New host records of *Ganoderma* in northern Thailand and determination of nutritional contents of selected *Ganoderma* species

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Abstract
    Ganoderma P. Karst is a group of wood-degrading mushrooms, and some are medicinal mushrooms that are ecologically and economically important. *Ganoderma* has distinctive non-laccate and laccate basidiocarps and double-wall basidiospores. This fungus is known to cause infections in hardwood hosts in tropical and temperate regions. This study reports non-laccate (*Ganoderma gibbosum*) and laccate (*G. tropicum*) species on a new host species, *Anthocephalus chinensis*, from Chiang Rai Province in Thailand. Comprehensive details of the two *Ganoderma* reported herein were proposed, described, and illustrated based on macro- and micro-morphology. The phylogenetic position was evaluated using the ITS sequence. The phylogenetic tree is provided to show the placement of taxa. Medicinal *G. tropicum* was selected to investigate the nutritional content. A high value was observed on energy (187.43) and dried matter content (75.92 ± 1.96 g/100g), followed by crude fiber, carbohydrates, protein, and moisture contents 51.53 ± 2.65 g/100g, 49.86 ± 1.98 g/100g, 14.64 ± 1.24 g/100g, 7.24 ± 0.40 g/100g, 1.86 ± 0.23 g/100g, and crude fat of 1.23 ± 0.19 g/100g, respectively.

Keywords – molecular identification – proximate analysis – saprobic fungi – taxonomy – white rot fungi

Introduction

        The genus *Ganoderma* was established by Karsten (1881) with *G. lucidum* (Curtis) P. Karst as the type species in the Ganodermataceae family (Moncalvo & Ryvarden 1997). *Ganoderma lucidum* was accepted as the binomial scientific name of "Lingzhi". This fungus has been compiled as a monograph on traditional Chinese medicinal fungi (Liu 1974, Tan et al. 2015) and is widely used, particularly in China, Japan, and Korea (Cao et al. 2012). They contain an abundance and variety of biological actions initiated by the primary metabolites (De Silva et al. 2012), and they have been used to prevent and treat many immunological diseases (Paterson 2006, Wang et al. 2012, Tan et al. 2015). Consequently, this mushroom species holds significant economic value (Dai et al. 2007). However, *Ganoderma* species are not classified as edible mushrooms (Sheikha 2022).
        There are 492 records of *Ganoderma* in Index Fungorum (2023), while 420 in Species Fungorum. *Ganoderma* species are distinctive by one of the two types of basidiocarps produced,

depending on the species: a laccate fruiting body with a shiny upper surface and a non-laccate fruiting body with a dull upper surface (Pilotti et al. 2004). The double-walled basidiospores with interwall pillars are a key diagnostic feature for the genus, and they bear an apical umbo, often truncated apex (Li et al. 2015). *Ganoderma* species are distributed worldwide in green ecosystems in tropical and temperate geographical regions (Pilotti et al. 2004). *Ganoderma* species grow as facultative parasites that can live as saprobes on rotting stumps and roots. It causes white rot in hardwoods by decomposing lignin, cellulose, and related polysaccharides (Kües et al. 2015).

The taxonomic situation within *Ganoderma* is unclear as morphologically similar members are found in other genera (Wang et al. 2010, Cao et al. 2012, Zhou et al. 2015, Galappaththi et al. 2022). Many mycologists have used various criteria to illustrate the taxonomic situation and identification of *Ganoderma* species, such as the identity based on host-specificity, geographical distribution, and macromorphology of basidiomes. In contrast, others focus primarily on taxonomic characteristics (Bhosle et al. 2010). Environmental factors, variability, interhybridization, and individual morphological bias mean that identifying *Ganoderma* species is complicated (Zheng et al. 2007). However, the majority of the members in the genus *Ganoderma* have yet to be subjected to systematic studies (Baby et al. 2015). This present study aims to report an additional new host record for *Ganoderma* species collected from the tropical region of Thailand. *Ganoderma* species were confirmed based on both morphological characteristics and phylogenetic evidence.

Materials & Methods

Sample collections
Fresh fruiting bodies of *Ganoderma* were collected in Chiang Rai Province, Thailand, in 2022. Details of the color of samples, host type, and location were recorded and photographed in the field and taken back to the laboratory. The samples were then air-dried using a hot-air oven at 40 °C for 48 hours until completely dehydrated. Dried collections were deposited in the Fungarium of Mae Fah Luang University.

Morphological identification
Macro-morphological characteristics were described following the method by Lodge et al. (2004), and colors were recorded following Ridgeway (1912). Micro-morphological characteristics were described based on dried specimens sectioned and mounted in 5% KOH and Congo red solutions. The micro-morphological examination was conducted using a Nikon Eclipse 80i compound microscope (Nikon, Tokyo, Japan), and the photographs were taken with a Canon 750D digital camera (Canon Inc., Tokyo, Japan) fitted to the microscope. Fifty basidiospores per collection were measured, and their sizes and shapes were recorded, photographed, and measured (Tulloss 2005). Faces of Fungi numbers were registered as instructed by Jayasiri et al. (2015).

