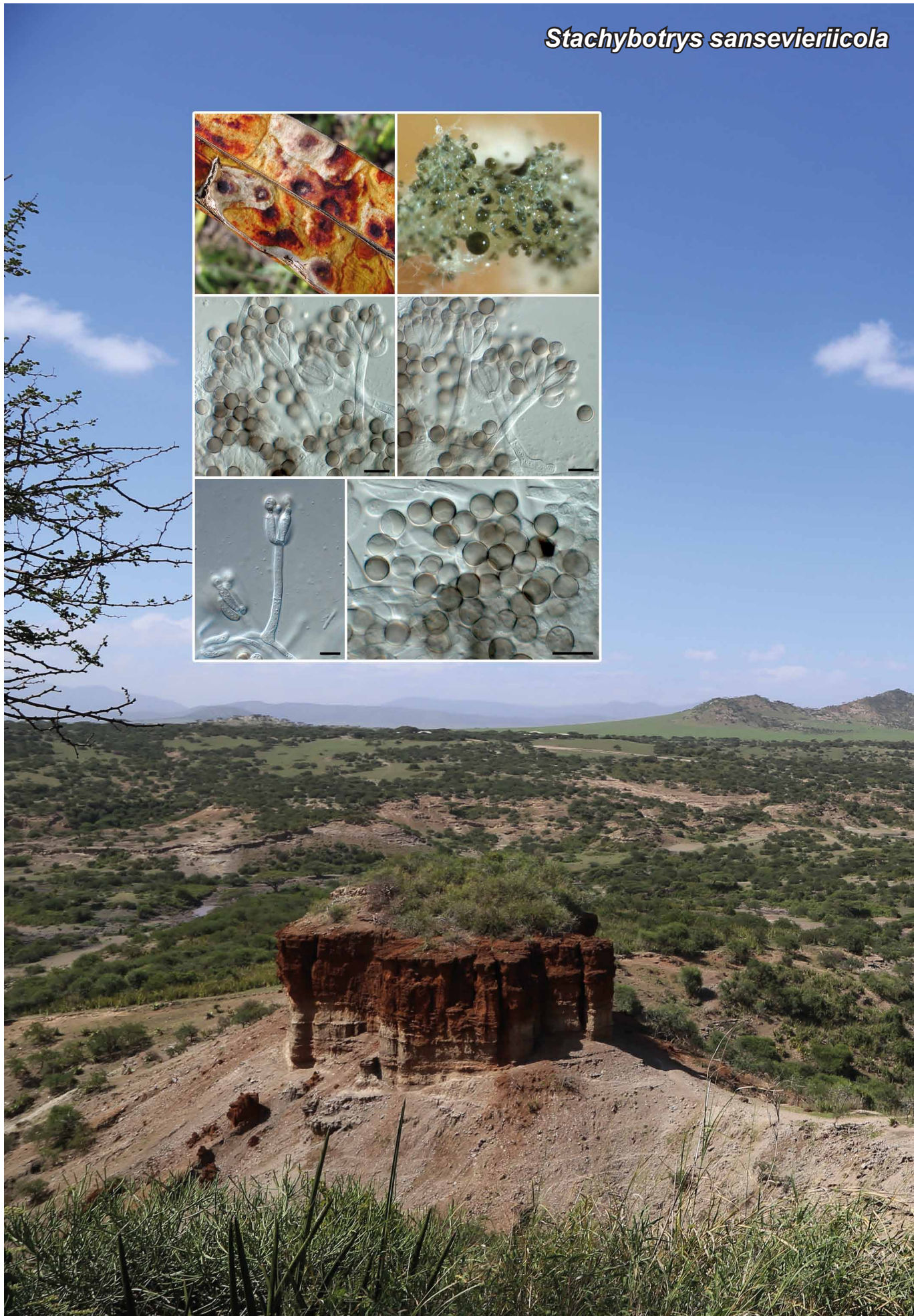


Stachybotrys sansevieriicola



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***Stachybotrys sansevieriicola* Crous & M.J. Wingf., sp. nov.**

Etymology. Name reflects the host genus *Sansevieria*, from which the species was isolated.

