Phytotaxa

Table of Contents

Article

Correspondence

ISSN 1179-3155 (print); ISSN 1179-3163 (online)

Published by Magnolia Press, Auckland, New Zealand

Phytotaxa 432 (2): 111–118
https://www.mapress.com/j/pt/

Article

ISSN 1179-3155 (print edition)
PHYTOTAXA
ISSN 1179-3163 (online edition)

https://doi.org/10.11646/phytotaxa.432.2.1

Gloeodontia yunnanensis sp. nov. (Russulales, Basidiomycota) from China, evidenced by morphological characters and phylogenetic analyses

LU CHEN[2], ZHENG-JUN SHI[3], CHUN-HUA WU[3] & CHANG-LIN ZHAO[1,2,3*]

[1]*Key Laboratory for Forest Resources Conservation and Utilization in the Southwest Mountains of China, Ministry of Education, Southwest Forestry University, Kunming 650224, P.R. China.*
[2]*College of Biodiversity Conservation, Southwest Forestry University, Kunming 650224, P.R. China.*
[3]*School of Chemical Engineering, Southwest Forestry University, Kunming 650224, P.R. China.*
[*]*Corresponding author: fungichanglinz@163.com*

Abstract

A new wood-inhabiting fungal species, *Gloeodontia yunnanensis*, is proposed based on a combination of morphological features and DNA data. The species is characterized by an annual, resupinate basidiomata with smooth hymenial surface, a monomitic hyphal system with thin-walled, clamped generative hyphae and obclavate cystidia and subglobose to globose, hyaline, thick-walled, asperulate, strongly amyloid, acyanophilous basidiospores measuring 3.3–4.3 × 2.5–3.5 µm. Sequences of ITS and 28S gene regions of the studied samples were generated and phylogenetic analyses were performed with Maximum Likelihood, Maximum Parsimony and Bayesian Inference methods. The analyses based on ITS+28S sequences showed that *G. yunnanensis* nested in the *Gloeodontia* clade and formed a monophyletic lineage with strong support (100% BS, 100% BP, 1.00 BPP).

Keywords: Gloeodontiaceae, *Gloeocystidiellum*, taxonomy, Yunnan Province

Introduction

The genus *Gloeodontia* Boidin (1966: 22) was typified by *G. discolor* (Berk. & M.A. Curtis) Boidin (1966: 22) (Boidin 1966), and characterized by a combination of resupinate or effused-reflexed basidiomata of ceraceous to membranaceous consistency, smooth to odontioid hymenophore, a monomitic or dimitic hyphal structure, clamped hyphae, presence of cystidia, cylindrical to urniform basidia, and hyaline to pale yellow, thick-walled, asperulate, ellipsoid to globose, acyanophilous and amyloid basidiospores (Boidin 1966, Bernicchia & Gorjón 2010). So far eight species have been accepted in the genus (Burdsall & Lombard 1976, Hjortstam 1987, Rajchenberg 1987, Telleria *et al*. 2008, Larsson & Larsson 2003, Gorjón & Jesus 2012, Zhou & Dai 2013).

Recently, molecular studies involving *Gloeodontia* have been carried out (Larsson & Larsson 2003, Zhou & Dai 2013, Leal-Dutra *et al*. 2018). Phylogenetic relationships of russuloid basidiomycetes with an emphasis on non-gilled taxa revealed that four species of *Gloeodontia* formed a monophyletic clade that grouped with Russulales and Stereales clades, and additionally, one new combination *G. subasperispora* (Litsch.) E. Larss. & K.H. Larss. (2003: 1062) was proposed (Larsson & Larsson 2003). Later, a taxonomic work on wood-inhabiting hydnoid species in the Russulales showed that five *Gloeodontia* species grouped together as a well-supported clade (Zhou & Dai 2013). Leal-Dutra *et al*. (2018) studied Lachnocladiaceae and Peniophoraceae (Russulales) and showed that *Gloeodontia* formed a single clade and then grouped with the clades Amylostereaceae, Auriscalpiaceae, Bondarzewiaceae, *Gloeocystidiellum*, Russulaceae and Stereaceae.

During studies of wood-inhabiting fungi in southern China, an additional taxon resembling a *Gloeodontia* with a smooth hymenophore could not be assigned to any described species. In this paper, the authors examine the taxonomy and phylogeny of this new species, based on the internal transcribed spacer (ITS) regions and 28S sequences.