DNA extraction, PCR amplification, and sequencing
Genomic DNA was extracted from the dried internal tissues of the samples. Total DNA was extracted using the Genomic DNA Extraction Kits (OMEGA Bio-Tek Inc.) following the manufacturer's protocol. The nuclear rDNA internal transcribed spacer region ITS1–5.8S–ITS2 (ITS) was amplified using the primers, ITSF and ITS4 by Polymerase Chain Reaction (PCR). The PCR conditions were adjusted and performed (Vilgalys & Hester 1990, White et al. 1990). Polymerase chain reaction (PCR) amplifications were performed in a total volume of 25 μL, including 12.5 μL of 2× Power Taq PCR Master Mix, 1μL of each primer (20 μM), 1 μL genomic DNA, and 9.5 μL of deionized water, using the primers and conditions demonstrated at 94 °C for 3 min, 35 cycles of 94 °C for 30 s, 55 °C for 50 s, 72 °C for 1 min, and 72 °C for 10 min for a final extension (White et al. 1990). The sequencing of PCR products was performed by Biogenomed Co., Ltd (South Korea).

Alignments and phylogenetic analyses

The obtained raw sequences were trimmed at the ends using BioEdit (Hall 1999) to remove ambiguous bases. The generated sequences were subjected to a BLAST search against the nucleotide database in GenBank (https://blast.ncbi.nlm.nih.gov/Blast.cgi), and the homogenous sequences were obtained from the BLAST search to identify the closest taxa or species in GenBank. All sequences used to construct the phylogenetic tree are listed in Table 1. *Perenniporia subtephropora* (Dai 10962) was used as the outgroup. Sequences for each strain were aligned using Clustal X (Thompson et al. 1997) to allow maximum sequence similarity. Gaps were treated as missing data.

Phylogenetic analyses of the ITS gene were performed with maximum likelihood (ML) and Bayesian inference posterior probabilities (BIPP). Max trees were unlimited, branches of zero length were collapsed, and all multiple parsimonious trees were saved. Maximum likelihood analyses, including 1,000 bootstrap replicates, were performed using the RAxML-HPC2 on XSEDE v. 8.2.12 in the CIPRES Science Gateway (Stamatakis 2014) and carried out using raxmlGUI v. 1.3.1 (Silvestro & Michalak 2011). The Bayesian inference posterior probabilities (PP) distribution was performed by Markov Chain Monte Carlo sampling (MCMC) in MrBayes v. 3.2.2, discarding the first 25% of generations as the "burn-in" (Huelsenbeck & Ronquist 2001). Trees were viewed in Treeview and exported to graphics programs.

Table 1. The names, voucher numbers, references and corresponding GenBank accession numbers of sequences were used in this study. The superscript "T" refers to the type.

Taxa	Voucher	GenBank accession number of ITS	References
Ganoderma acaciicola	Cui 16815	MZ354895	Sun et al. (2022)
G. acontextum	JV 0611/21G	KF605667	Sun et al. (2022)
G. adspersum	FGA1	AM269771	Guglielmo et al. (2008)
G. adspersum	SFC20150918-07	KY364248	Jargalmaa et al. (2017)
G. adspersum	Dai 13191	MG279153	Xing et al. (2018)
G. alpinum	Cui 17467	MZ354912	Sun et al. (2022)
G. alpinum	Cui 17325	MZ354911	Sun et al. (2022)
G. applanatum	Wei5787	KF495001	Unpublished
G. applanatum	Dai8924	KU219987	Song et al. (2016)
G. australe	HUEFS DHCR417	MF436676	Coetzee et al. (2015)
G. australe	HUEFS DHCR411	MF436675	Coetzee et al. (2015)
G. australe	CTRA1	KU569531	Bolaños et al. (2016)
G. australe	CTRA12	KU569541	Bolaños et al. (2016)
G. austroafricanum	CMW41454	KM507324	Crous et al. (2015)
G. bubalinomarginatum	Dai 20075[T]	MZ354927	Sun et al. (2022)
G. chalceum	URM80457	JX310812	De Lima Júnior et al. (2014)
G. chocoense	QCAM 3123	MH890527	Sun et al. (2022)
G. destructans	CBS139793	NR132919	Coetzee et al. (2015)
G. destructans	CMW43670	KR183856	Coetzee et al. (2015)
G. dianzhongense	L4331	MW750237	He et al. (2021)
G. enigmaticum	CBS 139792[T]	NR 132918	Song et al. (2016)
G. enigmaticum	CMW43669[T]	KR183855	Coetzee et al. (2015)
G. esculentum	L4935	MW750242	He et al. (2021)
G. fallax	JV 1009/27	KF605655	Sun et al. (2022)
G. gibbosum	SFC20150918-08	AY593860	Jargalmaa et al. (2017)

Table 1. Continued.

