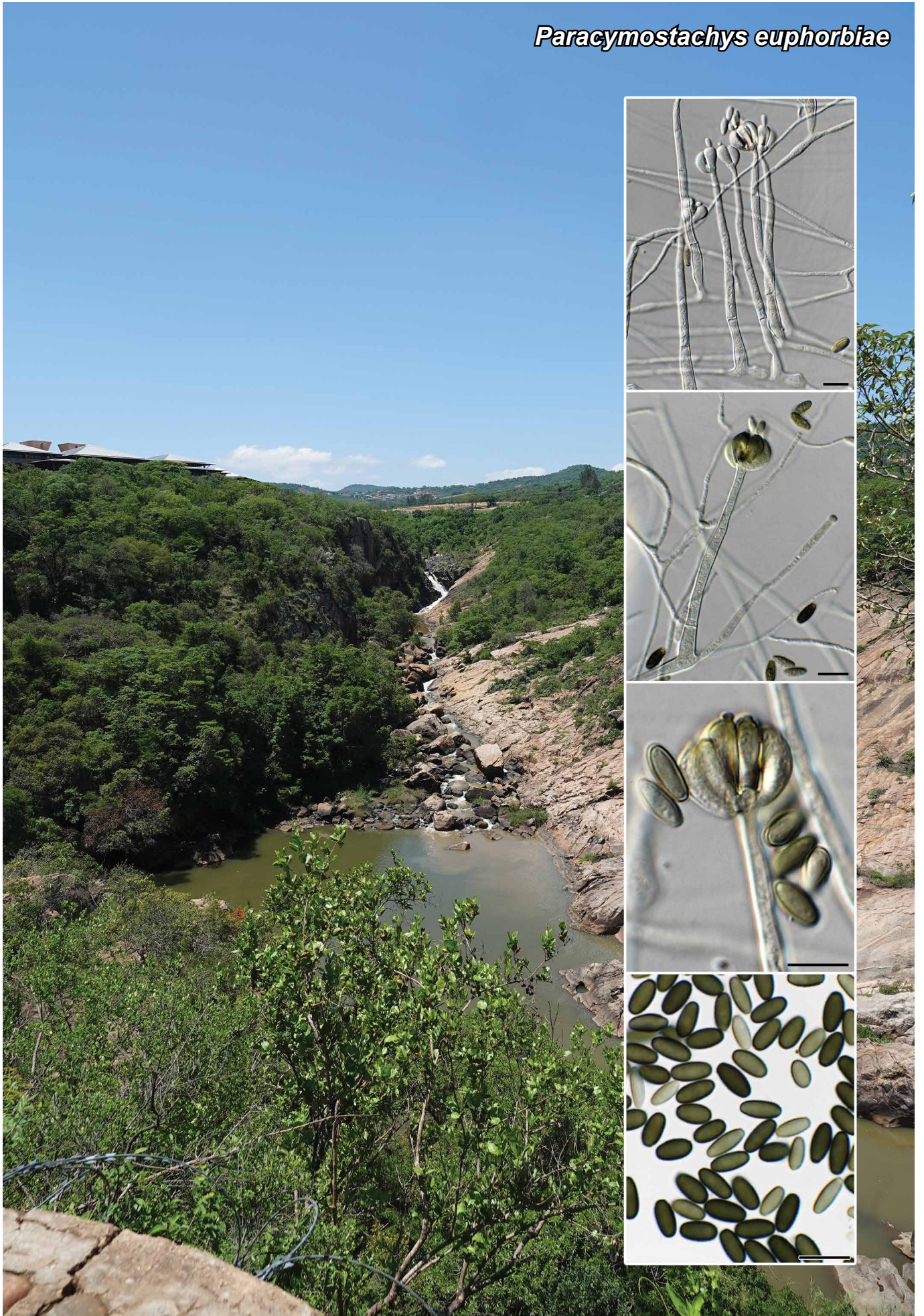


*Paracymostachys euphorbiae*





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***Paracymostachys* Crous, gen. nov.***Etymology.* Name reflects its close relationship to *Cymostachys*.Classification — *Stachybotryaceae*, *Hypocreales*, *Sordariomycetes*.*Conidiophores* macronematous, mononematous, erect, mostly in groups, mostly unbranched, thick-walled, hyaline to pale olivaceous brown, smooth, 1–2-septate, with 4–6 conidiogenous cells radiating from the apex. *Conidiogenous cells* phialidic, clavate to elongate doliiform, smooth to slightly verrucose, oli-

vaceous brown at the apex becoming subhyaline towards the base, with inconspicuous collarettes. Conidia in a mucoid droplet, aseptate, olivaceous brown to dark brown, thick-walled, guttulate, smooth to verrucose, fusoid, rarely subcylindrical, apex rounded, base truncate.

*Type species.* *Paracymostachys euphorbiae* Crous  
Mycobank MB 839506.***Paracymostachys euphorbiae* Crous, sp. nov.***Etymology.* Name refers to the host genus *Euphorbia* from which it was isolated.*Conidiophores* macronematous, mononematous, erect, solitary or in groups, mostly unbranched, thick- and smooth-walled, hyaline to pale olivaceous brown, 70–120 × 3–4 µm, 1–2-septate, with 4–6 conidiogenous cells arranged in a cluster at apex. *Conidiogenous cells* phialidic, clavate to fusoid or elongate doliiform, hyaline, becoming olivaceous brown and verruculose with inconspicuous collarettes, 7–11 × 3–5 µm. *Conidia* in a mucoid droplet, aseptate, olivaceous brown to dark brown, smooth, becoming verruculose, thick-walled, guttulate, fusoid, with rounded apex and truncate base, (7.5–)8–9(–10) × (3–)3.5–4 µm; rarely subcylindrical, up to 17 µm long. Germinating conidia dark brown, verrucose, 1-septate (constricted at septum) with polar germination, 13–17 × 6–7 µm.

