
Neocamarosporium chichastianum

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Neocamarosporium chichastianum Papizadeh, Crous, Shahzadeh Fazeli & Amoozegar, *sp. nov.*

Etymology. Name reflects the location, Lake Urmia (formerly known as Chichast), from which the species was isolated.

Conidiomata pycnidial, solitary, uniloculate, black, up to 200 µm diam, with 1–3 papillate necks (up to 150 µm diam), with central ostioles 5–10 µm diam. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, subcylindrical, 7–15 × 4–5 µm, proliferating percurrently at apex. *Paraphyses* intermingled between conidiogenous cells, hyaline, smooth, subcylindrical, 1–2-septate with obtuse ends, up to 35 µm long, 4–5 µm diam. *Conidia* solitary, brown, finely roughened, ellipsoid, widest in middle, apex obtuse, muriformly septate, thick-walled, base truncate, 2–3 µm diam, (11–)15–19(–22) × (6–)8–9(–11) µm; 3 transverse septa, 1–2 oblique or vertical septa.

Culture characteristics — Colonies flat, spreading with sparse aerial mycelia. On OA surface olivaceous-grey. On MEA surface pale olivaceous-grey to olivaceous-grey. Optimum growth occurred at 25 °C, but the fungus grew at 15 °C up to 35 °C. Furthermore, optimum growth was recorded at pH values between 5.5 and 6.5, although it could grow at a broad range of pH values (4–10).

Typus. Iran, Lake Urmia, soil, 2011, *M. Papizadeh & M.R. Soudi* (holotype CBS H-21989, culture ex-type IBRC-M 30126 = CBS 137502; ITS sequence GenBank KP004455, LSU sequence GenBank KP004483, MycoBank MB810602).

Notes — *Neocamarosporium chichastianum* clusters with *N. goegapense*, the type species of the genus *Neocamarosporium*, which is morphologically similar to the genus *Camarosporium* based on its pycnidial conidiomata, hyaline, percurrently proliferating conidiogenous cells, and brown, muriformly septate conidia (Crous et al. 2014). *Neocamarosporium chichastianum* is the second species described in this genus, and interestingly has paraphyses, which were not observed in *N. goegapense.*

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Neocamarosporium goegapense* (GenBank KJ869163; Identities = 550/579 (95 %), Gaps = 5/579 (0 %)), *Phoma betae* (GenBank KC460811; Identities = 463/493 (94 %), Gaps = 7/493 (1 %)) and *Ascochyta obiones* (GenBank GU230752; Identities = 463/498 (93 %), Gaps = 4/498 (0 %)). Our ITS sequence is 98 % (517/529) identical to the sequence of *Chaetosphaeronema hispidulum* CBS 826.88 in Q-bank (www.q-bank.eu).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Neocamarosporium goegapense* (GenBank KJ869220; Identities = 804/806 (99 %), no gaps), *Chaetosphaeronema hispidulum* (GenBank EU754145; Identities = 848/851 (99 %), no gaps) and *Coniothyrium obiones* (GenBank DQ678054; Identities = 849/853 (99 %), no gaps).

Colour illustrations. Lake Urmia in Iran; conidiomata on OA and PNA, conidiomatal neck, conidiogenous cells and conidia. Scale bars = 10 µm.

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