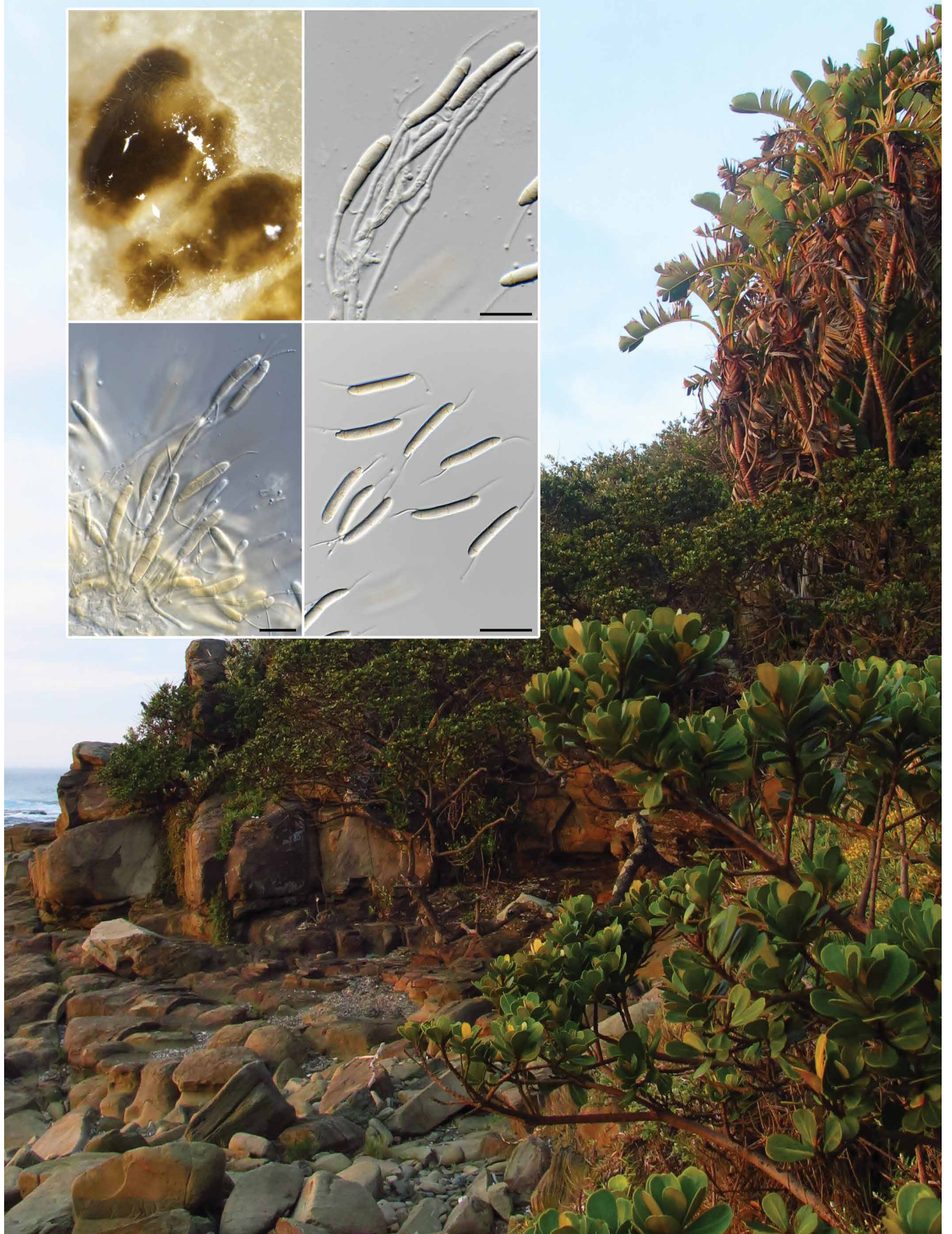
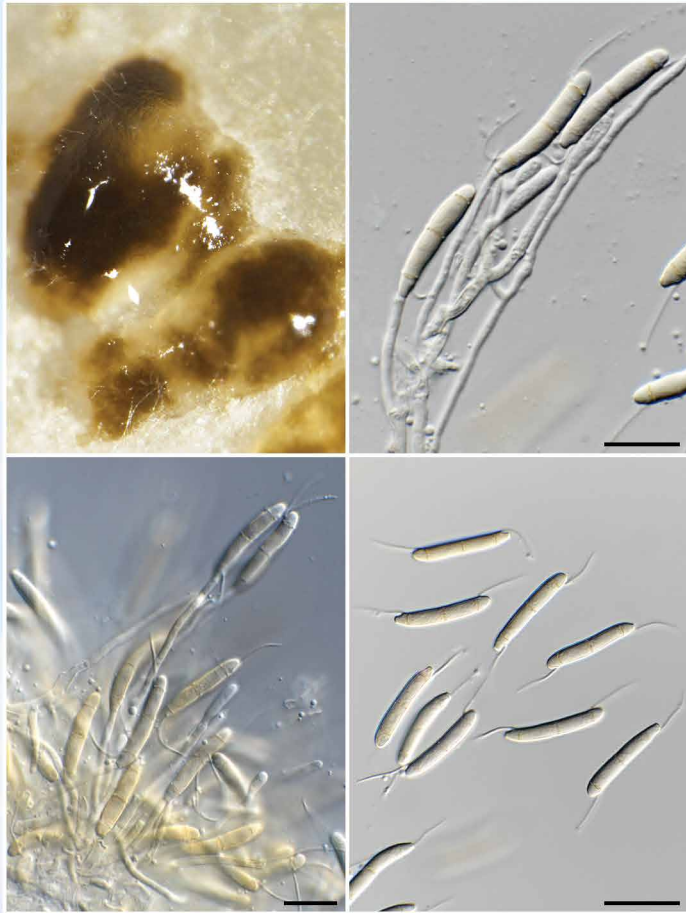


