Species diversity of *Ganoderma* (Ganodermataceae, Polyporales) with three new species and a key to *Ganoderma* in Yunnan Province, China

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*Ganoderma* is a globally distributed genus that encompasses species with forestry ecological, medicinal, economic, and cultural importance. Despite the importance of this fungus, the studies on the species diversity of *Ganoderma* in Yunnan Province, China (YPC) have poorly been carried out. During this study, opportunistic sampling was used to collect 21 specimens of *Ganoderma* from YPC. Morphology and multigene phylogeny of the internal transcribed spacer (ITS) regions, the large subunit of nuclear ribosomal RNA gene (nrLSU), the translation elongation factor 1-α gene (TEF1-α), and the second largest subunit of RNA polymerase II (RPB2) were used to identify them. Morphological and molecular characterization of the 21 specimens showed that they belong to 18 species of *Ganoderma* in Yunnan Province, China. With the help of an extensive literature survey and the results of this study, a checklist of 32 *Ganoderma* species from YPC was established, which accounts for 71.11% of the known species in China. In addition, a key to the *Ganoderma* in YPC is also provided.

**KEYWORDS**
3 new taxa, basidiomycetes, Lingzhi, medicinal mushroom, multigene phylogeny, taxonomy
Introduction

_Ganoderma_ P. Karst. 1881 is a genus of white rot fungi in the Polyporales and Ganodermataceae containing species that were originally described in the United Kingdom (Moncalvo and Ryvarden, 1997). _Ganoderma_ worldwide distribution from warm temperate to tropical, and is a facultative parasite on living, dead or rotting trees (Zhou et al., 2015). _Ganoderma_ species cause white rot of hardwoods by decomposing lignin, cellulose, and related polysaccharides. Generally associated with the decay of roots and the lower trunk or stems flare, which can lead to hazardous tree conditions and tree failures, resulting in serious damage to property and life (Loyd et al., 2017). Previous studies have reported that some species of _Ganoderma_ can cause diseases as pathogens of living trees such as Areca catechu (betel nut palm), Elaeis guineensis (oil palm), Hevea brasiliensis (rubber), and cause wood rot of forest trees and can contribute to tree mortality and failure by wind throw (Adaskaveg et al., 1991; Elliott and Broschat, 2001; Tonjock and Afui, 2015). Several species are responsible for stem and butt rots of commercially important crops such as stem rot of betel nut palm and oil palm caused by _G. boninense_ or _G. zonatum_ (Elliott and Broschat, 2001; Nur et al., 2019), and rubber root rot caused by _G. philippi_ (Glen et al., 2009). Other species, such as _G. australis_, _G. sessile_ and _G. curtisi_ seem to be opportunistic pathogens and typically only cause serious decay in old or stressed trees (Sinclair and Lyon, 2005). On the other hand, some of _Ganoderma_ have been shown to selectively delignify wood and are recognized as a potentially important source of lignin degrading enzymes (Otjen et al., 1997). Obviously, _Ganoderma_ are ecologically indispensable, but some of them are pathogenic and can cause diseases in forest trees.

Moreover, most _Ganoderma_ species have biologically active components with nutritional and medicinal effects, which are economically important (Dai et al., 2009). _Ganoderma_ has been used in Asian countries for over two millennia as a traditional medicine for maintaining vivacity and longevity, for its perceived health benefits, has gained wide popular use as a dietary supplement (Hapuarachchi et al., 2018a). _Ganoderma lucidum_ ("lingzhi") and _G. sinense_ have been included in the Chinese Pharmacopoeia, and are used for anti-cancer treatment, lowering blood pressure, and improving immunity (Dai et al., 2009; Sun et al., 2022). Research of _Ganoderma_ is a hot topic since its high potential to use in biotechnology.

As a consequence of several taxonomic and molecular phylogenetic studies on _Ganoderma_, an unexpectedly high level of species diversity has been uncovered worldwide, with the description of many new species (Cao et al., 2012; Cao and Yuan, 2013; Li et al., 2015; Xing et al., 2016, 2018; Hapuarachchi et al., 2018b, 2019; Liu et al., 2019; Wu et al., 2020; He et al., 2021). However, many taxonomy confusions have resulted from the great variability in the macroscopic characters of the _Ganoderma_ basidiomata. As of 20 September 2022, there were 488 records of _Ganoderma_ recorded in Index Fungorum,¹ and 529 records in MycoBank.² Nearly two-thirds of these records have been identified as synonyms. Up to now, 181 species are taxonomically accepted in _Ganoderma_, making it as one of the most species-rich genera in Ganodermataceae (Costa-Rezende et al., 2020). The genus is unique with characteristic double-walled basidiospores with a thin hyaline exosporium and ornamented endospore (Karsten, 1881; Moncalvo and Ryvarden, 1997).

China has a complex and diverse plant diversity, and a diversified three-dimensional climate environment that breeds abundant wild _Ganoderma_ resources, thus, a total of 40 species of _Ganoderma_ have been reported in China (Cao et al., 2012; Cao and Yuan, 2013; Li et al., 2015; Xing et al., 2018; Hapuarachchi et al., 2018b, 2019; Liu et al., 2019; Wu et al., 2020; He et al., 2021; Sun et al., 2022). Yunnan is an inland Province with low latitude and high altitudes in southwest China, which is a hotspot of global biodiversity and has abundant wildlife resources Nine type species of _Ganoderma_ viz. _Ganoderma alpinum_, _G. chuxiongensis_, _G. dianzhongensis_, _G. esculetum_, _G. mutabile_, _G. puerensis_, _G. subangustisporum_, _G. weixiensis_ and _G. yunlingensis_ have been reported in this region. In addition, several researchers have reported the diversity of _Ganoderma_ in southwestern China, such as Luangharn et al. (2021), which reported 13 _Ganoderma_ species viz. _G. applanatum_, _G. australis_, _G. calidophilum_, _G. flexipes_, _G. gibbous_, _G. leucocontextum_, _G. lucidum_, _G. multiplicatum_, _G. resinaceum_, _G. sanduense_, _G. sichuanensis_, _G. sinensis_, and _G. tsgae_ from YPC based on comprehensive morphological characteristics and molecular analyses. Apparently, there are many economically and medicinally important _Ganoderma_ species in YPC (Figure 1; He et al., 2021; Luangharn et al., 2021; Sun et al., 2022). However, with the exception of the taxonomic and new species description studies, very little efforts have been made to identify the _Ganoderma_ species diversity in YPC. Thus, the objectives of this research are, to identify and describe different species of _Ganoderma_ including three new species in YPC based on morphology and multigene phylogeny, and to prepare a checklist of _Ganoderma_ and a key to _Ganoderma_ in YPC.

Materials and methods

Specimen collection

Twenty-one _Ganoderma_ specimens were collected during the rainy season from July 2016 to September 2021 from jungle hill forests in Yunnan Province, China. They were photographed in the field, then collected and wrapped in aluminium foils or kept separately in a plastic collection box. Macro-morphology of fresh basidiomata was described, on the same day of collection. Specimens were then thoroughly dried at 40°C in a food drier, stored in sealed

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1. http://www.indexfungorum.org/
2. http://www.mycobank.org/
plastic bags with anhydrous silica gel, and deposited in the herbarium of Kunming Institute of Botany, Chinese Academy of Sciences (HKAS section, KUN). MycoBank numbers were obtained as described in Jayasiri et al. (2015).

