Type locality of *Coronosporidium ecuadorianum* gen. & sp. nov.  
(Sosa & al.— Fig. 1, p. 112)
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VOLUME ONE HUNDRED THIRTY-FOUR (1) — TABLE OF CONTENTS

Nomenclatural novelties .......................................................... vii
Errata ......................................................................................... viii
Reviewers .................................................................................... ix
2019 submission procedure .......................................................... x
From the Editor .......................................................................... xi

History & Nomenclature
North American mycology comes of age:
the 19th century participants and their roles Ronald H. Petersen 1

Taxonomy
Coronosporidium ecuadorianum gen. & sp. nov.
from submerged decaying leaf from Ecuador Daynet Sosa,
Adela Quevedo, Fernando Espinoza, Lizette Serrano,
Freddy Magdama, Marcos Vera, Simón Pérez-Martinez,
Elaine Malosso, Rafael F. Castañeda-Ruiz 111

Trichoglossum tetrasporum, newly recorded from India
Sanjit Debnath, Kripamoy Chakraborty,
Badal Kumar Datta, Panna Das, Ajay Krishna Saha 119

Perenniporia mopanshanensis sp. nov. from China
Chang-Lin Zhao & Xiang Ma 125

New records of Bilimbia and Toninia from China Mei-jie Sun,
Shu-kun Yan, Rong Tang, Chun-xiao Wang, Lu-lu Zhang 139

Anamylopsora altaica sp. nov. from Northwestern China
Parida Ahat, Anwar Tumur, Shou-Yu Guo 147

Four Pyrenula species new to China Jie-Meng Fu, André Aptroot,
Zhong-Liang Wang, Lu-Lu Zhang 155

Spadicoides matsushimae sp. nov., and
Anisospadicoides gen. nov. for two atypical Spadicoides species
Min Qiao, De-Wei Li, Ze-Fen Yu, Kai Zhang, Rafael F. Castañeda-Ruiz 161

New records of Hymenoscyphus, Parascutellinia, and
Scutellinia for Turkey Ali Keleş 169

Lemonniera yulongensis sp. nov. from Yunnan, China
Ze-fen Yu, Yi-fan Lv, Bo Feng, Min Qiao 177
Contributions to species of Xylariales in China—2.  
Rosellinia pervariabilis and R. tetrastigmae spp. nov.,  
and a new record of R. caudata  
Xin Xie, Lili Liu, Xu Zhang, Qingde Long, Xiangchun Shen,  
Saranyaphat Boonmee, Jichuan Kang, Qirui Li 183  

Catalog of *Penicillium* spp. causing blue mold on  
bulbs, roots, and tubers  
Frank M. Dugan & Carl A. Strausbaugh 197  

*Sulzbacheromyces yunnanensis*, a new record for Thailand  
Nakarin Suwannarach, Jaturong Kumla, Kanitta Satienperakul,  
Witchaphart Sungpalee, Sutheera Hermhuk, Piyawan Suttiprapan,  
Kriangsak Sri-Ngernyum & Saisamorn Lumyong 215  

Mycobiota (Funga) new to the Mycotaxon website  
A checklist of the non-gilled fleshy fungi (*Basidiomycota*)  
of Kerala State, India (summary)  
T.K. Arun Kumar, Anjitha Thomas,  
Krishnapriya Kuniyil, Salna Nanu, Vinjusha Nellipunath 221
Nomenclatural novelties and typifications proposed in Mycotaxon 134(1)

Anamylopsora altaica Ahat, A. Abbas, S.Y. Guo & Tumur
[FN 570571], p. 150

Anisospadicoides R.F. Castañeda, Qiao & Z.F. Yu
[MB 827953], p. 162

Anisospadicoides macrocontinua (Matsush.) R.F. Castañeda, Qiao & Z.F. Yu
[MB 827954], p. 165

Anisospadicoides macroobovata (Matsush.) Qiao, Z.F. Yu & R.F. Castañeda
[MB 827955], p. 165

Coronosporidium R.F. Castañeda, Quevedo & D. Sosa
[IF 554557], p. 113

Coronosporidium ecuadorianum R.F. Castañeda, Quevedo & D. Sosa
[IF 554558], p. 113

