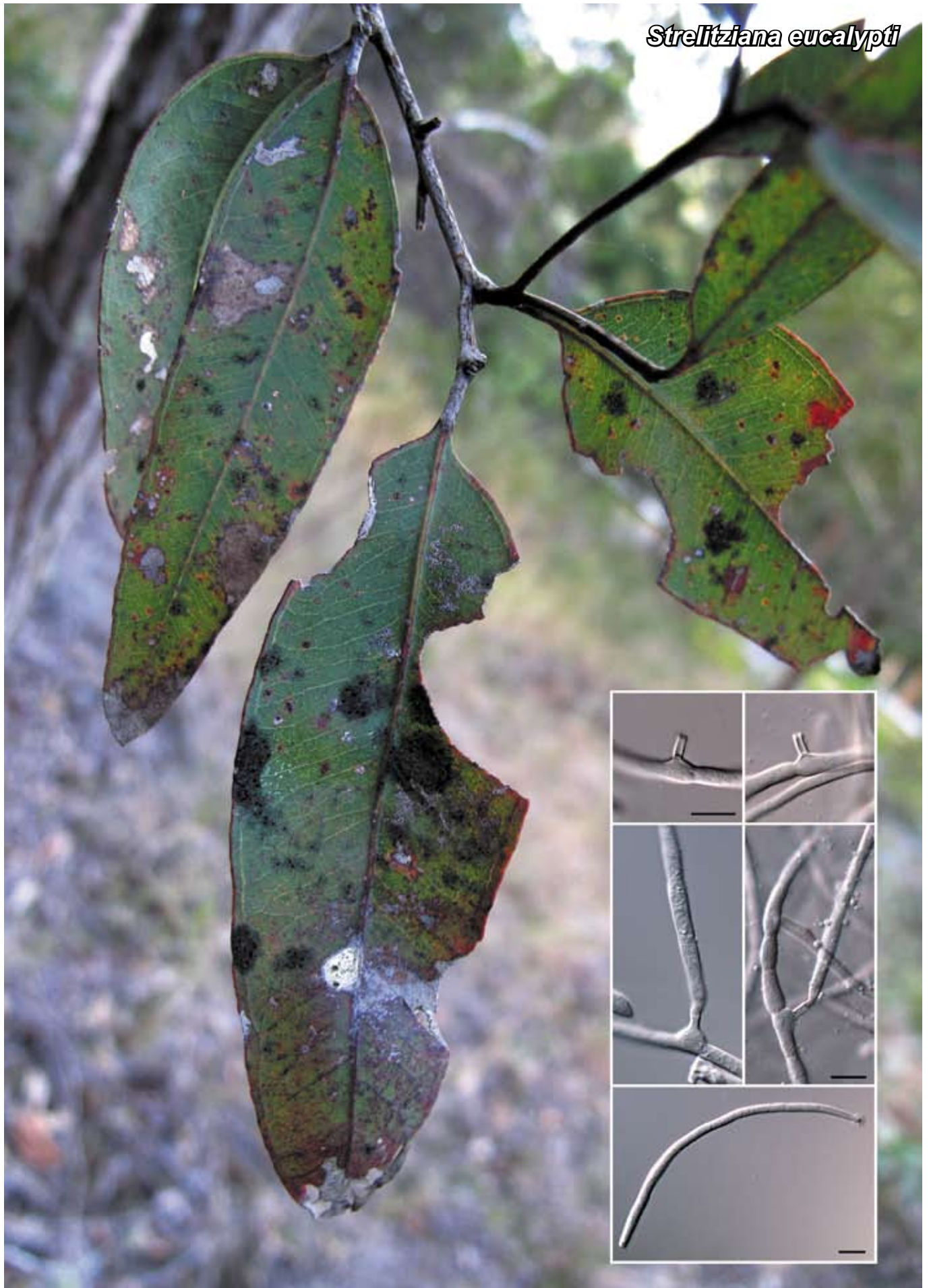


Strelitziana eucalypti



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Strelitziana eucalypti Crous & R.G. Shivas, *sp. nov.*

Strelitziana australiensis similis, sed conidiis majoribus, (40–)60–80(–130) × (3–)3.5(–4) µm, discernitur.