**Morphological study**

Macro-morphological studies were conducted following the protocols provided by Torres-Torres and Guzmán-Dávalos (2012). Key colors were obtained from Kornerup and Wanscher (1978). Micro-morphological data were obtained from the dried specimens and observed under a light microscope (Nikon). The temporary prepared microscope slides were placed under magnification up to 1,000 × using Nikon ECLIPSE80i (Nikon, Japan) compound stereomicroscope for observation and microscopic morphological photography. Microscopic observations were made from slide preparations stained with 10% potassium hydroxide (KOH), Melzer’s reagent, and Cotton Blue. Measurements were made using the Image Frame work v.0.9.7. To represent variation in the size of basidiospores, 5% of measurements were excluded from each end of the range and extreme values were given in parentheses (He et al., 2021).

The following abbreviations are used: IKI = Melzer’s reagent, IKI – = neither amyloid nor dextrinoid, KOH = 10% potassium hydroxide, CB = Cotton Blue, CB + = cyanophilous, L = mean spore length (arithmetic average of all spores), W = mean spore width (arithmetic average of all spores). The abbreviation for spore measurements (x/y/z) denote “x” spores measured from “y” basidiocarps of “z” specimens. Basidiospore dimensions (and “Q” values) are given as (a) b–av–c (d). Where “a” and “d” refer to the lower and upper extremes of all measurements, respectively, b-c are the range of 95% of the measured values, and Q is the length/width ratio of basidiospores, which is given as Qm ± standard deviation, where Qm is the average Q of all basidiospores.

**DNA extraction, PCR amplification, and sequencing**

Genomic DNA isolation and PCR of the studied material were performed at the Yunnan Academy of Agricultural Sciences,
TABLE 1 PCR primers and conditions used in this study.

| Locus   | Primers     | PCR conditions* | References               |
|---------|-------------|-----------------|--------------------------|
| ITS     | ITS1F, ITS4 | 94°C: 30 s, 53°C: 30s, 72°C: 50 s. (38 cycles) | White et al. (1990)     |
| nrLSU   | LR0R, LR5   | 94°C: 30 s, 52°C: 30 s, 72°C: 1 min. (38 cycles) | Vilgalys and Hester (1990)|
| TEF1-α  | 983E, 1567R | 94°C: 30 s, 52°C: 1 min, 72°C: 1 min. (38 cycles) | Matheny et al. (2007)  |
| RPB2    | RPB2-6f, fRPB2-7cR | 94°C: 30 s, 58°C: 30 s, 72°C: 1 min. (38 cycles) | Liu et al. (1999)     |

*The three steps given for each primer pair were repeated for 38 cycles, preceded by an initial denaturation step of 5 min at 94°C, and followed by a final elongation step of 10 min at 72°C and a final hold at 4°C.

Chin. Genomic DNA was extracted from dried specimens using Ezup Column Fungi Genomic DNA Purification Kit (Sangon Biotech Limited Company, Kunming, Yunnan, China) based on the manufacturer’s protocol. Primer pairs used for PCR were ITS1F/ITS5 (White et al., 1990) for ITS, L5R/L0R (Vilgalys and Hester, 1990) for nrLSU, TEF1–983/TEF1–1567R (Matheny et al., 2007) for TEF1–α, and RPB2–6f/RPB2–7cR (Liu et al., 1999) for RPB2. Primer sequences of the primers used in this study are available in the WASABI database of the AFTOL website (aftol.org). Gene regions were amplified in 30 μl reactions containing 15 μl 2 × Taq Plus Master Mix II (Sangon Biotechnology Co., Kunming, China), 13 μl ddH2O, 0.5 μl 10 μM of forward and reverse primers, 1 μl DNA. PCR conditions were used as in the Table 1, using a C1000 thermal cycler (Bio-Rad China). The PCR amplicons were sent to Sangon Biotech (China) for Sanger sequencing. Raw DNA sequences were assembled, and edited in Sequencher 4.1.4 and the assembled DNA sequences were deposited in GenBank (Table 2).

Sequencing and sequence alignment

The sequences of the new species were subjected to standard BLAST searches in GenBank to find the most closely related sequences. All the sequences except those obtained from this study (Table 2), were retrieved from GenBank for phylogenetic analyses. Sequences were aligned using the online version of MAFFT v7 (Katoh and Standley, 2013) and adjusted using BioEdit v.7.0.9 by hand (Hall, 1999) to minimize gaps and align properly. Ambiguous regions were excluded from the analyses and gaps were treated as missing data. The phylogeny website tool “ALTER” (Glez-Peña et al., 2010) was used to convert the Fasta alignment file to Phylip format for RAxML analysis and, AliView and PAUP 4.0b 10 were used to convert the Fasta alignment file to a Nexus file for Bayesian analysis (Swoford, 2003).

Phylogenetic analyses

Maximum likelihood (ML) analysis was performed for both gene regions separately using RAxML-HPC2 v. 8.2.12 (Stamatakis, 2014) as implemented on the CIPRES portal (Miller et al., 2010), with the GTR + G model for both genes and 1,000 rapid bootstrap (BS) replicates. Since no supported conflict (BS ≥ 60%) was detected among the topologies, the four single-gene alignments were concatenated using SequenceMatrix (Vaidya et al., 2011).

Bayesian analysis was performed in MrBayes 3.2 (Ronquist et al., 2012) and the best-fit model of sequences evolution was estimated via MrModeltest 2.3 (Guindon and Gascuel, 2003; Nylander, 2004; Darriba et al., 2012). The Markov Chain Monte Carlo (MCMC) sampling approach was used to calculate posterior probabilities (PP; Rannala and Yang, 1996), Bayesian analysis of six simultaneous Markov chains was run for 10,000,000 generations and trees were sampled every 1,000 generations. The first 5,000 trees, representing the burn-in phase of the analyses, were discarded, while the remaining 1,500 trees were used for calculating posterior probabilities in the majority rule consensus tree (the critical value for the topological convergence diagnostic is 0.01).

Phylogenetic trees were visualized using FigTree v1.4.0, editing and typesetting using Adobe Illustrator CS5 (Adobe Systems Inc., United States). Sequences derived in this study were deposited in GenBank.5 The final sequence alignments and the phylogenetic trees are available at TreeBase (http://www.treebase.org, accession number: 29691).

Results

Phylogenetic analyses

In this study, 71 Ganoderma sequences were newly generated from the specimens collected from YPC, and were deposited in GenBank (Table 2), i.e., 19 sequences of ITS, 21 sequences of nLSU, 18 sequences of tef1, and 13 sequences of rpb2. The combined two-gene dataset ITS + nLSU (Figure 2) included sequences from 174 Ganodermaeae specimens representing 86 species. The dataset had an aligned length of 1,463 characters including gaps (ITS: 1–611; nLSU: 612–1,463), of which Amauroderma ragusum Cui 9,011 and Sanguinoderma rude Cui 16,592 as the outgroup taxa (Figure 2; Sun et al., 2020, 2022). The Maximum likelihood analysis based on the concatenated ITS + nLSU dataset resulted in a similar topology as Bayesian Inference analysis. The RAxML analysis of the
### TABLE 2: Specimens used for phylogenetic analyses and their corresponding GenBank accession numbers.

