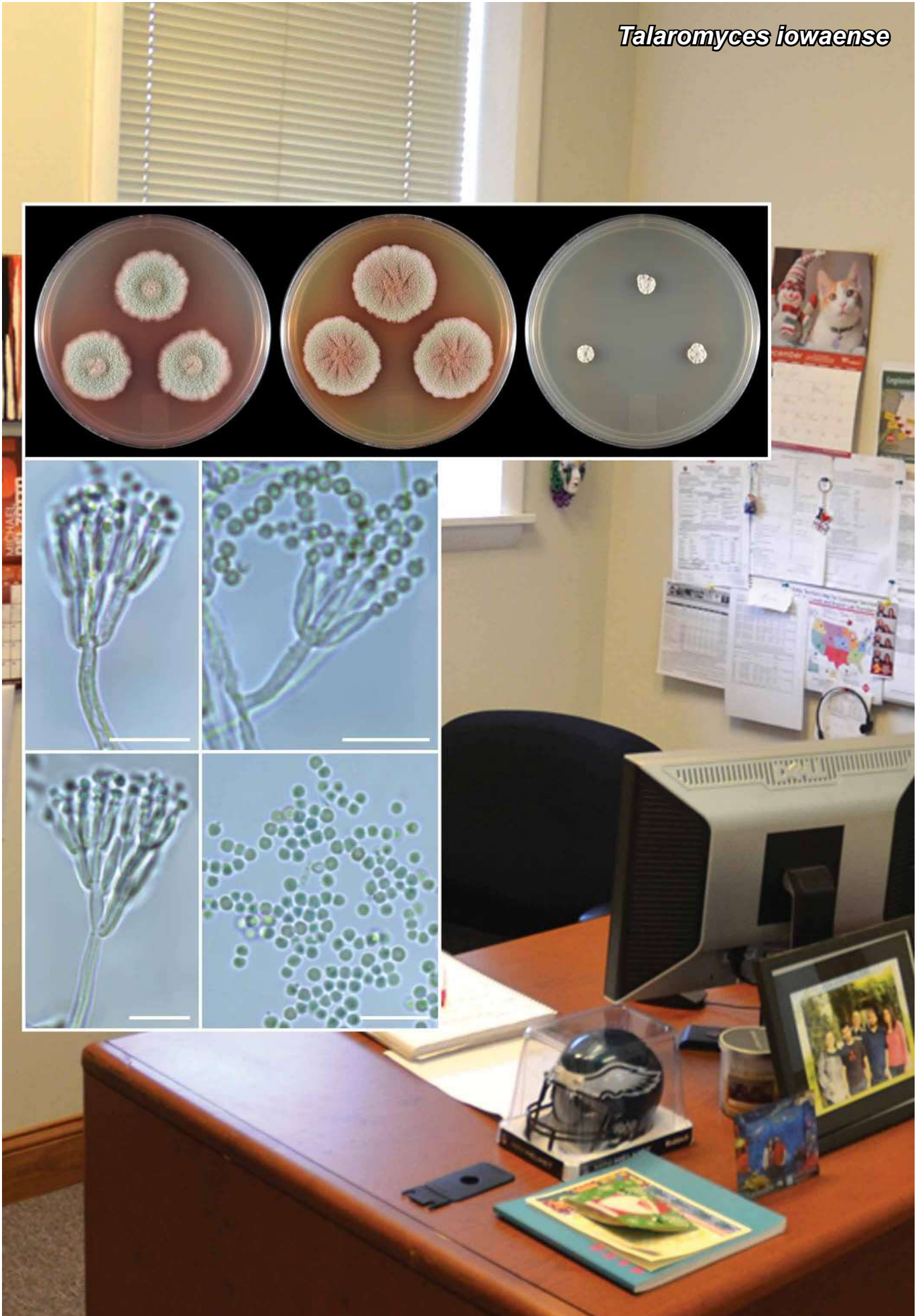
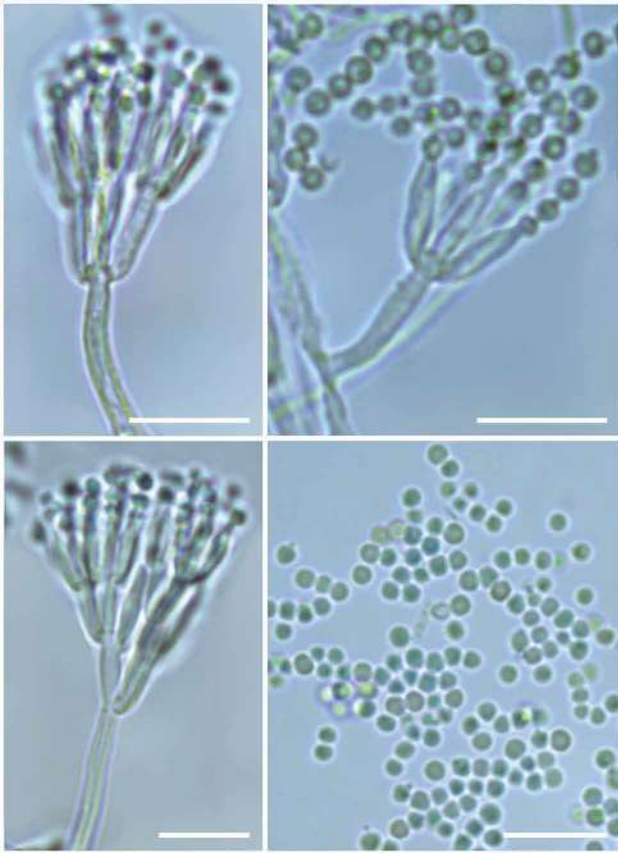
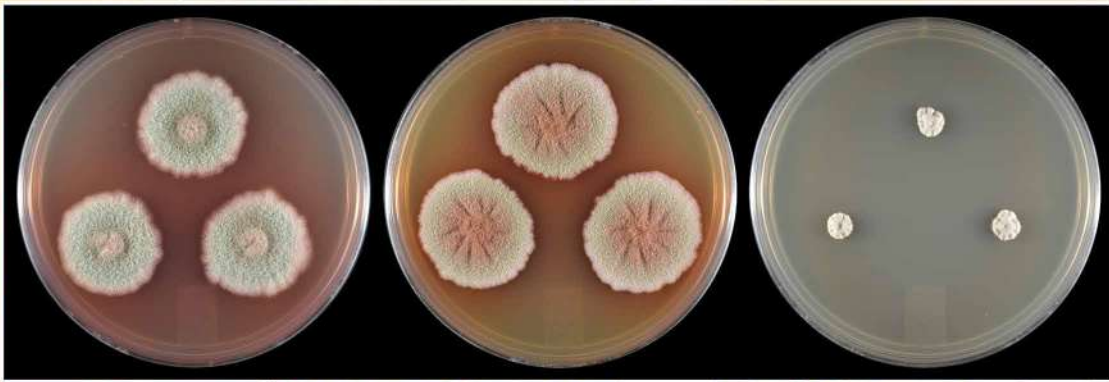
Notes — The geographical origin of the strains (USA and Spain) and the nature of the substrates from which they were isolated (human and environmental ones) probably indicates a wide distribution of this new taxon. *Superstratomyces tardicrescens* is distinguished from the rest of the species of the genus by its small conidia produced on well-developed conidiophores (larger, and produced on single phialides in the rest of the species) (Van Nieuwenhuijzen et al. 2016). Based on a megablast search of NCBI's GenBank nucleotide database, the closest hit using the LSU sequences is *S. atroviridis* CBS 140272 (GenBank NG_058271; Identities = 762/766 (99 %), 1 gaps (0 %)). Closest hits using the ITS sequence is *S. albomucosus* DTO 277-H8 (GenBank KX950421; Identities = 778/790 (98 %), 2 gaps (0 %)). The closest hits using *tef-1α* sequence is *S. flavomucosus* DTO 305-C3 (GenBank KX950470; Identities = 869/889 (98 %), no gaps).



