



Fungal Planet 1118 – 19 December 2020

***Parasarocladium tasmanniae* Crous, sp. nov.**

Etymology. Name refers to the host genus *Tasmannia* from which it was isolated.

Classification — *Sarocladiaceae*, *Hypocreales*, *Sordariomycetes*.

Ascomata perithecial, hyaline, smooth-walled, globose to obpyriform, 50–100 × 50–80 µm; wall of 3–6 layers of hyaline *textura angularis*. *Asci* obovoid to subcylindrical, hyaline, 8-spored, unitunicate with apical mechanism, not straining in Melzer's reagent, apex slightly flattened, 23–30 × 5–8 µm, stipitate, intermingled among cellular, hyaline paraphyses that dissolve at maturity. *Ascospores* hyaline, smooth, guttulate, fusoid-ellipsoid, straight to slightly curved, constricted at median septum, (9–)10–11(–12) × (2.5–)3(–3.5) µm. *Mycelium* consisting of hyaline, smooth, septate, branched, 1.5–2 µm diam hyphae. *Conidiophores* hyaline, smooth, subcylindrical, branched below, 1–2-septate, 20–35 × 2–3 µm. *Conidiogenous cells* at times solitary, arising directly from superficial hyphae, or on conidiophores, terminal or intercalary, phialidic, subcylindrical with slight apical taper, 12–30 × 2–3 µm; collarette minute, 1 µm tall, not flared. *Conidia* hyaline, smooth, granular, subcylindrical to fusoid, straight to slightly curved, aseptate, apex subobtuse, base slightly tapered to truncate hilum, 0.5 µm diam, (5–)7–8(–9) × (1.5–)2(–2.5) µm.

Culture characteristics — Colonies flat, spreading, surface folded, with sparse aerial mycelium and lobate, even margin, reaching 60 mm diam after 2 wk at 25 °C. On MEA and PDA surface and reverse dirty white; on OA surface buff.

Typus. AUSTRALIA, New South Wales, Limpinwood Nature Reserve, Mt Merino, on leaves of *Tasmannia insipida* (*Winteraceae*), 26 May 2015, B.A. Summerell, HPC 2953 (holotype CBS H-24402, culture ex-type CPC 38162 = CBS 146807, ITS, LSU, *actA*, *tef1* and *tub2* sequences GenBank MW175340.1, MW175380.1, MW173094.1, MW173121.1 and MW173134.1, MycoBank MB837830).

Notes — *Parasarocladium* was recently introduced by Summerbell et al. (2018) to accommodate a distinct clade of acremonium-like fungi, which are commonly isolated from soil (Crous et al. 2018a). As shown here, however, species can also be foliicolous, and have a sexual morph, which has thus far not been observed for any member of *Parasarocladium*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Parasarocladium radiatum* (strain CBS 142.62, GenBank NR_161112.1; Identities = 546/581 (94 %), 11 gaps (1 %)), *Parasarocladium debruynii* (strain CBS 144942, GenBank NR_163316.1; Identities = 540/581 (93 %), 17 gaps (2 %)), and *Parasarocladium gamsii* (as *Acremonium gamsii*; strain CBS 726.71, GenBank NR_159615.1; Identities = 538/584 (92 %), 17 gaps (2 %)). Closest hits using the **LSU** sequence are *Parasarocladium breve* (as *Acremonium breve*; strain CBS 150.62, GenBank FJ176882.1; Identities = 886/901 (98 %), two gaps (0 %)), *Parasarocladium gamsii* (strain CBS 726.71, GenBank MH872068.1; Identities = 885/900 (98 %), two gaps (0 %)), and *Sarocladium strictum* (strain CBS 147.49, GenBank HQ232139.1; Identities = 833/849 (98 %), four gaps (0 %)). Closest hits using the **actA** sequence had highest similarity to *Parasarocladium debruynii* (strain CBS 144942, GenBank MK069413.1; Identities = 594/648 (92 %), 19 gaps (2 %)), *Cordyceps militaris* (strain ATCC 34164, GenBank CP023327.1; Identities = 400/422 (95 %), no gaps), and *Fusarium striatum* (strain CBS 101573, GenBank KM231195.1; Identities = 462/515 (90 %), six gaps (1 %)). Closest hits using the **tef1** sequence had highest similarity to *Parasarocladium debruynii* (strain CBS 144942, GenBank MK069410.1; Identities = 241/289 (83 %), 19 gaps (6 %)). Closest hits using the **tub2** sequence had highest similarity to *Parasarocladium debruynii* (strain CBS 144942, GenBank MK069407.1; Identities = 586/668 (88 %), 27 gaps (4 %)), *Sarocladium spirale* (strain 3-22, GenBank LC464483.1; Identities = 396/482 (82 %), 29 gaps (6 %)), and *Chaetopsina acutispora* (strain CBS 667.92, GenBank KM232029.1; Identities = 317/370 (86 %), 16 gaps (4 %)).

Colour illustrations. Rainforest at Limpinwood Nature Reserve (photo B. Summerell). Ascomata and ascospores; ascus; conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.