| Species                     | Voucher/strain | Origin                  | GenBank accession numbers |
|-----------------------------|----------------|-------------------------|---------------------------|
| Gomphus acaciicola          | Cui 16,815    | Australia               | MZ354895                  |
| G. acaciicola               | Cui 16,813    | Australia               | MZ354893                  |
| G. aconetxstum              | JV 0611/21G   | Guatemala               | KF605667                  |
| G. aconetxstum              | JV 1208/111   | Guatemala               | KF605668                  |
| G. adspersum                | HSRU-200894   | China                   | MG279154                  |
| G. adspersum                | Dai 13,191    | China                   | MG279153                  |
| G. alpinum                  | Cui 17,467    | Yunnan, China           | MZ354912                  |
| G. alpinum                  | Dai 15,402    | Yunnan, China           | MZ354910                  |
| G. angustisporum            | Cui 13,817    | Fujian, China           | MZ354917                  |
| G. angustisporum            | Dai 18,245    | Malaysia                | MZ354979                  |
| G. applanatum               | L5370         | Yunnan, China           | ON994241                  |
| G. applanatum               | SFC20150930-02 | Inje gun,Gangwon do       | KY364258                  |
| G. arctocarpica             | HL173         | Yunnan, China           | ON994239*                 |
| G. arctocarpica             | HL188         | Yunnan, China           | ON994240*                 |
| G. aridica                  | Dai 12,588    | South Africa            | KU572491                  |
| G. australae                | DHCR417 HUEFS | Australia               | MF436674                  |
| G. australae                | DHCR411 HUEFS | Australia               | MF436675                  |
| G. australophyllum          | CBS138724     | South Africa            | KM507324                  |
| G. australophyllum          | CMW25884      | South Africa            | MH571693                  |
| G. bambusicolor             | Wu 1,207-1    | Taiwan, China           | MN957782                  |
| G. bambusicolor             | Wu 1,207-151  | Taiwan, China           | MN957781                  |
| G. boninense                | WD 2085       | Japan                   | KI43906                   |
| G. boninense                | WD 2028       | Japan                   | KI43905                   |
| G. brownii                  | JV 1105/9J    | United States           | MG279159                  |
| G. brownii                  | JV 0709/109   | United States           | MG056562                  |
| G. bublaminomarginatum      | Dai 20,075    | Guangxi, China          | MZ354926                  |
| G. bublaminomarginatum      | Dai 20,074    | Guangxi, China          | MZ354927                  |
| G. calidophyllum            | MFLU 19-2,174 | Yunnan, China           | MN398337                  |
| G. calidophyllum            | H36            | Yunnan, China           | MW750241                  |
| G. carnarius                | JV 8709/8     | Czech R, Europe         | KU572493                  |
| G. carnarius                | MJ 21/08      | Czech R, Europe         | KU572492                  |
| G. carocallacrum            | DMC 513       | Cameroon                | EU089970                  |
| G. carocallacrum            | DMC 322       | Cameroon                | EU089969                  |
| G. casasianicornica         | HKAS 104639   | Thailand                | MK817650                  |
| G. casasianicornica         | Dai 16,336    | Guangdong, China        | MG279173                  |
| G. choconense               | QCAM5123      | Ecuador                 | MH890527                  |
| G. constrictogonse          | Cui 17,262    | MZ354907                | –                        |
| G. cocoicola                | Cui 16,791    | Australia               | MZ354984                  |
| G. cocoicola                | Cui 16,792    | Australia               | MZ354985                  |
| G. concinnum                | Robledo 3,235 | Brazil                  | MN077523                  |
| G. concinnum                | Robledo 3,192 | Brazil                  | MN077522                  |
| G. curtissi                 | CBS 100132    | NC, United States       | JQ781849                  |
| G. curtissi                 | CBS 100131    | NC, United States       | JQ781848                  |
| G. destructans              | CBS 130979    | South Africa            | NR132919                  |
| G. destructans              | Dai 16,431    | South Africa            | MG279177                  |
| G. dianzhongense            | L4331         | Yunnan, China           | MW750237                  |
| G. dianzhongense            | L4969         | Yunnan, China           | MW750240                  |
| G. dianzhongense            | L4759         | Yunnan, China           | MW750239                  |

(Continued)
| Species          | Voucher/strain | Origin          | GenBank accession numbers |
|------------------|----------------|----------------|---------------------------|
|                  |                |                | ITS | nLSU | TEF1–α | RPB2 |
| G. dunense       | CMW 42150      | South Africa   | MG020249       | –    | MG020228   | –    |
| G. dunense       | CMW 42157 T    | South Africa   | MG020255       | –    | MG020227   | –    |
| G. ecuadorense   | URM 89449      | Ecuador        | MK119828       | MK119908 | MK121577   | MK121535 |
| G. ecuadorense   | URM 89441      | Ecuador        | MK119827       | MK119907 | MK121576   | MK121534 |
| G. eickeri       | CMW 49692 T    | South Africa   | MHS71690       | –    | MHS76278   | –    |
| G. eickeri       | CMW 50325      | South Africa   | MHS71689       | –    | MHS76290   | –    |
| G. ellipsoidesum | GACP1408966 T  | Hainan, China  | –             | –    | –          | –    |
| G. ellipsoidesum | Dai 20,544     | China          | MZ354971       | MZ355033 | MZ221654   | MZ245400 |
| G. enigmaticum   | L4954          | Yunnan, China  | ON994242       | OP380257 | OP508446   | –    |
| G. enigmaticum   | Dai 15,977     | Africa         | KU572487       | –    | KU572497   | MG367514 |
| G. enigmaticum   | Dai 15,970     | Africa         | KU572486       | –    | KU572496   | MG367513 |
| G. esculentum    | L4935 T        | Yunnan, China  | MW750242       | –    | MW838998   | MW839004 |
| G. esculentum    | HL 107         | Yunnan, China  | ON994243       | OP380258 | OP508437   | OP508424 |
| G. fallax        | JV 1009/27 T   | United States  | KF605655       | –    | –          | –    |
| G. fallax        | JV 0709/39     | United States  | KF605658       | –    | –          | –    |
| G. flexipes      | Cui 13,841     | Hainan, China  | MZ354923       | MZ355063 | MZ221655   | MZ245401 |
| G. flexipes      | HL 137         | Yunnan, China  | ON994244       | OP380259 | OP508439   | OP508426 |
| G. fornicatum    | BCRC35374      | Taiwan         | JX840349       | –    | –          | –    |
| G. gibbosum      | Cui 13,940     | China          | MZ354972       | MZ355021 | MZ221658   | MZ245404 |
| G. gibbosum      | HL 10          | Yunnan, China  | ON994245       | OP380260 | OP508434   | OP508421 |
| G. guangxiense   | Cui 14,453 T   | Guangxi, China | MZ354939       | MZ355037 | MZ221661   | MZ245407 |
| G. guangxiense   | Cui 14,454     | Guangxi, China | MZ354941       | MZ355039 | MZ221662   | MZ245408 |
| G. leucocitatum  | Cui 13,982     | Guangxi, China | MG279178       | –    | MG675750   | MG675715 |
| G. leucocitatum  | Dai 11,995     | Yunnan, China  | KU219988       | KU220016 | MG675550   | MG67497 |
| G. hochiminhense | MFLU 19–2,225  | Vietnam        | MN396662       | MN396391 | MN423177   | –    |
| G. hochiminhense | MFLU 19–2,224 T| Vietnam        | MN398324       | MN396390 | MN423176   | –    |
| G. knysnamense   | CMW 47756      | South Africa   | MHS71684       | –    | MHS67274   | –    |
| G. knysnamense   | CMW 47755 T    | South Africa   | MHS71681       | –    | MHS67261   | –    |
| G. leucocontextum| GDGM 40200     | Vietnam        | KP11548        | –    | –          | –    |
| G. leucocontextum| L4913          | Yunnan, China  | ON994246       | OP380261 | OP508445   | OP508431 |
| G. longhi        | Dai 20,895     | Liaoning, China| MZ354904       | MZ355006 | MZ221668   | MZ245413 |
| G. longhi        | HL 56          | Yunnan, China  | ON994247       | OP380262 | –          | OP508423 |
| G. lobatum       | JV 1008 32     | United States  | KF605670       | –    | MG675544   | MG675000 |
| G. lobatum       | JV 1008 31     | United States  | KF605671       | –    | MG675553   | MG674999 |
| G. lucidum       | Cui 14,404     | Sichuan, China | MG279181       | MZ355051 | MG675753   | MG67519 |
| G. lucidum       | LS 478         | Yunnan, China  | ON994248       | OP380263 | OP508449   | OP508433 |
| G. magniporum    | Zhou 439       | Guangxi, China | MZ354936       | MZ355097 | –          | –    |
| G. magniporum    | Dai 19,966     | Yunnan, China  | –             | MZ355098 | MZ221670   | MZ345728 |
| G. martinicense  | 246TX          | TX, United States| MG654185      | –    | MG754737   | MG754858 |
| G. martincense   | LIP SW-Mart08-35 T | Martinique, France | KP66256  | –    | –          | –    |
| G. mastoporium   | TNM-F0018838   | China          | JX840350       | –    | –          | –    |
| G. mexicanum     | MCUL 55832     | Martinique     | MK31815        | –    | MK31829    | MK31839 |
| G. mexicanum     | MCUL 49453     | Martinique     | MK31811        | –    | MK31825    | MK31836 |
| G. mizohamadai   | Cui 18,271     | Malaysia       | MZ354958       | MZ355067 | MZ221672   | MZ345729 |
| G. mizohamadai   | Cui 18,283     | Malaysia       | MZ354959       | MZ355069 | MZ221673   | MZ345730 |
| G. mizoramense   | UMN MZ5        | India          | KY643751       | KY747490 | –          | –    |
| G. mizoramense   | UMN MZ4 T      | India          | KY643750       | –    | –          | –    |

