Article

Insight into the Taxonomic Resolution of the Pleosporalean Species Associated with Dead Woody Litter in Natural Forests from Yunnan, China

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Abstract: In the course of investigating the systematics of woody litter micromycete associates in Yunnan Province, China, we found one new species in Phaeocephalaceae, one new genus and three new species in Sulcatisporaceae from 16 specimens collected (ten collections of ascomycetes telemorphs, four collections of hyphomycetes and two collections of coelomycetes anamorphs) from Ailaoshan, Chuxiong, Diqing, Honghe, Kunming, Lancang, Mengla and Yuxi in Yunnan Province. These taxonomic novelties were recognized with the aid of morphological comparisons and phylogenetic analyses of multiple gene sequences (non-translated loci and protein-coding regions). Pleosporalea menglaense sp. nov. is accommodated in Phaeocephalaceae (Pleosporales) based on its hyphomycetous anamorph, which is characterized by superficial sporodochia on the host surface, macronematous, mononematous, cylindrical, unbranched, aspartate, hyaline and smooth-walled conidiophores, monoblastic, terminal, hyaline conidiogenous cells, hyaline, muriform conidia, and brown, muriform conidia with tri-lobed wing like basal cells. Kazuakitanaka gen. nov. (type: K. yuxiensis) is introduced in Sulcatisporaceae (Massarinae, Pleosporales) for a saprobiic ascomycete with teleomorphic and anamorphic (coelomycetous) features. The teleomorph possesses globose to subglobose ascomata with an eccentric ostiole, a peridal wall of textura prismatic, cylindrical-clavate, pedicellate asci with an ocular chamber, and 1–2-septate, hyaline, fusiform, guttate ascospores with a distinct mucilaginous sheath. The anamorph features pycnidial conidiomata, phialidic, ampulliform to cylindrical, hyaline conidiogenous cells and ampulliform to cylindrical, one-to-three-septate, hyaline, guttulate conidia. Loculosulcatispora was known only from its anamorph of L. thailandica. We observed the teleomorph of Loculosulcatispora hongheensis sp. nov. and amended the generic description of Loculosulcatispora accordingly. Loculosulcatispora hongheensis is characterized by globose to subglobose ascocoma with a central ostiole, a peridal wall of textura angularis to globosa, branched, septate, pseudoparaphyses, clavate asci with a short pedicle and a minute ocular chamber and hyaline, fusiform, 1-septate ascospores with a thick irregular mucilaginous sheath. This study provides some insights into the diversity of fungi on dead wooden litter in terrestrial habitats.

Keywords: Ascomycota; anamorph; Dothideomycetes; Greater Mekong Subregion; teleomorph

1. Introduction

Despite estimates that ~2.2–3.8 million or more fungal species exist on Earth [1], we know of only 146,150 [2], suggesting that 96% of fungal species remain unknown [3]. Some
fungal groups are well researched because of their impact on human lives, while others remain seriously neglected. This could potentially distort our understanding of fungal diversity [4]. Owing to their abundance across ecosystems, the importance of fungi cannot be discounted in any region [5]. There are numerous understudied habitats that harbor abundant species, and if they were to be thoroughly studied, many new species could be found [6]. Most species of plant-associated fungi can be pathogens, endophytes, saprobes or epiphytes on a wide range of hosts that reside in terrestrial as well as aquatic habitats [7]. Particularly, microfungi play important functional roles in almost all ecosystems, functioning as decomposers that degrade dead organic materials and recycle nutrients for reuse in the ecosystem [8,9]. Given the omnipresent nature of microfungi, additional taxonomic and ecological knowledge is prerequisites to understanding microfungal biology and their environmental significance.

Ascomycota is the most species-rich phylum of Fungi, comprising more than 92,700 species [2], and Dothideomycetes is the largest and most ecologically diverse class of the phylum [10]. This class comprises saprobes, human and plant pathogens, endophytes, epiphytes, ectomycorrhizal, lichens, lichenicolous, nematode-trapping and rock-inhabiting members [11]. In the Dothideomycetes, Pleosporales is the most species-rich order, consisting of 10,142 species [2] recognized in more than 90 families and 650 genera [12]. In recent years, molecular studies coupled with morphological evidence have revealed numerous novel families, genera and species within Pleosporales [12]. Recently, many new woody litter pleosporalean lineages from terrestrial [5,11,13–19] or freshwater [20–25] environments have been reported in Yunnan Province, China.

At the Center for Mountain Futures (Kunming Institute of Botany), we are investigating the diversity of microfungi on woody litter [3,15–17,26,27]. During this survey of lignicolous ascomycetes in Yunnan, we encountered numerous undescribed pleosporalean fungi. This study aimed to document taxonomic novelties in Phaeoseptaceae and Sulcatisporaceae. We used sequence data from relevant members of Pleosporales, three functional ribosomal RNA genes, the small and large subunit of the nuclear ribosomal RNA (nc18S and nc28S), the internal transcribed spacer region (ITS) and two protein-coding genes, the second largest subunit of RNA polymerase II (rpb2) and translation elongation factor 1-alpha gene (tef1-α) to perform an in-depth phylogenetic study. We present morphological and molecular phylogenetic evidence that supports the recognition of a new species in Phaeoseptaceae and four new species in Sulcatisporaceae, including a new genus.

2. Materials and Methods

2.1. Isolates and Specimens

During our fieldwork across the Ailaoshan, Chuxiong, Dqing, Honghe, Kunming, Lancang, Mengla and Yuxi regions of Yunnan Province, China, typical black ascomata/conidiomata appearing on dead twigs were collected during both dry (January, March and April) and wet (May, June and July) seasons. In total, sixteen specimens were included in this study. The collected samples were placed in Ziploc bags and taken to the mycology laboratory of the Kunming Institute of Botany and stored inside paper envelopes. Single spore isolation was conducted, and germinated spores were handled in accordance with the methods described in Wanasinghe et al. [15]. Dried specimens (at room temperature) were preserved in the fungarium of the Cryptogams Kunming Institute of Botany, Academia Sinica (KUN-HKAS). Representative cultures were deposited in the Kunming Institute of Botany Culture Collection (KUMCC), Kunming, China and China General Microbiological Culture Collection Center (CGMCC). Nomenclatural data of fungal novelties were deposited in MycoBank [28].