Millesimomyces rhoicissi



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Millesimomyces Crous & M.J. Wingf., *gen. nov.*

Etymology. Composed of *millesimus* (thousandth; for species No. 1000 described in Fungal Planet) and the suffix *-myces* (múkēs, Greek, fungus).

Classification — *Sporocadaceae*, *Xylariales*, *Sordariomycetes*.

Conidiomata gregarious, black, stromatic, acervular, exuding a brown conidial mass. *Conidiophores* hyaline, smooth, septate, branched, flexuous or reduced to conidiogenous cells. *Conidiogenous cells* discrete, subcylindrical or lageniform, hyaline,

smooth. *Conidia* subcylindrical, straight or slightly curved, pale brown, 3-septate, smooth, not constricted at septa, basal cell cylindrical, thin-walled, subhyaline; median two cells cylindrical, hyaline, thin-walled, unequal; apical cell subcylindrical with obtuse apex; appendages tubular, slender, flexuous; apical appendage single, unbranched, excentric; basal appendage single, unbranched, excentric.

Type species. *Millesimomyces rhoicissi* Crous & M.J. Wingf.
Mycobank MB832917.

Millesimomyces rhoicissi Crous & M.J. Wingf., *sp. nov.*

Etymology. Name refers to *Rhoicissus*, the host genus from which this fungus was isolated.

Conidiomata gregarious, black, stromatic, acervular, exuding a brown conidial mass. *Conidiophores* hyaline, smooth, septate, branched, flexuous or reduced to conidiogenous cells. *Conidiogenous cells* discrete, subcylindrical or lageniform, hyaline, smooth, 5–30 × 2–2.5 µm. *Conidia* subcylindrical, straight or slightly curved, pale brown, 3-septate, smooth, not constricted at septa, (18–)22–25(–27) × (3.5–)4 µm, basal cell cylindrical, thin-walled, subhyaline, 3–4 µm long; median two cells cylindrical, hyaline, thin-walled, unequal, second cell from base 8–10 µm long, third cell from base 8–9 µm long, apical cell subcylindrical with obtuse apex, 2.5–4 µm long; appendages tubular, slender, flexuous; apical appendage single, unbranched, excentric, 10–16 µm long, inserted c. 1.5 µm from apex; basal appendage single, unbranched, excentric, 11–14 µm long, inserted 2–3 µm from basal septum.

Culture characteristics — Colonies flat, spreading, with folded surface, moderate aerial mycelium and smooth, lobate margin, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface peach, reverse fulvous with patches of sienna.