(Continued)
### TABLE 2 (Continued)

| Species | Voucher/strain | Origin       | GenBank accession numbers                  |
|---------|---------------|--------------|---------------------------------------------|
|         |               |              |                 ITS                nLSU   | TEF1–α  | RPB2                   |
| G. multipileum | Cui 13,597 | Hainan, China | MZ354899, MZ355043, MZ221675, MZ345732     |
| G. multipileum | L4989     | Yunnan, China | ON994249, OP380264, OP508447, OP508432     |
| G. multiplicatum | CC8 | China          | KU569515, KU570915                           |
| G. multiplicatum | Dai 17,395 | Brazil         | MZ354903 –, MZ221678, MZ345734              |
| G. mutabile      | Yuan 2,289  | Yunnan, China  | MN957785 –, MZ345734                        |
|                  | Dai 20,414  | China          | MZ354977 –, MZ345734                        |
| G. myanmarense   | MFLU 19–2,167 | Myanmar    | MN963330, MN28672                           |
| G. nasalanense   | GACP17060211 | Laos        | MZ354903, MZ221678, MZ345734              |
|                  | CC8        | China          | KU569515, KU570915                           |
| G. neojaponicum  | FFPRI WD 1532 | Chiba, Japan | MN957785 –, MZ345734                        |
|                  | FFPRI WD 1285 | Tokyo, Japan | MN957785 –, MZ345734                        |
| G. obscuratum    | Lsh88      | Yunnan, China  | ON994237*, OP508450*, OP508451*             |
| G. obscuratum    | Lsh89      | Yunnan, China  | ON994237*, OP508450*, OP508451*             |
| G. orbiforme     | Cui 13,918  | Hainan, China  | MG279186 –, MG367576, MG367522              |
| G. orbiforme     | HL43       | Yunnan, China  | ON994250, OP380265, OP508435               |
| G. oreogense     | CBS 266.88  | United States | JQ/81876, –, –, KJ143975                    |
| G. oreogense     | CBS 265.88  | United States | JQ/81875, KJ143933, KJ143974               |
| G. ovisporum     | HKAS 123193 | China          | MZ354903, MZ221678, MZ345734              |
| G. parvulum      | MFLU 52655  | Guiana, French | MM545770, MM545747, MM545745              |
|                  | MFLU 47096  | Cuba           | MM545783, MM545721, MM545742              |
| G. pfeifferi     | JV 0511/11  | United States | KF605660 –, –, –                         |
|                  | 120,818     | British        | AY884185 –, –, –                         |
|                  | Yunnan, China | – | MG279188 –, MG367576, MG367522              |
| G. philippinum   | Cui 14,443  | Hainan, China  | ON994250, OP380265, OP508435               |
|                  | L4989      | Yunnan, China  | ON994249, OP380264, OP508447, OP508432     |
|                  | L4951      | Yunnan, China  | ON994249, OP380264, OP508447, OP508432     |
| G. polychromum   | 330OR      | OR, United States | MG654196, MG654197, –, –                  |
|                  | MS343OR    | OR, United States | MG654196, MG654197, –, –                  |
| G. psiarum       | Dai 20427   | Yunnan, China  | –, MZ35012, MZ221688, MZ345738             |
| G. ravenelli     | MS187FL    | FL, United States | MG654211, MG754745, MG345865            |
| G. ravenelli     | NC-8349    | United States | AY456341 –, –, –                           |
|                  | LGA462     | Greece         | MG706250, MG706196, MG387858, MG387821     |
|                  | LGA448     | Greece         | MG706249, MG706195, MG387857, MG387820     |
| G. ryvardenii    | HKAS 58053  | South Africa   | HM138670 –, –, –                           |
| G. ryvardenii    | HKAS 58054  | South Africa   | HM138671 –, –, –                           |
|                  | Yunnan, China | – | MG279188 –, MG367576, MG367522              |
| G. sandanense    | GACP 18012501 | China       | MK345450 –, –, –                           |
|                  | L4906      | Yunnan, China  | ON994251, OP380266, OP508444, OP508430     |
| G. sessile       | 113FL      | FL, United States | MG654307, MG754748, MG345866            |
|                  | 111TX      | TX, United States | MG654306, MG754747, MG345866            |
| G. shaxiensis    | BJTC FM423  | Shangxi, China | MK764268, MK783937, MK783940               |
| G. shaxiensis    | Dai 18,921  | Shangxi, China | MZ354909, MZ355044, MZ221691, MZ345740     |
| G. shunanense    | Cui 16,343  | China          | MZ354928, MZ355011, MZ221692, MZ345741     |
| G. sinense       | Wei 5,327  | Hainan, China  | MF499988, MF49976, MF49976, MG367529       |

(Continued)
TABLE 2 (Continued)

| Species                  | Voucher/strain | Origin                  | GenBank accession numbers | ITS          | nLSU         | TEF1-α    | RPB2      |
|--------------------------|---------------|-------------------------|---------------------------|--------------|-------------|-----------|-----------|
| G. steyaraeum            | MEL 2382783   | Australia               |                           | KPO12964     | –           | –         | –         |
| G. steyaraeum            | 6 WN 208      | Indonesia               |                           | KJ654462     | –           | –         | –         |
| G. subangustissporum     | Cui 18,592 T  | Yunnan, China           |                           | MZ354981     | MZ355027    | MZ221697  | –         |
| G. subangustissporum     | Cui 18,597    | Yunnan, China           |                           | MZ354980     | MZ355025    | MZ221700  | MZ345746  |
| G. thailandicum         | HKAS 10460 T | Thailand                |                           | MK848681     | MK848879    | MK875829  | MK875831  |
| G. thailandicum         | HKAS 10461    | Thailand                |                           | MK848682     | MK848880    | MK875830  | MK875832  |
| G. tongshanense          | Cui 17,168 T  | Hubei, China            |                           | MZ354975     | MZ355024    | MZ221706  | –         |
| G. tornatum              | TBJG01AM2009  | Brazil                  |                           | JQ514108     | JX310808    | –         | –         |
| G. tornatum              | URM 82776     | Brazil                  |                           | JQ514110     | JX310800    | –         | –         |
| G. tropicum              | Dai 16,434    | Hainan, China           |                           | MG279194     | MZ355026    | MG367585  | MG367532  |
| G. tropicum              | Dai 19,679    | China                   |                           | MZ354900     | MZ355009    | MZ221707  | MZ358825  |
| G. yunlingense           | MZ354932      | Yunnan, China           |                           | Yunnan, China|              |           |           |
| G. yunlingense           | MZ354930      | Yunnan, China           |                           | Yunnan, China|              |           |           |
| G. yunlingense           | Cui 16,592    | Yunnan, China           |                           | Yunnan, China|              |           |           |
| G. yunlingense           | Cui 19,043    | Yunnan, China           |                           | Yunnan, China|              |           |           |
| G. yunlingense           | MZ354916      | Yunnan, China           |                           | Yunnan, China|              |           |           |
| G. yunnanense            | HL45 T        | Yunnan, China           |                           | Yunnan, China|              |           |           |
| G. yunnanense            | L4812         | Yunnan, China           |                           | Yunnan, China|              |           |           |
| G. zonatum               | FL 03         | FL, United States       |                           | KJ143922     | –           | KJ143940  | KJ143978  |
| G. zonatum               | FL 02         | FL, United States       |                           | KJ143921     | –           | KJ143941  | KJ143979  |
| Amauroderma rugosum      | Cui 9,011     | Guangdong, China        |                           | KJ31664      | –           | KU357204  | MG367506  |
| Sanguinoderma rude       | Cui 16,592    | Australia               |                           | MK119836     | MK119916    | MK121586  | MK121521  |