2.2. DNA Extraction, PCR Amplifications and Sequencing

The extraction of genomic DNA was performed using fresh mycelia in accordance with the methods of Wanasinghe et al. [5], using the Biospin Fungus Genomic DNA Extraction Kit-BSC14S1 (BioFlux, Shanghai, China) and following manufacturer guidelines. When
cultures could not be maintained for certain collected samples, DNA was extracted directly from the fruiting bodies of the fungus as outlined by Wanasinghe et al. [29]. The reference DNA for the polymerase chain reaction (PCR) was stored at 4 °C for regular use and stored at −20 °C for long-term storage.

Primers ITS5/ITS4 [30], LR0R/LR5 [31,32], NS1/NS4 [30], EF1-983F/EF1-2218R [33,34] and fRPB2-5f/fRPB2-7cR [35] were used to amplify the DNA sequences of the internal transcribed spacers (ITS), partial 28S large subunit rDNA (LSU), partial 18S small subunit rDNA (SSU), translation elongation factor 1-α (tef1), and RNA polymerase II second largest subunit (rpb2). Protocols used for PCR amplification (SSU, LSU, ITS and tef1) were used as in Wanasinghe et al. [15]. PCR amplification conditions of rpb2 were set as initial denaturation at 98 °C for 2 min, followed by 35 cycles of denaturation at 98 °C for 10 s, annealing at 52 °C for 10 s and extension at 72 °C for 20 s, with a final extension step at 72 °C for 5 min. The amplified PCR fragments were then sent to a private company for sequencing (BGI, Ltd., Shenzhen, China).

2.3. Molecular Phylogenetic Analyses

2.3.1. Sequencing and Sequence Alignment

BLAST searches using the BLASTn algorithm were performed to retrieve similar sequences from GenBank (http://www.ncbi.nlm.nih.gov, accessed on 29 December 2021) and relevant publications [36,37]. The collection/strain numbers for these sequences (Table 1) are presented in the corresponding phylogenetic trees (Figures 1 and 2). All alignments were produced with the server version of MAFFT v.7 [38], checked and refined using BioEdit v.7.0.5.2 software [39].

| Species                          | Strain | GenBank Accession Numbers       |
|---------------------------------|--------|----------------------------------|
|                                |        | SSU                             | LSU | ITS | tef1 | rpb2 |
| Alfoldia vorosii                | CBS 145501 T | MK589346 MK589354 JN859336 MK599320 |
| Amorocoelophoma cassiae         | MFLUCC 17-2283 T | NG_065775 NG_066307 NR_163330 MK360041 MK434894 |
| Angustimassarina acerina        | MFLUCC 14-0505 T, NG_063573 | KP888637 NR_138406 KR075168 |
| Angustimassarina populii        | MFLUCC 13-0034 T, NG_061204 | KP888642 KP899137 KR075164 |
| Angustimassarina quercicola     | MFLUCC 14-0506 T, NG_063574 | KP888638 KP899133 KR075169 |
| Anthosulcatispora brunnea       | MFLU 18-1393 T | MH644791 MH644792 - - |
| Anthosulcatispora subglobosa    | MFLUCC 17-2065 T | MT267205 MT214592 MT310636 MT394649 MT394706 |
| Bambusicola bambusae           | MFLUCC 11-0614 T | JX442039 JX442035 JX442031 KU671227 KP761718 |
| Bambusicola didymospora         | MFLUCC 10-0557 T | KU872110 KU863105 KU940116 KU940188 KL940163 |
| Bambusicola didymospora         | MFLUCC 15-0189 T | KU872111 KU863106 KU940117 KU940189 KL940164 |
| Bambusicola irregulispora       | MFLUCC 11-0437 T | JX442040 JX442036 JX442032 KP761723 KP761719 |
| Bambusicola loculata            | MFLUCC 13-0856 T | KP761735 KP761729 KP761732 KP761724 KP761715 |
| Bambusicola massarinia          | MFLUCC 11-0135 T | KU872115 KU863111 KU940122 KU940192 KL940169 |
| Bambusicola pustulata           | MFLUCC 15-0190 T | KU872112 KU863107 KU94018 KL940190 KL940165 |
| Bambusicola sichuanensis        | SICAUCC 16-0002 T | MK255328 MK255352 MK254373 MK262829 MK262830 |
| Bambusicola splendida           | MFLUCC 11-0439 T | JX442042 JX442038 JX442034 KP761726 KP761717 |
| Bambusicola subthailandensis    | SICAU 16-0005 T | MK253529 MK253533 MK253474 MK262829 MK262831 |
| Brillantella spathulifera        | MFLUCC 11-0147 T | KU872113 KU863108 KU940119 KU940191 KL940166 |
| Crassictyphus aquaticus         | CBS 143643 T | LC312472 LC312530 LC312501 LC312559 LC312588 |
| Decaisnella formosa             | BCC 25516 | GQ928533 GQ928546 - - |
| Decaisnella formosa             | BCC 25517 | GQ928534 GQ928547 - - |
| Flabellascoma caudicola         | CBS 143644 T | LC312473 LC312531 LC312502 LC312560 LC312589 |
| Forliomyces uniseptata          | MFLUCC 15-0765 T | NG_061234 NG_059659 NR_154006 KU727897 |
| Glotonipsis praelonga          | MFLUCC 12-1245 T | JF161134 JF161173 FJ161090 FK161113 |
| Guttulispora crataegi           | MFLUCC 13-0442 T | KP899125 KP888639 KP899134 KR075161 - |
| Halothia posidoniae            | BBH 22481 | GU79752 GU79786 - - - |
| Hysterium angustatum           | MFLUCC 16-0623 T | GU397359 FJ161180 - FJ161096 MH535875 |
Table 1. Cont.

