Bambusicolous Fungi in Pleosporales: Introducing Four Novel Taxa and a New Habitat Record for *Anastomitrabeculia didymospora*

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Abstract: While conducting a survey of bambusicolous fungi in northern Thailand and southwestern China, several saprobic fungi were collected from dead branches, culms and twigs of bamboos, which were preliminarily identified as species belonging to Pleosporales (Dothideomycetes) based on a morphological approach. Multigene phylogenetic analyses based on ITS, LSU, SSU, rpb2, tef1-α and tub2 demonstrated four novel taxa belonging to the families Parabambusicolaceae, Pyrenochaetopsidaceae and Tetraploasphaeriaceae. Hence, *Paramultiseptospora bambusae* sp. et gen. nov., *Pyrenochaetopsis yunnanensis* sp. nov. and *Tetraploa bambusae* sp. nov. are introduced. In addition, *Anastomitrabeculia didymospora* found on bamboo twigs in terrestrial habitats is reported for the first time. Detailed morphological descriptions and updated phylogenetic trees of each family are provided herein.

Keywords: Dothideomycetes; morphology; multigene phylogeny; Parabambusicolaceae; Pyrenochaetopsidaceae; Tetraploasphaeriaceae

1. Introduction

Bamboo is one of the most useful perennial woody grasses that contains the highest amount of living biomass [1]. It belongs to the subfamily Bambusoideae, family Poaceae, comprising about 127 genera, with approximately 1680 species, covering around 25 million hectares in tropical, subtropical, and mild temperate regions of Africa, America, Asia and Oceania, but it is rarely found in Europe [1–5]. Bamboo is important for ecological and socioeconomic sustainability throughout the world. Bamboo forests are crucial for the environmental benefits and climate change mitigation; they are sustainable in soil erosion control, carbon sequestration, soil and water conservation, windbreaks and shelterbelts, land rehabilitation, as well as releasing negative oxygen ions [4,6–9]. Bamboo has also been utilized for traditional Chinese medicine, food sources, furniture and building construction, musical instruments, paper and textile industries, reinforcing fibers, as well as feedstock...
for bioethanol and biomethane productions [1,4,7,9,10]. Bamboo is considered to be an eco-friendly plant, but there are also potential problems associated with bamboo’s cultivations such as decreasing biodiversity and soil fertility, soil and water loss, and surface water pollution [7].

Bamboo are highly diverse, distributed worldwide, contain high biomass and are a sustainable carbon source; hence, they host a high diversity of fungi [3,8,11–13]. Study into bambusicolous fungi has being carried out since the 18th century, which was first started by Léveillé [14]. Subsequently, many mycologists have described an increasing number of fungi on bamboo, especially ascomycetes [3,11–13,15–19]. Recently, more than 1300 fungi have been reported on bamboo, including 150 basidiomycetes and 800 ascomycetes, of which 350 species are reported as asexual morphs [13]. However, many bambusicolous fungi remain poorly clarified in taxonomic classification due to the lack of molecular–phylogenetic approaches [3,12].

Over the last two decades, taxonomic studies of bambusicolous fungi have become an interesting research topic for many Asian mycologists [3,12,13,20–54]. The taxonomic classification of bambusicolous fungi based on molecular phylogeny was initially carried out by Tanaka et al. [12], who introduced a novel family Tetraplosphaeriaceae to accommodate tetraploa-like taxa in Pleosporales. Noteworthily, major studies of bambusicolous ascomycetes with modern taxonomic treatments have been carried out by Dai et al. [3], Liu et al. [31,32], Phookamsak et al. [39], and Tanaka et al. [27]. Up to now, more than 175 bambusicolous ascomycetes have been described based on morphological and phylogenetic evidence [13,42–53,55–70]. However, there have been few thorough studies into the phylogeny-based taxonomy of bambusicolous fungi preceding 2002 [11], causing more than 80% of bambusicolous fungi to lack molecular data that could clarify their phylogenetic placement.