The newly generated sequences are shown in black bold. Superscript “T” is used after the number to show the type specimens. *New species sequences generated in this study.

Combined dataset yielded the best scoring tree with a final ML likelihood value of −8472.680716 (Figure 2). The matrix had 475 distinct alignment patterns, with 33.97% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.230978, C = 0.222798, G = 0.276648, T = 0.269576; substitution rates AC = 1.230871, AT = 1.401201, CG = 1.020212, CT = 9.538270, GT = 1.000000, α = 0.177171, Tree-Length: 1.586199. The best model for the ITS + nLSU dataset estimated and applied in the Bayesian analysis was HKY + I + G for ITS [Lset nst = 2, rates = invgamma; Prset statefreqpr = Dirichlet (1,1,1,1)] and GTR + I + G for nLSU. The RAxML analysis of the combined dataset yielded the best scoring tree with a final ML likelihood value of −33599.741722 (Figure 3). The matrix had 1.087 distinct alignment patterns, with 36.13% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.223924, C = 0.253042, G = 0.274308, T = 0.248726; substitution rates AC = 1.353439, AG = 6.944619, AT = 1.408316, CG = 1.653377, CT = 9.538270, GT = 1.000000, α = 0.194286, Tree-Length: 1.880697. Best model for the ITS + nLSU + TEF1-α + RPB2 dataset estimated and applied in the Bayesian analysis were HKY + I + G for ITS [Lset nst = 2, rates = invgamma; Prset statefreqpr = Dirichlet (1,1,1,1)] and GTR + I + G for nLSU, TEF1-α and RPB2 [Lset nst = 6, rates = invgamma; Prset statefreqpr = Dirichlet (1,1,1,1)]. ML and BI analyses generated nearly identical tree topologies with minimal
variations in statistical support values. Thus, only a ML tree is shown. Bootstrap support values in maximum likelihood (ML) equal to or greater than 60%, and Bayesian posterior probabilities (PP) equal to or greater than 0.90 are given above the nodes (Figures 2, 3).

The multigene phylogenetic analyses showed that 18 of our new specimens are nested in *Ganoderma*, of which three are described as new species. *Ganoderma artocarpicola* sp. nov. was sister to *G. bubalinomarginatum* B.K. Cui, J.H. Xing and Y.F. Sun with high statistical supports (−ML/1.00PP, Figure 3). *Ganoderma obscuratum* sp. nov. clustered as a sister clade with *G. yunlingense* B.K. Cui, J.H. Xing & Y.F. Sun and *G. acontextum* B.K. Cui, J.H. Xing & Vlasák with high statistical support (100%ML/1.00PP, Figure 3). The third species, *G. yunnanense* sp. nov. closely clustered with *G. ovisporum* H.D. Yang, T.C. Wen, *G. magniporum* J.D. Zhao & X.Q. Zhang and *G. sandunense* Hapuar., T.C. Wen and K.D. Hyde with high statistical support (100%ML/1.00PP), and a distinct lineage.

**Taxonomy**

*Ganoderma artocarpicola* J. He and S.H. Li, sp. nov. (Figure 4). MycoBank number: MB845720

**Diagnosis:** *Ganoderma artocarpicola* is characterized by its sessile and concrescent basidiomata, reddish brown to yellowish brown pileus surface with shallow concentric furrows and radial rugose, heterogeneous context, wavy margin and ellipsoid to ovoid basidiospores (8.0–10.5 × 5.0–7.5 μm).

**Etymology:** The epithet ‘*artocarpicola*’ refers to the host tree genus *Artocarpus*.

**Holotype:** CHINA. Yunnan Province., Lincang City, Yongde County (24°54′1″N, 99°15′31″E), on living tree of *Artocarpus pithecogallus*, alt. 1,506 m, Jun He, 21 September 2021, HL188 (HKAS 123782).

**Description:** Basidiomata: annual, sessile and broadly attached, usually concrescent, woody hard. Pileus: imbricate, flabelliform to reniform, slightly convex to applanate, projecting up to 9 cm, 8 cm wide and 2 cm thick at the base. Pileus surface reddish brown (9E8) to yellowish brown (5C7), weakly to strongly laccate, with shallowly concentric furrows and radial rugose, concentrically zonate or azonate. Margin: buff (1A3) to grayish orange (6D8), entire, obtuse, irregularly wavy. Context: up to 1.8 cm thick, heterogeneous, the upper layer greyish white (2B1), the lower layer cinnamon brown (6D7) to chestnut brown (8E5), without black melanoid lines, hard corky and fibrous. Tubes: 0.2–0.5 cm long, dark brown (6E8), woody hard, unstratified. Pores: 5–7 per mm, circular to angular, dissepiments thick, entire; pores surface cream (2B2) to greyish white (2B1) when fresh, golden grey to greyish brown when bruising and drying.
Hyphal system trimitic: generative hyphae 2.0–3.5 μm in diameter, colorless, thin-walled, with clamp connections; skeletal hyphae 2.0–5.0 μm in diameter, thick-walled with a narrow lumen to sub-solid, arboriform and flexuous, pale yellow to yellowish brown; binding hyphae 1.5–3.0 μm in diameter, thick-walled, frequently branched, interwoven, colorless, scarce; all the hyphae IKI–, CB+; tissues darkening in KOH.

Pileipellis: a crustohymeniderm, cells 35–50 × 5–10 μm, thick-walled to sub-solid, apical cells clavate, inflated and flexuous, pale yellow to golden yellow, without granulations in the apex, moderately amyloid at maturity.

Basidiospores: ellipsoid to ovoid, not obviously truncated, with apical germ pore, yellowish to golden yellow, IKI–, CB+, inamyloid; double walled with slightly thick walls, exospore wall smooth, endospore wall with inconspicuous spinules; (60/3/2) 8.0 (8.5)–9.3–10.0 (10.5) × 5.0 (5.5)–6.2–7.0 (7.5) μm, L = 9.25 μm, W = 6.20 μm, Q = (1.23) 1.31–1.50–1.72 (1.78), Qm = 1.50 ± 0.14 (including myxosporium). Basidia: barrel-shaped to utriform, colorless, with a clamp connection and four sterigmata, thin-walled, 10–15 × 5–9 μm; basidioles pear-shaped to fusiform, colorless, thin-walled, 8–10 × 4–7 μm.

Additional specimen examined: China, Yunnan Province, Lincang City, Yongde County, Dedang Town (24°01’12”N, 99°15’34”E), on a living tree of Artocarpus pithecogallus, alt. 1,484 m, Qian-Qiu Luo, 22 August 2021, HL173 (HKAS 123783).

