

Calonectria blephiliae



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Calonectria blephiliae Crous & Hodges, *sp. nov.*

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

Conidiophores with a stipe bearing a suite of penicillate, fertile branches, a stipe extension, and a terminal vesicle; stipe septate, hyaline, smooth, 90–220 × 5–7 µm; stipe extensions septate, straight to flexuous, 200–280 µm long, 3.5–4.5 µm wide at apical septum, terminating in a clavate to ellipsoid vesicle, 7–10 µm diam. *Conidiogenous apparatus* 100–150 µm long and 90–110 µm wide; primary branches aseptate or 1-septate, 33–70 × 6–8 µm; secondary branches aseptate, 15–25 × 4–5 µm; tertiary and additional branches (–4), aseptate, 8–22 × 3–5 µm, each terminal branch producing 2–4 phialides; phialides doliform to reniform, hyaline, aseptate, 7–12 × 3–4 µm; apex with minute periclinal thickening and inconspicuous collarette. *Macroconidia* cylindrical, rounded at both ends, straight, (42–)48–52(–55) × (4–)4.5(–5) µm, 1-septate, aggregated in parallel cylindrical clusters. *Megaconidia* and *microconidia* not seen.

Culture characteristics — Colonies with moderate aerial mycelium and feathery margin. On PDA surface and reverse chestnut; on MEA surface bay, reverse chestnut; on OA surface bay, reverse umber.

Typus. USA, North Carolina, Ellerbe, associated with dead lower stems of *Blephilia ciliata* (*Lamiaceae*), 18 Sept. 2012, T. Sharp (holotype CBS H-21434, culture ex-type CPC 21859 = CBS 136425, ITS sequence GenBank KF777141, LSU sequence GenBank KF777197, TEF sequence GenBank KF777243, TUB sequence GenBank KF777246, MycoBank MB805839).

Notes — Morphologically *Calonectria blephiliae* is part of the *C. morganii* species complex (Schoch et al. 1999, 2000).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Calonectria variabilis* (GenBank GQ280785; Identities = 874/874 (100 %), no gaps), *C. sulawesiensis* (GenBank GQ280760; Identities = 874/874 (100 %), no gaps) and *C. insularis* (GenBank GQ280710; Identities = 874/874 (100 %), no gaps). Closest hits using the ITS sequence had highest similarity to *C. sulawesiensis* (GenBank GQ280638; Identities = 569/571 (99 %), Gaps = 2/571 (0 %)), *C. cerciana* (GenBank GQ280560; Identities = 569/571 (99 %), Gaps = 1/571 (0 %)) and *C. morganii* (GenBank GQ280626; Identities = 568/571 (99 %), Gaps = 3/571 (0 %)). Closest hits using the TEF sequence had highest similarity to *C. morganii* (GenBank FJ918557; Identities = 483/488 (99 %), Gaps = 1/488 (0 %)), *C. sulawesiensis* (GenBank GQ267343; Identities = 483/490 (99 %), Gaps = 3/490 (0 %)) and *C. variabilis* (GenBank GQ267335; Identities = 486/494 (98 %), Gaps = 7/494 (1 %)). Closest hits using the TUB sequence had highest similarity to *C. morganii* (GenBank DQ521600; Identities = 536/537 (99 %), Gaps = 1/537 (0 %)), *C. pauciramosa* (GenBank FJ795548; Identities = 516/517 (99 %), Gaps = 1/517 (0 %)) and *C. pseudonaviculata* (GenBank GQ267214; Identities = 562/564 (99 %), Gaps = 1/564 (0 %)).

Colour illustrations. Symptomatic *Blephilia ciliata*; conidiophores sporulating on CLA; conidiogenous cells, cylindrical, 1-septate conidia and terminal vesicles. Scale bars = 10 µm.