Taxa	Voucher	GenBank accession number of ITS	References
G. gibbosum	SFC20140702-12	AY593861	Jargalmaa et al. (2017)
G. gibbosum	KUMCC17-0005	MH035682	Luangharn et al. (2020)
G. gibbosum	KUMCC17-0008	MH035683	Luangharn et al. (2020)
G. gibbosum	KUMCC17-0009	MH035684	Luangharn et al. (2020)
G. gibbosum	KUMCC17-0010	MH035685	Luangharn et al. (2020)
G. gibbosum	MFLU 19-2176	MN396311	Luangharn et al. (2020)
G. gibbosum	MFUL23-0346	OR335811	This study
G. guangxiense	Cui 14453[T]	MZ354939	Sun et al. (2022)
G. hochiminhense	MFLU 19-2224	MN398324	Luangharn et al. (2021)
G. multipileum	CWN04670	KJ143913	Zhou et al. (2015)
G. multiplicatum	URM83346	JX310823	De Lima Júnior et al. (2014)
G. orbiforme	URM83332	JX310813	De Lima Júnior et al. (2014)
G. parvulum	URM83339	JX310817	De Lima Júnior et al. (2014)
G. parvulum	URM83340	JX310818	De Lima Júnior et al. (2014)
G. resinaceum	URM83400	JX310824	De Lima Júnior et al. (2014)
G. subflexipes	Cui 17247	MZ354921	Sun et al. (2012)
G. tropicum	HMAS 263143	JF915410	Wang et al. (2012)
G. tropicum	Yuan 3490	JQ781880	Cao et al. (2012)
G. tropicum	Dai 16434	MG279194	Xing et al. (2018)
G. tropicum	KUMCC18-0046	MH823539	Luangharn et al. (2019)
G. tropicum	MFLU 23-0347	OR335812	This study
G. thailandicum	HKAS104640	MK848681	Luangharn et al. (2019)
G. thailandicum	HKAS104641	MK848682	Luangharn et al. (2019)
Perenniporia subtephropora	Dai10962	JQ861752	Zhao & Cui (2013), Xing (2019)

Nutritional analysis

Proximate analysis was conducted based on the standard procedure of the AOAC (1995). Laccate *Ganoderma tropicum* (MFLU 23-0347) was selected to determine the nutritional contents. One hundred grams of dried samples were powdered and used to determine the nutritional contents for each test. Moisture content was tested at 105°C in a hot air oven (UM500, Memmert), and ash content was analysed using an electric furnace (Eurotherm 2416CG, Lento) at 600°C, and crude fiber by acid treatment and subsequent heating at 600°C in the Fibertec System M1020 Extractor (Foss Tecator). The Kjeldahl method was performed to analyze nitrogen-free extract, in which the protein content was estimated with a conversion factor of 6.25, and the analysis was performed using the Soxtec 2055 Extraction Unit (Foss Tecator) with petroleum ether to determine fat content. All the analyses were carried out in five replications.

Results

Phylogenetic study

The ITS data set comprised 49 taxa that belong to *Ganoderma* and *Perenniporia subtephropora* B.K. Cui & C.L. Zhao (Dai 10962) was used as an outgroup taxon. The data set

