

Ganoderma austroafricanum



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***Ganoderma austroafricanum* M.P.A. Coetzee, M.J. Wingf, Marinc., Blanchette, sp. nov.**

Etymology. Name reflects the geographical origin from which the fungus was collected.

Mature *basidiomata* annual, pileate, sessile, dimidiate, pileus dark to reddish brown when dry, margin rounded, thickened, red brown when dry. *Pore surface* smooth, pores 3–4 per mm, round to angular, radially elongated, 150–390 µm long, 85–245 µm wide, dissepiments 60–200 µm diam. *Hyphal system* dimitic, generative hyphae, usually collapsed, thin-walled, hyaline. *Vegetative hyphae* observed in the tubes. *Tube trama* intricate and agglutinated skeletal hyphae 4–8 µm thick, with extremities tapering to elongate apices of 2–2.5 µm diam, hyaline to pale yellowish in 5 % KOH. *Basidia* not observed. *Basidiospores* brown, subglobose with a truncate base, bitunicate, verruculose, 8–11 × 5.5–7 µm. *Chlamydospores* on 2 % malt extract agar medium (MEA) ellipsoidal with a hyphal extension at the base, apex occasionally papillated, terminal or intercalary, 10.5–19.5 × 6.5–9.5 µm.

Culture characteristics — Colonies on 2 % MEA fertile, showing the best growth reaching 82 mm at 25 °C in the dark in 8 d, the second best 62 mm at 30 °C, 37 mm at 20 °C, 18 mm at 15 °C, no growth at 35 °C, circular with entire edge, flat, felt-like texture, white at all temperatures, with sporadic tint of yellow at inner 20 mm circle at 30 °C; chlamydospores present.

Typus. SOUTH AFRICA, Gauteng, Pretoria, Brooklyn, Jan. 2014, on *Jacaranda mimosifolia*, M.J. Wingfield (holotype PREM 61074, living culture ex-type CBS 138724 = CMW 41454; ITS sequence GenBank KM507324, LSU sequence GenBank KM507325, MycoBank MB810411).

Notes — *Ganoderma austroafricanum* is the causal agent of root and butt rot disease on large numbers of jacaranda trees in the suburb of Brooklyn (Pretoria, South Africa). ITS sequence comparisons using Blastn searches against sequences in GenBank yielded the closest hits with *G. subamboinense* var. *laevisporum* (JQ520205; query cover: 100 %, similarity 98 %). It can be differentiated from the closest related sequences of *G. subamboinense* var. *laevisporum* based on 13 nucleotide differences in the ITS sequence. Phylogenetic trees generated from ITS sequences placed *G. austroafricanum* within a clade that included sequences from GenBank representing *G. weberianum* and *G. stipitatum* but with low bootstrap support (parsimony bootstrap = 52 %). The latter group formed a sister group to a monophyletic clade (bootstrap support = 92 %) that included sequences from GenBank representing *G. lobatum*, *G. lucidum*, *G. neojaponicum*, *G. oregonense* and *G. resinaceum*.

Colour illustrations. *Jacaranda mimosifolia* (Jacaranda tree) growing as street tree in the suburb of Brooklyn, Pretoria, South Africa (background); crown of infected Jacaranda tree showing branch die-back; purple flowers of Jacaranda tree; basidiocarps; basidiospores (10 µm); skeletal hyphae refractive in phase contrast (25 µm); chlamydospores on 2 % MEA (10 µm).

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