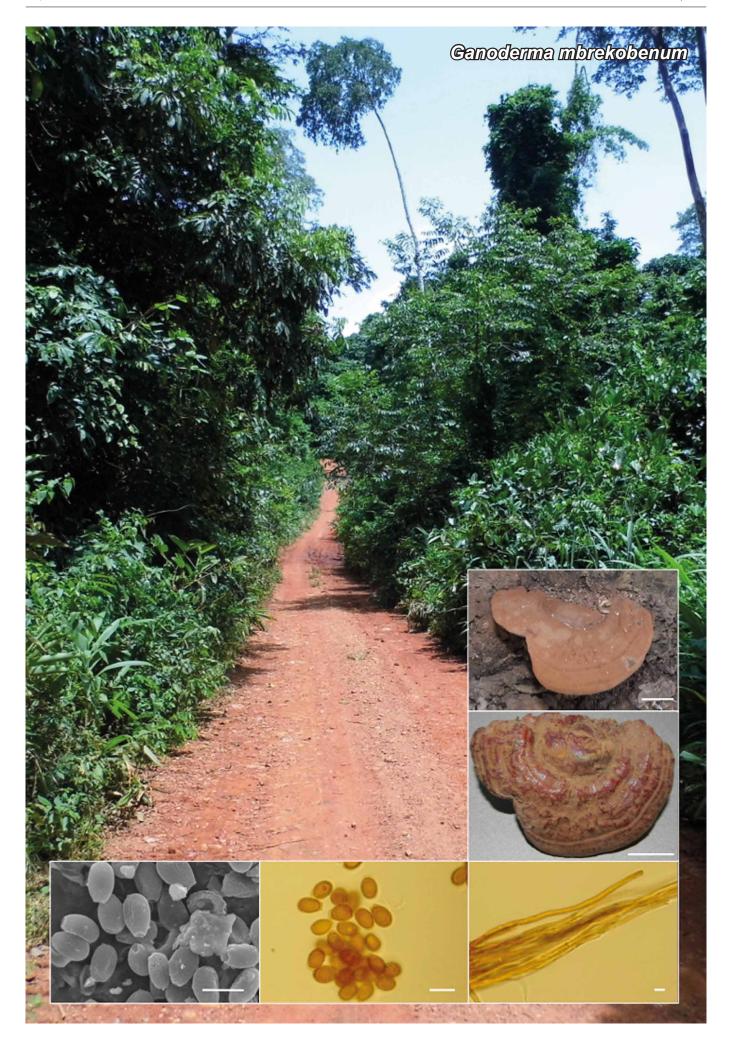
416 Persoonia – Volume 36, 2016



Fungal Planet description sheets 417

Fungal Planet 449 - 4 July 2016

Ganoderma mbrekobenum E.C. Otto, Blanchette, Held, C.W. Barnes & Obodai, sp. nov.

Etymology. Named after the Ghanaian Twi word 'mbrekoben', which translates to reddish brown mushroom.

Classification — Ganodermataceae, Polyporales, Agaricomycetes.

Mature basidiomata annual, pileate, stipitate, dimidiate, applanate, woody to corky when dried, homogenous context structure, pileus maroon to liver brown when dry, surface hard and glabrous, margin rounded, thickened, maroon to liver brown when dry. Stipe substibe (> 5 cm), lateral, columnar, with one solitary column, maroon; borders with hymenophore thickened. Pore surface smooth, creamy to snuff brown when dry, pores 4-6 per mm, round to somewhat irregular and slightly elongated, $105-247 \times 76-207 \ \mu m$ (av. $167.2 \times 123.8 \ \mu m$; SD 32, 26; n = 100), dissepiments 44-152 μm (av. 83.6 μm; SD 23; n = 100); tubes 0.1–0.7 mm long, dark brown. *Hyphal system* dimitic; generative hyphae slightly inconspicuous, branched, thin-walled and hyaline; skeletal hyphae most prevalent in the basidiocarp, occasionally branched, pale to dark brown, 2.5-7 µm thick, tapering towards the end. Basidia not observed. Basidiospores brown, ovoid to broadly ellipsoid with a truncate base, bitunicate, verruculose, $8-11.5 \times 6-8 \mu m$ (av. 10.4×7.1 μ m; SD 0.7, 0.4; n = 100), perisporium thin, smooth; exosporium with intermediate thick inter-walled pillars; endosporium thick, dark brown. Chlamydospores not observed.