Notes: In the phylogenetic analyses, G. artocarpicola is sister to G. bubalinomarginatum, which was described from the southwest Guangxi Province in China (Figure 3; Sun et al., 2022). Morphologically, both species share similar characteristics of the connate and sessile basidiomata, reddish brown to yellowish brown pileus surface, and non-stratified tubes. However, G. bubalinomarginatum differs from G. artocarpicola in having buff and obtuse pileus margin, smaller basidiospores (7.0–8.8 × 4.3–5.8 μm), and larger basidia (15–22 × 7–11 μm, Sun et al., 2022).

Ganoderma weberianum and G. artocarpicola are similar in having imbricate, sessile and hard basidiomata. However, G. weberianum has a pale-yellow pore surface when dry, homogeneous greyish brown context, smaller basidiospores (6.0–7.0 × 4.0–6.0 μm), and longer pileipellis (60.0–90.0 × 6.0–12.0 μm, Steyaert, 1972; Pan and Dai, 2001). In addition, the pileus of G. weberianum is more laccate than G. artocarpicola. The comparison of the ITS sequences of G. weberianum and G. artocarpicola showed 2.12% (13/614 bp) nucleotide differences.

Ganoderma obscuratum J. He and S.H. Li, sp. nov. (Figure 5). MycoBank number: MB845721.
**Diagnosis:** *Ganoderma obscuratum* is characterized by its small and dorso-laterally stipitate basidiomata, dark brown to greyish brown and laccate pileus surface, small pores (6–9 per mm), corky context, and almond-shaped to narrow ellipsoid basidiospores (8.0–9.5 × 4.5–5.5 μm).

**Etymology:** The epithet 'obscuratum' refers to the obscure pileus surface when dry.

**Holotype:** CHINA. Yunnan Province., Zhaotong City, Yiliang County (104°14'55"E, 27°47'56"N), on a dead tree of *Acer* sp. alt. 1,859 m, Shu-Hong Li, 12 August 2019, Lsh88 (HKAS 123786).
**Description:** Basidiomata: annual, sessile to subsessile, coriaceous to woody hard, light in weight. Pileus: single, flabelliform to reniform or shell-shaped, appinate, projecting up to 6 cm, 4.5 cm wide and 1 cm thick at the base. Pileus surface dark brown (8E8) when fresh becoming greyish brown (7E8) when dry, and covered by a thin hard crust, laccate, glabrous and shiny, with dense concentric furrows. Margin: buff (8B2) to generally concolorous, entire, subacute to obtuse, slightly wavy; cracked when dry. Context: up to 0.7 cm thick, homogeneous, yellowish brown (5D5) to chestnut brown (6E8), with black melanoid lines, hard corky. Tubes: 0.2–0.4 cm long, concolorous with the base of the context, corky, unstratified. Pores: 6–9 per mm, circular, disseminations slightly thick, entire; pores surface white to greyish white (2B1) when fresh, pale brown (6D6) to dark brown (7E7) when bruising and drying. Stipe: up to 6.5 cm long and 2.2 cm diam, flattened to cylindrical, fibrous to spongy, concolorous with pileus surface.

Hyphal system trimitic: generative hyphae 2.0–4.0 μm in diameter, colorless, thin-walled, with clamps connections; skeletal hyphae 2.0–8.0 μm in diameter, thick-walled with a wide to narrow lumen or sub-solid, arboriform with few branches, yellowish brown to golden yellow; binding hyphae 1.0–3.0 μm in diameter, thick-walled, branched and flexuous, colorless to pale yellow, scarce; all the hyphae IKI−, CB+, tissues darkening in KOH.

Basidiospores: almond-shaped to narrow ellipsoid, apex subacute, with apical germ pore, yellowish to yellowish brown, IKI−, CB+, inamyloid; double-walled with moderately thick walls, exospore wall smooth, endospore wall with inconspicuous spinules; (40/2/2; 8.0) 8.5–9.0–9.0 (9.5) × 4.5–5.2–5.0 (5.5) μm, L = 9.09 μm, W = 5.22 μm, Q = (1.58) 1.61–1.75–1.87 (2.08), Qn = 1.75 ± 0.11 (including myxosporium). Basidia: broadly clavate, colorless, with a clamp connection and four sterigmata, thin-walled, 15–25 × 5–9 μm; basidioles in shape like the basidia, colorless, thin-walled, 10–21 × 4–8 μm.

**Additional specimens examined:** China, Yunnan Province, Zhaotong City, Yiliang County, Xiaocaoaba Town (104°14′18″E, 27°47′59″N), on a dead tree of Acer sp., alt. 1,905 m, Shu-Hong Li, 12 August 2019, Lsh89 (HKAS 123772).

**Notes:** Phylogenetic analyses showed that *Ganoderma obscuratum* clusters as a sister taxon to *G. yunlingense* with good statistical support (100% ML/1.00 PP, Figure 3). Morphologically, *G. obscuratum* differs from *G. yunlingense* by having thin basidiomata, dark brown and laccate pileus surface when fresh, homogeneous context and non-stratified tubes, smaller pores (6–9 per mm), and narrow ellipsoid basidiospores with spinules on the endospore wall (Sun et al., 2022).

**Ganoderma alpinum** described from Yunnan Province is morphologically similar to *G. obscuratum* by having the hard basidiomata with greyish brown pileus surface, homogeneous context and non-stratified tubes. However, *G. alpinum* differs by the larger pores (5–7 per mm), and smaller basidiospores (6.2–7.8 × 4–5.5 μm, Sun et al., 2022). *Ganoderma applanatum* also has sessile basidiomata and homogeneous context, but it differs from *G. obscuratum* by having a perennial basidiomata with pale pileus surface and smaller basidiospores (5–8 × 4–6 μm, Moncalvo and Ryvarden, 1997; Hapuarachchi et al., 2019; Sun et al., 2022). Besides, *G. applanatum* and *G. obscuratum* were well separated in the phylogenetic analyses (Figure 3).

**Ganoderma yunnanense** J. He and S.H. Li, sp. nov. (Figure 6).

**Description.** Basidiomata: annual, centrally to laterally stipitate basidiomata with reddish brown to violet brown and strongly laccate pileus surface, cream color pore surface and context, and broadly ellipsoid basidiospores (8.0–12.5 × 7.0–9.0 μm).

**Etymology:** The epithet ‘yunnanense’ refers to Yunnan Province from where the holotype was collected.

**Holotype:** CHINA. Yunnan Province, Puer City, Jingdong County, Wuliang Mountains (100°48′48″E, 24°19′36″N), on a rotten broad-leaved tree, alt. 2,129 m, Song-Ming Tang, 8 August 2021, HL45 (HKAS 123771).

**Description.** Basidiomata: annual, centrally to laterally stipitate, hard corky. Pileus: single, flabelliform to reniform or suborbicular, projecting up to 9 cm, 6.5 cm wide and 0.5 cm thick at base. Pileus surface reddish brown (10F8) to violet brown (11F8), weakly to strongly laccate, glossy, with shallowly concentric furrows and radial rugose. Margin: pale yellow (3B2) to concolorous, entire, acute, incurred when dry. Context: up to 0.3 cm thick, homogeneous, white to cream (1B2), fibrous, corky, without black melanoid lines. Tubes: 0.1–0.2 cm long, concolorous with the base of the context, corky, unstratified. Pores: 4–6 per mm, round to angular, disseminations thick, entire; pore surface white when fresh, lead grey (3B1) when bruising and drying. Stipe: 15.0–17.5 × 1.0–2.0 cm, dorsally lateral to nearly dorsal, cylindrical and solid, concolorous with pileus surface, strongly laccate, fibrous to woody.