Culture characteristics — Colonies erumpent, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 8 mm diam after 2 wk at 25 °C. On MEA surface saffron, margin umber, reverse umber; on PDA surface and reverse pale luteous; on OA surface iron-grey with buff margins.

*Typus.* SOUTH AFRICA, Mpumalanga, Mbombela, Lowveld Botanical Garden, on leaf litter of *Euphorbia ingens* (*Euphorbiaceae*), Nov. 2018, P.W. Crous, HPC 3140 (holotype CBS H-24495, culture ex-type CPC 38954 = CBS 146983, ITS, LSU, *cmdA* and *rpb2* sequences GenBank MZ064419.1, MZ064476.1, MZ078163.1 and MZ078197.1, MycoBank MB 839507).Notes — Lombard et al. (2016) distinguished several genera in *Stachybotryaceae*. *Paracymostachys* can be distinguished from *Cymostachys* by having smooth, primarily unbranched conidiophores, and fusoid, rarely subcylindrical conidia. *Paracymostachys euphorbiae* is distinct from *Cymostachys* species in not having fabiform to globose conidia. Furthermore, it is distinct from *S. limonisporea* (conidia (6–)6.5–7.5(–9) × 3–4 µm) in lacking limoniform conidia, and from *S. phaeophialis* (conidia ellipsoidal to fusoid) in having larger conidia ((6–)6.5–7.5(–9) × 3–4 µm; Lombard et al. 2016).Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Stachybotrys dolichophialis* (strain DAOM 227011,*Colour illustrations.* Mbombela, Lowveld Botanical Garden. Conidiophores with conidiogenous cells giving rise to conidia on SNA; conidia. Scale bars = 10 µm.GenBank KU846734.1; Identities = 551/612 (90 %), 36 gaps (5 %)), *Stachybotrys zaeae* (voucher HGUP 0143, GenBank KC305346.1; Identities = 546/611 (89 %), 37 gaps (6 %)) and *Stachybotrys microspora* (voucher HGUP 0120, GenBank KC305353.1; Identities = 545/610 (89 %), 36 gaps (5 %)). Closest hits using the LSU sequence are *Memnoniella echinata* (strain CBS 216.32, GenBank MH866746.1; Identities = 852/863 (99 %), one gap (0 %)), *Memnoniella humicola* (strain CBS 463.74, GenBank NG\_058217.1; Identities = 813/825 (99 %), one gap (0 %)) and *Stachybotrys limonisporea* (strain CBS 128809, GenBank MH876595.1; Identities = 848/863 (98 %), one gap (0 %)). Closest hits using the *cmdA* sequence had highest similarity to *Stachybotrys phaeophialis* (strain KAS 525, GenBank KU846632.1; Identities = 386/466 (83 %), 11 gaps (2 %)), *Stachybotrys dolichophialis* (strain DAOM 227011, GenBank KU846628.1; Identities = 386/466 (83 %), 11 gaps (2 %)) and *Stachybotrys subsylvatica* (strain CBS 126205, GenBank KU846634.1; Identities = 365/441 (83 %), 19 gaps (4 %)). Closest hits using the *rpb2* sequence had highest similarity to *Striatibotrys rhabdospora* (strain CBS 136395, GenBank KU846986.1; Identities = 620/719 (86 %), no gaps), *Striatibotrys eucylindrospora* (strain CBS 203.61, GenBank KU846975.1; Identities = 630/732 (86 %), no gaps) and *Stachybotrys microspora* (voucher MFLU 18-2620, GenBank MW201479.1; Identities = 534/621 (86 %), no gaps).**Supplementary material****FP1194** Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 1.6.12 (Nguyen et al. 2015, Kalyaanamoorthy et al. 2017, Hoang et al. 2018) of the *Stachybotrys* and related genera multigene (LSU / *rpb2*) nucleotide alignment derived from the datasets of Lombard et al. (2016) and Samarakoon et al. (2021). GenBank accession numbers for the sequences used can also be obtained from Lombard et al. (2016) and Samarakoon et al. (2021), except for cultures where GenBank accession numbers are indicated in superscript text and which were obtained from other studies. Bootstrap support values (> 69 % shown; only values > 94 % are significant) from 5000 ultrafast bootstrap replicates are shown at the nodes. Culture collection numbers are indicated for all species. The tree was rooted to *Calonectria illicicola* (culture CBS 190.50) and the species described here are highlighted with coloured blocks and bold face. Alignment statistics: 91 strains including the outgroup; 1533 characters including alignment gaps analysed: 517 distinct patterns, 420 parsimony-informative, 70 singleton sites, 1043 constant sites. The best model identified for the entire alignment in IQ-TREE using the TESTNEWMERGE option was: TIM2+F+I+G4. The alignment and tree were deposited in TreeBASE (Submission ID 28129).Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl  
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