Accepted by Genevieve Gates: 24 Jan. 2020; published: 10 Feb. 2020

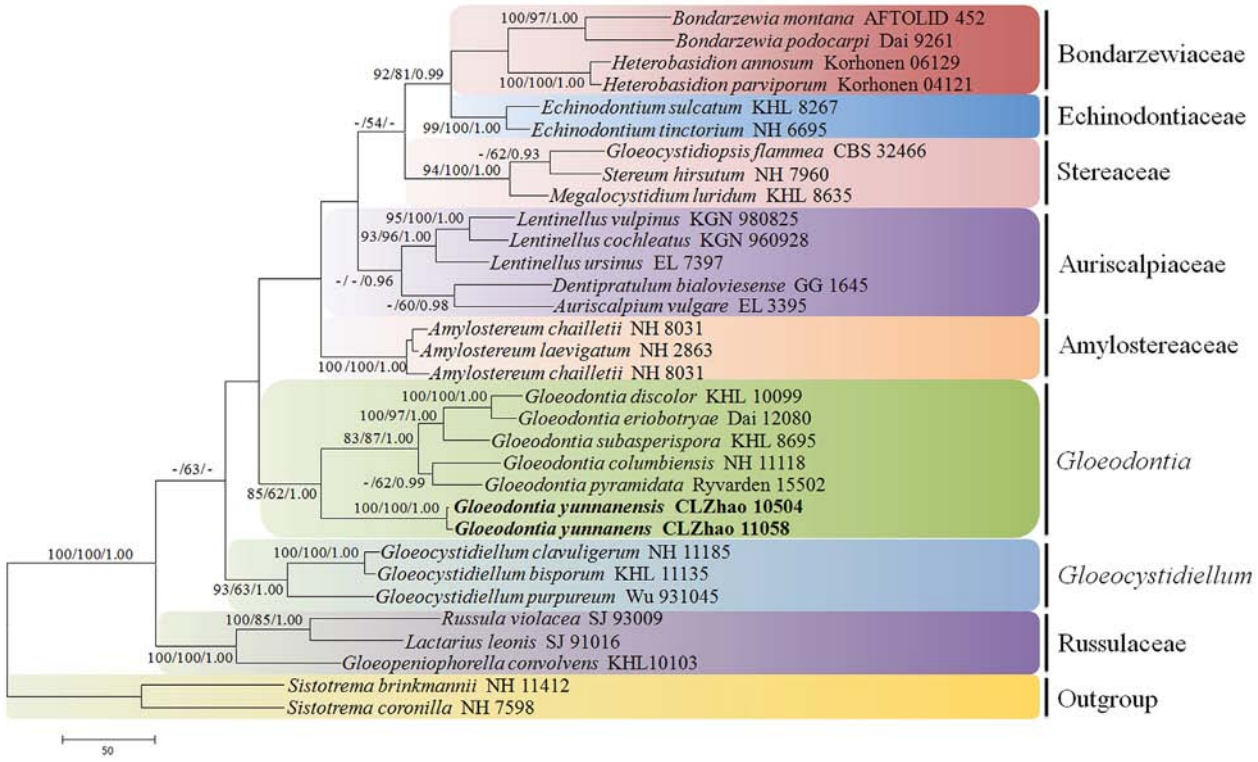

FIGURE 1. Maximum Parsimony strict consensus tree illustrating the phylogeny of *Gloeodontia yunnanensis* and related species in the Russulales based on ITS+28S sequences. Branches are labelled with maximum likelihood bootstrap values higher than 70%, parsimony bootstrap proportions higher than 50% and Bayesian posterior probabilities more than 0.95, respectively.

Materials and methods

Morphological studies:—The two specimens studied are deposited at the herbarium of Southwest Forestry University, Kunming, Yunnan Province, P.R. China (SWFC). Macromorphology descriptions are based on field notes. Micromorphology was studied on dried specimens using a light microscope following Dai (2012). The following abbreviations were used: KOH = potassium hydroxide 5% water solution, CB = Cotton Blue, CB– = acyanophilous, IKI = Melzer's reagent, IKI– = both inamyloid and non-dextrinoid, L = mean spore length (arithmetic average), W = mean spore width (arithmetic average of all spores), Q = variation in the L/W ratios between the specimens studied, n = a/b−number of spores (a) measured from given number (b) of specimens.

Molecular procedures and phylogenetic analyses:—CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd, Beijing) was used to obtain genomic DNA from dried specimens, according to the manufacturer's instructions. The ITS region was amplified with the primer pair ITS5 and ITS4 (White *et al.* 1990). The 28S region was amplified with the primer pair LR0R and LR7 (http://www.biology.duke.edu/fungi/mycolab/primers.htm). The PCR procedure for ITS was as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles at 94 °C for 40 s, 58 °C for 45 s and 72 °C for 1 min, and a final extension of 72 °C for 10 min. The PCR procedure for 28S was as follows: initial denaturation at 94 °C for 1 min, followed by 35 cycles at 94 °C for 30 s, 48 °C 1 min and 72 °C for 1.5 min, and a final extension of 72 °C for 10 min (Shen *et al*. 2019). The PCR products were purified and directly sequenced at Kunming Tsingke Biological Technology Limited Company. All newly generated sequences were deposited at GenBank (Table 1).