| Species | Strain 1 | GenBank Accession Numbers |
|---------|----------|---------------------------|
| **Pleopunctum pseudellipsoideum** | KUMCC 21-0820 | ON009084, ON009100, ON009116, ON009259, ON009285 |
| **Pleopunctum pseudellipsoideum** | KUMCC 21-0821 | ON009085, ON009101, ON009117, ON009258, ON009283 |
| **Phaeoseptum mali** | HKAS122920 | ON009088, ON009104, ON009120, ON009263, ON009266 |
| **Mangicamarosporium diospyricola** | MFLUCC 16-0419 | KT 2822 |
| **Loculosulcatispora thailandica** | MFLUCC 20-0108 | MG926559, MG926560, MG926562, MG926561 |
| **Sulcatispora berchemiae** | KUMCC 21-0823 | ON009094, ON009110, ON009126, ON009269, ON009292 |
| **Phaeoseptum Terricola** | MFLUCC 17-2423 | AB797219, AB807509, AB809640, AB808485 |
| **Pleopunctum pseudellipsoideum** | KUMCC 21-0820 | ON009084, ON009100, ON009116, ON009259, ON009285 |
| **Pleopunctum pseudellipsoideum** | KUMCC 21-0821 | ON009085, ON009101, ON009117, ON009258, ON009283 |
| **Phaeoseptum mali** | HKAS122920 | ON009088, ON009104, ON009120, ON009263, ON009266 |
| **Mangicamarosporium diospyricola** | MFLUCC 16-0419 | KT 2822 |
| **Loculosulcatispora thailandica** | MFLUCC 20-0108 | MG926559, MG926560, MG926562, MG926561 |
| **Sulcatispora berchemiae** | KUMCC 21-0823 | ON009094, ON009110, ON009126, ON009269, ON009292 |
| **Phaeoseptum Terricola** | MFLUCC 17-2423 | AB797219, AB807509, AB809640, AB808485 |
| **Pleopunctum pseudellipsoideum** | KUMCC 21-0820 | ON009084, ON009100, ON009116, ON009259, ON009285 |
| **Pleopunctum pseudellipsoideum** | KUMCC 21-0821 | ON009085, ON009101, ON009117, ON009259, ON009283 |
| **Phaeoseptum mali** | HKAS122920 | ON009088, ON009104, ON009120, ON009263, ON009266 |
| **Mangicamarosporium diospyricola** | MFLUCC 16-0419 | KT 2822 |
| **Loculosulcatispora thailandica** | MFLUCC 20-0108 | MG926559, MG926560, MG926562, MG926561 |
| **Sulcatispora berchemiae** | KUMCC 21-0823 | ON009094, ON009110, ON009126, ON009269, ON009292 |
| **Phaeoseptum Terricola** | MFLUCC 17-2423 | AB797219, AB807509, AB809640, AB808485 |

1 Ex-type strains are mentioned with superscripted “T”.

Figure 1. RAxML tree based on a combined dataset of a partial SSU, LSU, ITS, tef1 and rpb2 DNA sequence analysis in Phaeoseptaceae. Bootstrap support values for ML (MLB) equal to or greater than 70% and Bayesian posterior probabilities (BYPP) equal to or greater than 0.95 are shown as MLB/BYPP above the nodes. The new isolates are in blue. Species names given in bold indicate ex-type and ex-paratype strains. The scale bar represents the expected number of nucleotide substitutions per site.
2.3.2. Phylogenetic Analyses

The single-gene datasets were examined for topological incongruence among loci and the conflict-free alignments were concatenated into a multi-locus alignment that was subjected to maximum-likelihood (ML) and Bayesian (BI) phylogenetic analyses. The evolutionary models for Bayesian analysis and maximum-likelihood were selected independently for each locus using MrModeltest v.2.3 [40] under the Akaike Information Criterion (AIC) implemented in PAUP v.4.0b10.

The CIPRES Science Gateway platform [41] was used to perform RAxML and Bayesian analyses. ML analyses were made with RAxML-HPC2 on XSEDE v.8.2.10 [42] using the GTR+GAMMA swap model with 1000 bootstrap repetitions.
MrBayes analyses were performed setting GTR+I+G for two million generations, sampling every 1000 generations, ending the run automatically when the standard deviation of split frequencies dropped below 0.01, with a burnin fraction of 0.25. ML bootstrap values (MLB) equal to or greater than 70% and posterior probability in Bayesian statistics (BYPP) greater than 0.95 are given above each node of every tree.

Phylograms were visualized with the FigTree v1.4.0 program [43] and reorganized in Microsoft PowerPoint (2007) and Adobe Illustrator® CS5 (Version 15.0.0, Adobe®, San Jose, CA, USA). The finalized alignments and trees were deposited in TreeBASE, submission ID:29570 (http://purl.org/phylo/treebase/phylows/study/TB2:S29570, accessed on 19 March 2022).

2.4. Morphological Observations

Ascomata, conidiophores and conidia from the natural substrates were rehydrated with tap water and examined with a Motic SMZ 168 series stereo-microscope (Motic Asia, Kowloon, Hong Kong). Morphological characteristics were examined via hand sectioning of sporocarps placed on water-mounted glass slides. The following characteristics were evaluated: ascomata/conidiomata diameter, height, color and shape; width of peridium; and height and diameter of ostioles. Microscopic photography was conducted using a Nikon ECLIPSE Ni (Nikon Instruments Inc., Melville, NY, USA) compound microscope with differential interference contrast (DIC) and phase contrast (PC) illumination. Images of microscopic structures were captured with a Canon EOS 600D (Canon Inc., ¯Ota, Tokyo, Japan) camera. Macroscopic images of colonies were documented using an iPhone XS Max (Apple Inc., Cupertino, CA, USA) with daylight. Measurements were made with the Tarosoft (R) Image Frame Work program and images used for figures were processed with Adobe Photoshop CS6 (Adobe Systems, San Jose, CA, USA).

3. Results

3.1. Phylogenetic Analyses

The final concatenated SSU–LSU–ITS–tef1–rpb2 alignment (Figure 1) of Phaeoseptaceae comprised 48 strains, including the outgroup taxa Gloniopsis praelonga (CBS 112415) and Hysterium angustatum (MFLUCC 16-0623). The final alignment contained a total of 4478 characters used for the phylogenetic analyses, including alignment gaps (available in TreeBASE). The RAxML analysis of the combined dataset yielded a best scoring tree with a final ML optimization likelihood value of −30565.564394. The matrix had 1930 distinct alignment patterns, with 31.15% undetermined characters or gaps. Parameters for the GTR + I + G model of the combined amplicons were as follows: estimated base frequencies, A = 0.242181, C = 0.257106, G = 0.272525, T = 0.228188; substitution rates, AC = 1.247807, AG = 3.156565, AT = 1.478256, CG = 1.137163, CT = 7.093906, GT = 1.00; proportion of invariable sites, I = 0.397831; gamma distribution shape parameter, α = 0.56366. Bayesian analyses generated 3201 trees (average standard deviation of split frequencies: 0.009446) from which 2401 were sampled after 25% of the trees were discarded as burn-in. The alignment contained a total of 1932 unique site patterns.