Maximum likelihood tree obtained from the combined DNA sequences dataset from tree loci (ITS, LSU, *tef-1α*) of our isolates and sequences retrieved from the GenBank database. Ex-type strains of the different species are indicated with ^T. The new species proposed in this study is indicated in bold. The RAxML bootstrap support values (≥ 70 %) are provided at the nodes. *Superstratomyces albomucosus* was used as outgroup.

Nicomedes Valenzuela-Lopez, Mycology Unit, Medical School and IISPV, Universitat Rovira i Virgili (URV), Sant Llorenç 21, 43201 Reus, Tarragona, Spain; Microbiology Unit, Medical Technology Department, Faculty of Health Science, University of Antofagasta, Av. Universidad de Antofagasta s/n, 02800 Antofagasta, Chile; e-mail: nicomedes.vl@gmail.com
Ernesto Rodríguez-Andrade, Alberto M. Stchigel, Josep Guarro & José F. Cano-Lira, Mycology Unit, Medical School and IISPV, Universitat Rovira i Virgili (URV), Sant Llorenç 21, 43201 Reus, Tarragona, Spain; e-mail: dc.ernesto.roan@outlook.com, albertomiguel.stchigel@urv.cat, joSept.guarro@urv.cat & jose.cano@urv.cat

Talaromyces iowaense



Fungal Planet 864 – 14 December 2018

Talaromyces iowaense Jurjević, G. Perrone, S.W. Peterson, A. Susca, F. Epifani,
sp. nov.

Etymology. Named for Iowa, USA, where the fungal culture was isolated.

Classification — *Trichocomaceae*, *Eurotiales*, *Eurotiomycetes*.

On MEA. *Conidiophores* (8–)25–85(–135) × (2–)2.5–3(–4) µm, borne from surface and from aerial rope-like hyphal aggregations, with smooth to finely roughened walls, bearing terminal biverticillate, or more complex, occasionally monoverticillate penicilli, metulae (5–)6–10(–16) × 2–4 µm, smooth to finely roughened, in verticils of (2–)4–9(–11), phialides acerose, (6–)7–9(–11) × 2–3 µm, with long, gradually tapering collula, smooth to occasionally finely roughened, (2–)5–7(–9) per metula. *Conidia* sub-spherical to spherical, 2–2.5(–3) × 2–3 µm, with finely roughened walls, borne in short disordered chains. No *sexual morph* observed.