comprised 597 characters; 483 variable characters were constant, 22 were parsimony-uninformative, and 92 were parsimony-informative. The best-scoring ML tree is shown in Figure 1. The proportion of invariable sites was 0.380. Estimated base frequencies were A = 0.280, C = 0.173, G = 0.227, T = 0.320; substitution rates AC = 0.88182, AG = 3.77630, AT = 1.77105, CG = 0.6352, CT = 5.77334, GT = 1.000000; and the gamma distribution shape parameter α = 0.638.
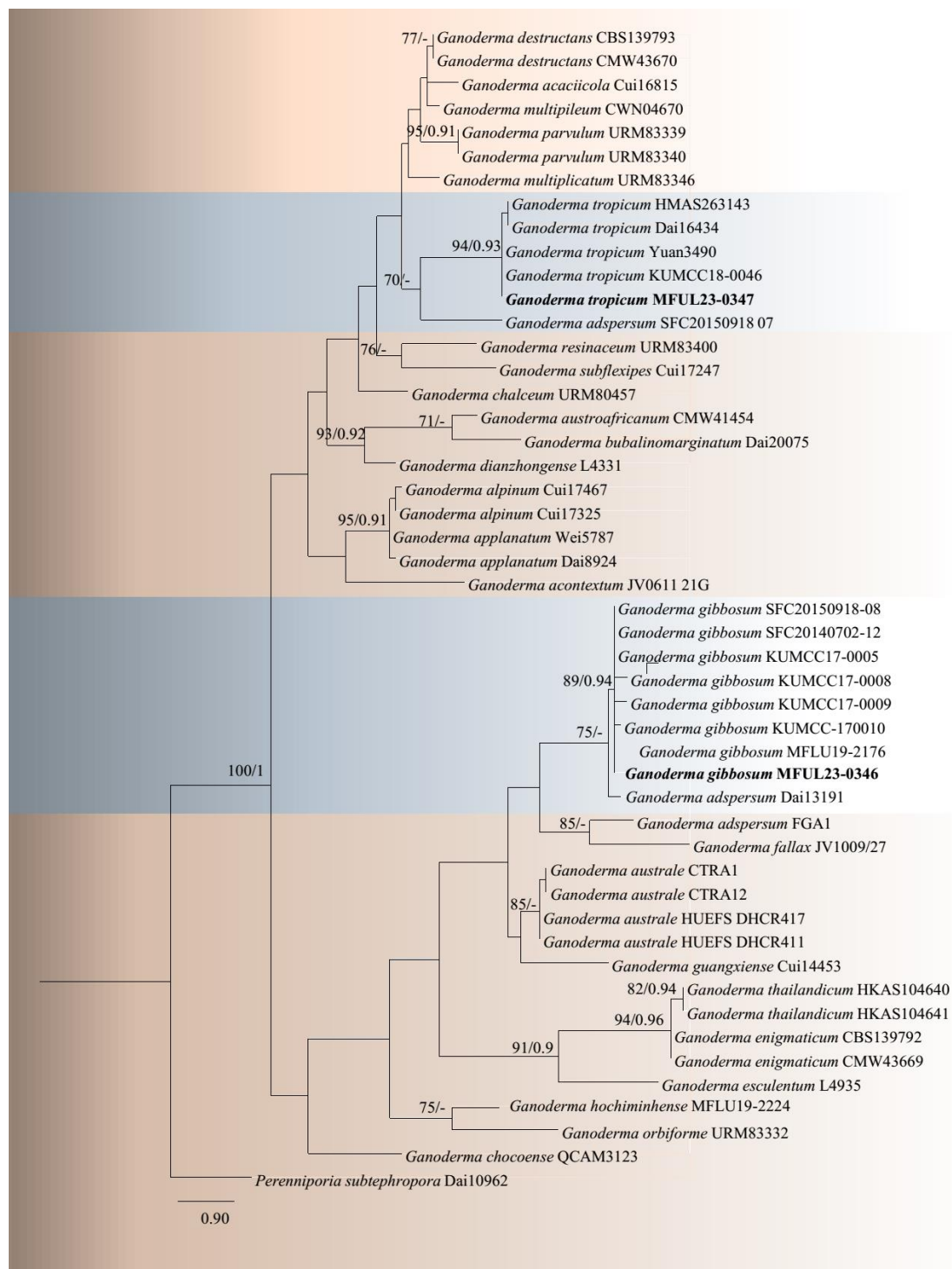

Fig 1 – Phylogram generated from the maximum likelihood (ML) analysis based on the ITS sequence matrix. The tree is rooted with *Perenniporia subtephropora* (Dai10962). The ML bootstrap supports (≥70%) and BI posterior probabilities (≥0.90) are denoted near the respective nodes. The taxa originating from this study are shown in black bold.

The alignments resulted in mostly similar topologies for both ML and BI analyses, so the topology from the ML tree is presented with statistical values from the MLBS/BIPP algorithms (Fig. 1). In our phylogeny, our sample *Ganoderma gibbosum* (MFLU 23-0346) is clustered in non-laccate species clades with 89% MLBS and 0.94 BIPP support, and our *G. tropicum* clustered to laccate *G. tropicum* isolate from with 94% MLBS and 0.93BIPP support.

Taxonomy
Ganoderma gibbosum (Blume and T. Nees) Pat. (1897)   (Fig 2)
      Facesoffungi number: FoF05652

      Basidiocarps sessile, annual, or perennial. *Pileus* 5–24 cm in length, 3–11cm in width, and 1.2–2.3 cm thick, shape convex, sub-flabellate, imbricate, umbonate, uneven, ungulate, broadly attached to its host, and usually wide at the base, slightly soft at the margin. *Pileus surface* non-laccate (dull), furrowed, sulcate, undulating on the upper surface, somewhat uneven, an irregularly ruptured crust, incised, woody, and cracked when old or older. *Pileus color* is usually pale orange (5A3) to light orange (5A4) and homogenous with pale yellow (1A3) when young, brownish to brown at the base, brown (7D8) at the center of mature fruiting bodies, and often reddish brown (8E6-7) to dark brown (8F5-8) and extending to the margin. *Context* up to 0.4–2.6 cm thick, usually reddish brown (8E6-7) to dark brown (8F5-8), hard when mature, and tough when dried. *Hymenophore* reddish-brown (8E7) with shading dark brown (7F6-7). *Tube layers* 0.3–1.8 cm, brown (7D7) to dark brown (8F6). *Margin* white (8A1), slippery when fresh, close to the underside of basidiomes. *Pore* 4–6 in per mm, subcircular to circular. *Pore surface* white (6A1) and turns reddish-brown (8E4-6) when touched. *Hyphal system* trimitic hyphal, hyaline, with abundant thick-walled with clamp connections, narrow and sparingly branched, and walls varying in thickness with simple septa; generative hyphae 1.1–3.4 μm broad ($n = 50$), mostly hyaline, thin-walled, and often brownish-orange (6C7) in Melzer's reagent; skeletal hyphae 3.1–4.6 μm broad ($n = 50$), mostly hyaline, abundant thick-walled, dextrinoid; binding hyphal 2.1–3.5 μm width ($n = 50$), usually thick-walled, hymenial with branched and reddish-brown (8E7), and mostly dark brown (8F8) in Melzer's reagent.

