

Chaetopsina pini
& *Chaetopsina pinicola*



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Chaetopsina pini Crous & Cheew., *sp. nov.*

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

Conidiophores erect, setiform, tapering towards acutely rounded apex, mostly flexuous, medium brown, turning red-brown in 3 % KOH, fertile in mid region, unbranched, verruculose, 130–180 × 6–8 µm, 7–10-septate, thick-walled (2 µm diam), base bulbous, up to 13 µm diam; fertile region consisting of irregularly branched, dense aggregated conidiogenous cells. *Conidiogenous cells* ampulliform to lageniform, hyaline, smooth, mono- to polyphialidic, 5–20 × 3–5 µm; apical collarette up to 2 µm long, not flared. *Conidia* hyaline, smooth, granular, cylindrical, aseptate, apex and base bluntly rounded, base rarely with flattened hilum, (13–)15–16(–18) × 2(–2.5) µm. Conidiophore base surrounded by cinnamon coloured ascomata, but these remained infertile.

Culture characteristics — Colonies reaching 50 mm diam after 2 wk, flat, spreading, with sparse aerial mycelium and even, lobate margins. On MEA surface and reverse cinnamon; on PDA surface and reverse brown-vinaceous; on OA surface vinaceous-buff.

Typus. THAILAND, Chiang Mai, Boa Keaw Silvicultural Research Station, on needle litter of *Pinus caribaea* (*Pinaceae*), 29 Oct. 2012, P.W. Crous (holotype CBS H-21454, culture ex-type CPC 21622, 21623 = CBS 136443, ITS sequence GenBank KF777144, LSU sequence GenBank KF777200, MycoBank MB805860).

Notes — Although morphologically similar, the genera *Chaetopsina* and *Kionochaeta* are phylogenetically distinct (Okada et al. 1997). Both genera have mono- to polyphialides, and setose conidiophores. However, species of *Chaetopsina* have conidiophores that turn yellow in lactic acid, while those of *Kionochaeta* are brown, and tend to have verticillate to penicillate fertile nodes (Seifert et al. 2011). Furthermore, the genus *Chaetopsina* has nectria-like sexual morphs that are accommodated in *Chaetopsinectria* (Luo & Zhuang 2010). The common species of *Chaetopsina* reported from *Pinus* is *C. fulva*, which has cylindrical conidia, 8–12 × 1.5 µm (Kirk & Sutton 1985), thus smaller than those reported here for *C. pini*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Chaetopsinectria chaetopsinae* (GenBank DQ119553; Identities = 869/880 (99 %), no gaps), *Chaetopsina fulva* (GenBank GU075867; Identities = 865/879 (98 %), no gaps) and *Cosmospora chaetopsinae-penicillatae* (GenBank GU075865; Identities = 857/879 (97 %), no gaps). Closest hits using the ITS sequence had highest similarity to *Volutella ciliata* (GenBank AJ301966; Identities = 633/730 (87 %), Gaps = 37/730 (5 %)), *Stachybotrys bisbyi* (GenBank AF081480; Identities = 636/735 (87 %), Gaps = 36/735 (4 %)) and *Chaetopsina penicillata* (GenBank HQ897798; Identities = 528/611 (86 %), Gaps = 30/611 (4 %)).

Chaetopsina pinicola Crous & Cheew., *sp. nov.*

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

Conidiophores erect, setiform, tapering towards acutely rounded apex, mostly flexuous, medium brown, turning red-brown in 3 % KOH, fertile in mid region, unbranched, verruculose, 130–250 × 8–12 µm, 11–15-septate, thick-walled (2 µm diam), base bulbous, up to 15 µm diam; fertile region consisting of irregularly branched, dense aggregated conidiogenous cells. *Conidiogenous cells* ampulliform to lageniform, hyaline, smooth, mono- to polyphialidic, 5–12 × 3–4 µm. *Conidia* hyaline, smooth, guttulate, subcylindrical, aseptate, apex and base bluntly rounded, base rarely with flattened hilum, (11–)13–15(–17) × 2(–2.5) µm.

Culture characteristics — Colonies reaching 45 mm diam after 2 wk, with sparse aerial mycelium, and flattened, lobate margins. On PDA surface and reverse sepia; on OA surface sepia with patches of honey; on MEA surface and reverse honey.

Typus. THAILAND, Chiang Mai, Chiang Mai Botanical Garden, pine arbo-retum, on needles of *Pinus* sp. (*Pinaceae*), 2 Nov. 2012, P.W. Crous (holotype CBS H-21455, culture ex-type CPC 21819, 21820 = CBS 136444, ITS sequence GenBank KF777145, LSU sequence GenBank KF777201, MycoBank MB805861).

Colour illustrations. Boa Keaw Silvicultural Research Station, Chiang Mai, Thailand; Left column *C. pini*: Conidiophores, conidiogenous cells and conidia. Right column *C. pinicola*: Conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — *Chaetopsina pinicola* differs from *C. pini* by having conidia with an average range shorter than those of *C. pini*, and having longer conidiophores and shorter conidiogenous cells. Conidiophores of *C. pini* were also surrounded by ascomatal initials, though these were never observed in cultures of *C. pinicola*, suggesting that the former may have a *Chaetopsinectria* state in vivo.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Chaetopsinectria chaetopsinae* (GenBank DQ119553; Identities = 881/889 (99 %), no gaps), *Chaetopsina fulva* (GenBank GU075867; Identities = 877/888 (99 %), no gaps) and *Volutella citrinella* (GenBank HQ843772; Identities = 859/876 (98 %), no gaps). Closest hits using the ITS sequence had highest similarity to *Chaetopsina fulva* (GenBank GU075861; Identities = 490/513 (96 %), Gaps = 8/513 (1 %)), *Cosmospora chaetopsinae* (GenBank GU075858; Identities = 472/505 (93 %), Gaps = 11/505 (2 %)) and *Chaetopsina penicillata* (GenBank HQ897798; Identities = 551/598 (92 %), Gaps = 10/598 (1 %)).