Culture characteristics — (in darkness, 25 °C after 14 d): Colonies on malt extract agar (MEA) 30–31 mm diam, colony texture floccose to funiculose, centrally rising c. 3 mm, occasional shallow radial sulci, mycelium white to pink (Venetian pink R13; Ridgway 1912) or reddish orange (orange rufous, R2), sporulation heavy, conidia *en masse*, light celandine green to Artemisia green (R47), exudate absent, soluble pigments red (light coral red to Pompeian red, R8), reverse mahogany red (R2) to light pinkish cinnamon (R29). Colonies on Czapek yeast autolysate agar (CYA) 3–4 mm diam, mycelium white, subsurface or submerged hyphae, sporulation not observed, exudate absent, soluble pigments absent, reverse cartridge buff to cream-buff (R30). Colonies on potato dextrose agar (PDA) 25–26 mm diam, colony texture floccose to funiculose, moderate deep to deep radial sulci, mycelium white to deep vinaceous (R27), sporulation moderate to heavy, in zones, conidia *en masse* pale green-blue grey to deep green-blue grey (R48), exudate clear, soluble pigments absent, reverse orange-vinaceous (R27) to orange-cinnamon (R29) to cream-buff (R30), marginally. Colonies on Czapek yeast agar with 20 % sucrose (CY20S) 2–3 mm diam, colony texture floccose to funiculose, mycelium white to ochraceous-orange (R15), sporulation moderate to very good, conidia *en masse* pale greenish blue grey to deep greenish blue grey (R48), pale green-blue grey to deep green-blue grey (R48), exudate absent, soluble pigments absent. Colonies on dichloran-glycerol agar (DG18) 11–12 mm diam, colony texture funiculose, at margins 2–3 mm diam subsurface to submerged hyphae, mycelium

white, sporulation moderate, conidia *en masse* not coloured, exudate absent, soluble pigments absent, reverse cartridge buff to cream-buff (R30). No growth on CYA with 5 % NaCl (CYAS). Colonies on oatmeal agar (OA) 9–10 mm diam, colony texture floccose to funiculose, abruptly rising c. 4–5 mm, mycelium white, inconspicuous, heavy sporulation, conidia *en masse* glaucous-grey to deep greyish blue-green (R48), exudate absent, soluble pigments absent. Colonies on creatine sucrose agar (CREA), up to 8 mm diam, no acid production. Colony diam, 14 d (mm): CYA/MEA 20 °C 2–3/22–24; 30 °C 3–4/33–35; 35 °C 1–2/9–11; no growth at 37 °C. Colony diam, 7 d (mm): CYA 1–2; MEA 17–18; PDA 10–12; CY20S no growth to germinate; DG18 3–4; CYAS no growth; OA 6–7 mm; CREA up to 4 mm; Colony diam, 7 d (mm): CYA/MEA 20 °C germinate/12–13; 30 °C 1–2/19–20; 35 °C germinate/5–6; no growth at 37 °C.

Typus. USA, Iowa, Jefferson, office, air, 27 Jan. 2014, Ž. Jurjević (holotype BPI 910643, cultures ex-type NRRL 66822 = ITEM 17527 = EMSL 2233, ITS, *BenA*, *CaM* and *rpb2* sequences GenBank MH281565, MH282578, MH282579 and MH282577, MycoBank MB828092).

Notes — BLAST searches of the sequences of *Talaromyces iowaense* showed β-tubulin (*BenA*) similarity to *T. rademirici* (83 %), calmodulin (*CaM*) similarity to *T. purpureus* (82 %), RNA polymerase II second largest subunit (*rpb2*) similarities to *T. rademirici* (89 %) and *T. purpureus* (87 %), and ITS similarity to *T. purpureus* was 91 %.

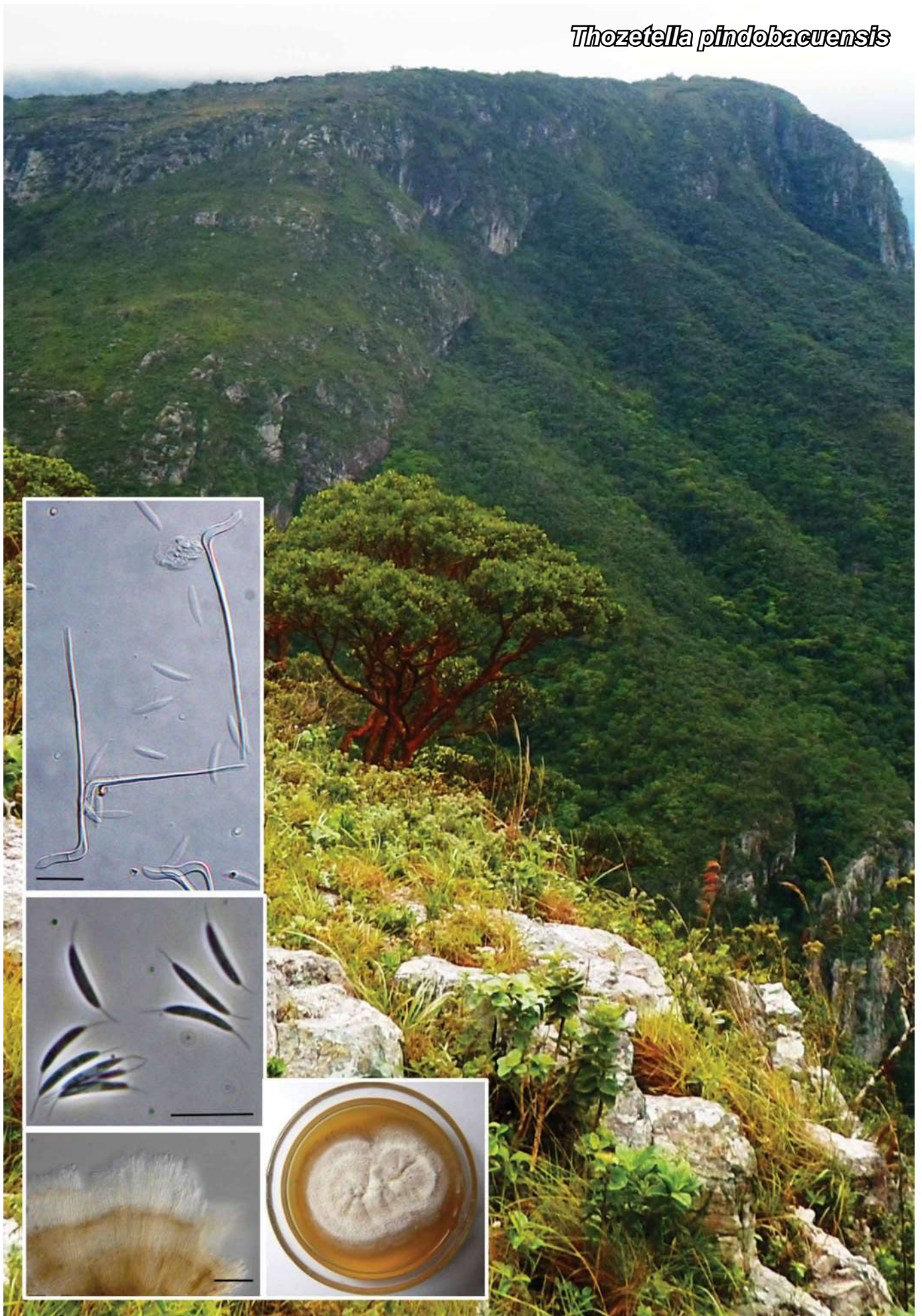
A phylogenetic tree with three genes was generated (no *T. rademirici* calmodulin sequence available), and the branch resolution improved when this species is included. The maximum likelihood analysis of DNA sequences show net separation of this new species from the other well-resolved branches. *Talaromyces iowaensis* clusters with the species from *Talaromyces* sect. *Purpurei*. *Talaromyces iowaense* is distinguished from other *Talaromyces* species by production of intense red (light coral red to Pompeian red, R8) soluble pigments on MEA, good growth on MEA but restricted on CYA, growth on CREA, no growth at 37 °C, and conidia 2–2.5(–3) × 2–3 µm. The closely related *T. rademirici* demonstrates no soluble pigments on MEA, good growth on CYA and MEA, no growth on CREA, growth at 37 °C, and has larger conidia 2.5–4 × 1.5–2.5 µm.