      Basidiospores usually ellipsoid to broadly ellipsoid with double walls, (4.2-)6.6–7.8–10.1(-11.2) × (4.3-)5.6–6.2–7.2(-7.9) μm ($\overline{x} = 7.9 \times 6.3$ μm, $n = 50$) μm, with Q = 1.45–1.58, L = 7.96 μm, W = 6.34 μm (including myxosporium), (4.8-)6.2–7.4–9.6(-10.6) × (4.2-)4.9–5.6–5.9(-6.7) μm ($\overline{x} = 6.4 \times 5.7$ μm, $n = 50$) μm, with Q = 1.08–1.14, L = 6.24 μm, W = 5.67 μm (excluding outer myxosporium), overlaid by hyaline, dextrinoid, echinulae, echinulate brownish-orange (6C7), light brown (7D6) to brown (7D8) of the inner wall, grayish-orange (6B4) in 5% KOH. Basidia not seen.

      Material examined – Thailand, Chiang Rai Province, Muang District, Thasud, 20°2′50″N, 99°53′44″E, 20 m, 24 September 2022, T. Luangharn, LT2022-11004, MFLU 23-0346.

      Host and habitat – solitary on the dead *Anthocephalus chinensis*

      GenBank numbers – ITS: OR335811

      Notes – *Ganoderma gibbosum* was first described from Java, and the holotype was lost (Moncalvo & Ryvarden 1997). This fungus was verified from the non-laccate *Ganoderma*, *G. applanatum*, and *G. applanatum–austral* complex (Moncalvo & Ryvarden 1997). This species is distinctive in having non-laccate basidiomes, lined or cracked crust, and woody basidiocarp from mature to older and produced ellipsoids with double-walled basidiospores (Zhao 1983). Based on macro-morphological features, *G. gibbosum* is similar to *G. adspersum*, *G. applanatum*, and *G. australe* (Zhao 1989, Luangharn et al. 2020). For the variations in *G. gibbosum*, see Luangharn et al. (2020). *Ganoderma* is a cosmopolitan genus of white-rot fungi and can be pathogens or saprobes on a wide range of hosts (Luangharn et al. 2021). This fungus is widely dispersed throughout tropical and temperate areas (Zhao 1983, Kaliyaperumal & Kalaichelvan 2008, Jargalmaa et al. 2017, Luangharn et al. 2019, 2021). It has been reported from China, India, Korea, Papua New Guinea, Laos, and Thailand on a wide range of host tree species (Pilotti et al. 2004, Kaliyaperumal & Kalaichelvan 2008, Wang et al. 2009, Jargalmaa et al. 2017, Luangharn et al. 2020, 2021, Sun et al. 2022).
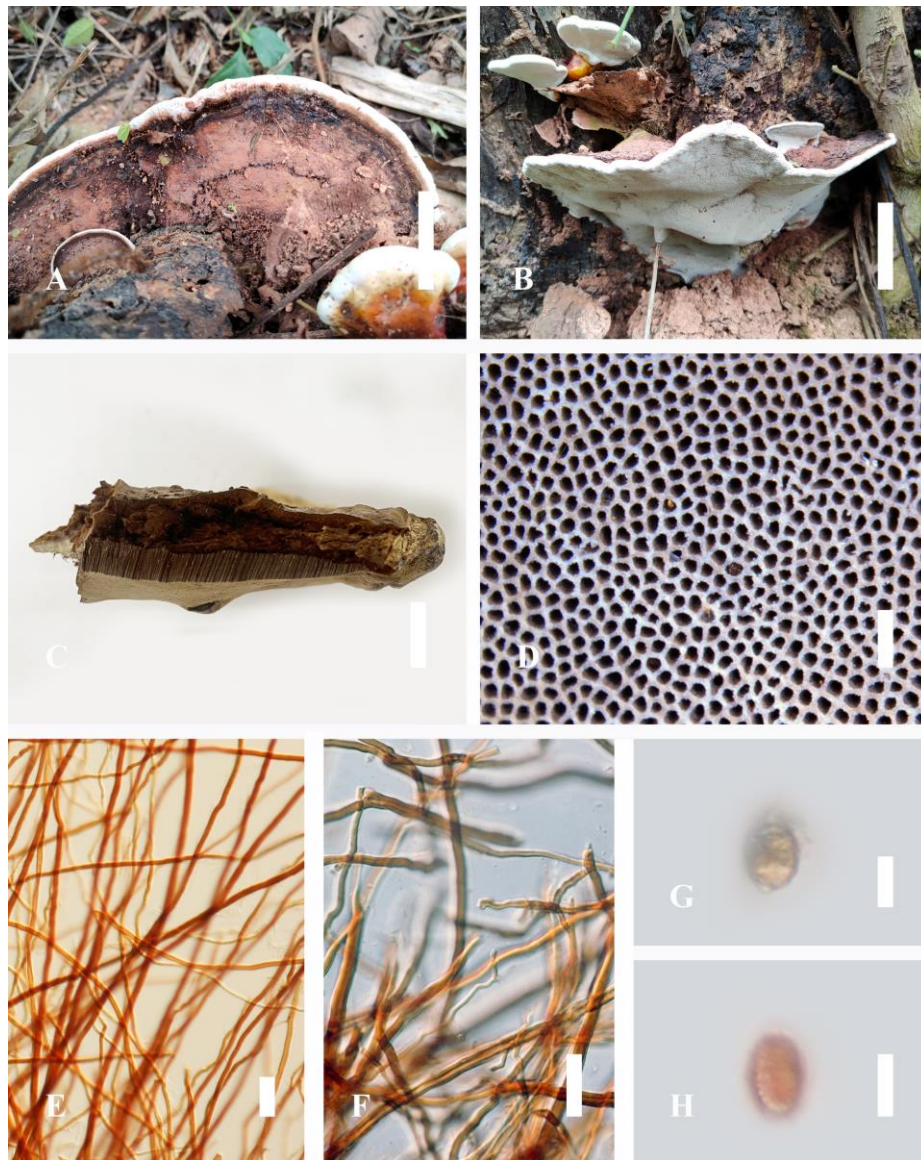
Fig 2 − *Ganoderma gibbosum* (MFLU 23-0346, new host record). A Upper view of mature basidiocarps on a host. B Side-view of mature basidiocarps on a host. C section of dried basidiocarp. D Pore characteristics. E–F Context hyphae. G–H Basidiospore. Scale bars: A–C = 5 μm, D = 500 μm, E–F = 20 μm, G–H = 5 μm.