Sequencher 4.6 (GeneCodes, Ann Arbor, MI, USA) was used to edit the DNA sequences. Sequences were aligned in MAFFT 7 (http://mafft.cbrc.jp/alignment/server/) using the "G-INS-i" strategy and adjusted manually in BioEdit (Hall 1999). The sequence alignment was deposited in TreeBase (ID 25437). Sequences of *Sistotrema brinkmannii* (Bres.) J. Erikss. (1948:134) and *S. coronilla* (Höhn.) Donk ex D.P. Rogers (1935: 23) obtained from GenBank were used as outgroup to root trees following Leal-Dutra *et al*. (2018).

Maximum parsimony analysis was applied to the ITS+28S dataset sequences. Procedure of this analysis followed Zhao & Wu (2017), and the tree construction was performed in PAUP* version 4.0b10 (Swofford 2002). All characters

were equally weighted and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1000 random sequence additions. Max-trees were set to 5000, branches of zero length were collapsed and all parsimonious trees were saved. Clade robustness was assessed using bootstrap (BT) analysis with 1,000 replicates (Felsenstein 1985). Descriptive tree statistics viz., tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI) were calculated for each Maximum Parsimonious Tree generated. The data matrix was also analyzed using the Maximum Likelihood (ML) approach with RAxML-HPC2 software through the Cipres Science Gateway (www.phylo.org, Miller *et al.* 2009). Branch support (BS) for ML analysis was determined through 1000 bootstrap replicates.

TABLE 1. List of species, specimens, and GenBank accession numbers of sequences used in this study.

Species name	Specimen No.	GenBank accession No.		References
		ITS	28S	
Amylostereum areolatum	NH 8041 (NH)	AF506405	AF506405	Larsson & Larsson 2003
A. chailletii	NH 8031 (NH)	AF506406	AF506406	Larsson & Larsson 2003
A. laevigatum	NH 2863 (NH)	AF506407	AF506407	Larsson & Larsson 2003
Auriscalpium vulgare	EL 3395	AF506375	AF506375	Larsson & Larsson 2003
Bondarzewia montana	AFTOL ID 452 (DAOM)	DQ200923	DQ234539	Larsson & Larsson 2003
B. podocarpi	Dai 9261	KJ583207	KJ583221	Chen & Shen 2014
Dentipratulum bialoviesense	GG 1645	AF506389	AF506389	Larsson & Larsson 2003
Echinodontium sulcatum	KHL 8267	AF506414	AF506414	Larsson & Larsson 2003
E. tinctorium	NH 6695 (NH)	AF506430	AF506430	Larsson & Larsson 2003
Gloeocystidiellum bisporum	KHL 11135	AY048877	AY048877	Larsson & Larsson 2003
G. clavuligerum	NH 11185 (NH)	AF310088	AF310088	Larsson & Hallenberg 2001
G. purpureum	Wu 9310-45	AF441338	AF441338	Larsson & Larsson 2003
Gloeocystidiopsis flammea	CBS 324.66 (CBS)	AF506437	AF506437	Larsson & Larsson 2003
Gloeodontia columbiensis	NH 11118 (NH)	AF506444	AF506444	Larsson & Larsson 2003
G. discolor	KHL 10099	AF506445	AF506445	Larsson & Larsson 2003
G. eriobotryae	Dai 12080	JQ349116	JQ349103	Zhou & Dai 2013
G. pyramidata	Ryvarden 15502 (LR)	AF506446	AF506446	Larsson & Larsson 2003
G. subasperispora	KHL 8695	AF506404	AF506404	Larsson & Larsson 2003
G. yunnanensis	CLZhao 10504	MN908252	MN908254	This study
G. yunnanensis	CLZhao 11058	MN908253	MN908255	This study
Gloeopeniophorella convolvens	KHL 10103	AF506435	AF506435	Larsson & Larsson 2003
Heterobasidion annosum	Korhonen 06129	KJ583211	KJ583225	Chen & Shen 2014
H. parviporum	Korhonen 04121	KJ583212	KJ583226	Chen & Shen 2014
Lactarius leonis	SJ 91016 (SJ)	AF506411	AF506411	Larsson & Larsson 2003
Lentinellus cochleatus	KGN 960928	AF506417	AF506417	Larsson & Larsson 2003
L. ursinus	EL 7397	AF506419	AF506419	Larsson & Larsson 2003
L. vulpinus	KGN 980825	AF347097	AF347097	Larsson *et al.* 2004
Megalocystidium luridum	KHL 8635	AF506473	AF506473	Larsson & Larsson 2003
Russula violacea	SJ 93009 (SJ)	AF506465	AF506465	Larsson & Larsson 2003
Sistotrema brinkmannii	NH 11412 (NH)	AF506473	AF506473	Larsson & Larsson 2003
S. coronilla	NH 7598 (NH)	AF506475	AF506475	Larsson & Larsson 2003
Stereum hirsutum	NH 7960 (NH)	AF506479	AF506479	Larsson & Larsson 2003

