

*Colletotrichum cliviigenum*



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***Colletotrichum cliviigenum* Crous, sp. nov.**

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

*Classification* — *Glomerellaceae*, *Glomerellales*, *Sordariomycetes*.

*Conidiomata* acervular, erumpent, brown, 200–300 µm diam. *Conidiophores* arising from a basal stroma, hyaline, smooth, branched, subcylindrical, 2–6-septate, 60–120 × 6–9 µm. *Conidiogenous cells* terminal and intercalary, hyaline, smooth, subcylindrical, phialidic, proliferating percurrently, 15–35 × 5–8 µm. *Conidia* solitary, aseptate, hyaline, smooth, guttulate, subcylindrical, apex obtuse, tapering at base toward truncate hilum, 2 µm diam, (18–)22–26(–30) × (6–)7–8 µm. Setae and appressoria not seen.

*Culture characteristics* — Colonies flat, spreading, with moderate aerial mycelium and smooth, even margin, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface buff to honey, reverse buff.

*Typus.* SOUTH AFRICA, Mpumalanga, Mbombela, Buffelskloof Nature Reserve, on leaves of *Clivia* sp. (*Amaryllidaceae*), Nov. 2018, P.W. Crous, HPC 3158 (holotype CBS H-24444, culture ex-type CPC 38800 = CBS 146825, ITS, LSU, *actA*, *chs-1*, *gapdh*, *his3* and *tub2* sequences GenBank MZ064415.1, MZ064472.1, MZ078143.1, MZ078161.1, MZ078178.1, MZ078180.1 and MZ078260.1, MycoBank MB 839502).

*Notes* — *Colletotrichum cliviigenum* is accommodated in the *C. boninense* species complex (Damm et al. 2012b). Several species are known from *Clivia*, namely *C. cliviae* (conidia 23–28 × 5–7 µm, the Netherlands), *C. cliviicola* (conidia (11–)15.5–20.5(–26.5) × (4–)5.5–6.5(–7) µm, China), and *C. himantophylli* (conidia 14–24 × 4–4.5 µm, Czech Republic) (Damm et al. 2019). *Colletotrichum cliviigenum* can be distinguished from those species in having larger conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Colletotrichum boninense* (strain ICMP 17904, GenBank NR\_165949.1; Identities = 588/593 (99 %), no gap), *Colletotrichum oncidii* (strain CBS 130242, GenBank MH865629.1; Identities = 588/593 (99 %), one gap (0 %)) and *Colletotrichum cymbidiicola* (strain JL-3, GenBank KX058529.1; Identities = 585/590 (99 %), no gaps). Closest hits using the **LSU** sequence are *Colletotrichum karsti* (strain CBS 130641, GenBank MH877253.1; Identities = 838/839 (99 %), no gaps), *Colletotrichum boninense* (strain CBS 130235, GenBank MH877209.1; Identities = 838/839 (99 %), no gaps) and *Colletotrichum novae-zelandiae* (strain CBS 130240, GenBank MH877051.1; Identities = 838/839 (99 %), no gaps). Closest hits using the **actA** sequence had highest similarity to *Colletotrichum beeveri* (strain CBS 128527, GenBank JQ005519.1; Identities = 259/267 (97 %), no gaps), *Colletotrichum brassicicola* (strain CD015-1, GenBank KC859967.1; Identities = 258/267 (97 %), no gaps) and *Colletotrichum colombiense* (strain CBS 129818, GenBank JQ005522.1; Identities = 258/267 (97 %), no gaps). Closest hits using the **chs-1** sequence had highest similarity to *Colletotrichum boninense* (strain SJSJH-Z43, GenBank MK992714.1; Identities = 271/273 (99 %), no gaps), *Colletotrichum philodendricola* (nom. inval.) (strain LZJZ1, GenBank MH105265.1; Identities = 271/273 (99 %), no gaps) and *Colletotrichum torulosum* (strain CBS 102667, GenBank JQ005339.1; Identities = 270/273 (99 %), no gaps). Closest hits using the **gapdh** sequence had highest similarity to *Colletotrichum boninense* (voucher HGUP HL8, GenBank MN542219.1; Identities = 532/547 (97 %), one gap (0 %)), *Colletotrichum karsti* (strain CkaCkLH20\_04883, GenBank XM\_038887602.1; Identities = 310/319 (97 %), no gaps) and *Colletotrichum aotearoa* (strain BRIP 62670, GenBank KU221340.1; Identities = 318/337 (94 %), no gaps). Closest hits using the **his3** sequence had highest similarity to *Colletotrichum boninense* (strain HJH-3, GenBank MH370543.1; Identities = 376/393 (96 %), five gaps (1 %)), *Colletotrichum cymbidiicola* (strain CBS 128543, GenBank JQ005428.1; Identities = 373/390 (96 %), five gaps (1 %)) and *Colletotrichum pseudoboninense* (nom. inval.) (strain LZJZ5, GenBank MK796580.1; Identities = 374/392 (95 %), five gaps (1 %)). Closest hits using the **tub2** sequence had highest similarity to *Colletotrichum cymbidiicola* (strain HTL126, GenBank MH305540.1; Identities = 676/696 (97 %), no gaps), *Colletotrichum boninense* (strain LF644, GenBank KJ955336.1; Identities = 688/709 (97 %), no gaps) and *Colletotrichum philodendricola* (nom. inval.) (strain LZJZ1, GenBank MH105277.1; Identities = 684/708 (97 %), no gaps).

*Colour illustrations.* Symptomatic leaf of *Clivia* sp. Conidiomata on OA; conidiogenous cells giving rise to conidia; conidia. Scale bars = 300 µm (conidiomata), 10 µm (all others).

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