Ganoderma tropicum (Jungh.) Bres., Annales Mycologici 8(6): 586 (1910)   (Figs 3,4)
        Facesoffungi number: FoF05068
        Basidiocarps sessile, dimidiate. *Pileus shape* up to 4–12 cm in length, 1–4 cm in width, 2 cm thick at the base, thicker at the base than the margin, and hard corky to woody. *Pileus surface* glabrous, weakly to strongly laccate, glossy and shiny, smooth, shallow sulcate layers, consistency furrows, covered by a thin and hard crust, plump when present, broadly attached and thick at the base, usually homogenous with orange (6A7) and deep orange (6A8) at the center, extending deep orange (5A8) from the center, and slight deep yellow (4A8) where the new hyphae are in active development on the upper surface, and light in weight when dried. *Tubes* 2–7 mm long, 80–170 μm wide, and sulcate at different levels. Margin white when present (5A1), pale orange (5A2), up to 0.8–2.3 cm thick, round, tough, and hard, thicker towards the margin. *Pore* angular, 4–6 per mm, and pore diameter up to 60–1150 μm. *Pore surface* white when present, turning brown (6E8) to dark brown (6F7) when touched. *Context* trimitic, irregular cuticle cells, mostly brown (6F6) to dark brown (9F5), near the tubes, dense context layer, and tough to break when dried.

Basidiospores mostly ellipsoid and broadly ellipsoid with the double wall (ganodermoid) at maturity, (6.9–)7.3–9.1(9.8) × (5.1)5.8–7.1(7.9) μm ($\overline{x}$ = 8.9 × 6.7 μm, *n* = 50) (including myxosporium), (5.8–)6.4–7.7(8.5) × (4.5)4.9–6.8(7.1) μm ($\overline{x}$ = 7.2 × 6.1μm, *n* = 50) μm (excluding outer myxosporium), light brown (6D6–6D8), reddish brown (9F6) to dark brown (9F8), usually with one end tapering, and usually overlaid by hyaline myxosporium. *Hyphal system* generative hyphae up to 2.28–3.17 μm ($\overline{x}$ = 2.84, *n* = 50) in diameter, colorless, thin-walled, some thick-walled, branched, with clamp connections; binding hyphae 1.12–2.73 μm ($\overline{x}$ = 1.86, *n* = 50), colorless, thick-walled, much-branched, clamped, and some thin-walled; skeletal hyphae up to 2.63–6.21μm ($\overline{x}$ = 5.15, *n* = 50), colorless, thick-walled, unbranched or with a few branches in the distal end, and arboriform and flexuous. *Cystidia* cystidioles, basidia, and basidioles are absent. *Cultures* usually white (4A1) that becomes orange white (5A2), pale orange (5A3), light orange (5A4–6A5), and some reddish yellow (4A6) to dark brown (9F8) around the plugged circle of active mycelium when old (over two months). *Odor* distinctive when fresh and dried.