Hyphal system trimitic: generative hyphae 2.0–3.0 μm in diameter, colorless, thin-walled, with clamps connections; skeletal hyphae 2.0–6.0 μm in diameter, non-septate, arboriform with few branches, colorless to pale yellow; binding hyphae 0.7–1.5 μm, slightly thick-walled, with clamps connections; skeletal hyphae 2.0–8.0 μm in diameter, thick-walled, with a wide to narrow lumen or sub-solid, arboriform with few branches, yellowish brown to golden yellow; binding hyphae 1.0–3.0 μm in diameter, thick-walled, branched and flexuous, colorless to pale yellow, scarce; all the hyphae IKI−, CB+, tissues darkening in KOH.

Pileipellis: a crustohymeniderm, composed of a palisade of vertical, cells 23–40 × 6–9 μm, slightly thick-walled, clavate to cylindrical, slightly inflated, straw yellow to golden-yellow, granulations in the apex, moderately clavate to cylindrical amyloid at maturity.

Basidiospores: broadly ellipsoid to ellipsoid, apex not obviously truncated, with apical germ pore, yellowish to pale yellowish brown, IKI−, CB+, inamyloid; double-walled with distinctly thick walls, exospore wall smooth, endospore walls with inter-wall pillars; (40/2/2) (8.0) 9.0–10.7–12.0 (12.5) × 7.0–7.6–8.0 (8.5) μm, Q = (11.0) 1.25–1.41–1.55 (1.60), Qn = 1.41 ± 0.12 (including myxosporium). Basidia: widely clavate to...
barrel-shaped, colorless, with a clamp connection and four sterigmata, thin-walled, 15–18 × 8–11 μm; basidioles clavate, colorless, thin-walled, 10–14 × 6–9 μm.

Additional specimens examined: China, Yunnan Province, Puer City, Jingdong County, Ailao Mountains (101°01’29”E, 24°30’03”N), on a rotten broad-leaved tree, alt. 2,326 m, Jun He, 4 August 2019, L4812 (HKAS 123769).

Notes: Our multi-locus phylogenetic analyses show that *Ganoderma yunnanense* is sister to *G. ovisporum* with high statistical support (84% ML/0.98 PP, Figure 3), and together they group with...
G. sandunense and G. magniporum (Zhao et al., 1984; Hapuarachchi et al., 2019; Yang et al., 2022). Ganoderma yunnanense resembles G. ovisporum in having reddish-brown pileus and broadly ellipsoid basidiospores. However, G. ovisporum has heterogeneous context, shorter pileipellis cells (18–29 × 6–11 μm) and larger basidiospores (12.5–15.5 × 9.0–11.5 μm, Yang et al., 2022). Moreover, Ganoderma sandunense has a larger basidiospores (10.8–15.7 × 8.6–12.5 μm) and thicker context than those of G. yunnanense (Hapuarachchi et al., 2019; Yang et al., 2022). Ganoderma magniporum can be easily distinguished from G. yunnanense by the larger pores (2–2.5 per
mm), black-brown to black pileus surface and ovoid basidiospores with truncated apex (8.7–10.4 × 5.2–7.0 μm, Zhao et al., 1984).

Morphologically, G. yunnanense resembles G. leucocontextum by white pore surface and context. However, G. leucocontextum has red to red brown pileus surface, white to yellowish margin, shorter stipe (5–10 cm) and broadly ellipsoid basidiospores with truncated apex (8.0–12.5 × 5.5–9.0 μm, Li et al., 2015). Among the species in the G. lucidum complex, G. yunnanense looks very similar to G. tsugae and G. weixiense morphologically, although they can be easily distinguished by phylogenetic analyses and ecological distribution (Murrill, 1902; Ye et al., 2019).

In addition, G. yunnanense also shares similarities with G. dianzhongense but the latter has dark-brown to putty context and wider pileipellis cells than those of G. yunnanense. The nucleotide comparison of ITS sequences of G. yunnanense and G. dianzhongense revealed 26 bp (26/614 bp, 4.23%) nucleotides differences (He et al., 2021).

### Key to the species of Ganoderma in Yunnan Province, China

| 1. Pileal surface non-laccate | 2 |
|-------------------------------|---|
| 1*. Pileal surface laccate    | 11 |
| 2. Pileus imbricate, margin lacerated like petals | G. puerense |
| 2*. Pileus solitary, margin entire | 3 |
| 3. Basidiospores subglobose | G. hoehnelianum |
| 3*. Basidiospores broadly ellipsoid to ellipsoid or ovoid | 4 |
| 4. Tubes stratified | 5 |
| 4*. Tubes non-stratified | 6 |
| 5. Context homogeneous; basidiospores 5.5–7 × 4.1–5.2 μm | G. applanatum |
| 5*. Context heterogeneous; basidiospores 7–12 × 5–8 μm | G. australe |
| 6. Pores > 6 per mm | G. obscuratum |
| 6*. Pores < 6 per mm | 7 |
| 7. Context without black melanoid lines; apical cells in cuticle branched | 8 |
| 7*. Context with black melanoid lines; apical cells in cuticle unbranched | 9 |
| 8. Distributed in higher altitudes | G. alpinum |
| 8*. Distributed in lower altitudes | 9 |
| 9. Apical cells in cuticle irregularly branched or with protuberances | G. williamsianum |
| 9*. Apical cells in cuticle unbranched or without protuberances | 10 |
| 10. Pileus surface reddish brown to greyish brown, pores angular | G. gibbusum |
| 10*. Pileus surface greyish brown to grey, pores circular | G. yunningsense |
| 11. Basidiomata sessile | 12 |
| 11*. Basidiomata stipitate or with constricted short stipe | 14 |
| 12. Apical cells in cuticle irregularly branched or with protuberances | G. mutable |
| 12*. Apical cells in cuticle unbranched or without protuberances | 13 |
| 13. Pileus surface reddish brown to yellowish brown; basidiospores > 8 μm in length | G. artocarpicola |
| 13*. Pileus surface pale brown to purplish black; basidiospores < 8 μm in length | G. philippi |
| 14. Pores < 3 per mm | G. magniporum |
| 14*. Pores > 3 per mm | 15 |
| 15. Pileus surface dark red to nearly black | 16 |
| 15*. Pileus surface pale brown to yellowish brown or reddish brown | 20 |
| 16. Stipe short or constricted at base, < 4 cm in length | 17 |
| 16*. Stipe obviously long, > 4 cm in length | 18 |
| 17. Basidiospores subglobose to broadly ellipsoid, < 6 μm in width | G. weberianum |
| 17*. Basidiospores ellipsoid to ovoid, > 6 μm in width | G. oribiforme |
| 18. Basidiomata central stipitate; basidiospores truncated | G. sanduense |
| 18*. Basidiomata laterally stipitate; basidiospores not obviously truncated | 19 |
| 19. Context homogeneous, pores 5–6 per mm; basidiospores > 7 μm in width | G. dianzhongense |
| 19*. Context heterogeneous, pores 3–5 per mm; basidiospores 11.0–13.7 × 7.0–8.8 μm | G. sibangustiaporium |
| 20. Pore surface yellowish to buff when fresh | 21 |
| 20*. Pore surface white to greyish white or cream when fresh | 22 |
| 21. Pileus surface oxblood red to violet brown; basidiospores > 7 μm in width | G. lucidum |
| 21*. Pileus surface reddish brown to yellowish brown; basidiospores < 7 μm in width | 23 |
| 22. Distributed in temperate areas | 28 |
| 22*. Distributed in tropical areas | 28 |
| 23. Growing on coniferous trees | G. tsugae |
| 23*. Growing on broad-leaf trees | 24 |
| 24. Basidiospores < 5 μm in width | G. weixiense |
| 24*. Basidiospores > 5 μm in width | 25 |
| 25. Context with black melanoid lines | G. sibangustiaporium |
| 25*. Context without black melanoid lines | 26 |
| 26. Context heterogeneous, buff to dark brown | G. lucidum |
| 26*. Context homogeneous, white to cream or greyish white | 27 |
| 27. Pileus surface red to red brown; basidiospores truncated | G. leucocontextum |
| 27*. Pileus surface violet brown; basidiospores not obviously truncated | G. yunnanense |
| 28. Stipe short or constricted at base, < 6 cm in length | G. tropicam |
| 28*. Stipe obviously long, > 6 cm in length | 29 |
| 29. Pileus imbricate, upper surface orange yellow to orange red | G. multipileum |
| 29*. Pileus solitary, upper surface reddish brown to black brown | 30 |
| 30. Growth on broad-leaved forests | G. flexipes |
| 30*. Growth on bamboo forests. | 31 |
| 31. Context heterogeneous, pores 4–6 per mm; basidiospores 8.0–10.5 × 5.5–9.1 μm | G. calidophilum |
| 31*. Context homogeneous, pores 5–8 per mm; basidiospores 8.0–12.5 × 5.0–8.0 μm | G. esculentum |
### TABLE 3 Species, hosts, and geographical locations and corresponding references of *Ganoderma* in Yunnan Province, China.