The family Phaeoseptaceae (SSU, LSU, ITS, tef1 and rpb2 phylogeny) was resolved into four distinct clades with 100 MLB and 1.00 BYPP support values. Four strains of Pleopunctum (KUMCC 21-0820, KUMCC 21-0025, KUMCC 21-0026 and HKAS122915) isolated in the study formed a well-supported clade with P. clematidis (MFLUCC 17-2091), P. ellipsoideum (MFLUCC 19-0390) and P. pseudollipoideum (MFLUCC 19-0391). Three strains of Thyridaria macrostomoides (GKM 224N, GKM 1033, GKM 1159) constituted a strongly supported monophyly with the ex-type strain of Lignosphaeria fusispora (MFLUCC 11-0377). Two of our new strains, HKAS122916 and HKAS122917, nested with the ex-type strain of Phaeoseptum mali MFLUCC 17-2108 with 100 MLB and 1.00 BYPP statistical support. Strains of Phaeoseptum aquaticum, P. carolsharerianum, P. hydei, P. mali, P. manglicola and P. terricola grouped as a monophyletic clade with strong support values in both maximum likelihood and Bayesian analyses. Finally, the two strains of Decaisnella formosa (BCC 25616,
BCC 25617) formed a basal terminal clade in *Phaeoseptaceae* with 100 MLB and 1.00 BYPP support values.

The *Sulcatisporaceae* (SSU, LSU, ITS, *tef1* and *rpb2* phylogeny) alignment contained 38 isolates (Figure 2), and the tree was rooted to *Leptosphaeria dolicholium* (CBS 505.75) and *Stemphylium vesicarium* (CBS 191.86). The final alignment contained a total of 4931 characters used for the phylogenetic analyses, including alignment gaps (available in TreeBASE). The RAxML analysis of the combined dataset yielded a best scoring tree with a final ML optimization likelihood value of $-27594.247903$. The matrix had 1770 distinct alignment patterns, with 23.64% undetermined characters or gaps. Parameters for the GTR + I + G model of the combined amplicons were as follows: estimated base frequencies, $A = 0.241395$, $C = 0.257298$, $G = 0.268694$, $T = 0.232613$; substitution rates, $AC = 1.256046$, $AG = 2.926191$, $AT = 1.154561$, $CG = 0.858049$, $CT = 6.686514$, $GT = 1.000$; proportion of invariable sites, $I = 0.499455$; gamma distribution shape parameter, $\alpha = 0.532594$. The Bayesian analyses generated 401 trees (average standard deviation of split frequencies: 0.009088) from which 301 were sampled after 25% of the trees were discarded as burn-in. The alignment contained a total of 1771 unique site patterns.

The family Sulcatisporaceae was composed of distinct lineages that correspond to the genera Anthosulcatispora, Loculosulcatispora, Magnicamarosporium, Neobambusicola, Parasulcatispora, Pseudobambusicola and Sulcatispora. Four strains (HKAS122922, HKAS122923, HKAS122924, HKAS122925) obtained in the present study formed a well-separated clade in Sulcatisporaceae, featuring both a single locus and concatenated datasets. Thus, this new lineage is presented here as the new genus Kazuakitanaka gen. nov. Two of our new isolates, KUMCC 21-0821 and KUMCC 21-0822, were grouped with the ex-type strain of Sulcatispora acerina (KT 2982) with 95 MLB and 1.00 BYPP values. Another two new strains (KUMCC 21-0823 and KUMCC 21-0824) grouped with the ex-type strain of Sulcatispora berchemiae (KT 1607), with 100 MLB and 1.00 BYPP support values. Loculosulcatispora thailandica (MFLUCC 20-0108), a type of Loculosulcatispora, constituted a monophyletic clade with two of our new isolates (HKAS122920 and HKAS122921).

Neobambusicola strielitzia, Parasulcatispora clematidis and Pseudobambusicola thailandica were affiliated as monotypic genera. Two species of Magnicamarosporium, *M. diospyricola* (MFLUCC 16-0419) and *M. iriomotense* (KT 2822), grouped with 100 MLB and 1.00 BYPP support values. Anthosulcatispora brunnea (MFLU 18-1393) and *A. subglobosa* (MFLUCC 17-2065) formed a basal terminal clade in Sulcatisporaceae, with 100 MLB and 1.00 BYPP statistical support.

3.2. Taxonomy

**Pleosporales** Luttr. ex M.E. Barr, Prodromus to class Loculoascomycetes: 67 (1987).

**Phaeoseptaceae** Boonmee, Thambug. and K.D. Hyde, Mycosphere 9 (2): 323 (2018).

**Phaeoseptum** Y. Zhang, J. Fourn. and K.D. Hyde, Mycologia 105 (3): 606 (2013).

**Phaeoseptum mali** Phukhams. and K.D. Hyde, Asian Journal of Mycology 2 (1): 120 (2019).

Material examined: China, Yunnan, Honghe Hani and Yi Autonomous Prefecture, Kaiyuan, 23.863601° N, 103.407975° E, 1053 m, on dead woody litter, 17 March 2019, D.N. Wanasinghe (HKAS122916), ibid. Chuxiong Yi Autonomous Prefecture, Shuangbai County, 24.80527° N, 101.933887° E, 1736 m, on dead woody litter under the *Fagaceae* species, 25 June 2019 (HKAS122917).

Notes: Phukhamsakda et al. [44] introduced *Phaeoseptum mali* from the bark of fallen twigs of *Malus halliana* from the botanical garden of the Kunming Institute of Botany, Yunnan, China. *Phaeoseptum mali* fits well within the generic descriptions of *Phaeoseptum* based on its globose and immersed ascomata, cellular pseudoparaphyses, cylindrical-clavate, pedicellate asci, allantoid and brown muriform ascospores. In this study, we collected another two specimens of *Phaeoseptum mali* from Chuxiong and Honghe Prefectures in Yunnan, China on dead woody litter. Multi-gene phylogenetic analyses of combined SSU, LSU, ITS, *tef1* and *rpb2* DNA sequence showed that the ex-type strain of *Phaeoseptum mali* (MFLUCC 17-2108) and our two strains (HKAS122916 and HKAS122917) are monophyletic...
with 100% MLB and 1.00 BYPP support values. Morphologically, these new collections are not different from the holotype of *Phaeoseptum mali*.

*Pleopunctum* N.G. Liu, K.D. Hyde and J.K. Liu, Mycosphere 10 (1): 767 (2019).

*Pleopunctum menglaense* Wanas. sp. nov. (Figure 3).