Material examined – Thailand, Chiang Rai Province, Muang District, Thasud, 20°2′50″N, 99°53′44″E, 20 m, 24 September 2022, T. Luangharn, LT2022-11004, MFLU 23-0346.

Host and habitat – solitary on the dead *Anthocephalus chinensis*

GenBank numbers – ITS: OR335812

Notes – *Ganoderma tropicum* was introduced as *Polyporus tropicus* by Junghuhn (1838) from Indonesia. This fungus was mainly reported in tropical regions (Wang et al. 2012). *Ganoderma tropicum* is one of the *Ganoderma* species that share similarities to *G. flexipes*, *G. lucidum*, *G. multipileum*, *G. sichuanense*, and *G. tsugae* (Wang et al. 2012, 2014); however, this species is distinctive by its strongly echinulate basidiospores, dark brown context, concentric growth zones, and mostly irregular cuticle cells (Cao et al. 2012). *Ganoderma* species live as one of the most aggressive pathogens that cause diseases to several tree species, such as white rot fungi, and as pathogens to several plant species, such as *Elaeis guineensis* (oil palm), *Ficus carica* (Wang et al. 2012), *Acacia* sp. (Dai et al. 2007) and *Fabaceae* sp. (Cao et al. 2012). Luangharn et al. (2019) reported that a living *Dipterocarpus* was a host for *G. tropicum*, while *Anthocephalus chinensis* has yet to be reported from Thailand.

Fig 3 − *Ganoderma tropicum* (MFLU 23-0347, new host record). A–B Mature basidiocarps on the host. C Dried fruiting bodies. D Pore characteristics. Scale bars: A–C = 2 cm, D = 500 μm.
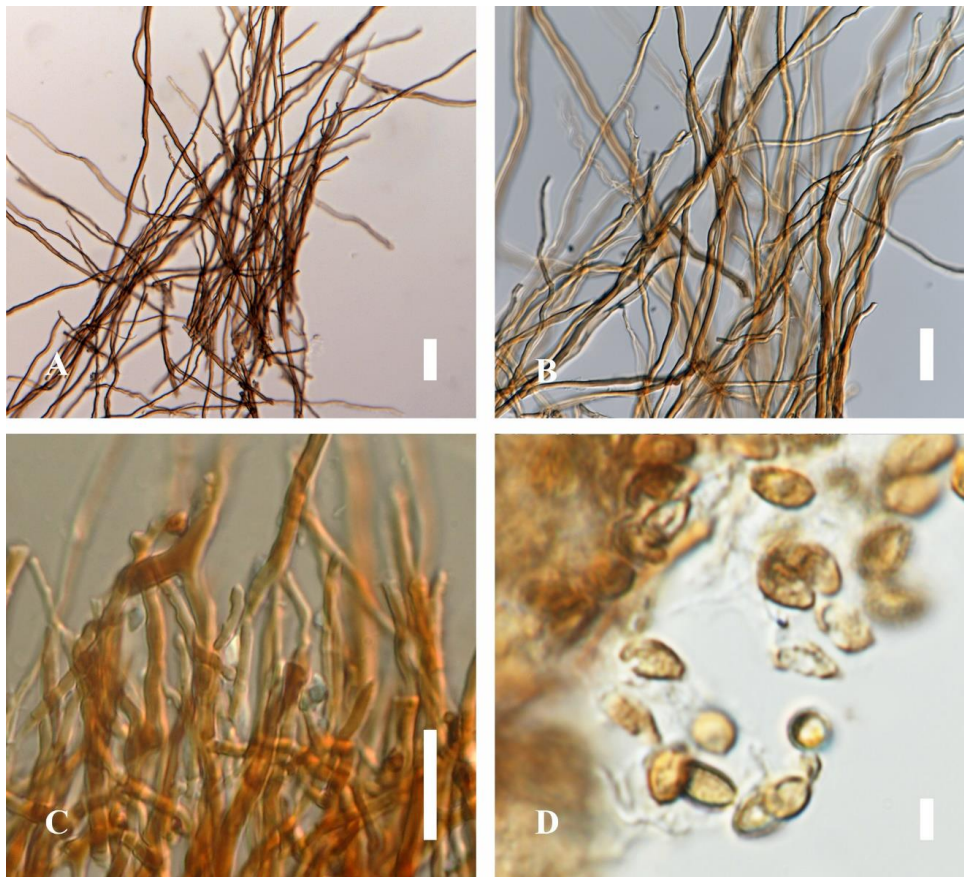
Fig 4 − *Ganoderma tropicum* (MFLU 23-0347, new host record). A–B Context hyphae. c Tube layer hyphae in Melzer's reagent. d Basidiospore. Scale bars: A–C = 20 μm, D = 5 μm.

