

*Ganoderma wiiroense*



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***Ganoderma wiiroense*** E.C. Otto, Blanchette, C.W. Barnes & Held, *sp. nov.*

*Etymology.* Named after the village of Wiiro where the fungus was found in the Sissala West District of the Upper West Region of Ghana.

*Classification* — *Ganodermataceae*, *Polyporales*, *Agaricomycetes*.

Mature *basidiomata* annual, pileate, sessile, dimidiate, applanate, woody to corky when dried, not completely homogeneous context structure, zonate, pileus surface hard and glabrous, yellowish brown to dark reddish brown when dry, margin rounded, thickened, yellowish brown to dark reddish brown when dry. *Pore surface* smooth, white to creamy yellow when dry, pores 3–5 mm, round to somewhat irregular and slightly elongated, 122–292 × 80–240 µm (av. 206.1 × 154.9), dissepiments 47–182 µm wide (av. 83.1); tubes 0.1–1 mm long, brown. *Hyphal system* trimitic, generative hyphae slightly inconspicuous, hyaline, thin-walled 2–4 µm diam, branched, clamped and hyaline; skeletal hyphae occasionally branched, pale to dark brown, 2.5–7.5 µm thick; binding and skeleton-binding hyphae hyaline, highly branched, tapering towards the end. *Basidia* not observed. *Basidiospores* ellipsoid to cylindrical-ellipsoid with a truncate base, bitunicate, verruculose, 10–13.5 × 6–8 µm (av. 11.8 × 7.1 µm), perisporium thin, smooth, exosporium with intermediate thick inter-walled pillars, endosporium thick, brown. *Chlamydospores* not observed.

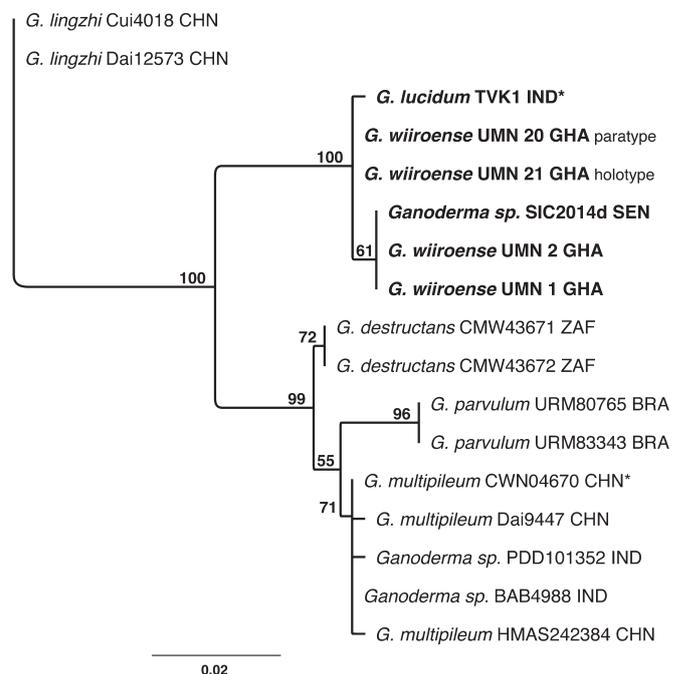
*Culture characteristics* — Colonies on MEA, showing optimum growth at 30 °C exceeding 40 mm in the dark in 7 d, followed by 35 mm at 35 °C, 33 mm at 25 °C, 20 mm at 20 °C; mycelial mats circular with entire edge, flat, white above and slight creaminess reverse at all temperatures, woolly to felty, superficial mycelium with medium density.

*Typus.* GHANA, Upper West Region, Sissala West District, Wiiro, on angiosperms, Aug. 2015, A.B. Wibonto & H.B. Babilwie (holotype MIN 938704, paratype MIN 938705, cultures ex-type UMN-21-GHA (also deposited at CBS), holotype ITS sequence GenBank KT952363, LSU sequence GenBank KT952364, paratype ITS sequence GenBank KT952361, LSU sequence GenBank KT952362, MycoBank MB814840).

Phylogenetic tree showing analysis done using the Maximum Likelihood plugin PHYML in Geneious v. R7 (<http://www.geneious.com>) (Kearse et al. 2012), and the substitution model was determined by jModelTest (Posada 2008) according to the Corrected Akaike Information Criterion (AICc). *Ganoderma lingzhi* (GenBank JQ781855 and JQ781856) is the outgroup. Bootstrap support values ≥ 50 % are given above branches. The phylogenetic position of *G. wiiroense* is indicated in **bold**. The *Ganoderma* species is followed by the sample ID and the three letter United Nations country code. The \* indicates the country is not specified in the Features section of the Blastn search and is assumed from author affiliations.

*Colour illustrations.* Field of cotton (*Gossypium hirsutum*) with shea trees (*Vitellaria paradoxa*) and other tree species dispersed throughout the field located near Wiiro, Ghana (background); basidiocarp; basidiocarp; basidiospores; skeletal hyphae. Scale bars = 3 cm (basidiocarp), 10 µm (microscopic structures).

*Notes* — *Ganoderma wiiroense* causes decay in the roots and trunks of angiosperm trees in the Upper West Region of Ghana in the village of Wiiro (a Sissali name). For Blastn ITS sequence comparisons, 530 bases were used from the *G. wiiroense* holotype sequence, starting at ITS1, after the CATT motif (Schoch et al. 2014). The Blastn results gave the highest score to an isolate *Ganoderma lucidum* (TVK1, GenBank FJ982798) submitted in 2009 by the Centre for Advanced Studies in Botany, University of Madra, Tamil Nadu, India, with three nucleotide differences. A second sequence from a collection in Senegal (SIC-2014d, GenBank KJ510534) has two nucleotide differences, but was 38 bases shorter at the 3' end than the holotype. Subsequently, two representative sequences of the next highest seven Blastn scores were downloaded for phylogenetic analysis. The sequence alignment was edited by hand to limit differences between sequences. The final alignment, ITS1-5.8S-ITS2, was trimmed at the 3' end following other ITS2 annotations from GenBank and being as conservative as possible not to lose any variable bases. Two additional DNA samples of *G. wiiroense*, along with the top two Blastn hits, showed two heterozygous sites in the alignment, thus forming two groups. The next closest species to *G. wiiroense* is *G. destructans*, with 30–33 nucleotide and gap differences. Eighty to ninety percent of the sequence variability occurs in ITS1.



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