Figure 3. The anamorph of *Pleopunctum menglaense* (HKAS122683, holotype). (a–c) Colonies on host surface; (d) β conidia with basal cells; (e,f) α conidia showing remnant of conidiogenous cells at base; (g) α conidia with the conidiophore; (h) β conidia with distinct basal cells; (i) germinating conidium; (j,k) colonies on PDA after 21 days. Scale bars: (d) 50 μm; (e–g) 10 μm; (h,i) 20 μm; (j,k) 2 cm.
MycoBank: MB843430.
Etymology: The specific epithet is derived from Mengla County, Yunnan Province, China. Holotype: HKAS122683.

The species is a saprobe on dead twigs of forest litter in terrestrial habitats. Teleomorph: undetermined. Anamorph: hyphomycetous. Colonies on host, sporodochial, superficial, black, scattered and punctiform. The conidiophores are arising from hyaline unbranched hyphae. They are 10–20 × 2.5–3.5 µm (M = 16.7 × 3.1, n = 15), macronematous, mononematous, cylindrical, unbranched, aseptate, hyaline and smooth-walled. The conidiogenous cells 5–8 × 2.8–3.5 µm (M = 6.9 × 3.2 µm, n = 30) are monoblastic, terminal, hyaline. The conidia are dimorphic, acrogenous and solitary. The α conidia are 18–25 × 10–14 µm (M = 23.1 × 11.7 µm, n = 30), hyaline, multi-septate, muriform, spatulate to obovate, notably constricted at septa, slightly obtuse to rounded at apex, notably narrow at base, often carrying remnants of conidiogenous cells at base. The β conidia are 38–55 × 20–26 µm (M = 45.6 × 24.4 µm, n = 30), brown, muriform, ellipsoidal to oblong shaped, moderately rough-walled, and slightly constricted at septa often with a hyaline, elliptical to globose, 1-3 basal cells, 7.5–12 × 4–6 µm (M = 9 × 5.1 µm, n = 25) with a tri-lobed wing-like appearance.

Culture characteristics: the conidia germinated on PDA within 12 h and germ tubes were produced from the basal cells of conidia. The colonies on PDA reached a 5 cm diameter after 2 weeks at 25 °C. They were effused, circular to lobed, with incised margin, flat or slightly hairy, pinkish brown in the center with concentric rings and pale brown at the periphery and reverse; three distinct color zones were present, namely greyish brown at the center, pinkish brown at the middle, golden brown at the periphery.

Material examined: China, Yunnan, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Wangtianshu, 21.61852° N, 101.58171° E, 747 m, on dead woody litter, 12 January 2021, D.N. Wanasinghe (HKAS122683, holotype), ex-type living culture, KUMCC 21-0826. ibid. 21.618839° N, 101.581098° E, 774 m (HKAS122684), living culture, KUMCC 21-0827.

Pleopunctum pseudoellipsoideum N.G. Liu, K.D. Hyde and J.K. Liu, Mycosphere 10 (1): 768 (2019)
Material examined: China, Yunnan, Diqing Tibetan Autonomous Prefecture, Mengla County, Wangtianshu, 21.61852° N, 101.58171° E, 747 m, on dead woody litter, 12 January 2021, D.N. Wanasinghe (HKAS122683, holotype), ex-type living culture, KUMCC 21-0826. ibid. 21.618839° N, 101.581098° E, 774 m (HKAS122684), living culture, KUMCC 21-0827.

Notes: Liu et al. [45] introduced Pleopunctum pseudoellipticum from decaying wood in Guizhou Province, China as a hyphomycetous muriform spored anamorph taxon in Phaeoseptaceae. During our investigation on the diversity of woody litter microfungi in Yunnan, China, two collections were made from the Diqing and Kunming areas. Morphological characteristics of our new collections, such as conidiophores and conidia, fit well within the anamorph of Pleopunctum pseudoellipticum. In our phylogenetic study (Figure 1), the new strains (KUMCC 21-0820, HKAS122915) cluster with Pleopunctum pseudoellipticum (MFLUCC 19-0391, ex-type strain) as a monophyletic clade with 100% MLB and 1.00 BYPP support values. Comparison of ITS, LSU and tef1 sequence data reveals there is no significant difference between our new isolates and Pleopunctum pseudoellipticum. Therefore, we recognize our new isolates as additional collections of Pleopunctum pseudoellipticum, and we provide SSU and rpb2 sequence data that were not provided by Liu et al. [45].

Sulcatisporaceae Kaz. Tanaka and K. Hiray., Studies in Mycology 82: 119 (2015).
Kazuakitanaka Wanas. gen. nov.
MycoBank: MB843431.

Etymology: The generic epithet stems from the combined two words “kazuaki” and “tanaka”, referring to Kazuaki Tanaka, who introduced the family Sulcatisporaceae.

The genus comprises saprobic fungi on woody substrates in terrestrial habitats. Teleomorph: the ascomata is a solitary or gregarious, semi-immersed, erumpent through the host
surface, coriaceous, dark brown to black, globose to subglobose, ostiolate. The ostiole is central, with hyaline to pale-brown pseudoparenchymatous cells. The peridium is broader at the apex and thinner at the base, comprising two strata with several layers of brown or lightly pigmented to hyaline cells building textura angularis to textura prismatica, indistinguishable from the host tissues. The hamathecium comprises many branched, septate, cellular pseudoparaphyses, located between and above the asci, embedded in a gelatinous matrix. The asci are eight-spored, bitunicate, fissitunicate, cylindric-clavate, pedicellate, and apically rounded, with an ocular chamber. The ascospores are uni- to bi-seriate, partially overlapping in lateral view, and are hyaline. They are fusiform, 1–2-septate, slightly curved, deeply constricted at the central septum, conically rounded at the ends, and smooth-walled, with a distinct mucilaginous sheath, comprising a large guttule in each cell. Anamorph: Coelomycetous. The conidiomata are pycnidial, solitary, gregarious, dark brown to black, immersed or slightly erumpent, coriaceous to carbonaceous, papillate or apapillate. The conidiomatal wall is multi-layered; the outer layers are pseudoparenchymatous, with brown-walled cells, with the innermost layer thin and hyaline. The conidiophores are reduced to conidiogenous cells. The conidiogenous cells are phialidic, ampulliform to cylindrical, determinate, hyaline, smooth-walled and formed from the inner layer of the pycnidium wall. The conidia are hyaline, one-to-three-septate, straight to curved, fusiform, with conical ends, thick-walled, smooth, with large guttules in each cell.

Type species: *Kazuakitanaka yuxiensis* Wanas. sp. nov. (Figure 4). MycoBank: MB843432.