Nutritional content

The nutritional composition and content of dried *Ganoderma tropicum* fruiting bodies (MFLU 23-0347) indicated a high significance of energy (187.43), with 75.92 ± 1.96 g/100g of dried matter. The content of crude fiber and carbohydrates were the most abundant compounds (51.53 ± 2.65 g/100g and 49.86 ± 1.98 g/100g, respectively), followed by total protein (14.64 ± 1.24 g/100g), moisture (7.24 ± 0.40 g/100g), ash (1.86 ± 0.23 g/100g), and lowest crude fat contents (1.23 ± 0.19 g/100g). The nutritional compositions are listed in Table 2.

Table 2. The nutrient content of dried *Ganoderma tropicum* (MFLU 23-0347).

Component	Content
Dry matter	75.92 ± 1.96
Moisture	7.24 ± 0.40
Ash (g/100g)	1.86 ± 0.23
Crude fat (g/100g)	1.23 ± 0.19
Crude fiber (g/100g)	51.53 ± 2.65
Protein (g/100g)	14.64 ± 1.24
Carbohydrate (g/100g)	49.86 ± 1.98
Energy (Kcal)	187.43 ± 2.28

Notes: Moisture content was presented based on air-dried weight.

Discussion

This study reports *Anthocephalus chinensis* as a new host record for *Ganoderma* in Chiang Rai Province, Thailand. Molecular and morphological data were used to confirm the identity of non-laccate species (*G. gibbosum*) and laccate species (*G. tropicum*). Although a combination of

the ITS, nLSU, rpb2, tef1, mtSSU, and nSSU genes is typically used to identify the species level of *Ganoderma* (Song et al. 2021), in this work, we only used the ITS gene and obtained strong support.

Our sample, *Ganoderma gibbosum* (MFLU 23-0346), clustered in the clade comprising *G. gibbosum* from Korea, Thailand, and China, forming a well-supported lineage (89% MLBS/0.94 BIPP). This result is in line with earlier research by Luangharn et al. (2020, 2021) and Sun et al. (2022), who stated that *G. gibbosum* collections were found in the Chinese provinces of Kunming, Yunnan, Guangdong, Guangxi, and Sichuan. Our laccate *G. tropicum* (MFLU 23-0347) clustered in the same clade as Chinese *G. tropicum* (89% MLBS/0.94 BIPP), which is a sister clade to laccate *G. destructans*, *G. multipileum*, and *G. multiplicatum*. In addition, Xing et al. (2018) demonstrated that *G. tropicum* forms a sister clade to *G. casuarinicola*. In this study, *G. gibbosum* agrees well with the description by Hapuarachchi et al. (2019) and Luangharn et al. (2019, 2021).

Previously, Venkatarayan (1936) reported that *Ganoderma* species have a diverse host range, with more than 44 species recognized from 34 probable host genera. This fungal genus has not been reported as host-specific. They are often found in natural forests (deciduous forests) and are dominated by various plantations. *Ganoderma gibbosum* is a common non-laccate *Ganoderma* species found in natural forests and is usually parasitic or pathogenic on a wide range of dead and living broadleaved deciduous trees.

Ganoderma is the one that causes wood deterioration, wood rots, and infections in living trees, which cause root and stem rots. Luangharn et al. (2021) updated the *Ganoderma* species distributed across the Greater Mekong Subregions (GMS), including both *G. gibbosum* and *G. tropicum* collections from Thailand. They can be important in horticulture since they infect landscapes, fruit tree crops, and economic trees. Several tree species have been reported as *Ganoderma* hosts, including *Areca catechu*, *Camellia sinensis*, *Cocos nucifera*, *Elaeis guineensis*, *Hevea brasiliensis*, *Castanopsis* spp., *Dipterocarpus* spp., *Indochinese* spp., *Pinus* spp., and *Pterocarpus* spp. from temperate and tropical regions (Hapuarachchi et al. 2019, Liu et al. 2019, Luangharn et al. 2019, 2020, 2021, Xing 2019, He et al. 2022, Jayawardena et al. 2023). In Thailand, many hardwood trees such as *Albizia lebbeck*, *Dendrocalamus strictus*, *Mangifera indica*, *Peltophorum pterocarpum*, *Dipterocarpus* spp., and *Pinus* spp. were hosts to *Ganoderma*; however, *Anthocephalus chinensis* has not been reported.

Generally, wild mushrooms are protein-rich and low in fat content compared to cultivated mushrooms. Given medicinal mushroom consumption trends, our *G. tropicum* was selected to determine the nutritional composition. It showed abundant energy, crude fiber, carbohydrates, protein, moisture, ash, and low-fat contents. Our results agree with Ghulam et al. (2016), who reported the nutritional contents of wide *G. lucidum*, and Sanmee et al. (2003), who reported that the protein content of Thai wild mushrooms was between 14–24%. However, mushroom development stages, such as young or old fruiting bodies, can affect the nutritional content of mushrooms. *Ganoderma tropicum* is medicinally used in China but is less prevalent in Thailand. Based on its high nutritional content, we recommend using *G. tropicum*, which has a high potential for commercial production. More research will be considered to identify more medicinal *Ganoderma* possibilities, including mycelium yield for potential food applications, fruiting body production for potential medical applications, and commercialization strategies for Thai *G. tropicum*.

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