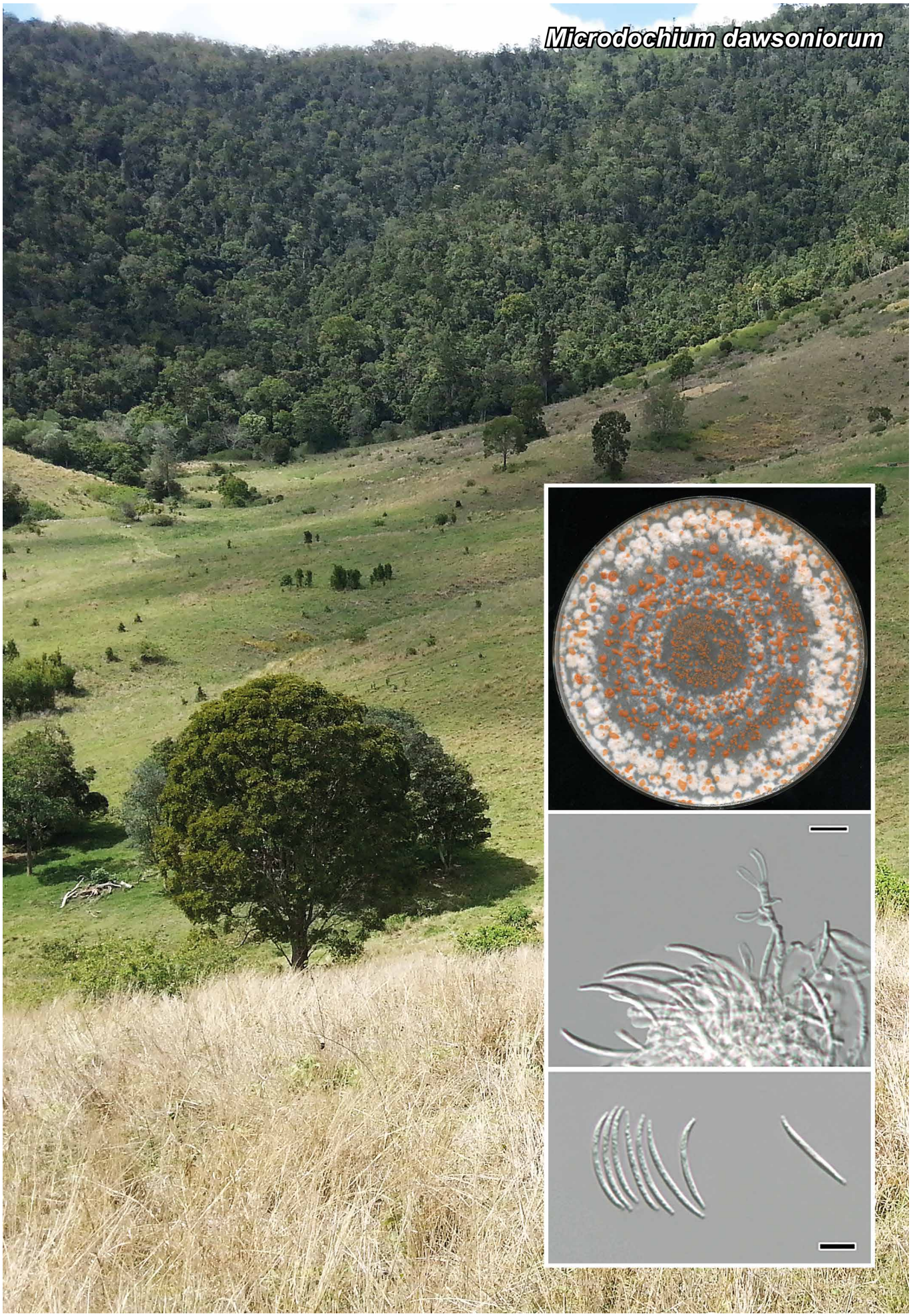
Microdochium dawsoniorum

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Microdochium dawsoniorum C. Lock, Vitelli, Holdom, Y.P. Tan & R.G. Shivas, *sp. nov.*

Etymology. Named after the Dawson family from Taunton, Queensland, on whose property the fungus was first collected.

Classification — *Michrodochiaceae*, *Xylariales*, *Sordariomycetes*.

Conidiophores abundant in a dense compact layer, occasionally branched, mostly reduced to conidiogenous cells. *Conidiogenous cells* cylindrical to irregular, flexuous, 20–30 × 1–2 µm, narrowed towards the tip, hyaline, smooth. *Conidia* flexuous to falcate, 0–3-septate, sometimes with a geniculation, 25–75 × 1–2 µm, acute at the tip, narrow at the base. *Sexual morph* not seen.