Etymology: The specific epithet is derived from Yuxi, Yunnan Province, China.

Holotype: HKAS122924.

The species is a saprobe on dead twigs of forest litter in terrestrial habitats. Teleomorph: the ascomata is 350–400 μm high, 220–260 μm diam. (M = 386.6 × 249.9 μm, n = 5), scattered to gregarious, semi-immersed to erumpent, coriaceous, dark brown to black, globose to subglobose ostiolate. The ostiole is 110–140 μm long, 90–115 μm diam. (M = 125.6 × 98.7 μm, n = 5), centrally papillate, comprising hyaline cells. The peridium is 10–15 μm wide at the base, 12–20 μm wide at the sides, broad at the apex (30–40 μm), comprising two strata, with the outer stratum composed of small, pale brown to brown, slightly flattened, thick-walled cells of textura angularis, fusing and indistinguishable from the host tissues. The inner stratum is composed of several layers with lightly pigmented to hyaline cells centrally textura angularis to textura prismatica. The hamathecium is 1–2 μm wide, branched, septate, cellular pseudoparaphyses, situated between and above the asci, embedded in a gelatinous matrix. The asci are 80–120 × 17–21 μm (M = 102.2 × 18.5 μm, n = 20), eight-spored, bitunicate, fissitunicate, cylindric-clavate, with a pedicel, and is rounded at the apex, with an ocular chamber. The ascospores are 25–32 × 7–9 μm (M = 29.1 × 7.9 μm, n = 30), uni- to bi-seriate, overlapping, and hyaline. They are fusiform, 1–2-septate. They are slightly curved, deeply constricted at the central septum, conically rounded at the ends, and smooth-walled, surrounded by a distinct mucilaginous sheath, each cell with a large guttule. Anamorph: undetermined.

Material examined: China, Yunnan, Yuxi, Xinping Yi and Dai Autonomous County, 24.09083° N, 101.935124° E, 2091 m, on dead woody litter, 25 May 2019, D.N. Wanasinghe (HKAS122924, holotype). ibid. 24.09083° N, 101.935124° E, 2095 m (HKAS122925).

*Kazuakitanaka lancangensis* Wanas. sp. nov. (Figure 5). MycoBank: MB843433.

Etymology: The specific epithet is derived from Lancang, Yunnan Province, China.

Holotype: HKAS122922.
Figure 4. The teleomorph of Kazuakitanaka yuxiensis (HKAS122924, holotype). (a,b) Ascomata on dead woody twigs; (c,d) vertical section of ascomata; (e) closeup of ostiole; (f) peridium; (g) pseudoparaphyses; (h–j) asci; (k) ascospores. Scale bars: (c) 500 μm; (d) 100 μm; (e,f,h–k) 20 μm; (g) 10 μm.
**Figure 5.** *Kazuakitanaka lancangensis* (HKAS122922, holotype). (a,b) Conidiomata on host surface; (c,d) sections through conidiomata; (e) conidioma wall; (f–i) conidiogenous cells and developing conidia; (j–n) conidia. Scale bars: (c) 500 μm; (d) 50 μm; (e) 15 μm; (f–n) 10 μm.
It is saprobic on dead twigs of forest litter in terrestrial habitats. Teleomorph: undetermined. Anamorph: coelomycetous. The conidiomata is 130–150 \(\mu m\) high, 160–190 \(\mu m\) diam. (M = 140 \(\times\) 170 \(\mu m\), n = 5), pycnidial, solitary, gregarious, globose to subglobose, coriaceous, uniloculate, dark brown to black, and immersed, with a central ostiole. The conidiomata wall is 10–20 \(\mu m\) wide, multi-layered, with brown-walled pseudoparenchymatous cells, with a hyaline inner most layer. The conidiophores are reduced to conidiogenous cells. The conidiogenous cells are 7–10 \(\times\) 2–3.5 \(\mu m\) (M = 8.3 \(\times\) 2.7 \(\mu m\), n = 15), phialidic, ampulliform to cylindrical, determinate, hyaline, smooth-walled and formed from the inner layer of the pycnidium wall. The conidia are 17–23 \(\times\) 3.7–4.7 \(\mu m\) (M = 20 \(\times\) 4.2 \(\mu m\), n = 30), fusiform, straight, hyaline, one-to-three-septate, not constricted at septa, tip and base rounded, thick-walled, and smooth, with numerous large guttules in each cell.

Material examined: China, Yunnan, Pure, Lancang Lahu Autonomous County, 23.164681° N, 99.969248° E, 1990 m, on dead woody litter, 11 April 2019, D.N. Wanasinghe (HKAS122922, holotype). ibid. 23.164686° N, 99.969492° E, 1975 m (HKAS122923).

*Loculosulcatispora* G.C. Ren and K.D. Hyde, *Phytotaxa* 475 (2): 70 (2020) amended
MycoBank: MB557580

The genus comprises saprobic species on dead wood or twigs. Teleomorph: the ascomata are scattered, immersed to semi-immersed, globose to subglobose, brown to dark-brown, with a central ostiole. The peridium is composed of small, pale brown to brown, thick-walled cells forming textura angularis to globosa. The hamathecium comprises branched, septate, cellular pseudoparaphyses. The asci are eight-spored, bitunicate, clavate, straight to curved, with a short pedicel. They are apically rounded, with or without an ocular chamber. The ascospores are overlapping uni- to bi-seriate, hyaline, fusiform with acute ends, 1-septate, smooth-walled, surrounded by a thick irregular mucilaginous sheath. Anamorph: see Ren et al. [36].

Type species: *Loculosulcatispora thailandica* G.C. Ren and K.D. Hyde, *Phytotaxa* 475 (2): 73 (2020).

*Loculosulcatispora hongheensis* Wanas. sp. nov. (Figure 6).
MycoBank: MB843434.

Etymology: The specific epithet is derived from Honghe, Yunnan Province, China. Holotype: HKAS122920.

