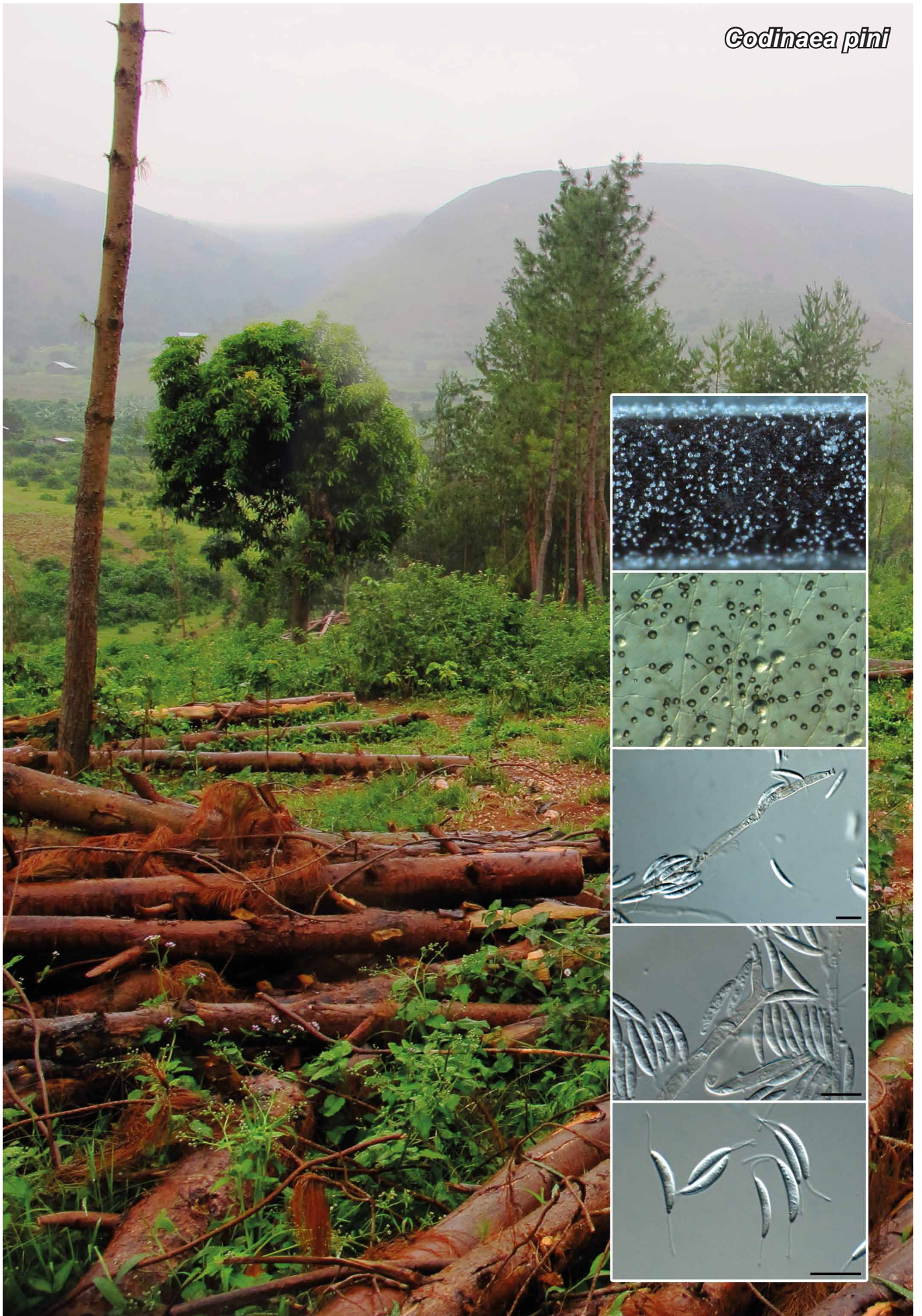


*Codinaea pini*



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***Codinaea pini* Crous & M.J. Wingf., sp. nov.**

*Etymology.* Name reflects the host genus *Pinus*, from which this species was isolated.

*Conidiophores* erect, brown, flexuous, finely verruculous, appearing somewhat granular, unbranched, arising from superficial mycelium, mononematous, macronematous, cylindrical, 1–3-septate, 30–100 × 2.5–4 µm. *Conidiogenous cells* terminal, pale to medium brown, mono- to rarely polyphialidic, with one lateral aperture, 25–60 × 3–3.5 µm; collarette funnel-shaped, 3–4 µm diam, 2–3 µm deep, pale brown. *Conidia* (12–)13–15 × (2–)2.5(–3) µm, solitary, aggregating in a globose mucoid mass, hyaline, smooth, granular, fusoid, slightly curved or straight, widest in middle, tapering towards acute apices that give rise to setulae at each end, 8–9(–10) µm.

*Culture characteristics* — Colonies flat, appressed, spreading, with sparse aerial mycelium and smooth, even, lobate margin, reaching 35 mm diam after 2 wk at 25 °C in the dark. On OA surface iron-grey in centre, crystalline in outer region. On MEA surface olivaceous-grey, pale olivaceous-grey in outer region, olivaceous-grey in reverse. On PDA surface olivaceous-grey in centre, pale olivaceous-grey in outer region; in reverse olivaceous-grey in centre, pale olivaceous-grey in outer region.

*Typus.* UGANDA, on dead needles of *Pinus patula* (*Pinaceae*), Jan. 2014, M.J. Wingfield (holotype CBS H-21998, culture ex-type CPC 24400 = CBS 138866; ITS sequence GenBank KP004465, LSU sequence GenBank KP004493, MycoBank MB810611).

*Notes* — The species is described in the genus *Codinaea* because Réblová & Winka (2000) suggested separating *Codinaea* (setulate conidia) from *Dictyochoaeta* (asetulate conidia). Based on the keys provided by Kuthubutheen & Nawawi (1991) and Whitton et al. (2000), *C. pini* appears to be distinct from presently known taxa. Phylogenetically, it is part of the *C. simplex* species complex (Hughes & Kendrick 1968).

*ITS.* Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Dictyochoaeta simplex* (GenBank EF029193; Identities = 472/515 (92 %), Gaps = 21/515 (4 %)), *Pseudolachnella guaviyunis* (GenBank KJ834524; Identities = 493/548 (90 %), Gaps = 27/548 (4 %)) and *Dictyochoaeta fertilis* (GenBank AF178540; Identities = 463/507 (91 %), Gaps = 23/507 (4 %)).

*LSU.* Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Dictyochoaeta simplex* (GenBank AF178559; Identities = 827/832 (99 %), Gaps = 1/832 (0 %)), *Rattania setulifera* (GenBank HM171322; Identities = 811/838 (97 %), Gaps = 1/838 (0 %)) and *Pseudolachnella guaviyunis* (GenBank KJ834525; Identities = 803/831 (97 %), Gaps = 1/831 (0 %)).

*Colour illustrations.* *Pinus patula* plantation in Uganda; colonies sporulating on PNA and SNA, conidiophores and conidia. Scale bars = 10 µm.

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