MrModeltest 2.3 (Nylander 2004) was used to determine the best-fit evolution model for each data set for Bayesian inference of the phylogeny (BI). BI was calculated with MrBayes 3.1.2 (Ronquist & Huelsenbeck 2003). Four Markov chains were run for 2 runs from random starting trees for 460,000 generations and trees were sampled every 100 generations. The first one-fourth of the generations was discarded as burn-in. A majority rule consensus tree of all remaining trees was calculated. Branches were considered as significantly supported if they received maximum

likelihood bootstrap (ML) >70%, maximum parsimony bootstrap (MP) >50%, or Bayesian posterior probability (PP) >0.95.

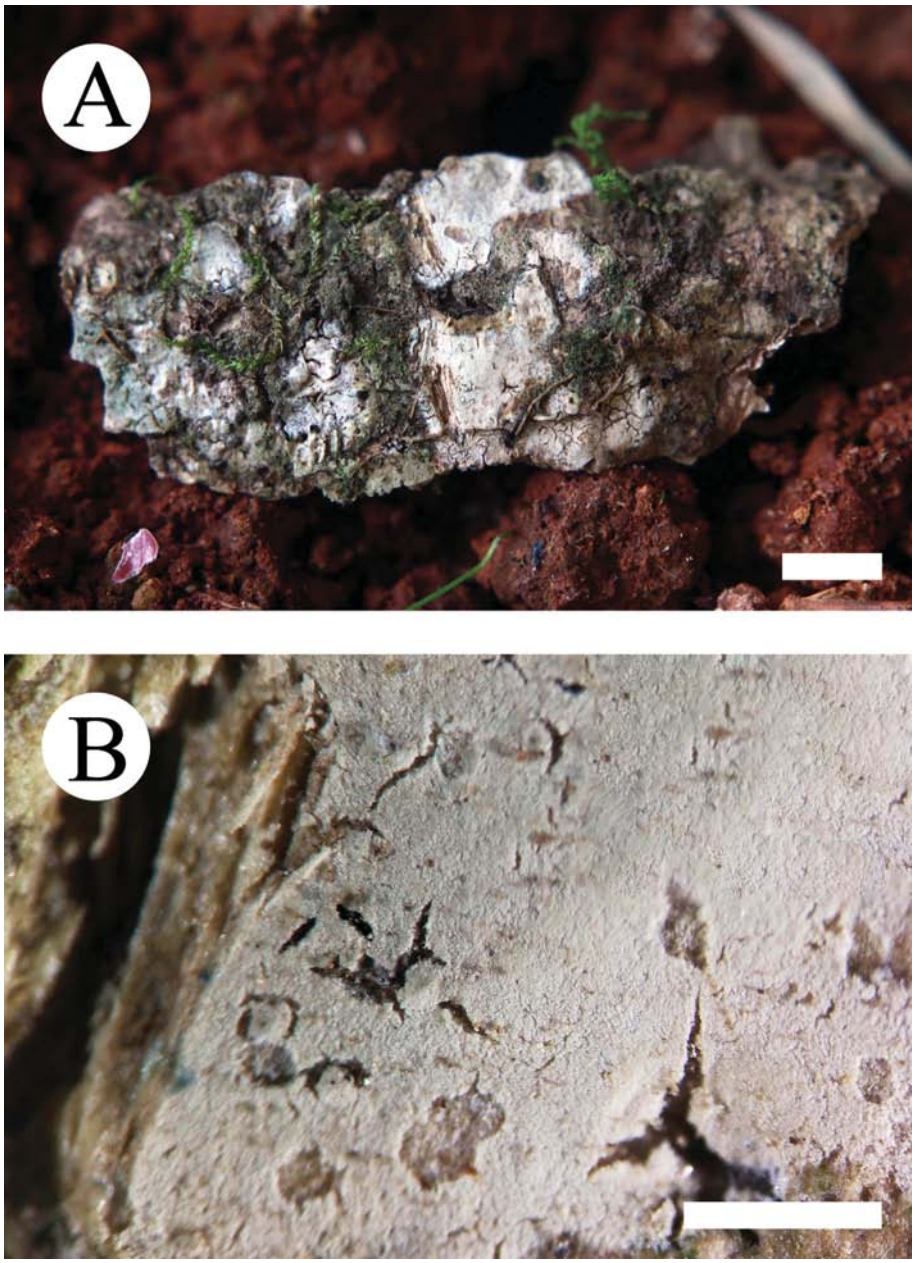

FIGURE 2. Basidiomata of *Gloeodontia yunnanensis* (holotype). Bars: A = 0.5 cm, B = 1 mm. Photos by: Changlin Zhao.

