Table of Contents

Article

Gloeoendontia yunnanensis sp. nov. (Russulales, Basidiomycota) from China, evidenced by morphological characters and phylogenetic analyses
LU CHEN, ZHE-NING SHI, CHUN-HUA WU, CHANG-LIN ZHAO

Akanthomyces neolecoteraeorum, a new verticillium-like species
YAN-HAO CHEN, YAN-FENG HAN, JIAN-DONG LIANG, ZONG-QI LIANG

Nepenthes fractiflora (Nepenthaceae), a new Bornean pitcher plant exhibiting concave-lobed metapoty and a high degree of axillary bud activation
MICHAL R. GOLOŚ, ALASTAIR S. ROBINSON, MARC BARER, MARTIN DANČÍK, JEAN DE WITTE, ADRIEN LIMBERG, NOORHANA BINTI MOHD SAPAWI, WEWIN TIIASMANTO

Typifications, a new synonym and new distribution data in Ficaria (Ranunculaceae)
BEATA PASZKO, WOJCIECH PAUL, AGNIESZKA NIKEL, LUCYNA MUSIĄŁ

Stanhopinnae Mesoamericanae VI. On the identity of Polycycnis barbata (Orchidaceae), and other notes on the genus Polycycnis
GUENTER GERLACH, FRANCO PUPULIN

A New Aerophilic Neidiium Pilsteri (Nelidiaceae, Bacillariophyta) species from Guangxi Zhuang Autonomous Region, China
YAN LIU, JOHN PATRICK KOCIOLEK, QI LIU, XIANG TAN, YAWEN FAN

Plutos kovaljovi (Plutoaceae, Agaricostlos), a new species in section Collulodorma
HANA ŠEVČÍKOVÁ, PIERRE-ARTHUR MOREAU, JAN BOROVÍČKA

Lectotypification of the name Chenopodium hirsutum, a wild relative of the pseudocereal crop species C. quinoa (Chenopodiaceae)
SERGEI L. MOSYAKIN, IRINA V. SOKOLOVA

A new species of Calea (Neuralean, Astereaceae) from the Espinhaço Range, Minas Gerais, Brazil
GENILSON ALVES DOS REIS E SILVA, JIMI NAOKI NAKAJIMA

Plastome data provide insights into intra and interspecific diversity and rpd gene loss in Capparis (Capparaceae)
SATISH MAURYA, ASHWINI M. DARSHETKAR, MANDAR N. DATAR, SHUBHADA TAMHANKAR, PAN LI, RITESH KUMAR CHOUHARY

Correspondance

Second-step lectotypification of the name Wurmaia mansonii, the basionym of Dilleria mansonii (Dilleniaceae)
SATISH MAURYA, SARANG A. BOKIL, ASHWINI M. DARSHETKAR, MANDAR N. DATAR, RITESH KUMAR CHOUHARY
Gloeodontia yunnanensis sp. nov. (Russulales, Basidiomycota) from China, evidenced by morphological characters and phylogenetic analyses

LU CHEN², ZHENG-JUN SHI³, CHUN-HUA WU³ & CHANG-LIN ZHAO¹²³*
¹Key Laboratory for Forest Resources Conservation and Utilization in the Southwest Mountains of China, Ministry of Education, Southwest Forestry University, Kunming 650224, P.R. China.
²College of Biodiversity Conservation, Southwest Forestry University, Kunming 650224, P.R. China.
³School of Chemical Engineering, Southwest Forestry University, Kunming 650224, P.R. China.
*Corresponding author: fungichanglin@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.
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.

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

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
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%).


**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* 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**

GLOEODONTIA YUNNANENSIS SP. NOV. FROM CHINA

Phytotaxa 432 (2) © 2020 Magnolia Press • 117


https://doi.org/10.1080/00275514.1925.12020457


https://doi.org/10.7872/crym.v35.iss3.2014.271

https://doi.org/10.1007/s13225-019-00427-4

https://doi.org/10.1007/S10267-010-0068-1

https://doi.org/10.1007/S10267-011-0134-3

https://doi.org/10.1111/j.1558-5646.1985.tb00420.x

https://doi.org/10.11646/phytotaxa.67.1.3


https://doi.org/10.1080/15572536.2004.11833020

https://doi.org/10.1080/00275514.2001.12063225

https://doi.org/10.1017/S0953756204000851

https://doi.org/10.3897/mycokeys.37.26303


https://doi.org/10.11646/phytotaxa.404.6.3

https://doi.org/10.11646/phytotaxa.408.2.3


https://doi.org/10.1111/j.1756-1051.1987.tb02023.x


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
https://doi.org/10.11646/phytotaxa.373.3.2

https://doi.org/10.3767/persoonia.2019.42.05


https://doi.org/10.3852/07-200R1

https://doi.org/10.1016/B978-0-12-372180-8.50042-1

https://doi.org/10.11646/phytotaxa.387.3.2

https://doi.org/10.1016/j.myc.2013.11.006

https://doi.org/10.3852/12-011