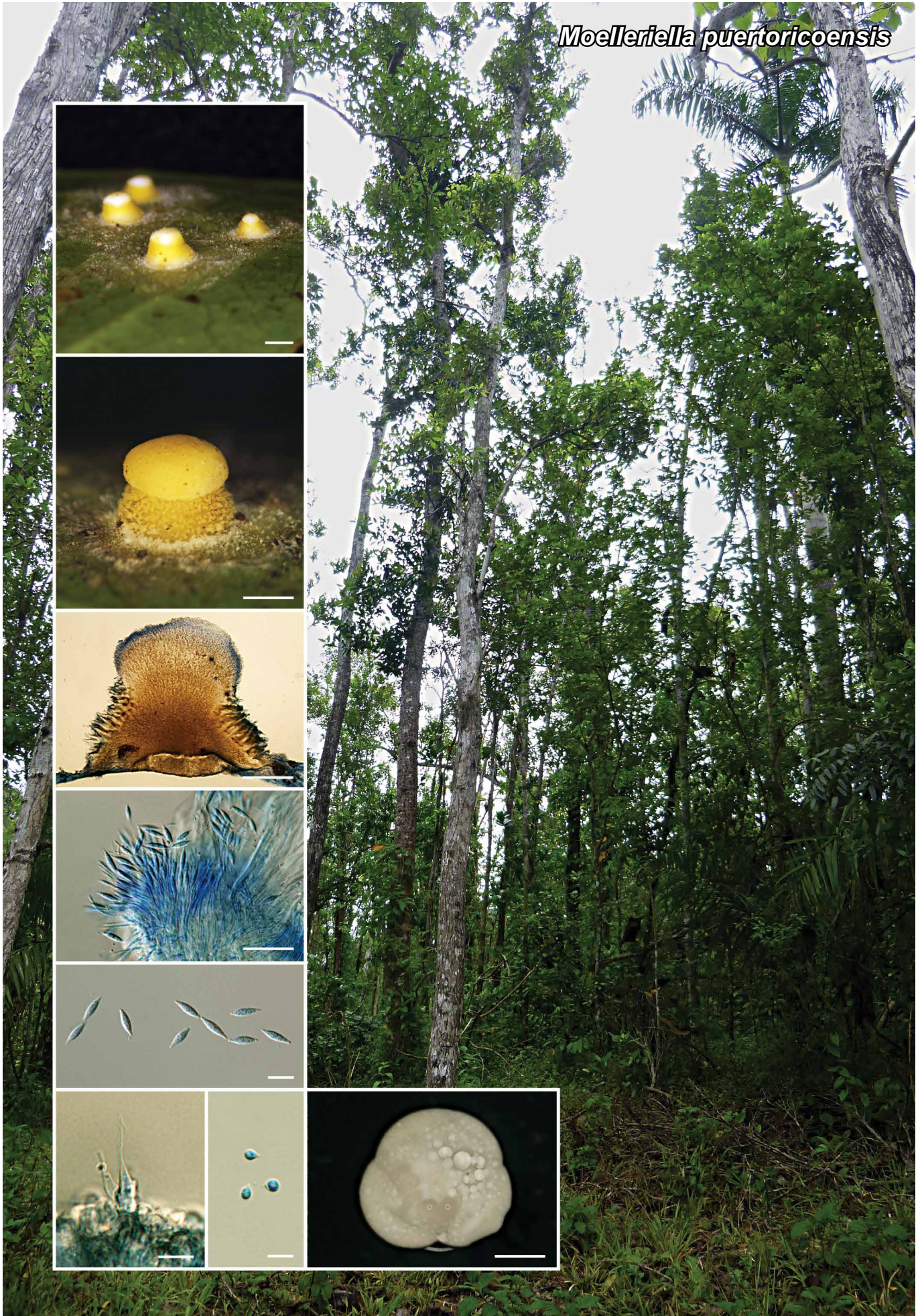


*Moelleriella puertoricensis*





Fungal Planet 1162 – 19 December 2020

***Moelleriella puertoricensis* Mongkolsamrit, Noisripoom & Luangsa-ard, sp. nov.**

*Etymology.* Name refers to Puerto Rico, the location where this species was collected.

*Classification* — *Clavicipitaceae*, *Hypocreales*, *Sordariomycetes*.

*Specimens* found on the underside of dicotyledonous leaves of forest plants. Hosts are scale insect nymphs (Hemiptera). *Stromata* discoid, distinctly stud-shaped, up to 3 mm diam, and 1–2.5 mm high, pale yellow, base surrounded by a white membranous hypothallus. *Conidiomata* scattered around a narrow neck, with a pale yellow to yellow mass of conidia. *Conidiogenous cells* phialidic, aschersonia-like, cylindrical, straight, up to 55 µm long, 1–2 µm wide, forming a compact layer. *Conidia* hyaline, fusoid, with acute ends, aseptate, (10–)11–12.5(–14) × 2–3 µm. *Paraphyses* absent. Hirsutella-like synasexual morph scattered on the upper surface of stroma, *phialides* with a long thin neck, entire phialides up to 25 µm, 3–5 µm wide, *conidia* globose, 4–5 µm diam. *Sexual morph* not observed.

