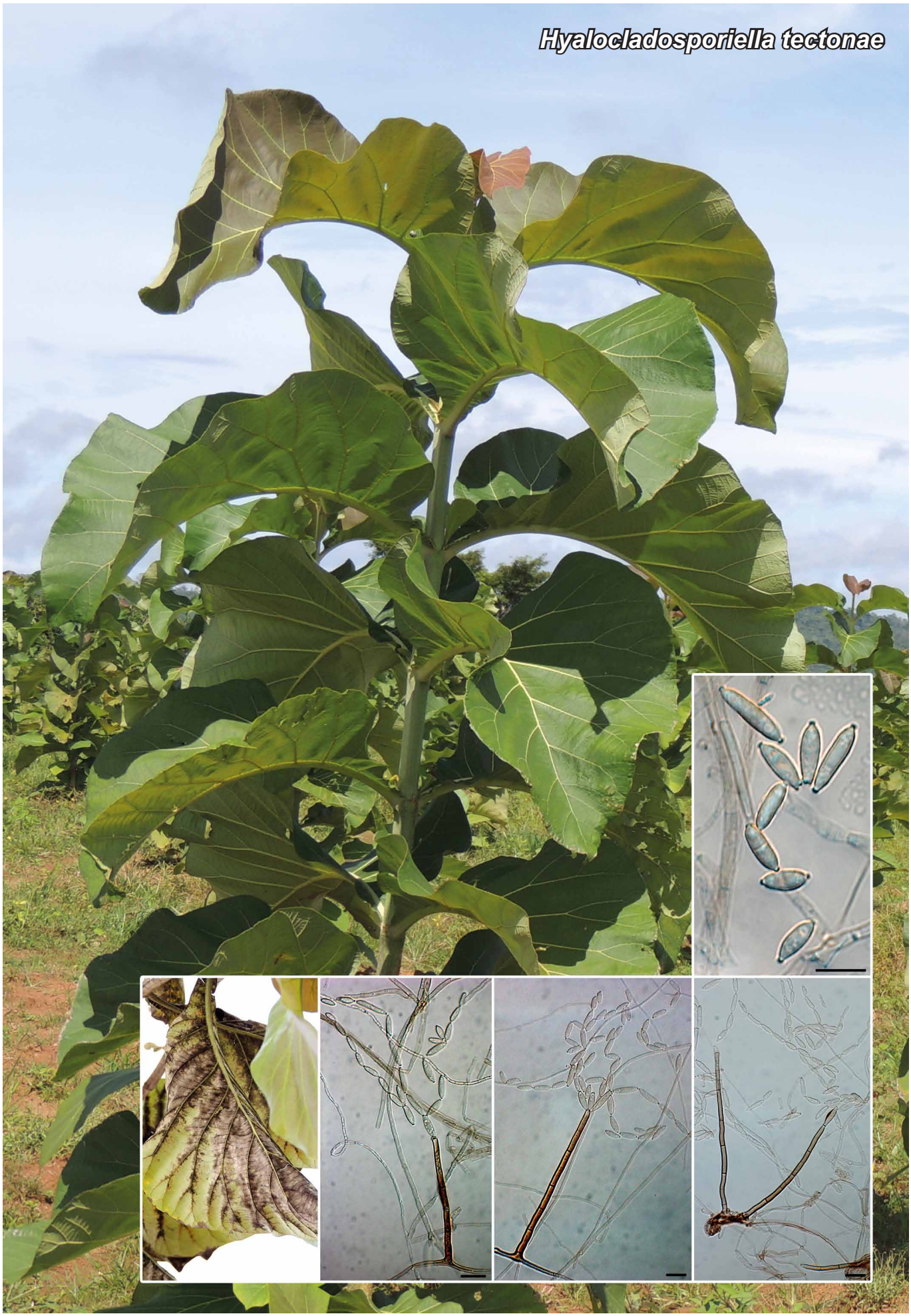
Hyalocladosporiella tectonae

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Hyalocladosporiella Crous & Alfenas, *gen. nov.*

Etymology. Named after its hyaline conidia and cladosporium-like morphology.