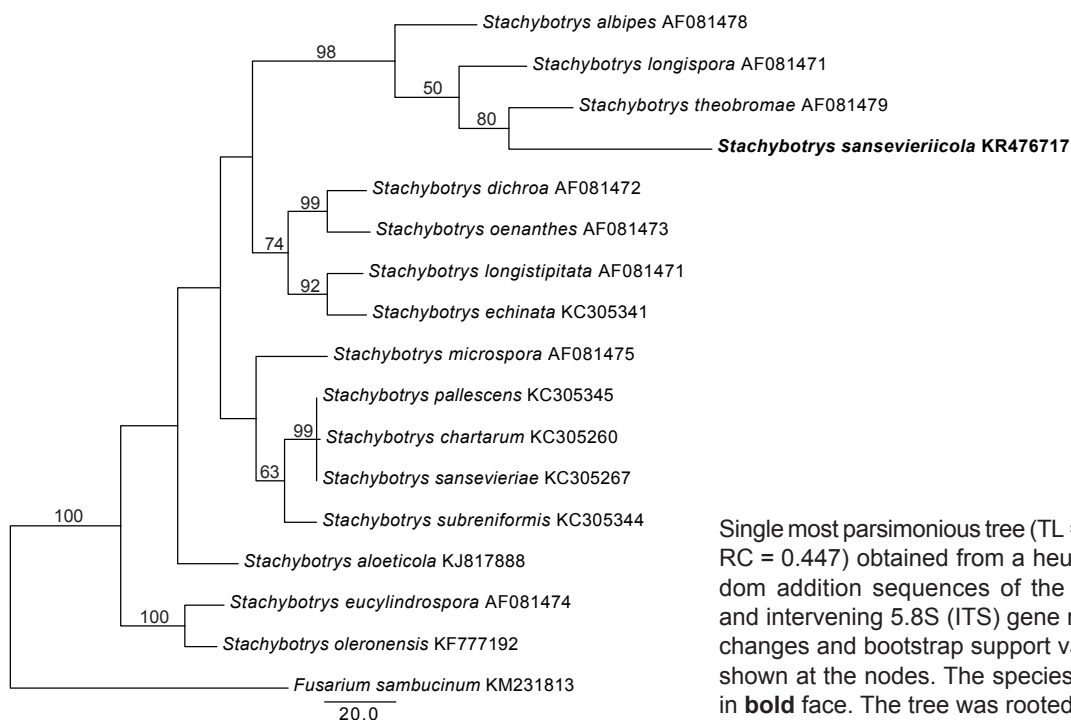
Classification — *Stachybotriaceae*, *Hypocreales*, *Sordariomycetes*.

Conidiophores simple, macronematous, mononematous, single or in groups, mostly unbranched, erect, straight to slightly flexuous, 1–3-septate, smooth, hyaline, 40–70 × 3–5 µm, bearing a whorl of 3–8 phialides. *Phialides* terminal, clavate to broadly reniform or subcylindrical, hyaline, becoming pale brown, 10–15 × 4–5 µm, smooth with conspicuous collarettes. *Conidia* acrogenous, aggregated in slimy masses, aseptate, globose to ellipsoid with truncate hilum, 3 µm diam, smooth, 7–9 × 6–8 µm (av. 8 × 7 µm), containing one or two guttules.

Culture characteristics — Colonies spreading, erumpent, with sparse aerial mycelium on OA and PDA, but with fluffy aerial mycelium on MEA, margin smooth, lobate, and surface folded. On MEA surface dirty white, reverse sienna in centre, orange in outer region. On PDA surface dirty white with luteous pigment, similar in reverse. On OA dirty white.

Typus. TANZANIA, Olduvai Gorge, on leaves of *Sansevieria ehrenbergii* (*Asparagaceae*), Feb. 2014, M.J. Wingfield (holotype CBS H-22220, culture ex-type CPC 24316 = CBS 138872; ITS sequence GenBank KR476717, LSU sequence GenBank KR476752, TEF sequence GenBank KR476793, TUB sequence GenBank KR476794, MycoBank MB812416); CPC 24317.

Notes — *Stachybotrys sansevieriicola* is closely related to *S. theobromae*, a species easily differentiated by its black, ovate to limoniform conidia (Hansford 1943). However, the conidia of *S. sansevieriicola* are much smaller than those of *S. theobromae* (21–28 × 15–18 µm). Another species, *S. sansevieriae*, has been reported from decayed leaves of *Sansevieria roxburghiana* in India, and is characterised by ellipsoid or boat-shaped, dark brown conidia (Ellis 1976), distinct from *S. sansevieriicola*.



Single most parsimonious tree (TL = 523, CI = 0.704, RI = 0.635, RC = 0.447) obtained from a heuristic search with 1 000 random addition sequences of the internal transcribed spacer and intervening 5.8S (ITS) gene regions. Scale bar shows 20 changes and bootstrap support values (1 000 repetitions) are shown at the nodes. The species described here is indicated in bold face. The tree was rooted to *Fusarium sambucinum*.

Colour illustrations. Olduvai Gorge in Tanzania; symptomatic leaf, colony, conidiophores and conidia. Scale bars = 10 µm.

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