The species is a saprobe on dead twigs of forest litter in terrestrial habitats. Teleomorph: the ascomata is 130–490 \(\times\) 120–560 (M = 260 \(\times\) 280, n = 5) \(\mu m\), scattered, immersed, coriaceous, globose to subglobose, brown to dark-brown, with a central ostiole. The peridium is 10–15 \(\mu m\) wide; the outer stratum composed of small, pale brown to brown, thick-walled cells forming textura angularis to globosa indistinguishable from the host tissues. The inner stratum is composed of hyaline cells forming textura angularis. The hamathecium is 1–2.5 \(\mu m\) wide, branched, septate, cellular pseudoparaphyses, situated between and above the asci, embedded in a gelatinous matrix. The asci are 60–100 \(\times\) 10–18 \(\mu m\) (M = 84 \(\times\) 13.7 \(\mu m\); n = 15) \(\mu m\), eight-spored, bitunicate, fissionsunicate, clavate, straight to curved, with a minute ocular chamber. The ascospores are 20–30 \(\times\) 4–6.5 \(\mu m\) (M = 25 \(\times\) 5 \(\mu m\), n = 30), overlapping uni- to bi-seriate, hyaline, fusiform with acute ends, 1-septate, smooth-walled, surrounded by a thick irregular mucilaginous sheath. Anamorph: undetermined.

Material examined: China, Yunnan, Honghe Hani and Yi Autonomous Prefecture, Mengzi, 23.18604° N, 103.413838° E, 1854 m, on dead woody litter, 16 March 2019, D.N. Wanasinghe (HKAS122921, holotype). ibid. 23.186552° N, 103.414063° E, 1866 m (HKAS122922).

*Sulcatispora* Kaz. Tanaka and K. Hiray., *Studies in Mycology* 82: 120 (2015).

*Sulcatispora acerina* Kaz. Tanaka and K. Hiray., *Studies in Mycology* 82: 120 (2015).

Material examined: China, Yunnan, Pure, Jingdong Yi Autonomous County, 24.548691° N, 101.027802° E, 2546 m (HKAS122927), living culture, KUMCC 21-0822.
Figure 6. *Loculosulcatispora hongheensis* (HKAS122920, holotype). (a) Dead wood host substrate; (b,c) section of ascoma; (d); close-up of ostiole; (e) peridium; (f) pseudoparaphyses; (g,h) asci; (i,j) ascospores. Scale bars: (b) 500 μm; (c) 100 μm; (d,g,h) 20 μm; (e,i,j) 10 μm; (f) 5 μm.

Notes: *Sulcatispora acerina*, introduced by Tanaka et al. [46], was collected from *Acer palmatum* in a terrestrial habitat. Based on phylogenetic analysis of combined SSU, LSU, ITS, tef1 and rpb2 sequence data, two of our isolates, KUMCC 21-0821 and KUMCC 21-0822, were clustered with the ex-type strain of *Sulcatispora acerina* (KT 2982) with 95% MLB and 1.00 BPP support (Figure 2). Our isolate resembles *Sulcatispora acerina* in shape and size of the ascomata, asci and ascospores. Moreover, there are no base pair differences of the SSU and LSU nucleotides and only four and seven nucleotide differences in the ITS and tef1 regions, respectively. Therefore, we recognize that our new isolates belong to *Sulcatispora*...
Phaeoseptum mali was initially described as an accepted species in 2015, with high bootstrap support (100% MLB, 1.00 BYPP). These three strains share similar morphological features in ascomata, ascii and ascospores. KT 1607 was collected from Japan on Berchemia racemosa, whereas KUMCC 21-0823 and KUMCC 21-0824 were collected from China on dead woody litter. Based on both morphology and molecular data, we consider our new isolates and Sulcatispora berchemiae to be conspecific. While extending the biogeography of Sulcatispora berchemiae, we also provide the rpb2 gene region for the species, which was not accounted for earlier.

4. Discussion

Hyde et al. [47] established Phaeoseptaceae in Pleosporales to accommodate Phaeoseptum. However, this family is now recognized as a group of heterogenous taxa that have diversified habitats with different types of anamorphs and diverged morphological characteristics [37]. In the recent outlines of Hongsanan et al. [10] and Wijayawardane et al. [12], only Phaeoseptum and Pleopunctum are accepted in Phaeoseptaceae. In the combined multi-gene phylogenetic analyses, the ex-type strains of Lignospheria diospyrosa, L. fusiispora and L. thailandica also clustered in Phaeoseptaceae [48]. Therefore, Lignospheria should be an accepted genus within Phaeoseptaceae. Even though the putative strains of Deccaisnella formosa (BCC 25616, BCC 25617) and Thyridaria macrosomoides (GKM 1033, GKM 1159, GKM 224N) are phylogenetically affiliated in Phaeoseptaceae [37,47], they are not related to any type specimens. Therefore, it is necessary to recollect and epitypify them with DNA sequence data in order to ensure correct generic placement of these two species [49,50].

Phaeoseptum was introduced by Zhang et al. [51] to accommodate P. aquaticum, and it was initially described as an accepted species in Halotthiaceae based on phylogenetic analysis of LSU sequence data. Currently, six species are accepted in Phaeoseptum viz.: P. aquaticum, P. carolshearerianum, P. hydei, P. mali, P. manglicola and P. terricola [10]. Phaeoseptum aquaticum was reported from freshwater habitats, and later Hyde et al. [47] added P. terricola from a terrestrial environment. In recent studies, Phukhamsakda et al. [44] and Wanasinghe et al. [37] collected Phaeoseptum mali and P. hydei from terrestrial habitats, respectively. Dayarathne et al. [52] showed that these species can be found in tropical coastlines, while introducing Phaeoseptum carolshearerianum and P. manglicola from mangroves. In this study, we accounted for another two records of Phaeoseptum mali from Chuxiong and Honghe Prefectures in Yunnan (China) from terrestrial habitats.

Pleopunctum, typified by P. ellipsoideum, is a hyphomycetous genus established in Phaeoseptaceae by Liu et al. [45]. Species in the genus are characterized by macronematous, mononematous conidiophores with monoblastic conidiogenous cells and oval to ellipsoidal, muriform conidia mostly with a hyaline, elliptical to globose basal cell [45]. Currently, five Pleopunctum species (viz. P. bauhiniae, P. clenatiidis, P. ellipsoideum, P. pseudoellipsoideum, P. thailandicum) are accepted in Species Fungorum [53]. However, Koukol and Delgado [54] argued that Pleopunctum clenatiidis should be a synonym of P. bauhiniae (=Hermatomyces bauhiniae), Members in the genus have appeared to be saprobic on dead twigs of deciduous hosts in terrestrial habitats [45-57]. In this study, morphological characteristics and multi-gene phylogenetic analysis of combined SSU, LSU, ITS, tef1 and rpb2 DNA sequence data reveals a new species of Pleopunctum from the dead woody litter collected in Yunnan, China. In a multi-gene (concatenated LSU, SSU, ITS, tef1 and rpb2) phylogenetic analysis, two of our strains (KUMCC 21-0025, KUMCC 21-0026) clustered with Pleopunctum...
species as a monophyletic clade with 100 MBP and 1.00 BYPP bootstrap support (Figure 1). Morphological features of KUMCC 21-0025 and KUMCC 21-0026 are similar to extant species of Pleopunctum in having sporodochial colonies, holoblastic, monoblastic conidiogenous cells and brown muriform conidia [45]. We introduce these two isolates as a novel species belonging to this genus, Pleopunctum menglaense. Within the Pleopunctum clade, P. menglaense strains constitute a sister lineage to P. pseudoellipsoideum (MFLUCC 19-0391, KUMCC 21-0820, HKAS122915). Pleopunctum menglaense has contrasting morphological features to P. pseudoellipsoideum by its distinct, hyaline, 1–3 basal cells in β conidia, whereas P. pseudoellipsoideum has a single basal cell in β conidia [45].