Results

Molecular phylogeny

The ITS+28S dataset included sequences from 32 fungal specimens and 31 species. The dataset had the aligned length of 1999 characters, of which 1303 characters are constant, 243 are variable and parsimony-uninformative, and 453 are parsimony-informative. Maximum parsimony analysis yielded 2 equally parsimonious trees (TL = 2058, CI = 0.4956, RI = 0.5506, RC = 0.2729, HI = 0.5044). Best model for the ITS+28S dataset estimated and applied in BI was GTR+I+G. Bayesian analysis and ML analysis resulted in a similar topology as MP analysis, with an average standard deviation of split frequencies in BI = 0.005526.

The phylogenetic tree (Fig. 1) revealed that the new species nested in the *Gloeodontia* clade and then formed a monophyletic lineage with a high support (100% BS, 100% BP and 1.00 BPP).

In addition, the results of BLAST queries in NCBI based on ITS and nLSU separately showed the sequences

producing significant alignments descriptions: in ITS blast results, the top one taxon is *Gloeodontia subasperispora* (Maximum record descriptions: Max score 523; Total score 523; Query cover 95%; E value 3e-144; Ident 83%). In nLSU blast results, the top one taxon is *G. subasperispora* (Maximum record descriptions: Max score 2281; Total score 2281; Query cover 98%; E value 0.0; Ident 96.85%).