For supplementary information see MycoBank.

Colour illustrations. Air, office; 14-d-old cultures of *Talaromyces iowaense* on MEA (left: 25 °C, middle: 30 °C, right: 35 °C), conidia and conidiophores on MEA. Scale bars = 10 µm.

Željko Jurjević, EMSL Analytical, Inc., 200 Route 130 North, Cinnaminson, NJ 08077, USA; e-mail: zjurjevic@emsl.com
Giancarlo Perrone, Antonia Susca & Filomena Epifani, Institute of Sciences of Food Production, CNR, Via Amendola 122/O, 70126 Bari, Italy; e-mail: giancarlo.perrone@ispa.cnr.it
Stephen W. Peterson, Mycotoxin Prevention and Applied Microbiology Research Unit, Agricultural Research Service, U.S. Department of Agriculture, 1815 North University Street, Peoria, IL 61604, USA; e-mail: stephen.peterson@ars.usda.gov

Thozetella pindobacuensis



Fungal Planet 865 – 14 December 2018

Thozetella pindobacuensis T.A.B. Santos, L.B. Conç. & Gusmão, *sp. nov.*

Etymology. Referring to the municipality of Pindobaçu where this fungus was collected.

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

Colonies on natural substrata effuse, whitish. *Mycelium* partly superficial, partly immersed in the substrata, hyphae septate, branched, cylindrical cells, 1.5–2.5 µm diam, smooth-walled, pale brown. *Stromata* absent. *Conidiomata* synnematal, infundibuliform, campanulate, convex and wide at the apex, straight, unbranched, brown, pale brown to pale yellowish brown, 154–200 µm high, 30–65.5 µm wide at the base, 255–311 µm wide at the apex, with synchronous extensions. *Conidiophores* macronematous, septate, cylindrical, smooth, pale brown. *Conidiogenous cells* monophialidic, integrated, determinate, terminal, cylindrical, smooth, pale brown, 10–21 × 1.5–2.5 µm, collarette absent. *Conidia* lunate, fusiform, ellipsoid-fusoid, rarely naviculate, continuous, guttulate or eguttulate, hyaline, 13.5–18 × 1.5–2 µm, provided with a single setula at each end, setulae 4.5–7 µm long. *Microawns* awn-like, L-shaped to almost straight, 0–1-septate, smooth, refractive, hyaline, 19–75 × 1.5–3.5 µm, basal part thin-walled.

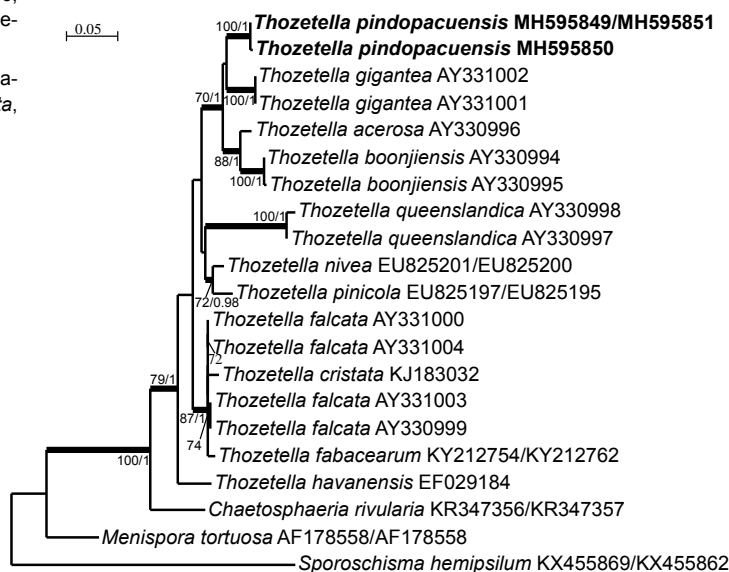
Culture characteristics — Colonies on 2 % malt extract agar (MEA), reaching 55 mm diam after 15 d at 25 °C, immersed mycelium, semicircular, entire edges, whitish. Reproductive structures and microawns present on the surface of the culture medium and abundant in the centre and the edge of the colony.