| Species            | Host plant                          | Location           | References                        |
|--------------------|-------------------------------------|--------------------|-----------------------------------|
| *G. alpinum*       | *Populus* sp.                       | Shangri-La         | Sun et al. (2022)                 |
| *G. applanatum*    | *Eriobotrya japonica*               | Nujiang Prefecture | This study                        |
| *G. artocarpicola* | *Artocarpus* sp.                    | Lincang City       | This study                        |
| *G. austrole*      | *Fagus* sp.                         | Kunming City       | Luangharn et al. (2021)           |
| *G. calidophilum*  | On bamboo roots                     | Dehong Prefecture  | This study, He et al. (2021)      |
| *G. dianzhongense* | *Cyclobalanopsis glauca*            | Central Yunnan Province | This study, He et al. (2021) |
| *G. ellipsoideum*  | Broad-leaved tree                   | Honghe Prefecture  | This study                        |
| *G. esculentum*    | *Bambusa intermedia*                | Honghe Prefecture  | He et al. (2021)                  |
| *G. flexipes*      | *Castanopsis fargesii*              | Puer City          | This study                        |
| *G. gibbosum*      | *Carya cathayensis*                 | Zhaotong City      | This study, Wang and Wu (2010), Xing (2019) |
| *G. hoehnelianum*  | Broad-leaved tree                   | Jinghong City      | This study                        |
| *G. leucocontextum*| *Cyclobalanopsis glauca*            | Dali Prefecture    | This study                        |
| *G. lingzhi*       | Broad-leaved tree                   | Kunming City       | This study                        |
| *G. lucidum*       | *Quercus* sp.                       | Chuxiong Prefecture| This study                        |
| *G. magniporum*    | Broad-leaved tree                   | Yunnan Province    | Sun et al. (2022)                 |
| *G. multiplexum*   | *Acacia farnesiana*                 | Yuxi City          | This study                        |
| *G. mutabile*      | *Angiosperm tree*                   | Chuxiong Prefecture| Cao (2013)                        |
| *G. otsunum*       | *Acer* sp.                          | Zhaotong City      | This study                        |
| *G. philippii*     | *Hevea brasiliensis*                | Sipsongpanna       | Zhao (1988)                       |
| *G. puerense*      | *Cinnamomum sp.*                    | Puer City          | Sun et al. (2022)                 |
| *G. sandanense*    | *Quercus* sp.                       | Honghe Prefecture  | This study                        |
| *G. sienense*      | *Cyclobalanopsis sp.*               | Kunming City       | Luangharn et al. (2021)           |
| *G. subangustiporum*| Broad-leaved tree                   | Wenshan Prefecture | This study                        |
| *G. tsugae*        | *Picea* sp.                         | Wenshan Prefecture | Sun et al. (2022)                 |
| *G. tropicum*      | *Acacia* sp.                        | Kunming City       | Luangharn et al. (2021)           |
| *G. weixiensis*    | coniferous forest                   | Puer City          | This study                        |
| *G. weberianum*    | *Ficus* sp.                         | Dingqin Prefecture | Ye et al. (2019)                  |
| *G. yunnanense*    | Broad-leaved tree                   | Jinghong City      | Pan and Dai (2001)                |
| *G. yunlingense*   | *Quercus* sp.                       | Puer City          | Cao and Yuan (2013)               |

### Discussion

Sun et al. (2022) revealed the species diversity, taxonomy and phylogeny of *Ganoderma* with emphasis on Chinese collections, which showed that 40 species of *Ganoderma* in China were confirmed by morphology and DNA sequence data. Among the 40 species, five new species of *Ganoderma* were discovered in YPC, namely *G. alpinum*, *G. chuxiongense*, *G. puerense*, *G. subangustiporum*, and *G. yunlingense*. Besides, Sun et al. (2022) summarized known species of *Ganoderma* in YPC viz. *G. ellipsoideum*, *G. flexipes*, *G. hoehnelianum*, *G. lingzhi*, and *G. magniporum*. However, results of our research showed that *Ganoderma* chuxiongense and *G. dianzhongense* are similar in morphology and phylogeny, and based on the time priority, *G. chuxiongense* is considered as a synonym of *G. dianzhongense*. In consideration of the authors’ contributions, it is suggested to use the sample Cui 17,262 (BJFC034120) as a paratype of *Ganoderma dianzhongense* (He et al., 2021; Sun et al., 2022).

To date, 25 species of *Ganoderma* have been recorded in YPC (Cao et al., 2012; Ye et al., 2019; He et al., 2021; Sun et al., 2022), however, the species diversity of *Ganoderma* is still not well known, especially in the subtropical and tropical areas. According to our survey of different sample sites in Yunnan Province from 2016 to 2021, a total of 268 samples of *Ganoderma* were collected. Based on comprehensive morphological characteristics and phylogenetic evidence, we report 15 known species of *Ganoderma* from YPC viz. *Ganoderma applanatum*, *G. calidophilum*, *G. dianzhongense*, *G. ellipsoideum*, *G. esculentum*, *G. flexipes*, *G. gibbosum*, *G. magniporum*. In consideration of the authors’ contributions, it is suggested to use the sample Cui 17,262 (BJFC034120) as a paratype of *Ganoderma dianzhongense* (He et al., 2021; Sun et al., 2022).
G. leucocontextum, G. lingzhi, G. lucidum, G. multiplex, G. orbiforme, G. sandunense, G. sinense and G. tricolor. In addition, three new species viz. G. articarpola, G. obscuratum and G. yunnanense are proposed in this study. Up to now, 183 species of Ganoderma have been described all over the world, of which 42 species have been recorded in China (Wu et al., 2020; Sun et al., 2022; Yang et al., 2022). The discovery of three new species of Ganoderma in this study raises the known Ganoderma species in Yunnan Province to 32, accounting for 71.11% of the known Ganoderma species in China. Thus, Yunnan Province can be considered as one of the biodiversity center hot spots for Ganoderma.

A checklist of Ganoderma in YPC is given in Table 3. In addition, a key to Ganoderma in YPC is also provided. This paper enriches the knowledge of Ganoderma in YPC, and it is likely that more new taxa will be discovered in the future with extensive sampling in different areas and comprehensive molecular analyses.

Data availability statement

The original contributions presented in the study are included in the article-supplementary material, further inquiries can be directed to the corresponding author.

Author contributions

S-HL and Z-LL: conceptualization. JH: methodology, formal analysis, data curation, and writing—original draft preparation. JH and XH: investigation. S-HL and Z-ZL: resources. K-YN, S-MT, E-XL, H-ML, and S-HL: writing—review and editing. S-HL: funding acquisition. All authors contributed to the article and approved the final version of the manuscript.

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Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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