

*Amorocelophoma neoregeliae*  
& *Cadophora neoregeliae*



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***Amorocoelophoma neoregeliae* Crous, sp. nov.**

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

Classification — *Amorosiaceae*, *Pleosporales*, *Dothideomycetes*.

*Conidiomata* solitary, erumpent, globose, pycnidial, brown with central ostiole, 200–350 µm diam; wall of 6–8 layers of brown *textura angularis*. *Conidiophores* lining the inner cavity, reduced to conidiogenous cells or with a supporting cell, branched at base, hyaline, smooth, 7–15 × 2–3 µm. *Conidiogenous cells* hyaline, smooth, subcylindrical with apical taper, 7–12 × 2–2.5 µm, phialidic with periclinal thickening. *Conidia* solitary, hyaline, smooth, guttulate, straight, subcylindrical, apex obtuse, base bluntly rounded, (3–)3.5–4.5(–5) × (1.5–)2(–2.5) µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface olivaceous grey, reverse isabelline; on PDA surface and reverse olivaceous grey; on OA surface olivaceous grey.

*Typus.* NEW ZEALAND, Tauranga port, from leaf spots of *Neoregelia* sp. (*Bromeliaceae*), 22 Aug. 2019, *D. Brunt* (holotype CBS H-24438, culture ex-type CPC 38740 = T19\_05712A = CBS 146820, ITS, LSU, *rbp2* and *tef1* (second part) sequences GenBank MZ064410.1, MZ064467.1, MZ078193.1 and MZ078247.1, MycoBank MB 839497).

Notes — *Amorocoelophoma neoregeliae* is related to *A. cassiae*, but distinct in that the latter has longer conidia (9–11 × 2–3 µm) (Jayasiri et al. 2019).

***Cadophora neoregeliae* Crous, sp. nov.**

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

Classification — *Ploettnerulaceae*, *Helotiales*, *Leotiomyces*.

*Mycelium* consisting of hyaline, smooth, septate, branched, 2–3 µm diam hyphae. *Conidiophores* hyaline, smooth, erect, penicillate (at times reduced to solitary phialides on hyphae), branched or not, with clusters of conidiogenous cells, terminal and intercalary, 30–90 × 2–3 µm, 2–7-septate. *Conidiogenous cells* hyaline, smooth, curved, phialidic, 7–15 × 2.5–3 µm, with visible periclinal thickening, arranged in rosettes of up to seven per conidiophore, mostly terminal. *Conidia* solitary, aseptate, globose, guttulate to granular, smooth, hyaline, 2.5–4 µm diam. *Chlamydospores* rare, terminal on hyphae, ellipsoid to subglobose, brown, smooth, guttulate, 8–12 × 6–8 µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 50 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse brown vinaceous.

*Colour illustrations.* *Neoregelia* sp. Left column: *Amorocoelophoma neoregeliae*. Conidiomata on PDA; conidioma with ostiole; conidiogenous cells giving rise to conidia; conidia. Right column: *Cadophora neoregeliae*. Colony sporulating on OA; conidiogenous cells; chlamydospore; conidiophore giving rise to conidia; conidia. Scale bars = 10 µm.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Hermatomyces* sp. 1-2018 (strain KZP352, GenBank LS398262.1; Identities = 671/776 (86 %), 32 gaps (4 %)), *Acrocallymma vagum* (strain 0101-2, GenBank MN540314.1; Identities = 651/778 (84 %), 38 gaps (4 %)) and *Alfoldia vorosii* (strain CBS 145501, GenBank NR\_171211.1; Identities = 396/409 (97 %), four gaps (0 %)). Closest hits using the LSU sequence are *Amorocoelophoma cassiae* (strain MFLUCC 17-2283, GenBank NG\_066307.1; Identities = 871/877 (99 %), one gap (0 %)), *Alfoldia vorosii* (strain CBS 145501, GenBank NG\_068885.1; Identities = 869/877 (99 %), no gaps) and *Angustimassarina populi* (strain MFLUCC 17-1069, GenBank MF409166.1; Identities = 861/878 (98 %), two gaps (0 %)). Closest hits using the *rbp2* sequence had highest similarity to *Opegrapha varia* (voucher KAG981017-42, GenBank AY485628.1; Identities = 833/921 (90 %), one gap (0 %)), *Amorocoelophoma cassiae* (strain MFLUCC 17-2283, GenBank MK434894.1; Identities = 810/908 (89 %), three gaps (0 %)) and *Angustimassarina rosarum* (strain MFLUCC 17-2155, GenBank MT394678.1; Identities = 725/823 (88 %), no gaps). Closest hits using the *tef1* sequence had highest similarity to *Alfoldia vorosii* (strain REF117, GenBank MK599321.1; Identities = 874/907 (96 %), no gaps), *Pseudohelminthosporium clematidis* (strain MFLUCC 17-2086, GenBank MT394627.1; Identities = 833/868 (96 %), no gaps) and *Amorocoelophoma cassiae* (strain MFLUCC 17-2283, GenBank MK360041.1; Identities = 868/907 (96 %), no gaps).

*Typus.* NEW ZEALAND, Tauranga port, from leaf spots of *Neoregelia* sp. (*Bromeliaceae*), 22 Aug. 2019, *D. Brunt* (holotype CBS H-24439, culture ex-type CPC 38741 = T19\_05712B = CBS 146821, ITS and LSU sequences GenBank MZ064411.1 and MZ064468.1, MycoBank MB 839498).

Notes — Species of *Cadophora* (dematiaceous hyphomycetes with monophialidic conidiophores with distinct flask-shaped, hyaline collarettes, and aseptate conidia) are commonly isolated from soil, but are also known as plant pathogens or saprobes (Bien & Damm 2020, Crous et al. 2020b). *Cadophora neoregeliae* is distinguished from other species known in the genus by its globose conidia, 2.5–4 µm diam, and the production of chlamydospores in culture.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Cadophora fastigiata* (strain CBS 869.69, GenBank MH859469.1; Identities = 554/569 (97 %), no gaps), *Phialophora dancoi* (strain IFM 50357, GenBank AB190869.1; Identities = 551/566 (97 %), no gaps) and *Cadophora malorum* (strain NW-FVA5175, GenBank MT561395.1; Identities = 563/579 (97 %), one gap (0 %)). Closest hits using the LSU sequence are *Mollisia cinerella* (strain CBS 312.61, GenBank MH869631.1; Identities = 860/864 (99 %), no gaps), *Cadophora bubakii* (as *Phialophora bubakii*; strain CBS 198.30, GenBank MH866559.1; Identities = 860/864 (99 %), no gaps) and *Cadophora melinii* (strain CBS 120273, GenBank MH874636.1; Identities = 859/864 (99 %), no gaps).