Typus. BRAZIL, Bahia, Pindobaçu, Serra da Fumaça, on decaying leaves of unidentified plant, 19 Feb. 2017, L.B. Conceição (holotype HUEFS239376, isotype HUEFS239377, cultures ex-type LAMIC0122/17, ITS and LSU sequences GenBank MH595849 and MH595851, MycoBank MB827077).

Additional specimen examined. BRAZIL, Ceará, Ubajara, Serra de Ibiapaba, on decaying leaves of *Vismia guianensis*, 5 July 2012, L.A. Costa, LAMIC0134/12, ITS sequence GenBank MH595850.

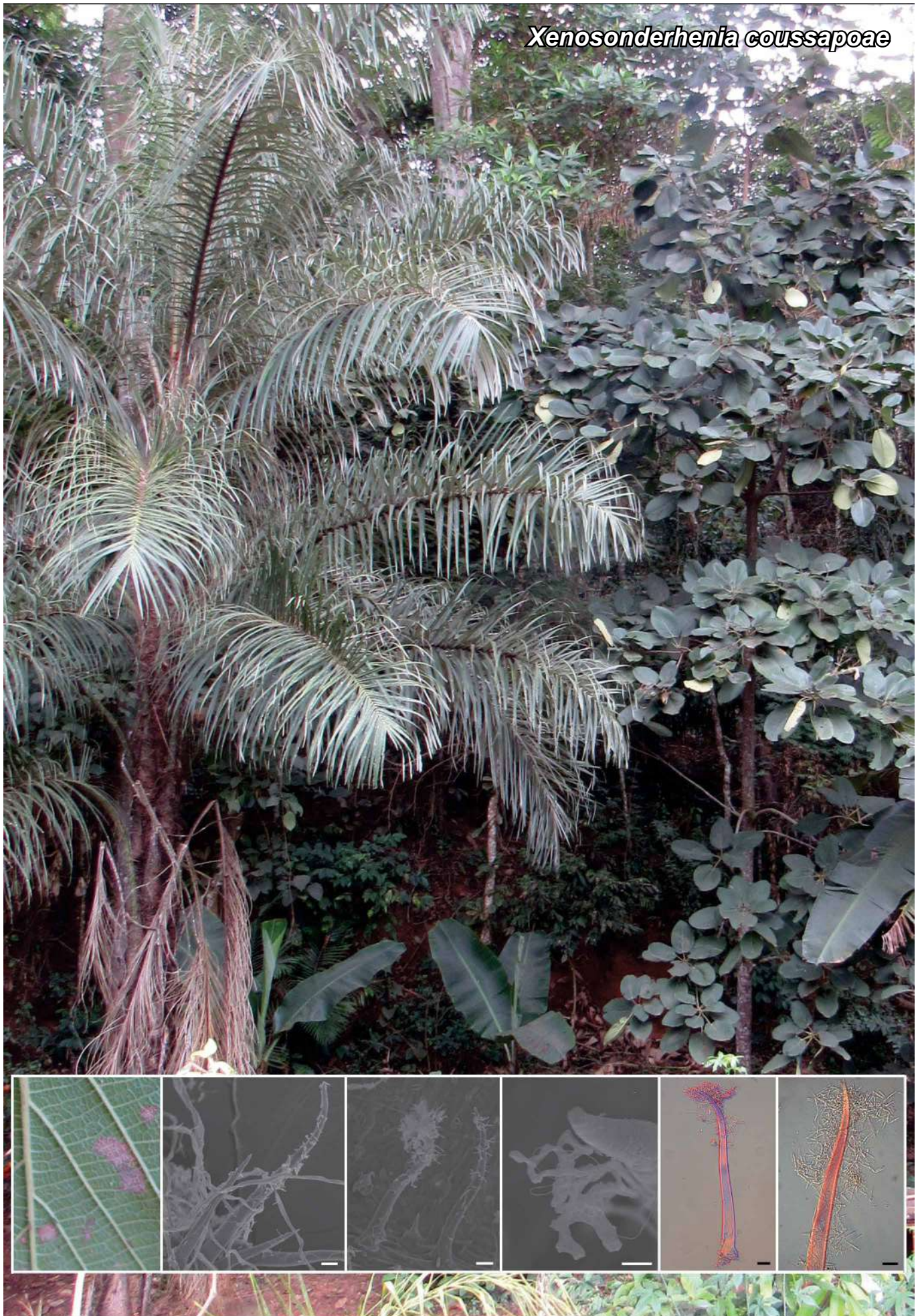
Colour illustrations. Background photo of Serra da Fumaça; 15-d-old culture on MEA, conidiomata with synchronous extensions, conidiogenous cells, conidia and microawns. Scale bars = 20 µm.