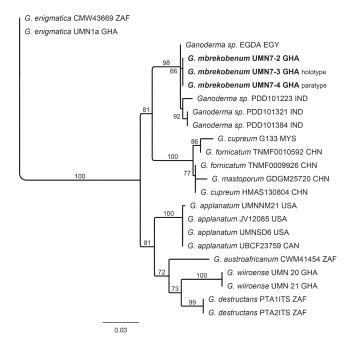
Culture characteristics — No live culture obtained.

Typus. Ghana, Brong Ahafo and Greater Accra Regions, on angiosperms, June 2015, M. Obodai (holotype MIN 850481, paratype MIN 850482, holotype ITS sequence GenBank KX000896, LSU sequence GenBank KX000897; paratype ITS sequence GenBank KX000898, LSU sequence GenBank KX000899, holotype MycoBank MB816172).

The phylogenetic tree with *G. mbrekobenum* was constructed using the Maximum Likelihood plugin PHYML in Geneious R9 (http://www.geneious.com, Kearse et al. 2012), and the substitution model determined by jModelTest (Posada 2008) according to Corrected Akaike Information Criterion (AICc). *Ganoderma enigmatica* (GenBank KR183855 and KR150678) is the outgroup. Bootstrap support values ≥ 50 % are given above branches. The phylogenetic position of *G. mbrekobenum* is indicated in **bold**. The *Ganoderma* species is followed by the sample ID and the three letter United Nations country code, in order of appearance ZAF: South Africa, GHA: Ghana, EGY: Egypt, IND: India, MYS: Malaysia, CHN: China, USA: United States.

Colour illustrations. Ghana, Brong Ahafo Region, native tree species along the road of the Ayum forest (background); basidiocarp in the field with basidiospores covering the pileus, basidiocarp in lab with basidiospores cleaned off; skeletal hyphae, basidiospores by light microscopy and SEM. Scale bars = 3 cm (basidiocarps), 10 μm (microscopic structures).

Notes — Ganoderma mbrekobenum causes decay in the roots and trunks of angiosperm trees in the southern regions of Ghana. Sequences were downloaded from GenBank for phylogenetic analysis with G. mbrekobenum sequences using the program Geneious R9 (http://www.geneious.com, Kearse et al. 2012). The complete ITS sequence of the G. mbrekobenum holotype was used for the Blastn search. The results gave the highest score to an isolate Ganoderma sp. (EGDA, GenBank LN774971) from Egypt, with a single nucleotide difference. The next 14 Blastn hits were to Ganoderma sp. sequences from a single institution in India. The analysis included only the top three of these sequences, having four to six differences from the G. mbrekobenum holotype. A few isolated sequences with various Ganoderma species names had relatively high Blastn scores, but were excluded from the analysis because they did not align with their respective species and are likely G. mbrekobenum, or closely related. The closest legitimate Ganoderma species were G. applanatum and G. fornicatum, both with 94 % identity. Additional sequences of other recently described Ganoderma species from Africa (Coetzee et al. 2015, Crous et al. 2015b) were included in the analysis. The final alignment was edited by hand for alignment errors.



Eric C. Otto, Robert A. Blanchette & Benjamin W. Held, Department of Plant Pathology, University of Minnesota, 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA; e-mail: ottox136@umn.edu, robertb@umn.edu & bheld@umn.edu Charles W. Barnes, Departamento Nacional de Protección Vegetal, Estación Experimental Santa Catalina, Instituto Nacional de Investigaciones Agropecuarias, Panamericana Sur Km. 1 vía Tambillo, Cantón Mejía, Provincia de Pichincha, Quito, Ecuador; e-mail: cbarnes333b@gmail.com Mary Obodai, CSIR-Food Research Institute, P.O. Box M20, Accra, Ghana; obodaime@yahoo.com