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

Mycelium superficial, consisting of smooth, septate, branched hyphae, pale brown, 2–3 µm diam. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* intercalary on hyphae, pale brown, concolorous with hyphae, basal part swollen, ellipsoid to globose, up to 6 µm tall, with a single conspicuous denticle, 2–5 × 1.5–2 µm; conidiogenesis rhexolytic with remnants of separating cell clearly visible on conidiogenesis cell, rarely visible on conidium hilum as a minute marginal frill. *Conidia* pale brown, smooth, guttulate, long obclavate, widest at basal septum, tapering to a subobtusely rounded apex and truncate base with inconspicuous marginal frill, (40–)60–80(–130) × (3–)3.5(–4) µm, 6–10-septate; conidial hila neither thickened nor darkened, 1.5–2 µm wide; conidial apex frequently with globose mucoid appendix; microcyclic conidiation present in culture.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies erumpent, spreading, with sparse aerial mycelium and feathery margins; reaching up to 7 mm diam. On potato-dextrose agar pale olivaceous-grey (centre), olivaceous-grey (margin), and olivaceous-grey in reverse; on oatmeal agar olivaceous-grey; on malt extract agar pale olivaceous-grey (surface), olivaceous-grey (reverse).

Typus. AUSTRALIA, Queensland, Brisbane, 27°21'41.5"S 152°47'18.3"E, on leaves of *Eucalyptus* sp. infected with black mildew, 15 July 2009, P.W. Crous & R.G. Shivas, CBS-H 20495 holotype, cultures ex-type CPC 17261, 17260 = CBS 128214, ITS sequence of CPC 17260 GenBank HQ599596 and LSU sequence of CPC 17260 GenBank HQ599597, MycoBank MB517543.

Notes — A megablast search in GenBank using the LSU sequence retrieved as closest sisters *Strelitziana australiensis* (GenBank GQ303326; Identities = 820/825 (99 %), Gaps = 3/825 (0 %)) and *Strelitziana africana* (GenBank DQ885895; Identities = 798/830 (97 %), Gaps = 13/830 (1 %)). These same two species, as well as *Pseudoramichloridium henryi* (GenBank GQ303289; Identities = 680/686 (99 %), Gaps = 2/686 (0 %)), were obtained when a megablast was performed with the ITS sequence, albeit with a slightly different sequence identity (*S. australiensis* GenBank GQ303295, Identities = 699/706 (99 %), Gaps = 2/706 (0 %) and *S. africana* GenBank DQ885895, Identities = 665/724 (92 %), Gaps = 23/724 (3 %)). Based on DNA sequence data of the ITS gene, *S. eucalypti* is related to *S. australiensis*. However, *S. eucalypti* has much longer conidia than *S. australiensis* (conidia 30–73 × 2.8–3.2 µm, 4–8-septate)^{1,2}. There is also a significant difference in the ITS sequence between *S. eucalypti* and *S. albisiae* (described in Fungal Planet 56 elsewhere in this volume), Identities = 665/724 (92 %), Gaps = 28/724 (3 %).

An important ecological observation is that *S. albisiae* was isolated from leaves of *Albizia julibrissin* heavily infected with *Camptomeris albisiae*, while *S. eucalypti* was isolated from leaves of a *Eucalyptus* sp. infected with a black mildew. In both cases the causal organism failed to grow in culture, and eventually a species of *Strelitziana* was isolated, suggesting that members of this genus may be fungicolous.

Colour illustrations. *Eucalyptus* leaves with black mildew, including *Strelitziana eucalypti*; hyphae with separating cells attached to conidiogenous cells; conidia attached to conidiogenous cells; conidium with apical mucoid appendage. Scale bars = 10 µm.

References. ¹Arzanlou M, Crous PW. 2006. *Strelitziana africana*. Fungal Planet No. 8. ²Cheewangkoon R, Groenewald JZ, Summerell BA, Hyde KD, To-anun C, Crous PW. 2009. Myrtaceae, a cache of fungal biodiversity. Persoonia 23: 55–85.

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