Notes — Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *T. gigantea* (GenBank AY331002 and AY331001; Identities = 432/442 and 431/442 (98 %), no and 1 gap, respectively), *T. acerosa* (GenBank AY330996; Identities = 440/455 (97 %), 1 gap) and *T. boonjiensis* (GenBank AY330995; Identities = 424/442 (96 %), 1 gap). Closest hits using the LSU sequence had highest similarity to *T. fabacearum* (GenBank NG_059767 and KY212762; Identities = 499/518 (96 %), 6 gaps (1 %)), *T. nivea* (GenBank EU825200; Identities = 497/518 (96 %), 6 gaps (1 %)) and *Chaetosphaeria rivularia* (GenBank KR347357; Identities = 490/519 (94 %), 7 gaps (1 %)). Morphologically, *T. pindobacuensis* differs from *T. gigantea* based on the size of the microawns (65–280 × 2.5–8 µm) and conidial setula (6–12.5 µm long) (Paulus et al. 2004, Silva & Grandi 2013). Furthermore, the new species has synnematal conidiomata with synchronic extensions and 0–1-septate microawns. *Thozetella pindobacuensis* differs from *T. acerosa*, *T. boonjiensis* and *T. nivea* in the production of sporodochial conidiomata and the shape of its microawns. In this paper, we considered *T. acerosa* and *T. boonjiensis* as distinct species based on molecular data (Paulus et al. 2004, Jeewon et al. 2009, Perera et al. 2016).



Maximum likelihood (ML) tree based on combined dataset of ITS and LSU sequences. The ML analysis was performed using RAxML v. 8.2.10. The Bayesian inference (MrBayes v. 3.2.6) was performed under a GTR+G+I model for 2 M generations. The values of ML bootstrap (BP-ML) and posterior probabilities (PP-BI) were plotted at the nodes for which threshold values (BP-MP: > 50 % / BP-ML: > 70 % / PP: > 0.95) were achieved. One access number = ITS; two access numbers ITS and LSU sequences, respectively. The novel species is indicated in bold face.

Xenosonderhenia coussapoeae



Fungal Planet 866 – 14 December 2018

Xenosonderhenia coussapoe J.L. Alves & R.W. Barreto, *sp. nov.*

Etymology. Name reflects the host genus from which it was isolated, *Coussapoa*.

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

Leaf spots amphigenous, irregular, 1–7 mm diam, medium brown with irregular edges, white patches due to raised epidermis, surrounded by a wide, red-purple border and with abundant fungal structures abaxially. *Internal mycelium* indistinct. *External mycelium* superficial, up to 2–3 µm diam, branched, septate, pale brown, smooth. *Stromata* absent. *Conidiophores* arising from external mycelium, either isolated or clustering on trichomes, cylindrical, 17.5–40 × 5–7.5 µm, 1–3-septate, not branched, hyaline to subhyaline, smooth. *Conidiogenous cells* terminal or intercalary, subcylindrical, 18–39.5 × 5–7 µm, smooth. *Conidiogenous loci* protuberant, 3–7 per cell up to 1 µm diam, not thickened nor darkened. *Conidia* cylindrical, straight, 10–29 × 1–4 µm, 1–3-septate, base truncate, 1–2 µm diam, apex rounded, hyaline to subhyaline, smooth.

Culture characteristics (under 12 h light regime, at 25 °C) — Slow growing (12–15 mm diam after 12 d), aerial mycelium sparse, lobate margins, white to buff with some overlapping areas smoke grey, reverse pale luteus to honey. Cultures sterile.

Typus. BRAZIL, Viçosa, campus of Universidade Federal de Viçosa, on *Coussapoa floccosa* (*Cecropiaceae*), 18 July 2014, R.W. Barreto (holotype VIC44404, culture ex-type COAD1824; ITS and LSU sequences GenBank MG780415 and MH716814, MycoBank MB827438).

