

*Passalora pseudotithoniae*



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***Passalora pseudotithoniae* Crous & Cheew., sp. nov.**

*Etymology.* Named after its morphological similarity to *Passalora tithoniae*.

*Leaf spots* amphigenous, brown, angular, confined by leaf veins, 2–5 mm diam. *Conidiophores* amphigenous, fasciculate, 40–100 µm tall, 3–4 µm wide, straight to geniculate-sinuous, mostly unbranched, subcylindrical, 1–3-septate, brown, smooth to finely verruculose, arising from a weakly developed brown stroma, up to 50 µm wide and 60 µm tall. *Conidiogenous cells* integrated, brown, smooth to finely verruculose, terminal, subcylindrical to once geniculate, 15–35 × 3–4.5 µm; loci thickened and darkened, 2 µm diam, mostly solitary and terminal, but also lateral on conidiogenous cells. *Conidia* occurring in long branched chains, brown, granular, smooth, subcylindrical to narrowly obclavate, apex obtuse to truncate, base obconically truncate, 1–6-septate, scars 2 µm diam, thickened and darkened, (30–)40–65(–130) × (4–)5(–5.5) µm.

*Culture characteristics* — Colonies reaching 25 mm diam after 2 wk, flat, spreading with sparse aerial mycelium and even, smooth margins. On PDA surface olivaceous-grey, reverse iron-grey; on MEA surface folded, olivaceous-grey with patches of pale olivaceous-grey, reverse olivaceous-grey.

*Typus.* THAILAND, Royal Project, N18°09'24.8" E98°23'19.6", on leaves of *Tithonia diversifolia* (Asteraceae), 5 Nov. 2012, P.W. Crous (holotype CBS H-21453, culture ex-type CPC 21688, 21689 = CBS 136442, ITS sequence GenBank KF777179, LSU sequence GenBank KF777231, MycoBank MB805859).

*Notes* — *Passalora pseudotithoniae* is morphologically similar to *P. tithoniae* (on *Tithonia diversifolia*, Trinidad; conidia 1–5-septate, 20–65 × 3–5.5 µm) (Ellis 1976), but distinct in that it has much longer conidia. Another recently described species from this host is *P. stromatica* (on *Tithonia diversifolia*, Brazil) which has wider conidiophores (4–8 µm) and 0–2-septate, subcylindrical to obclavate, 15.5–61.5 × 2.5–6.5 µm conidia (Fernandes et al. 2013).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are '*Passalora* sp.' (GenBank GU214668; Identities = 879/880 (99 %), no gaps), *Passalora tithoniae* (GenBank KC677927; Identities = 854/855 (99 %), no gaps) and *P. ageratinae* (GenBank GU214453; Identities = 855/857 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to '*Passalora* sp.' (GenBank GU214668; Identities = 670/677 (99 %), Gaps = 1/677 (0 %)), *P. ageratinae* (GenBank GU214639; Identities = 630/638 (99 %), no gaps) and *Dothistroma septosporum* (GenBank GU256362; Identities = 538/552 (97 %), Gaps = 3/552 (0 %)). Our ITS sequence differs from the sequence of *P. tithoniae* on GenBank (KC677895) with the presence of an 8-bp indel (Identities = 459/467 (98 %), Gaps = 8/467 (1 %)).

*Colour illustrations.* *Tithonia diversifolia* in Thailand; symptomatic leaves; conidiophores and conidia. Scale bars = 10 µm.

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