Sulcatisporaceae currently accommodates seven genera: viz. Anthosulcatispora, Loculosulcatispora, Magnicamarosporium, Neobambusicola, Parasulcatispora, Pseudobambusicola and Sulcatispora [12]. The species in this family are mostly restricted to terrestrial habitats excluding Neobambusicola streltzieae, which was found from the coastal region (Eastern Cape Province) of South Africa [58]. The conidia of anamorphs of Sulcatisporaceae can vary from hyaline, aseptate or septate (Anthosulcatispora, Loculosulcatispora, Neobambusicola, Pseudobambusicola), to pigmented phragmo-conidia (Sulcatispora) or muriform conidia (Magnicamarosporium), with or without striation [36,46,56,58–60]. The anamorph of Parasulcatispora is yet to be discovered. Shared characteristics within the family consist of immersed ascomata, peridium comprising pseudoparenchymatous cells with a thickened apex, cellular or trabeculate pseudoparaphyses and having cylindrical to cylindric-clavate ascis with a long pedicel. However, the ascospore arrangement inside an ascus and the features of ascospores can differ between species belonging to this group. The spore arrangement can be uniseriate (Anthosulcatispora) and 2–3-seriate in others. Spores are hyaline and fusiform with conical ends that are completely surrounded by a sheath excluding Anthosulcatispora brunnea, which is brown to dark brown, oblong to ellipsoidal and lacking a sheath.

Kazuakitanaka is introduced in Sulcatisporaceae as a new genus, based on LSU, ITS, tef1 and rpb2 sequence data. Kazuakitanaka morphologically resembles Parasulcatispora and Sulcatispora with its cylindrical-clavate ascis and fusiform, 1-septate hyaline ascospores. However, these genera were revealed as phylogenetically distant in multi-gene phylogenetic analysis (Figure 2). The coelomycetous anamorph of Kazuakitanaka is similar to species of Neobambusicola and Pseudobambusicola by its pycnidial conidiomata, phialidic conidiogenous cells and hyaline, fusiform, multi-septate conidia. The new genus has a close phylogenetic proximity to Pseudobambusicola even though this relationship is not statistically significant, and Neobambusicola was placed in a distinct branch apart from the Kazuakitanaka clade (Figure 2). The teleomorph for these genera is still undetermined and therefore they cannot be morphologically compared with the teleomorph of the new genus.

Ren et al. [36] introduced Loculosulcatispora as a monotypic genus to accommodate L. thailandica, and it was known only from its anamorph. Loculosulcatispora thailandica was introduced as a decaying woody-based saprobe from Thailand (Chiang Rai). The genus was characterized by multilocular conidiomata, phialidic, discrete, determinate, doliform to cylindrical, hyaline conidiogenous cells, unbranched and aseptate paraphyses, and 1-celled, oblong conidia with guttules. During our sample collections, we found a teleomorphic species characterized by globose to subglobose, immersed ascomata with a central ostiole, peridium composed of textura angularis, hamathecium comprises branched, septate, cellular pseudoparaphyses, clavate, short pedicellate ascis with a minute ocular chamber, hyaline, fusiform, and 1-septate ascospores with a mucilaginous sheath. In the multi-gene phylogenetic analyses, two of the isolates of this teleomorphic species (HKAS122920, HKAS122921) constituted a monophyletic clade (100% MLB and 1.00 BYPP, Figure 2) with the type strain of Loculosulcatispora thailandica (MFLUCC 20-0108). Therefore, we introduce our new collections as Loculosulcatispora hongheensis sp. nov. and amended the generic descriptions herein to accommodate its teleomorphic characteristics. The Loculosulcatispora clade has a sister affiliation to Parasulcatispora clematidis, which is known only from its teleomorph [56]. It could also be a species in Loculosulcatispora. For us to
combine these two genera here would require an extensive taxonomic reassessment and describing anamorphic morphology, which is beyond the scope of the current study.

Tanaka et al. [46] introduced *Sulcatispora* to accommodate *S. acerina* and *S. berchemiae*, which were collected as saprobes on *Sapindaceae* (*Acer palmatum*) and *Rhamnaceae* (*Berchemia racemosa*) hosts. The teleomorph of the genus is characterized by globose, subglobose to hemispherical and immersed to erumpent ascomata, short papillate, central ostioles with periphyses, peridium composed of several layers of compressed angular cells, trabeculate pseudoparaphyses, clavate asci with a short pedicel and fusiform, 1-septate, hyaline ascospores with a large sheath. The anamorph is characteristic with globose, pycnidial conidiomata, cylindrical and annellidic conidiogenous cells, ellipsoid, yellowish brown, multi-septate conidia with striate ornamentation. These teleomorphic characteristics are somewhat similar to those in *Massarina*. The most distinctive feature of *Sulcatispora* is the longitudinal striae on the surface of conidia. Some species in *Barriopsis* (e.g., *B. iraniana*), *Dwiroopa* (e.g., *D. ramya*), *Endomelanconium* (e.g., *E. pini*), *Lasiodiplodia* (e.g., *L. theobromae*), *Mucoharknessia* (e.g., *M. cortaderiae*), *Neodeightonia* (e.g., *N. phoenicum*) and *Phaeophleospora* (e.g., *P. striae*) are known to have such conidia [61].

In the present study, we identified five genera and eight species associated with dead woody litter in Yunnan, China. Among them, one genus and four species are new to science. Our results emphasize that Yunnan Province has not yet been properly studied and is an open field for new fungal discoveries.

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