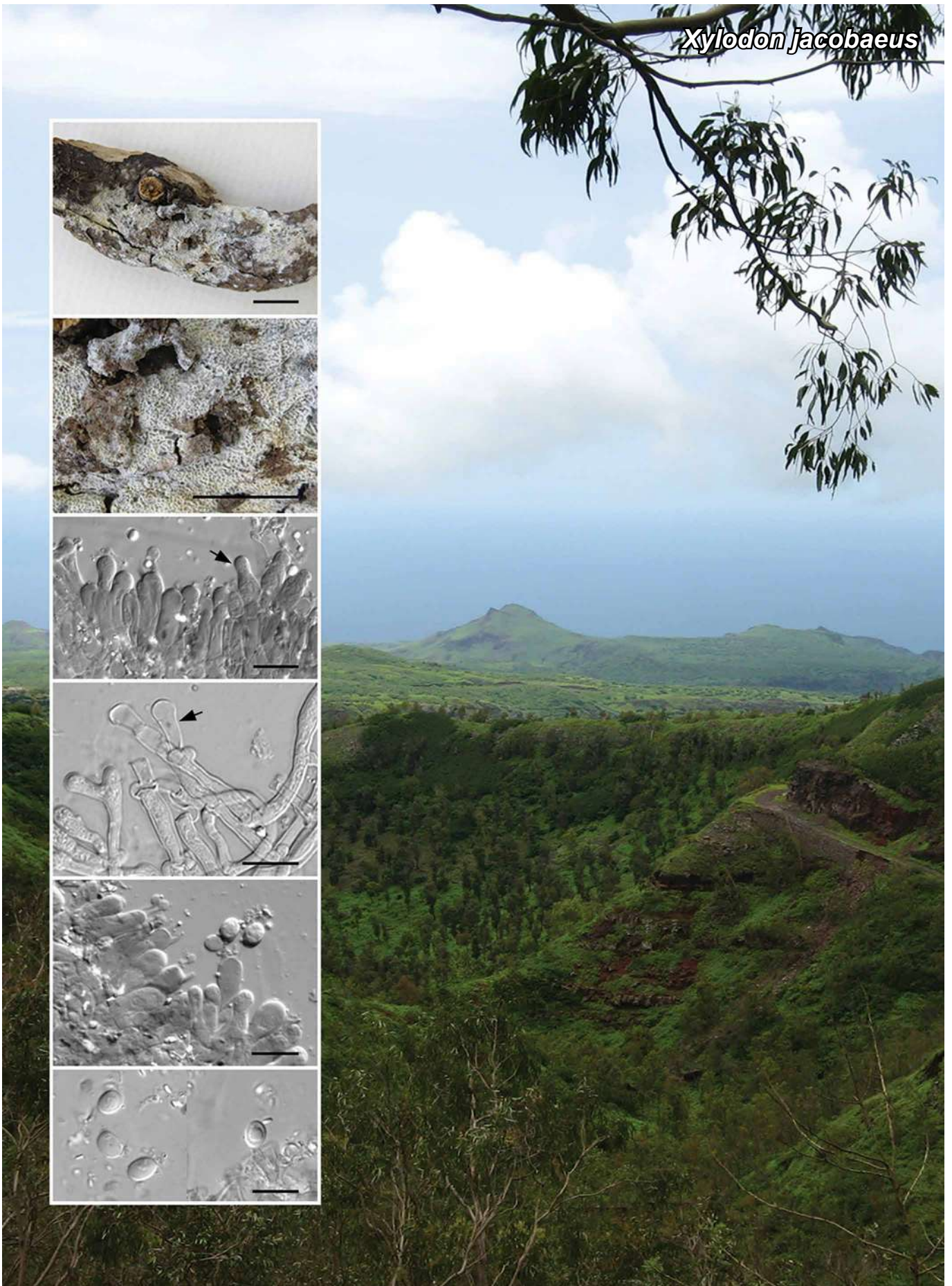
Colour illustrations. Leaf spots on *Coussapoa floccosa*; leaf spot, conidiophores and conidia on trichomes (SEM). Scale bars = 20, 20, 5, 40 and 20 µm, respectively.

Notes — *Xenosonderhenia* was recently established to accommodate two leaf spot fungal pathogens belonging to the *Mycosphaerellaceae*. *Xenosonderhenia* is a pleomorphic genus including the type species *X. syzygii* – with no known sexual morph but described as having two asexual morphs: a pycnidial morph and a hyphomycete synasexual morph seen only in culture (Crous et al. 2012b) and *X. eucalypti* – known only from its ascotal morph (Crous et al. 2014b). Phylogenetically, COAD1824 clusters with *Mycosphaerella elaeocarpi* – a fungus lacking an asexual morph – and with *Xenosonderhenia*. Morphological features such as size and surface of conidia (finely verruculose in *X. syzygii* but smooth in the newly proposed species) and phylogenetic data indicated that the fungus on *C. floccosa* represents a new species of *Xenosonderhenia*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence were *X. syzygii* (GenBank NR_111763; Identities = 461/492 (94 %), 7 gaps (1 %)), *X. eucalypti* (GenBank NR_137937; Identities = 457/492 (93 %), 6 gaps (1 %)) and *Mycosphaerella elongata* (GenBank EF394833; Identities = 456/492 (93 %), 8 gaps (1 %)). Closest hits for LSU were *M. elaeocarpi* (GenBank EU040212; Identities = 858/868 (99 %), 4 gaps (0 %)), *X. syzygii* (GenBank NG_042685; Identities = 852/864 (99 %), 2 gaps (0 %)) and *X. eucalypti* (GenBank NG_058120; Identities = 812/823 (99 %), no gaps).

Xenosonderhenia coussapoe represents an addition to the known mycobiota of *C. floccosa* and, if proven specific to this host, may represent an endangered species of microfungi, as are other fungal species described from this highly endangered Brazilian tree species (Rocha et al. 2010).

Xylodon jacobaeus



Fungal Planet 867 – 14 December 2018

Xylodon jacobaeus J. Fernández-López, M. Dueñas, M.P. Martín & Telleria, *sp. nov.*

Etymology. Named after Santi Jacobi Insula, Latin name for Santiago Island, Cape Verde Archipelago, where it was collected.

Classification — *Schizoporaceae*, *Hymenochaetales*, *Agaricomycetes*.

Basidioma resupinate, effuse, adnate; hymenophore reticulate to poroid, 1–2 pores/mm, yellowish white to pale yellow (92. y White – 89. p. Y; Kelly & Judd 1976) margin not clearly differentiated, sometimes paler. *Hyphal system* monomitic; hyphae hyaline, thin to slightly thickened walls, sparsely branched, with clamps, 2.5–3.5 µm wide; subicular hyphae loosely interwoven, parallel to substratum; subhymenial hyphae more densely interwoven, perpendicular to substratum, usually slightly encrusted. *Cystidia* or rather cystidial elements present: 1) capitate cystidia arise from the hymenium, subcylindrical to utriform, thin-walled, basal clamped, 20–24 × 4–7 µm; and 2) capitate hyphae arise from the subiculum, basal clamped, 15–35 × 2.5–3.5 µm, apex up to 7 µm diam. *Basidia* claviform to subclaviform, sometimes pedunculated, 17–20 × 4–5 µm, internal linear repetition seems to occur occasionally, four sterigmata, with basal clamp. *Spores* ellipsoid, (5–)6–7 × (3.5–)4–4.5 µm, hyaline, thin-walled, smooth, guttulate, L = 6.24, W = 4.35, Q = 1.43 (n = 32/3).