Lemonniera yulongensis Z.F. Yu
[MB 827810], p. 178

Perenniporia mopanshanensis C.L. Zhao
[MB 827580], p. 132

Rosellinia pervariabilis Q.R. Li & J.C. Kang
[MB 827512], p. 188

Rosellinia tetrastigmae Q.R. Li & J.C. Kang
[MB 828157], p. 190

Spadicoides matsushimae R.F. Castañeda & D.W. Li
[MB 809530], p. 165
Errata from previous volumes

Volume 133(2)
Front cover, bottom line  FOR:  133(#)  READ:  133(2)

Volume 133(4)
p. 729, line 3 (masthead)  FOR:  pp. 729  READ:  p. 729
Back cover (online edition only):
   REPLACE single bottom line by
   (Kaur & al.—Figs 2,3; p. 678)
   Maninder Kaur, ARTIST
Back cover (printed hard copy only): after bottom line
   ADD:  Maninder Kaur, ARTIST
The Editors express their appreciation to the following individuals who have, prior to acceptance for publication, reviewed one or more of the papers prepared for this issue.

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Dinushani Anupama Daranagama
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2019 Mycotaxon submission procedure

Prospective Mycotaxon authors should download the Mycotaxon 2019 guide, review & submission forms, and Mycotaxon sample manuscript by clicking the ‘file download page’ link on our Instructions to Authors page before preparing their manuscript. This page briefly summarizes our ‘4-step’ submission process.

1—Peer review: Authors first contact peer reviewers (two for journal papers; three for mycobiota/fungae) before sending them formatted text & illustration files and the appropriate 2019 Mycotaxon journal or weblist reviewer comment form. Experts return revisions & comments to both the Editor-in-Chief <editor@mycotaxon.com> and authors. All co-authors must correct and proof-read their files before submitting them to the Nomenclature Editor.

2—Nomenclatural review: Authors email all error-free text & illustration files to the Nomenclature Editor <PennycookS@LandcareResearch.co.nz>. Place first author surname + genus + ‘Mycotaxon’ on the subject line, and (required) attach a completed submission form. The Nomenclature Editor will (i) immediately assign the accession number and (ii) after a few weeks return his notes and suggested revisions to the author(s) and Editor-in-Chief.

3—Final submission: All coauthors thoroughly revise and proof-read files to prepare error-free text and images ready for immediate publication. Poorly formatted copy will be rejected or returned for revision. They email the final manuscript to the Editor-in-Chief <editor@mycotaxon.com>, adding the accession number to the message and all files, which include a (i) revised 2019 submission form, all (ii) text files and (iii) jpg images, and (iv) FN, IF, or MB identifier verifications for each new name or typification. The Editor-in-Chief acknowledges submissions within two weeks of final submission but requests authors to wait at least 14 days before sending a follow-up query (without attachments).

4—Final editorial review & publication: The Editor-in-Chief conducts a final grammatical and scientific review and returns her editorial revisions to all expert reviewers and coauthors for final author approval. Author-approved files are placed in the publication queue.

The PDF proof and bibliographic & nomenclatural index entries are sent to all coauthors for final inspection. After PDF processing, the Editor-in-Chief corrects only PDF editorial/conversion and index entry errors; corrections of all other errors are listed in the Errata of a subsequent issue for no charge. Authors will pay fees for mycobiota uploads, optional open access, and correction of major author errors to the Business Manager <subscriptions@mycotaxon.com> at this time.

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The Mycotaxon journal publishes four quarterly issues per year. Both open access and subscription articles are offered.
From the Editor-in-Chief

On time! (for a change)—Loyal Mycotaxon authors and readers are undoubtedly weary of the constant stream of editorial apologies following yet another issue released 1–2 months after the end of a March, June, September, or December quarter. We are equally tired of apologizing to you. Thus it is with immense pleasure that we announce the release of Mycotaxon 134(1) in March! To ensure future timely journal delivery, we [i] urge authors to send their manuscripts to the Editor-in-Chief immediately after receiving their final review from the Nomenclature Editor and [ii] set a June 15 closure deadline for 134(2), the 2019 April–June issue. Submissions received after that date will be scheduled for the following (July–September) issue.

