Corynespora thailandica
**Fungal Planet 817 – 13 December 2018**

**Corynespora thailandica** Crous, *sp. nov.*

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

*Classification.* — *Corynesporascaceae, Pleosporales, Dothideomycetes."

*Mycelium* consisting of brown, finely roughened, branched, septate, 3–4 µm diam hyphae. **Conidiophores** solitary, erect, flexuous, subcylindrical, unbranched, brown, thick-walled, finely roughened, base swollen, up to 12 µm diam, conidiophores extremely long in culture, 5–6 µm diam, multi-septate. **Conidiogenous cells** integrated, terminal, monotretic, subcylindrical, brown, finely roughened, slightly darkened at apex, 3–4 µm diam, 25–30 (–60) × 5–6 µm. **Conidia** obclavate, mostly solitary, thick-walled, brown, finely roughened, 4–8-distoseptate, (50–) 80–110 (–200) × (9–)10–12 (–13) µm; hila darkened, thickened, 3–4 µm diam.

**Culture characteristics.** — Colonies erumpent, spreading, with moderate aerial mycelium and feathery, lobate margin, reaching 10 mm diam on PDA, 60 mm diam on OA and MEA after 2 wk at 25 °C. On MEA, PDA and OA surface olivaceous grey, reverse iron-grey.


**Notes.** — The genus *Corynespora* is polyphyletic (Voglmayr & Jaklitsch 2017). Species occur on a range of substrates, varying from leaves to twigs, with several being regarded as serious plant pathogens. Based on the species treated by Ellis (1971, 1976), and those known from DNA sequence data, the present collection appears to represent a new taxon, described here as *Corynespora thailandica.*

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Corynespora cassicola* (GenBank FJ852592.1; Identities = 537/557 (96 %), 6 gaps (1 %)), *Corynespora smithii* (GenBank KY984300.1; Identities = 536/558 (96 %), 9 gaps (1 %)) and *Corynespora torulosa* (GenBank NR_145181.1; Identities = 530/556 (95 %), 6 gaps (1 %)). Closest hits using the **LSU** sequence are *Corynespora cassicola* (GenBank MH869486.1; Identities = 840/847 (99 %), 2 gaps (0 %)), *Corynespora torulosa* (GenBank NG_058866.1; Identities = 839/847 (99 %), 2 gaps (0 %)) and *Corynespora smithii* (GenBank KY984299.1; Identities = 839/847 (99 %), 2 gaps (0 %)). Closest hits using the **tef1** sequence had highest similarity to *Corynespora smithii* (GenBank KY984436.1; Identities = 396/464 (85 %), 19 gaps (4 %)), *Pyrenochaeta nobilis* (GenBank MF795880.1; Identities = 289/348 (83 %), 27 gaps (7 %)) and *Neocucurbitaria acerina* (GenBank MF795856.1; Identities = 286/347 (82 %), 17 gaps (4 %)).

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*Colour illustrations.* Indigenous forest in Thailand; conidiogenous cells and conidia. Scale bars = 10 µm.