Topology of ITS tree obtained by Maximum Likelihood Inference conducted in RAxML v. 8.2.10 on CIPRES Science Gateway v. 3.3 (Miller et al. 2010). Two sequences of *X. paradoxus* were used as outgroup. Bootstrap support values (> 50 %) are indicated on the branches (bootstrap iterations = 1000). The *X. jacobaeus* clade is marked with a green block; the accession numbers from the EMBL/GenBank database are indicated at the terminal nodes. The asterisk (*) after the EMBL/GenBank accession numbers are sequences obtained for this study.

Habitat & Distribution — On debris of *Eucalyptus camaldulensis* and *Lantana camara*; known from two localities of Santiago Island, Cape Verde Archipelago.

Typus. CAPE VERDE, Santiago island, São Domingos, Rui Vaz, N15°01'59" W23°37'06", 873 msl, on *Eucalyptus camaldulensis* (Myrtaceae), 21 Sept. 2010, J. Cardoso, L.M. Catarino, M. Dueñas, M.P. Martín, I. Melo, I. Salcedo & M.T. Telleria, 18975Tell. (holotype MA-Fungi 91340, ITS sequence GenBank MH430073, MycoBank MB826918).

Additional specimens examined. CAPE VERDE, Santiago island, Santa Catarina, Serra da Malagueta Natural Park, N15°10'41.5" W23°41'14.2", 907 msl, on *Lantana camara*, 20 Sept. 2010, J. Cardoso, L.M. Catarino, M. Dueñas, M.P. Martín, I. Melo, I. Salcedo & M.T. Telleria, 13224MD, MA-Fungi 91338, ITS sequence GenBank MH430074; *ibid.*, 13225MD, MA-Fungi 91339, ITS and LSU sequences GenBank MH430072 and MH430071).

Notes — Maximum likelihood phylogenetic analyses of ITS sequences under a GTR model grouped the new sequences in a well-supported clade (bootstrap support value > 95 %) with *Xylodon niemelaei*, *X. rhizomorphus* and *X. reticulatus*. No LSU GenBank sequences were available for *X. reticulatus*. Distribution and morphological diagnostic characters for each species are shown in Table 1. *Xylodon jacobaeus* is similar to these species, but differs in having subcylindrical to utriform cystidia, capitate hyphae and wider spores.

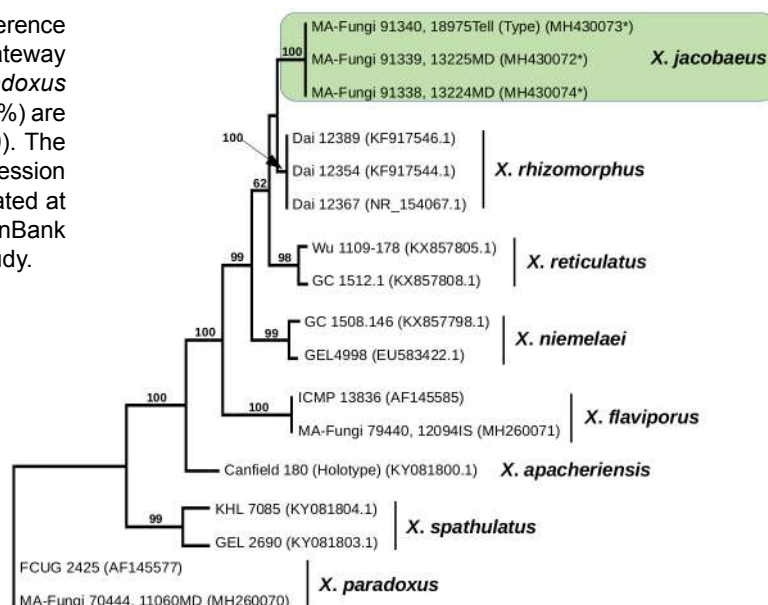


Table 1 Comparison of distribution and micromorphology of *Xylodon jacobaeus* and closely related species.

Species	Type locality	Cystidia and cystidial elements	Spores	References
<i>X. niemelaei</i>	Taiwan	Capitate and subulate cystidia	5–5.5(–6) × 3.5–4 µm	Wu (1990)
<i>X. rhizomorphus</i>	China	Bladder-like cystidia	(4.1–)4.3–5.5(–5.9) × (3.5–)3.7–4.1(–4.3) µm	Zhao et al. (2014)
<i>X. reticulatus</i>	Taiwan	Capitate, subclavate to clavate and slightly moniliform cystidia; short encrusted hyphal apices	(4.8–)5–6(–7) × 3–3.6(–4) µm	Chen et al. (2017)
<i>X. jacobaeus</i>	Cape Verde	Capitate, subcylindrical to utriform cystidia; capitate hyphae	(5–)6–7 × (3.5–)4–4.5 µm	Present study

Colour illustrations. Cape Verde, Santiago, São Domingos, Rui Vaz (photo credit M.T. Telleria); From top to bottom: basidioma (MA-Fungi 91340), cystidia, capitate hyphae, basidia and spores (MA-Fungi 91340). Scale bars = 1 cm (basidioma), 10 µm (all others).

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