Mycotaxon 134(1) presents 14 papers by 64 authors representing 10 countries and peer reviewed by 30 expert reviewers. The issue opens with Ronald H. Petersen's 110-page lively and welcome historical treatise on 19th century mycologists in North America. This provides us the opportunity to introduce two new journal divisions—History & Nomenclature and Taxonomy—to supplant our former ‘Research papers’ designation. [“Biodiversity & ecology” still find their home under the Mycobiota/Fungae summaries of papers posted on the Mycotaxon website, here announcing a checklist of fleshy non-gilled fungi from Kerala uploaded in February.]

The 2019 January–March Mycotaxon also proposes two new genera (Anisospadicoides with two species from Peru and Coronosporidium from Ecuador) and seven species new to science representing Anamylopsora, Lemonniera, Perenniporia, and Rosellinia from China; Coronosporidium from Ecuador; and Spadicoides from Peru.

New species range extensions represent ascomycetes Hymenoscyphus, Parascutellinia, and Scutellinia for Turkey and Trichoglossum for India, ascolichens Bilimbia, Pyrenula, Toninia for mainland China, and the basidiolichen Sulzbacheromyces for Thailand.

Plant pathologists especially will welcome the paper covering Penicillium causing blue mold on bulbs, roots, and tubers that tabulates where to find references to descriptions, culture methodologies, phylogenies, and hosts for each species.

Warm regards,

Lorelei Norvell (Editor-in-Chief)

22 March 2019
Anisospadicoides macrocontinua gen. & sp. nov.  
(Qiao & al.— Fig. 1, p. 163)  
RAFAEL F. CASTAÑEDA-RUIZ, artist
Perenniporia mopanshanensis sp. nov. from China

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Abstract—A new poroid, white-rot, wood-inhabiting fungal species, Perenniporia mopanshanensis, is proposed based on morphological and molecular characters. This species from Yunnan Province, China, is characterized by resupinate basidiomes with a cream to buff to straw pore surface, dimitic hyphal system with strongly dextrinoid, unbranched, interwoven skeletal hyphae, and ellipsoid, non-truncate basidiospores (5.5–6.5 × 4–5 µm) with hyaline, distinctly thick, smooth, strongly dextrinoid walls. Phylogenetic analyses of ITS+nLSU sequences showed that P. mopanshanensis is a distinct taxon in the Perenniporia sensu stricto clade and is sister to P. bannaensis.

Key words—molecular phylogenetics, Polyporaceae, taxonomy, Truncospora, wood-rotting fungi

Introduction

Perenniporia Murrill (Polyporaceae, Polyporales) is a large cosmopolitan genus characterized by poroid basidiomata with thick-walled, ellipsoid to distinctly truncate basidiospores that are cyanophilous and with variable dextrinoid reactions (Ryvarden 1991). The Perenniporia hyphal system is di- or trimitic: the generative hyphae with clamp connections and the skeletal hyphae with walls that are cyanophilous and variably dextrinoid (Decock & Stalpers 2006). About 100 species are accepted in the genus (Gilbertson & Ryvarden 1987; Hattori & Lee 1999; Núñez & Ryvarden 2001; Dai & al. 2002, 2011; Cui & al. 2007; Xiong & al. 2008; Choeyklin & al. 2009; Decock 2011, 2016; Zhao & al. 2013; Ryvarden & Melo 2014; Jang & al. 2015; Ji & al. 2017).
Recently, phylogenetic studies of *Perenniporia* based on sequences of the internal transcribed spacer (ITS) region and the large subunit nuclear ribosomal RNA gene (nLSU) have revealed several well-supported clades that could be recognized as distinct genera (Robledo & al. 2009, Zhao & al. 2013). Robledo & al. (2009) demonstrated that *Perenniporia* was phylogenetically related to *Abundisporus* Ryvarden, *Hornodermoporus* Teixeira, *Perenniporiella* Decock & Ryvarden, and *Truncospora* Pilát, while Zhao & al. (2013) have shown that *Perenniporia* itself is polyphyletic. Several new species of *Perenniporia* have been described based on ribosomal DNA sequences (Zhao & Cui 2013, Jang & al. 2015, Ji & al. 2017)

During research on polypore diversity in southern China, an undescribed species of *Perenniporia* was found. We present morphological and molecular phylogenetic evidence that support the recognition of *P. mopanshanensis* as a new species.