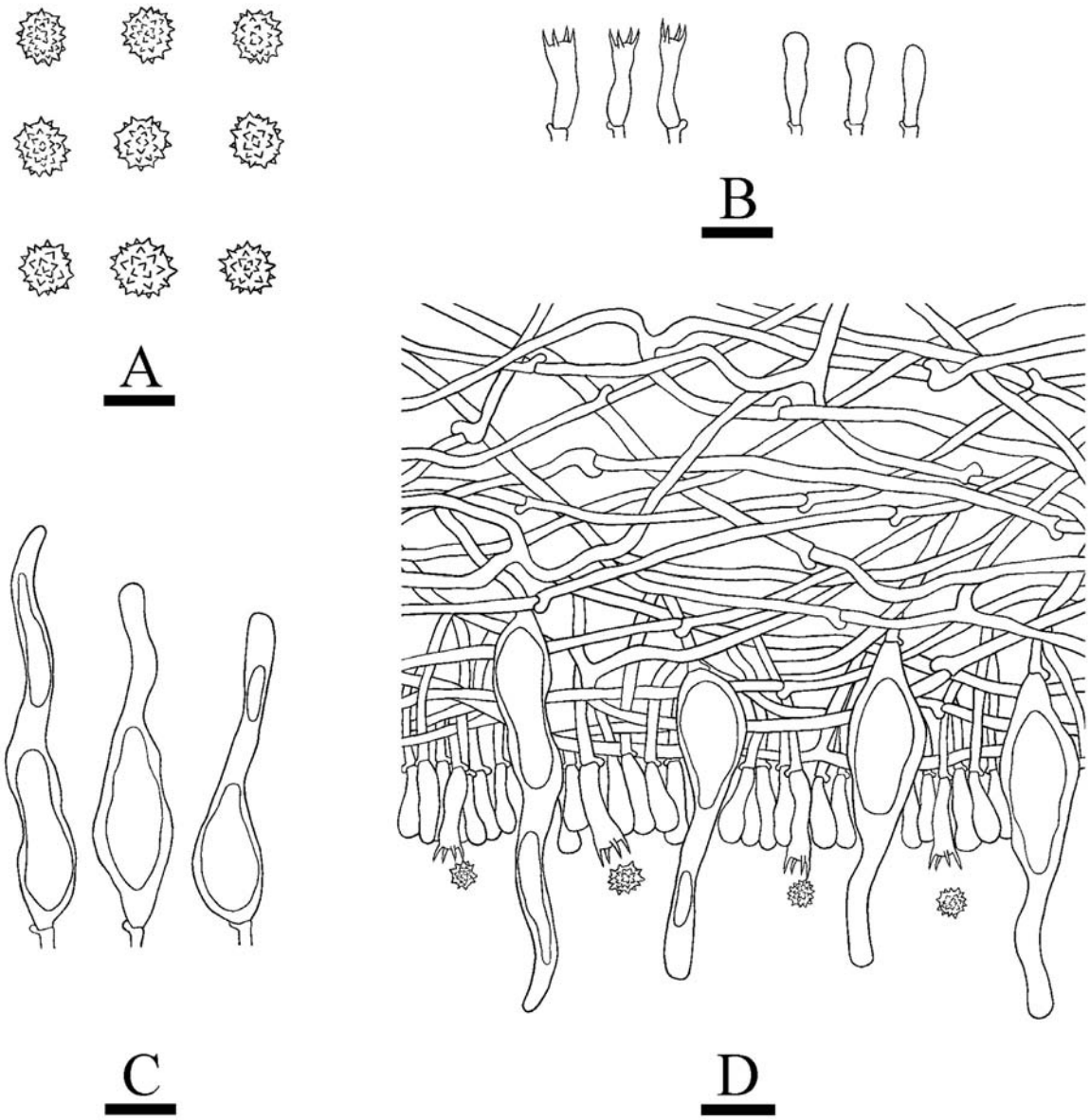

FIGURE 3. Microscopic structures of *Gloeodontia yunnanensis* (drawn from the holotype). a. Basidiospores. b. Basidia and basidioles. c. Cystida. d. A section of hymenium. Bars: a = 5 µm; b, c, d = 10 µm. Drawings by: Lu Chen.

Taxonomy

Gloeodontia yunnanensis C.L. Zhao *sp. nov*. (Figs. 2, 3)

Mycobank no.: MB 833888X

Holotype:—China. Yunnan Province: Dali, Nanjian County, Lingbaoshan National Forest Park, on angiosperm trunk, 10 January 2019, *CLZhao 10504* (SWFC).

Etymology:—the epithet refers to the locality (Yunnan Province) of the type specimens.

Description:—*Basidiomata* annual, effused, ceraceous, up to 8 cm long, 4 cm wide, 400–800 µm thick. Hymenial

surface smooth, cream to flesh pink when fresh, buff to brownish vinaceous upon drying. *Hyphal system* monomitic; generative hyphae with clamp connections, thin-walled, 1.5–2.5 µm in diameter, IKI–, CB–; tissues unchanged in KOH. *Hymenium* Gloeocystidia obclavate, widened in lower half and with flexuous-cylindrical apex, thin-walled, guttulate, 32–57 × 6–9 µm; basidia clavate, with four sterigmata and clamp connection at base, 9–14 × 3–4 µm, smooth, thin-walled; basidioles dominant, in shape similar to basidia, but slightly smaller. *Basidiospores* subglobose to globose, hyaline, thick-walled, asperulate, strongly amyloid, acyanophilous, 3.3–4.3 × 2.5–3.5 µm, L = 3.78 µm, W = 2.93 µm, Q = 1.22–1.38 (n = 60/2).

Additional specimen examined:—China. Yunnan Province: Wenshan, Xichou County, Xiaoqiaogou National Nature Reserve, on stump of angiosperm, 15 January 2019, *CLZhao 11058* (SWFC).

Discussion

Phylogenetically, Leal-Dutra *et al*. (2018) showed that 19 clades were found in the Russulales, in which eight clades were related to the *Gloeodontia* clade. According to our result based on the combined ITS+28S sequence data (Fig. 1), *G. yunnanensis* is nested in the *Gloeodontia* clade with strong support (100% BS, 100% BT, 1.00 BPP).

Gloeodontia yunnanensis belong to the common clade with other *Gloeodontia* species, for which sequences are available: *G. columbiensis* Burt ex Burds. & Lombard (1976: 17), *G. discolor* (Berk. & M.A. Curtis) Boidin (1966: 22), *G. eriobotryae* Y.C. Dai & L.W. Zhou (2013: 644), *G. pyramidata* (Berk. & M.A. Curtis) Hjortstam (1987: 58) and *G. subasperispora* (Litsch.) E. Larss. & K.H. Larss. Morphologically *G. yunnanensis* is different from other *Gloeodontia* species for which DNA data are available. *G. columbiensis* differs by having an odontioid hymenophore with white to pale yellowish hymenial surface and larger basidiospores (5.5–7 × 3.5–4.5 µm, Bernicchia & Gorjón 2010). *Gloeodontia discolor* differs in its hydnoid hymenophore with a white hymenial surface (Bresadola 1925). *Gloeodontia eriobotryae* differs from *G. yunnanensis* by having a dimitic hyphal system and encrusted cystidia (Zhou & Dai 2013). *Gloeodontia pyramidata* differs in its hydnoid hymenophore and larger basidiospores (5–6.5 × 4–5 µm, Hjortstam 1987). *Gloeodontia subasperispora* differs from *G. yunnanensis* by having reniform basidiospores (Litschauer 1941).