Typus. SOUTH AFRICA, Eastern Cape Province, Haga Haga, on leaves *Rhoicissus digitata* (*Vitaceae*) with dieback, 12 Dec. 2016, M.J. Wingfield, HPC 2296 (holotype CBS H-23936, culture ex-type CPC 35297 = CBS 145536, ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MN562156.1, MN567663.1, MN556817.1, MN556827.1 and MN556846.1, MycoBank MB832918).

Notes — *Millesimomyces* resembles the genus *Discosia* in morphology, having stromatic acervuli, and long, hyaline, subcylindrical or lageniform phialides that give rise to subcylindrical, pale brown, 3-septate conidia with excentric apical and basal appendages (Liu et al. 2019a). However, based on phylogenetic inference, the fungus clusters apart from species of *Discosia*, and hence *Millesimomyces* is established to accommodate it. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Monochaetia monochaeta* (strain CBS 118.66, GenBank MH858742.1; Identities = 569/595 (96 %), 3 gaps (0 %)), *Seimatosporium pistaciae* (strain CBS 138865, GenBank NR_137942.1; Identities = 559/586 (95 %), 9 gaps (1 %)),

and *Ciliochorella phanericola* (voucher MFLU 14-0776, GenBank NR_153928.1; Identities = 526/552 (95 %), 9 gaps (1 %)). Other more distant hits include *Discostroma fuscellum* (strain GSAA-0182, GenBank JF320818.1; Identities = 551/582 (95 %), 7 gaps (1 %)), *Discosia pseudoartocreas* (strain CBS 136438, GenBank NR_132068.1; Identities = 579/612 (95 %), 9 gaps (1 %)), and *Discosia artocreas* (strain CBS 241.66, GenBank MH858787.1; Identities = 559/592 (94 %), 8 gaps (1 %)). Closest hits using the LSU sequence are *Seiridium pseudocardinale* (as *Seiridium* sp. DW-2016a, strain MFLUCC 13-0525, GenBank KU848209.1; Identities = 843/847 (99 %), 2 gaps (0 %)), *Seiridium cardinale* (as *Seiridium unicorne*, strain CBS 908.85, GenBank DQ414532.1; Identities = 829/833 (99 %), 2 gaps (0 %)), and *Seiridium cupressi* (as *Seiridium unicorne*, strain CBS 320.51, GenBank MH868398.1; Identities = 853/858 (99 %), 3 gaps (0 %)). Other more distant hits include *Discosia querci* (strain MFLUCC 16-0642, GenBank MG815830.1; Identities = 841/858 (98 %), 3 gaps (0 %)), *Immersidiscosia eucalypti* (strain 17RA1, GenBank KY825092.1; Identities = 840/858 (98 %), 3 gaps (0 %)), and *Discosia fraxinea* (strain NTIT469, GenBank KF827439.1; Identities = 838/856 (98 %), 3 gaps (0 %)). Closest hits using the *rpb2* sequence had highest similarity to *Monochaetia monochaeta* (strain CBS 658.95, GenBank MH554977.1; Identities = 699/830 (84 %), no gaps), *Seiridium podocarpus* (strain CBS 137995, GenBank LT853148.1; Identities = 721/860 (84 %), no gaps), and *Monochaetia junipericola* (strain CBS 143391, GenBank MH108004.1; Identities = 674/805 (84 %), no gaps). Closest hits using the *tef1* sequence had highest similarity to *Pestalotiopsis jinchanghensis* (strain LC8191, GenBank KY464155.1; Identities = 215/241 (89 %), 8 gaps (3 %)), *Pestalotiopsis colombiensis* (strain CBS 118553, GenBank KM199488.1; Identities = 215/241 (89 %), 8 gaps (3 %)), and *Pestalotiopsis terricola* (strain CBS 141.69, GenBank MH554438.1; Identities = 217/244 (89 %), 17 gaps (6 %)). Closest hits using the *tub2* sequence had highest similarity to *Monochaetia ilexae* (strain CBS 101009, GenBank MH554612.1; Identities = 474/598 (79 %), 31 gaps (5 %)), *Nonappendiculata quercina* (strain CBS 270.82, GenBank MH554701.1; Identities = 331/405 (82 %), 27 gaps (7 %)), and *Monochaetia quercus* (strain CBS 144034, GenBank MH554844.1; Identities = 472/600 (79 %), 34 gaps (5 %)).

Colour illustrations. Collection site at Haga Haga. Conidiomata on oatmeal agar; conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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