**Materials & methods**

The specimens studied are deposited at the herbarium of Southwest Forestry University, Kunming, China (SWFC). Basidiomatal descriptions are based on field notes. Special colour terms follow Petersen (1996). Anatomical observations were obtained from the dried specimens and made using a light microscope following Dai (2010). The following abbreviations were used: KOH = 5% potassium hydroxide, CB = cotton blue, CB– = acyanophilous, IKI = Melzer’s reagent, IKI– = both inamyloid and non-dextrinoid, L = mean spore length (arithmetic average of all spores), 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.

The Omega EZNA HP Fungal DNA Kit was used to obtain genomic DNA from dried specimens according to the manufacturer’s instructions with some modifications. A 30 mg sample from a dried fungal specimen was ground to powder with liquid nitrogen. The powder was transferred to a 1.5 ml centrifuge tube, suspended in 0.4 ml of lysis buffer, and incubated in a 65°C water bath for 60 min. After that, 0.4 ml phenol-chloroform (24:1) was added to each tube, and the suspension was shaken vigorously. After centrifugation at 13,000 rpm for 5 min, 0.3 ml supernatant was transferred to a new tube and mixed with 0.45 ml binding buffer. This mixture was transferred to an adsorbing column (AC) for centrifugation at 13,000 rpm for 0.5 min. Then, 0.5 ml inhibitor removal fluid was added in AC for a centrifugation at 12,000 rpm for 0.5 min. After washing twice with 0.5 ml washing buffer, the AC was transferred to a clean centrifuge tube, and 100 ml elution buffer was added to the middle of adsorbed film to elute the genomic DNA. ITS region was amplified with primer pairs ITS5 and ITS4 (White & al. 1990). Nuclear LSU region was amplified with primer pairs LR0R and LR7 (http://www.biology.duke.edu/fungi/mycolab/primers.htm). The ITS region
was amplified by initial denaturation at 95°C for 3 min, then 35 cycles of 94°C for 40 s, 58°C for 45 s, and 72°C for 1 min with a final extension of 72°C for 10 min. The nLSU region was amplified by initial denaturation at 94°C for 1 min, then 35 cycles at 94°C for 30 s, 48°C for 1 min, and 72°C for 1.5 min, ending with a final extension of 72°C for 10 min. 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).

<table>
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<th>Species name</th>
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<td>Robledo &amp; al. 2009</td>
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<td>Cui 3643, FJ613655, AY336753</td>
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<td><em>T. ochroleuca</em></td>
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<td><em>Vanderbylia &quot;delavayi&quot;</em></td>
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<td><em>V. vicina</em></td>
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<td>Robledo &amp; al. 2009</td>
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</table>
Sequencher 4.6 (GeneCodes, Ann Arbor, MI, USA) was used to edit the DNA sequence. Sequences were aligned in MAFFT 7 using the "G-INS-I" strategy (https://mafft.cbrc.jp/alignment/server/index.html) and manually adjusted in BioEdit (Hall 1999). The sequence alignment was deposited in TreeBase (submission ID 22900). Donkioporia expansa (Desm.) Kotl. & Pouzar and Pyrofomes demidoffii (Lév.) Kotl. & Pouzar were used as outgroup to root trees following Zhao & al. (2013) in the ITS+nLSU analyses.

ITS+nLSU sequence analyses were performed using maximum parsimony, maximum likelihood, and Bayesian inference methods. Maximum parsimony (MP) analyses followed Song & al. (2016), and tree construction was performed in PAUP* version 4.0b10 (Swofford 2002). All characters were equally weighted, with gaps treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1000 random sequence additions. Max-trees was set to 5000, branches of zero length were collapsed, and all parsimonious trees were saved. Clade robustness was assessed using bootstrap (BT) analysis with 1000 replicates (Felsenstein 1985). Tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI) were calculated for each Maximum Parsimonious Tree (MPT) generated. Sequences were analyzed using Maximum Likelihood (ML) with RAxML-HPC2 through the Cipres Science Gateway (www.phylo.org; Miller & al. 2009). Branch support (BS) for ML analysis was determined by 1000 bootstrap replicates.