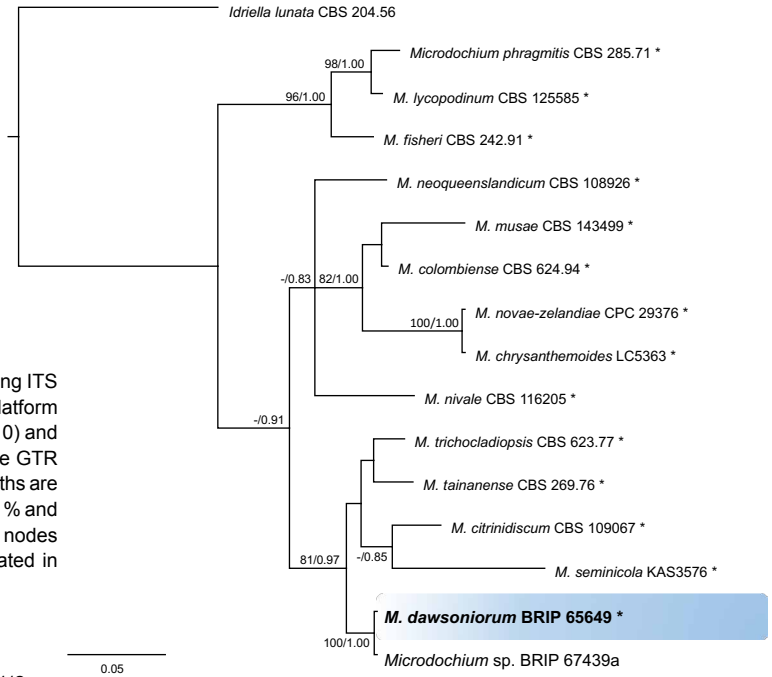
Culture characteristics — *Colonies* on oatmeal agar (OA) after 2 wk covering 9 cm diam plates, flat, mycelium in compact irregular to concentric scattered salmon tufts, with abundant slimy apricot sporodochia up to 3 mm arranged in irregular to concentric rings. Reverse pale saffron with sporodochia apparent as darker patches. *Mycelium* immersed or superficial, hyphae hyaline, septate, smooth.

Typus. Australia, Queensland, Taunton, Tableland Road, west side of road, S24°26'47.56" E151°47'13.27", isolated from leaves of *Sporobolus natalensis* (*Poaceae*), 8 Mar. 2017, *J. Vitelli* (holotype BRIP 65649, includes ex-type culture; ITS sequence GenBank MK966337, MycoBank MB831165).

Additional material examined. Australia, Queensland, Taunton, Tableland Road, east side of road, S24°26'51.98" E151°47'45.44", isolated from leaves of *S. elongatus*, 18 May 2018, *J. Vitelli*, BRIP 67439a; ITS sequence GenBank MN492650.

Notes — *Microdochium dawsoniorum* is sister to a clade that includes *M. citrinidiscum*, *M. seminicola*, *M. tainanense* and *M. trichocladiopsis*. Based on a mega-blast search of taxa within the sister clade, the ITS sequence of *M. dawsoniorum* differs from *M. citrinidiscum* (GenBank NR_155373; Identities = 529/556 (95 %), 9 gaps (1 %)), *M. seminicola* (GenBank KP859038; Identities = 488/541 (90 %), 34 gaps (6 %)), *M. tainanense* (GenBank NR_145248; Identities = 531/555 (96 %), 11 gaps (1 %)) and *M. trichocladiopsis* (GenBank KP858998; Identities = 536/557 (96 %), 13 gaps (2 %)). Morphologically, *M. dawsoniorum* has narrower conidia than *M. seminicola* (3–4.5 µm) and longer conidia than *M. citrinidiscum*, *M. tainanense* and *M. trichocladiopsis* (7–31 µm, 10–15 µm and 6–18 µm, respectively) (Hernández-Restrepo et al. 2016).

Microdochium dawsoniorum has only been found in Australia. Its close relatives include *M. citrinidiscum* from Peru; *M. seminicola* primarily from Canada and Switzerland; *M. tainanense* from Taiwan; and *M. trichocladiopsis* that has an unknown geographic origin (Hernández-Restrepo et al. 2016). *Microdochium dawsoniorum*, *M. tainanense* and *M. trichocladiopsis* have been isolated from the grasses *Sporobolus* spp., *Saccharum officinarum* and *Triticum aestivum*, respectively. *Microdochium seminicola* has been isolated from various grasses, including *T. aestivum*. *Microdochium citrinidiscum* has only been isolated from *Eichhornia crassipes* (*Pontederiaceae*) (Hernández-Restrepo et al. 2016). The origin of *M. dawsoniorum* is unclear as it has been isolated from both native Australian and established exotic *Sporobolus* spp.



Phylogenetic tree of *Microdochium* based on a Bayesian analysis using ITS sequences. Analyses were performed on the Geneious v. 11.1.2 platform (Biomatters Ltd.) using RAxML v. 8.2.11 (Stamatakis & Alachiotis 2010) and MrBayes v. 3.2.6 (Ronquist & Huelsenbeck 2003), both based on the GTR substitution model with gamma-distribution rate variation. Branch lengths are proportional to distance. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). *Idriella lunata* was used as outgroup. Novel taxon is indicated in **bold**. Ex-type strains are marked with an asterisk (*).

Colour illustrations. Forest trees close to collection site. Colony on 1/2 potato dextrose agar (PDA) after 2 wk; conidiomata on 1/2 PDA; conidiogenous cells; conidia. Scale bars = 200 µm (conidiomata) and 10 µm (conidiogenous cells and conidia).

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