*Culture characteristics* — Colonies developed from germinating conidia. The conidia germinated within 24 h on potato dextrose agar (PDA). Colonies reaching a diam of 1 cm after 3 wk at 25 °C. Colonies compact with white mycelium, colonies reverse uncoloured. Conidia produced after 30 d, hyaline thinly spreading on colonies, fusoid, with acute ends, aseptate, 9–12 × 2–3 µm.

*Typus.* USA, PUERTO RICO, Rio Abajo State Forest, on scale insect (Hemiptera) attached to underside of dicotyledonous leaves, 19 Jan. 2018, S. Mongkolsamrit, J.J. Luangsa-ard & S. Wongkanoun (holotype BBH43763, culture ex-type BCC88320, ITS, LSU and *tef1* sequences GenBank MW115297, MN954683 and MN944389, MycoBank MB834780).

*Additional materials examined.* USA, PUERTO RICO, Rio Abajo State Forest, on scale insect (Hemiptera) attached to underside of dicotyledonous leaves, 19 Jan. 2018, S. Mongkolsamrit, J.J. Luangsa-ard & S. Wongkanoun, BBH43763 (BCC88321), ITS, LSU and *tef1* sequences GenBank MW115298, MN954684 and MN944390; BBH43764 (BCC88322), ITS, LSU and *tef1* sequences GenBank MW115299, MN954682 and MN944391.

*Colour illustrations.* Background photo of side of a trail in Rio Abajo State Forest; fungi on hosts, side view of stroma showing stud-shaped and conidiomata, conidiogenous cells, conidia, hirsutella-like on stroma, conidia, culture derived from conidia on PDA (sporulation present). Scale bars = 1 and 2 mm (stromata), 20 µm (phialides), 10 µm (conidia, hirsutella-like phialides and conidia), 3 mm (culture).

*Notes* — The gross macromorphology of the natural samples of *M. puertoricensis* closely resembles the asexual morph of *M. basicystis* (Chaverri et al. 2008) and *M. pongdueatensis* (Li et al. 2016) that were found in Costa Rica and Thailand, respectively. These three species have discoid, distinctly stud-shaped stroma and conidiomata scattered around a narrow neck of the stroma, with a pale yellow to yellow mass of conidia. Conidia in *M. puertoricensis* and *M. pongdueatensis* are fusoid with acute ends and the width of conidia are in the same range (10–14 × 2–3 µm vs 9–12.5 × 1.5–2.5 µm). Conidia of *M. basicystis* are ventricose with acute ends (11–15.5 × 3–5 µm) and wider than those reported in *M. puertoricensis* and *M. pongdueatensis*. *Moelleriella puertoricensis* and *M. basicystis* lack paraphyses while they are present in *M. pongdueatensis*, linear, filiform, up to 110 × 1–2 µm. Additionally, *M. puertoricensis* and *M. pongdueatensis* have a hirsutella-like synasexual morph scattered on the upper surface of the stroma, phialides with a long thin neck (25 × 5 µm vs 20 × 1–2 µm), globose (4–5 µm) and citriform (2–3 × 1–2.5 µm) conidia, respectively. The results of our molecular phylogenetic study strongly support and separate *M. puertoricensis* from other known species. *Moelleriella puertoricensis* is therefore proposed as a new species belonging to *Moelleriella* from the Neotropics.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Moelleriella basicystis* (strain ROKI2770, GenBank EF190282.1; Identities = 546/594 (92 %), 21 gaps (3 %)), and *Orbiocrella* sp. (strain BCC33248, GenBank KJ138267.1; Identities = 300/349 (86 %), 22 gaps (6 %)).

Closest hits using the LSU sequence had highest similarity to *Moelleriella basicystis* (strain F183147, GenBank EU392577.1; Identities = 276/279 (99 %), 1 gap (0 %)), and *Moelleriella phyllogena* (strain CUP 67340, GenBank AY518372.1; Identities = 276/279 (99 %), 1 gap (0 %)).

Closest hits using the *tef1* sequence are *Moelleriella basicystis* (strain F183147, GenBank EU392653.1; Identities = 856/912 (94 %), no gaps (0 %)), and *Moelleriella basicystis* (strain P.C. 374, GenBank AY986928.1; Identities = 854/910 (94 %), no gaps (0 %)).

**Supplementary material**

**FP1162-1** Phylogenetic reconstruction of *M. puertoricensis* was done using a combined dataset comprising LSU and *tef1* sequences. The data was analysed using Maximum parsimony (MP), Maximum likelihood (ML) and Bayesian inference. The MP analysis was conducted on the combined data set using PAUP v. 4.0b10 (Swofford 2002), adopting random addition sequences (100 replications), with gaps being treated as missing data. A bootstrap (BP) analysis was performed using the maximum parsimony criterion in 1000 replications. The ML analysis was run with RAxML-VI-HPC2 v. 8.2.12 (Stamatakis 2014) under a GTR model, with 1000 bootstrap replicates. Bayesian phylogenetic inference was calculated with MrBayes v. 3.2.7a (Ronquist et al. 2012), with 5 M generations and under the same model. Numbers at the significant nodes represent MP bootstrap support values/RAxML bootstrap support values/Bayesian posterior probabilities (BPP) times 100. Thickened lines in the tree represent 99–100 % bootstrap support values and 99–100 BPP.

**FP1162-2** List of species and GenBank accession numbers of sequences used in this study.