Mycelium consisting of hyaline, smooth, branched, septate hyphae. *Conidiophores* dimorphic. *Microconidiophores* erect, subcylindrical, straight to geniculate-sinuous, septate, brown, smooth. *Macroconidiophores* erect, brown, smooth, cylindrical, flexuous, unbranched, lacking rhizoids, septate. *Conidiogenous cells* integrated, terminal, subcylindrical, smooth, brown; loci sympodially arranged, subdenticulate, slightly thickened and darkened. *Primary ramoconidia* fusoid-ellipsoidal to subcylindrical, hyaline to pale olivaceous, smooth, guttulate, septate; hila thickened and darkened. *Secondary ramoconidia* in branched chains, fusoid-ellipsoidal, hyaline, smooth, guttulate, with 1–3 apical loci that are thickened and darkened. *Intermediary conidia* hyaline, guttulate, fusoid-ellipsoid. *Terminal conidia* hyaline, smooth, guttulate, fusoid-ellipsoid, loci thickened and darkened.

Type species. Hyalocladosporiella tectonae.
MycoBank MB808921.

Hyalocladosporiella tectonae Crous & Alfenas, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Tectona.*

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* dimorphic. *Microconidiophores* erect, subcylindrical, straight to geniculate-sinuous, 1–2-septate, brown, smooth, 20–30 × 3–3.5 µm. *Macroconidiophores* erect, brown, smooth, cylindrical, flexuous, unbranched, lacking rhizoids, 60–200 × 3 µm, 5–15-septate. *Conidiogenous cells* integrated, terminal, subcylindrical, smooth, brown, 15–30 × 3 µm; loci sympodially arranged, subdenticulate, 0.5–1 × 1–1.5 µm, slightly thickened and darkened. *Primary ramoconidia* fusoid-ellipsoidal to subcylindrical, hyaline to pale olivaceous, smooth, guttulate, 1–3-septate, 30–35 × 3–3.5 µm; hila thickened and darkened, 1 µm diam. *Secondary ramoconidia* in branched chains, fusoid-ellipsoidal, hyaline, smooth, guttulate, with 1–3 apical loci that are thickened and darkened, 1 µm diam. *Intermediary conidia* hyaline, guttulate, fusoid-ellipsoid, 10–15 × 3 µm. *Terminal conidia* hyaline, smooth, guttulate, fusoid-ellipsoid, (7–)8–9(–10) × 2.5(–3) µm, loci thickened and darkened, 0.5 µm diam.

Culture characteristics — Colonies reaching 30 mm diam after 2 wk at 22 °C, erumpent, folded, with moderate aerial mycelium and even, smooth margins. On PDA surface smoke-grey in the middle, becoming olivaceous-grey toward the margin, reverse olivaceous-grey. On OA surface olivaceous-grey. On MEA surface smoke-grey, margins olivaceous-grey, reverse iron-grey.

Typus. Brazil, Minas Gerais, Verde Novo, Colider-MT, on leaves of *Tectona grandis* (*Lamiaceae*), Apr. 2013, *A.C. Alfenas* (holotype CBS H-21702, culture ex-type CPC 23133 = CBS 137989; ITS sequence GenBank KJ869142, LSU sequence GenBank KJ869199, MycoBank MB808922).

Notes — Based on phylogenetic and morphological data, the genus *Cladosporium* (type is *C. herbarum*) was separated into several allied genera within the *Cladosporiaceae* (Arzanlou et al. 2007, Crous et al. 2007a, b, Bensch et al. 2012). *Hyalocladosporiella* represents yet another genus in this complex, that is phylogenetically allied to *Metulocladosporiella* (*Chaetothyriales*). *Metulocladosporiella* has dimorphic, solitary, pigmented conidiophores with an apical conidiogenous apparatus consisting of conidiogenous cells that give rise to ramoconidia and branched conidial chains that are fusoid-ellipsoid, pale brown, smooth, and have slightly darkened, thickened scars. *Hyalocladosporiella* is morphologically different from *Metulocladosporiella* in that it has septate ramoconidia and lacks the apical conidiophore branches observed in macroconidiophores of *Metulocladosporiella*.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Phaeococcomyces chersonesos* (GenBank AJ507323; Identities = 632/713 (89 %), Gaps = 30/713 (4 %)), *Knufia perforans* (GenBank JN040506; Identities = 595/674 (88 %), Gaps = 32/674 (4 %)) and *Knufia petricola* (GenBank KC978734; Identities = 584/666 (88 %), Gaps = 31/666 (4 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Metulocladosporiella musae* (GenBank DQ008162; Identities = 819/841 (97 %), Gaps = 6/841 (0 %)), *Metulocladosporiella musicola* (GenBank DQ008159; Identities = 814/838 (97 %), Gaps = 2/838 (0 %)) and *Coniosporium perforans* (GenBank FJ358237; Identities = 809/840 (96 %), Gaps = 2/840 (0 %)).

Colour illustrations. *Tectona grandis* in Brazil; diseased leaf, conidiophores and conidia in culture. Scale bars = 10 µm.

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