MrModeltest 2.3 (Posada & Crandall 1998, Nylander 2004) was used to determine the best-fit evolution model for each data set for Bayesian inference (BI), which was calculated with MrBayes_3.1.2 using a general time reversible (GTR) model of DNA substitution and a gamma distribution rate variation across sites (Ronquist & Huelsenbeck 2003). Four Markov chains were run for 2 runs from random starting trees for 7 million generations (ITS+nLSU), and trees were sampled every 100 generations. The first 25% of the generations was discarded as burn-in. A majority rule consensus tree of all remaining trees was calculated. Branches that received bootstrap support for maximum likelihood (BS), maximum parsimony (BT), and Bayesian posterior probabilities (BPP) greater than or equal to 75% (BS, BT) and 0.95 (BPP) were considered significantly supported.

Molecular phylogeny

The ITS+nLSU dataset included sequences from 86 fungal specimens representing 46 species (Table 1). The dataset had an aligned length of 2100 characters, of which 1553 characters were constant, 86 variable and parsimony-uninformative, and 461 parsimony-informative. Maximum parsimony analysis yielded four equally parsimonious trees (TL = 1925, CI = 0.375, HI = 0.525, RI = 0.745, RC = 0.275). Best model for the ITS+nLSU dataset estimated and applied in the Bayesian analysis: GTR+I+G. Bayesian analysis and ML analysis produced similar topologies to MP analysis, with an average standard deviation of split frequencies = 0.006258 (BI).
Fig. 1. Maximum Parsimony strict consensus tree illustrating the phylogeny of *Perenniporia mopanshanensis* and related species in *Polyporales* based on ITS+nLSU sequences. Branches are labeled with maximum likelihood bootstrap >70%, parsimony bootstrap proportions >50% and Bayesian posterior probabilities >0.95.
The ITS+nLSU phylogeny places *Perenniporia mopanshanensis* in the *Perenniporia* sensu stricto clade (Fig. 1), where it forms a strongly supported monophyletic lineage (BS = 100%; BT = 100%; BPP = 1) and is sister to *P. bannaensis* B.K. Cui & C.L. Zhao.

**Taxonomy**

*Perenniporia mopanshanensis* C.L. Zhao, sp. nov. [Figs 2, 3]

Mycobank MB 827580

Differs from *Perenniporia luteola* by its larger pores, its smaller basidiospores, and its unbranched skeletal hyphae.

**Type**: China. Yunnan Province: Yuxi, Xinping county, Mopanshan National Forestry Park, on an angiosperm trunk, 19 August 2017, C.L. Zhao 2404 (Holotype, SWFC 002404; GenBank MH784911, MH784915).

**Etymology**: The specific epithet *mopanshanensis* (Lat.) refers to the locality (Mopanshan) of the type specimen.

**Basidiomata** perennial, resupinate, without odor or taste when fresh, becoming corky upon drying, ≤15 × 6 cm, 8 mm thick at center. Pore surface cream when fresh, cream to buff to straw upon drying; pores round, 3–5 per mm; dissepiments thin, entire. Sterile margin narrow, cream, ≤0.5 mm wide. Subiculum cream, thin, each layer ≤0.5 mm thick. Tubes cream to buff, corky, each layer ≤2 mm long.

**Hyphal structure** dimitic; generative hyphae with clamp connections; skeletal hyphae strong dextrinoid, CB+; tissues unchanged in KOH.

**Subiculum** generative hyphae infrequent, hyaline, thin-walled, unbranched, 2–3 µm in diam.; skeletal hyphae dominant, hyaline, thick-walled with a narrow to wide lumen, unbranched, interwoven, 2–3.5 µm in diam.

**Tube** generative hyphae infrequent, hyaline, thin-walled, unbranched, 1.5–3 µm in diam.; skeletal hyphae dominant, hyaline, thick-walled with a narrow to wide lumen, unbranched, interwoven, 2–3.5 µm. Plenty of crystals present among hyphae. Cystidia absent, fusoid cystidioles present, hyaline, thin-walled, 13–19 × 4.5–6.5 µm; basidia barrel-shaped to clavate, with four sterigmata and a basal clamp connection, 14–20 × 7–12 µm; basidioles dominant, mostly pear-shaped, but slightly smaller than basidia.

**Basidiospores** ellipsoid, non-truncate, hyaline, distinctly thick-walled, smooth, strong dextrinoid, CB+, (5–)5.5–6.5(–7) × 4–5(–5.5) µm, L = 6.15 µm, W = 4.6 µm, Q = 1.35–1.42 (n = 120/4).

