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***Setophoma vernoniae* Crous & Alfenas, sp. nov.**

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

Leaf spots amphigenous, angular, confined by leaf veins, 1–6 mm diam, brown to grey, at times surrounded by a broad dark purple margin. *Conidiomata* pycnidial, globose, superficial on SNA, pale brown, exuding a crystalline conidial mass, up to 300 µm diam, unilocular, with a central ostiole; conidiomatal wall of 3–4 layers of subhyaline *textura angularis*; outer wall with brown, unbranched setae, more prominent around upper part of conidioma, subcylindrical, flexuous to straight, base somewhat swollen, verruculose, apex obtusely rounded, smooth, thick-walled, 30–60 × 3–4 µm. *Conidiophores* reduced to conidigenous cells. *Conidigenous cells* hyaline, smooth, ampulliform, proliferating with aggregated percurrent proliferations at apex, or at same level, with periclinal thickening visible at apex, ovoid, 4–10 × 3–4 µm. *Conidia* solitary, hyaline, smooth, aseptate, granular, subcylindrical to narrowly fusoid-ellipsoid with obtuse ends, straight, (5–)6(–8) × 2.5(–3) µm.

Culture characteristics — Colonies reaching 40 mm diam after 2 wk at 22 °C, spreading with moderate aerial mycelium and smooth, even margins. On PDA surface grey-olivaceous, outer region iron-grey, reverse iron-grey. On OA surface isabel-line. On MEA surface olivaceous-grey, reverse cinnamon with patches of olivaceous-grey.

Typus. BRAZIL, Minas Gerais, Árvore de Natal, Viçosa, Viçosa - MG, on leaves of *Vernonia polyanthes* (*Compositae*), May 2013, A.C. Alfenas (holotype CBS H-21701, culture ex-type CPC 23123 = CBS 137988; ITS sequence GenBank KJ869141, LSU sequence GenBank KJ869198, MycoBank MB808920).

Notes — The genus *Setophoma* was introduced by de Gruyter et al. (2010) to accommodate phoma-like coelomycetes with setose pycnidia, phialidic conidigenous cells, and hyaline, aseptate conidia. The present collection closely matches other species of *Setophoma* and represents a new taxon on *Vernonia polyanthes* from Brazil.

ITS. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Setophoma chromolaena* (GenBank KF251244; Identities = 552/566 (98 %), Gaps = 2/566 (0 %)), *Coniothyria agaves* (GenBank JX681075; Identities = 491/543 (90 %), Gaps = 10/543 (1 %)) and *Shiraia bambusicola* (GenBank AB105798; Identities = 497/552 (90 %), Gaps = 12/552 (2 %)).

LSU. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Setophoma chromolaena* (GenBank KF251747; Identities = 834/834 (100 %), no gaps), *Setophoma sacchari* (GenBank GQ387586; Identities = 871/876 (99 %), no gaps) and *Phaeosphaeriopsis musae* (GenBank DQ885894; Identities = 895/907 (99 %), Gaps = 1/907 (0 %)).

Colour illustrations. *Vernonia polyanthes* in Brazil; conidiomata, setae, conidigenous cells and conidia in culture. Scale bars = 10 µm.

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