Among the species for which DNA data are not available *Gloeodontia americana* Rajchenb. (1987: 557) differs from *G. yunnanensis* in having larger basidiospores (6–7.5 × 4–4.5 µm, Hjortstam 1987). *Gloeodontia halocystidiata* Gorjón (2012: 43) differs in its odontioid hymenophore, a dimitic hyphal system and presence of halocystidia and encrusted skeletocystidia (Gorjón & Jesus 2012). *Gloeodontia xerophila* Tellería, M. Dueñas, Rodr.-Armas, Beltrán-Tej. & Melo (2008: 673) differs from *G. yunnanensis* in having a tuberculate to odontioid hymenophore and a dimitic hyphal system (Telleria *et al*. 2008).

Gloeodontia is a group of 'corticioid fungi' (Bernicchia & Gorjón 2010, Dai 2011), but only one species has been reported from China. Many recently described taxa of corticioid fungi from China were from subtropical and tropical areas (Zhao & Wu 2017, Shen *et al*. 2018, Cui *et al*. 2019, Liu *et al.* 2019, Luo *et al*. 2019, Wu *et al.* 2019). The new species in the present study, *Gloeodontia yunnanensis*, is also from the subtropics. It is possible that new taxa will be found after further investigations.

Acknowledgements

The research was supported by the National Natural Science Foundation of China (Project No. 31700023), and Yunnan Agricultural Foundation Projects (2017FG001-042), and the Science Foundation of Southwest Forestry University (Projects No. 111715, QN201904) and Biodiversity Survey, Observation and Assessment Program (2019–2023) of Ministry of Ecology and Environment of China (Project No. 1963049). We thank the two anonymous reviewers for their suggestions and corrections to improve our study.

References

Bernicchia, A. & Gorjón, S.P. (2010) *Fungi Europaei 12: Corticiaceae s.l.* Edizioni Candusso, Lomazzo, pp. 1–1007.

Boidin, J. (1966) Basidiomycètes Auriscalpiaceae de la république Centrafricaine. *Cahiers de la Maboké* 4: 18–25.

Bresadola, G. (1925) New species of fungi. *Mycologia* 17: 68–77.
https://doi.org/10.1080/00275514.1925.12020457

Burdsall, H.H. & Lombard, F.F. (1976) The genus *Gloeodontia* in North America. *Memoirs of the New York Botanical Garden* 28: 16–31.

Chen, J.J. & Shen, L.L. (2014) *Amylosporus succulentus* sp. nov. (Russulales, Basidiomycota) evidenced by morphological characters and phylogenetic analysis. *Cryptogamie Mycologie* 35: 271–282.
https://doi.org/10.7872/crym.v35.iss3.2014.271

Cui, B.K., Li, H.J., Ji, X., Zhou, J.L., Song, J., Si, J., Yang, Z.L. & Dai, Y.C. (2019) Species diversity, taxonomy and phylogeny of Polyporaceae (Basidiomycota) in China. *Fungal Diversity* 97: 137–392.
https://doi.org/10.1007/s13225-019-00427-4

Dai, Y.C. (2011) A revised checklist of corticioid and hydnoid fungi in China for 2010. *Mycoscience* 52: 69–79.
https://doi.org/10.1007/S10267-010-0068-1

Dai, Y.C. (2012) Polypore diversity in China with an annotated checklist of Chinese polypores. *Mycoscience* 53: 49–80.
https://doi.org/10.1007/s10267-011-0134-3

Felsenstein, J. (1985) Confidence intervals on phylogenetics: an approach using bootstrap. *Evolution* 39: 783–791.
https://doi.org/10.1111/j.1558-5646.1985.tb00420.x

Gorjón, S.P. & Jesus, M.A. (2012) Some new species and new records of corticioid fungi (Basidiomycota) from the Brazilian Amazon. *Phytotaxa* 67: 38–54.
https://doi.org/10.11646/phytotaxa.67.1.3

Hall, T.A. (1999) BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acids Symposium Series* 41: 95–98.

Hjortstam, K. (1987) A check-list to genera and species of corticioid fungi (Hymenomycetes). *Windahlia* 17: 55–85.

Larsson, E. & Larsson, K.H. (2003) Phylogenetic relationships of russuloid basidiomycetes with emphasis on aphyllophoralean taxa. *Mycologia* 95: 1037–1065.
https://doi.org/10.1080/15572536.2004.11833020

Larsson, E. & Hallenberg, N. (2001) Species delimitation in the *Gloeocystidiellum porosum-clavuligerum* complex inferred from compatibility studies and nuclear rDNA sequence data. *Mycologia* 93: 907–914.
https://doi.org/10.1080/00275514.2001.12063225

Larsson, K.H., Larsson, E. & Kóljal, U. (2004) High phylogenetic diversity among corticioid homobasidiomycetes. *Mycological Research* 108: 83–100.
https://doi.org/10.1017/S0953756204000851

Leal-Dutra, C.A., Neves, M.A., Griffith, G.W., Reck, M.A., Clasen, L.A. & Dentinger, B.T.M. (2018) Reclassification of *Parapterulicium* Corner (Pterulaceae, Agaricales), contributions to Lachnocladiaceae and Peniophoraceae (Russulales) and introduction of *Baltazaria* gen. nov. *MycoKeys* 37: 39–56.
https://doi.org/10.3897/mycokeys.37.26303

Litschauer, V. (1941) Neue Schwedische Corticieen aus dem Herbar L. Romell's. *Annales Mycologici* 39: 117–135.