**Type of rot**: white rot.

Additional specimens examined: CHINA. YUNNAN PROVINCE. Yuxi: Xinping county, Mopanshan National Forestry Park, on the angiosperm trunk, 19 August 2017,
Discussion

The new species, *Perenniporia mopanshanensis*, is supported by phylogenetic analyses and morphological characters. In the ITS+nLSU analyses (Fig. 1), it forms a strongly supported monophyletic lineage (BS = 100%; BT = 100%; BPP = 1) where it forms a clade with *P. bannaensis*. However, morphologically *P. bannaensis* differs from *P. mopanshanensis* by its annual basidiocarps with buff-yellow to pinkish buff pore surface and smaller pores (6–8 per mm; Zhao & al. 2013).

Morphologically, the presence of non-truncate basidiospores is shared by several other species in *Perenniporia* sensu stricto: *P. africana* Ipulet & Ryvarden, *P. ellipsospora* Ryvarden & Gilb., *P. koreana* Y. Jang & J.J. Kim, *P. luteola* B.K. Cui & C.L. Zhao, *P. rhizomorpha* B.K. Cui & al., and *P. subacida* (Peck) Donk. A morphological comparison between *P. mopanshanensis* and these six species is presented in Table 2.
Polypores are an extensively studied group in *Basidiomycota* (Gilbertson & Ryvarden 1987, Núñez & Ryvarden 2001, Ryvarden & Melo 2014), but Chinese polypore diversity is still not well known, especially in the subtropics and tropics. The new species, *Perenniporia mopanshanensis*, was found in the Chinese subtropics, where many new taxa in the *Polyporales* and *Hymenochaetales* have
Table 2. A comparison of Perenniporia species with non-truncate basidiospores

<table>
<thead>
<tr>
<th>Species</th>
<th>Habit</th>
<th>Pore surface</th>
<th>Pores / mm</th>
<th>Spores (µm)</th>
<th>Skeletal hyphae</th>
<th>Reference</th>
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<tbody>
<tr>
<td>africana</td>
<td>Annual</td>
<td>Pale orange to brown</td>
<td>6–8</td>
<td>4–5 × 3–4</td>
<td>Branched</td>
<td>Ipulet &amp; Ryvarden 2005</td>
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<tr>
<td>ellipsospora</td>
<td>Annual</td>
<td>Whitish to pale yellowish brown</td>
<td>3–4</td>
<td>4–5.5 × 3–4</td>
<td>Unbranched</td>
<td>Gilbertson &amp; Ryvarden 1987</td>
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<tr>
<td>koreana</td>
<td>Annual</td>
<td>Grayish orange</td>
<td>5–6</td>
<td>6–7 × 3.9–5.2</td>
<td>Rarely branched</td>
<td>Jang &amp; al. 2015</td>
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<td>luteola</td>
<td>Perennial</td>
<td>Buff-yellow</td>
<td>4–6</td>
<td>6–7 × 5–5.5</td>
<td>Frequently branched</td>
<td>Zhao &amp; Cui 2013</td>
</tr>
<tr>
<td>mopanshanensis</td>
<td>Perennial</td>
<td>Cream, buff to straw</td>
<td>3–5</td>
<td>5.5–6.5 × 4–5</td>
<td>Unbranched</td>
<td>This study</td>
</tr>
<tr>
<td>rhizomorpha</td>
<td>Annual</td>
<td>Yellow-buff to yellowish orange</td>
<td>4–6</td>
<td>5.3–6.5 × 4.1–5.2</td>
<td>Branched</td>
<td>Cui &amp; al. 2007</td>
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<tr>
<td>subacida</td>
<td>Perennial</td>
<td>Ivory to yellowish</td>
<td>5–6</td>
<td>4.5–6 × 3.5–4.5</td>
<td>Unbranched</td>
<td>Decock &amp; Stalpers 2006</td>
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</tbody>
</table>

been described (Cui & Dai 2008; Cui & al. 2009, 2010, 2011; Du & Cui 2009; Li & Cui 2010; He & Li 2011; Jia & Cui 2011; Yu & al. 2013; Yang & He 2014; Chen & al. 2015). We anticipate that additional polypore taxa will be found in China after further investigation and molecular analysis.

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