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Zasmidium commune Crous, sp. nov.

Eymology. Name refers to the common occurrence of this species.

Classification — Mycosphaerellaceae, Capnodiales, Dothideomycetes.

Mycelium consisting of branched, septate, medium brown, verruculose, 1.5–2.5 µm diam hyphae. Conidiophores solitary, erect, arising from superficial mycelium, 25–100 × 3–5 µm, subcylindrical, somewhat flexuous, medium brown, thick-walled, smooth, 1–8-septate, unbranched. Conidiogenous cells integrated, terminal, subcylindrical, medium brown, smooth, 5–20 × 3–4 µm; scars thickened, darkened, sympodial, 1 µm diam, proliferating sympodially. Secondary ramoconidia medium brown, verruculose, narrowly obclavate to somewhat subcylindrical, 30–150 × 3–5 µm, multisepitate; hila thickened, darkened, 0.5 µm diam. Conidia in short (1–2) branched chains, medium brown, verruculose, narrowly obclavate to somewhat subcylindrical, apex obtuse, base truncate, hilum 0.5 µm diam, thickened, darkened, (8–)15–35–(45) × (2.5–)3(–4) µm.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium, and feathery margins, reaching 15 mm diam after 2 wk at 25 °C. On MEA and PDA surface brown vinaceous, reverse isabelline. On OA surface olivaceous grey.

Typus. AUSTRALIA, Western Australia, Denmark, Mount Lindesay Walk Trail, on leaves of Xanthorrhoea sp. (Xanthorrhoeaceae), 19 Sept. 2015, P.W. Crous (holotype CBS H-23093, cultures CPC 29725 = CBS 142530, ITS, LSU, and actA sequences GenBank KY979765, KY979800, and KY979860, MycoBank MB820955); CPC 29547, CPC 29723, ITS, LSU, actA, and tub2 sequences GenBank KY979763–KY979764, KY979818–KY979819, KY979858–KY979859, and KY979929 (CPC 29547).

Notes — The genus Zasmidium (Mycosphaerellaceae) as it is presently defined is paraphyletic (Videira et al. in prep.). Most of the known species are associated with leaf spot diseases of various hosts. Some of these are agriculturally important, such as greasy leaf spot disease of Citrus (Huang et al. 2015). Zasmidium commune appears to be specific to leaves of a Xanthorrhoea sp. Phylogenetically, Z. commune is distinct from other Zasmidium spp. that are presently known based on their DNA sequences. Based on a megablast search using the ITS sequence, the best match was to Mycosphaerella pseudovespa (GenBank NR_137548; Identities = 501/507 (99%), no gaps), followed by Periconiella velutina (GenBank EU041781; Identities = 526/547 (96%), 1 gap (0%)). Based on the actA sequence, Z. commune was only 95 % similar to Mycosphaerella pseudovespa (GenBank KF903535; Identities = 502/531 (95 %), 10 gaps (1 %)).

Colour illustrations. Xanthorrhoea sp. at the Mount Lindesay Walk Trail; colony sporulating on SNA; conidiophores and conidia. Scale bars = 10 µm.