Liu, X.F., Shen, S. & Zhao, C.L. (2019) Morphological and molecular identification of a new species of *Eichleriella* (Auriculariales, Basidiomycota) in China. *Phytotaxa* 404: 245–254.
https://doi.org/10.11646/phytotaxa.404.6.3

Luo, K.Y., Ma, X. & Zhao, C.L. (2019) *Neofavolus yunnanensi*s sp. nov. (Polyporales, Basidiomycota) from China: evidence from morphology and DNA sequence data. *Phytotaxa* 408: 109–116.
https://doi.org/10.11646/phytotaxa.408.2.3

Miller, M.A., Holder, M.T., Vos, R., Midford, P.E., Liebowitz, T., Chan, L., Hoover, P. & Warnow, T. (2009) The CIPRES portals. CIPRES. Availalble from: http://www.phylo.org/sub_sections/portal (accessed 4 April 2009) [Archived by WebCite(r) at: http://www.webcitation.org/5imQlJeQa]

Nylander, J.A.A. (2004) *MrModeltest v2. Program distributed by the author*. Evolutionary Biology Centre, Uppsala University.

Rajchenberg, M. (1987) Type studies of Polyporaceae (Aphyllophorales) described by J. Rick. *Nordic Journal of Botany* 7: 553–568.
https://doi.org/10.1111/j.1756-1051.1987.tb02023.x

Rogers, D.P. (1935) Notes on the lower basidiomycetes. U*niversity of Iowa Studies in Natural History* 17:1–43.

Ronquist, F. & Huelsenbeck, J.P. (2003) MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* 19: 1572–1574.
https://doi.org/10.1093/bioinformatics/btg180

Shen, S., Ma, X., Xu, T.M. & Zhao, C.L. (2018) *Phlebia ailaoshanensis* sp. nov. (Polyporales, Basidiomycota) evidenced by morphological

characters and phylogenetic analyses. *Phytotaxa* 373: 184–196.
https://doi.org/10.11646/phytotaxa.373.3.2

Shen, L.L., Wang, M., Zhou, J.L., Xing, J.H., Cui, B.K. & Dai,Y.C. (2019) Taxonomy and phylogeny of *Postia*. Multi-gene phylogeny and taxonomy of the brown-rot fungi: *Postia* and its related genera. *Persoonia* 42: 101–126.
https://doi.org/10.3767/persoonia.2019.42.05

Swofford, D.L. (2002) PAUP*: phylogenetic analysis using parsimony (*and other methods). Version 4.0b10. Sinauer Associates, Massachusetts.

Telleria, M.T., Dueñas, M., Beltrán-Tejera, E., Rodríguez-Armas, J.L. & Melo, I. (2008) *Gloeodontia xerophila* (Aphyllophorales, Basidiomycota), a new species with corticioid basidioma from the Canary Islands. *Mycologia* 100: 673–676.
https://doi.org/10.3852/07-200R1

White, T.J., Bruns, T., Lee, S. & Taylor, J. (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis, M.A., Gelfand, D.H., Sninsky, J.J. & White, T.J. (Eds.) *PCR protocols: A guide to methods and applications*. Academic Press, San Diego, pp. 315–322.
https://doi.org/10.1016/B978-0-12-372180-8.50042-1

Wu, Y.X., Shen, S. & Zhao, C.L. (2019) *Podoscypha yunnanensis* sp. nov. (Polyporales, Basidiomycota) evidenced by morphological characters and phylogenetic analyses. *Phytotaxa* 387: 210–218.
https://doi.org/10.11646/phytotaxa.387.3.2

Zhao, C.L. & Wu, Z.Q. (2017) *Ceriporiopsis kunmingensis* sp. nov. (Polyporales, Basidiomycota) evidenced by morphological characters and phylogenetic analysis. *Mycological Progress* 16: 93–100.
https://doi.org/10.1016/j.myc.2013.11.006

Zhou, L.W. & Dai, Y.C. (2013) Taxonomy and phylogeny of wood-inhabiting hydnoid species in Russulales: two new genera, three new species and two new combinations. *Mycologia* 105: 636–649.
https://doi.org/10.3852/12-011