Many families in Pleosporales were initially introduced to accommodate bambusicolous fungi mainly such as Anastomitrabeculiaceae [71], Astrophaeriellaceae [39], Bambusicolaceae [72], Occultibambusaceae [3], Parabambusicolaceae [27], Pseudoastrophaeriellaceae [39], Roussellaceae [32], Shiriaiaceae [73] and Tetraplosphaeriaceae [12]. Furthermore, bambusicolous fungi are also distributed among many families in Pleosporales such as Aigialaceae, Dictyosporiaceae, Didymosphaeriaceae, Halothiaceae, Lentitheciaceae, Ligninsphaeriaceae, Longipedicellataceae, Lophiotremataceae, Periconiaceae, Phaeosphaeriaceae, and Pleosporaceae [27,31,41,49,52,74–81], suggesting that bambusicolous fungi are diverse in Pleosporales. In this study, we also found the bambusicolous fungi in Pleosporales with the intention of providing a better understanding of their taxonomy placement. The aim of this study is to introduce four novel taxa of bambusicolous fungi in Pleosporales based on the morpho-molecular approach.

2. Materials and Methods

2.1. Collection, Examination, Isolation, and Preservation

Samples were collected from the dead branches, culms, and twigs of bamboo in Chiang Mai and Chiang Rai Provinces of Thailand in 2011 and Yunnan Province of China in 2021. The samples were stored in paper bags and brought to the laboratory for observation and examination. Fungal fruiting bodies on host substrates were observed under an Olympus SZ61 series stereo microscope, and a centrum was mounted in sterilized distilled water on a clean slide for examination and captured under a Nikon ECLIPSE Ni compound microscope connected to a Nikon DS-Ri2 camera. Cotton blue was added to observe the fungal centrum, and Indian ink was used to check the mucilaginous sheath covering the ascospores. Morphological features were measured using Tarosoft (R) Image FrameWork version 0.9.7. Photographic plates were edited and combined in Adobe Photoshop CS6 software (Adobe Systems Inc., San Jose, CA, USA). The permanent slides were prepared by adding lacto-glycerol and sealed by nail polish and deposited with herbarium specimens at the Herbarium of Cryptogams Kunming Institute of Botany Academia Sinica (KUN-HKAS), China and the herbarium of Mae Fah Luang University, Chiang Rai, Thailand (MFLU).
Pure cultures were obtained from single-spore isolation based on a spore suspension technique [82]. Germinated ascospores were aseptically transferred to potato dextrose agar (PDA) and cultivated under normal light at 20–25 °C. Fungal colonies were observed and recorded after one week and four weeks. The asexual morph that sporulated in vitro was observed and examined after two months. Axenic living cultures were deposited in the Mae Fah Luang University Culture Collection (MFLUCC) and the Culture Collection of Kunming Institute of Botany (KUMCC). The newly described taxa were registered in Index Fungorum (http://www.indexfungorum.org/names/IndexFungorumRegister.htm; accessed on 13 May 2022).

2.2. DNA Extraction, Amplification, and Sequencing

Fresh mycelia were scraped from fungal colonies growing on PDA for a month and stored in a 1.5 mL sterilized microcentrifuge tube in an aseptic condition. Fungal genomic DNA was extracted by using Biospin Fungus Genomic DNA Extraction Kit (Bio Flux®, Hangzhou, China) following the manufacturer’s instructions (Hangzhou, China). Fungal genomic DNA was also extracted from fruiting bodies directly in case the fungi could not germinate on PDA using a Forensic DNA Kit (Omega®, Norcross, GA, USA). The generated fungal genomic DNA was stored at 4 °C for PCR amplification and duplicated at −20 °C for long-term storage.

Fungal genomic DNA was amplified by polymerase chain reaction (PCR) using informative phylogenetic markers of each family, including the internal transcribed spacers (ITS1-5.8S-ITS2), the 28S large subunit rDNA (LSU), the 18S small subunit rDNA (SSU), the partial RNA polymerase second largest subunit (rpb2), the translation elongation factor 1-alpha (tef1-α) and β-tubulin (tub2). The forward and reverse primer pairs ITS5 and ITS4 [83], LR0R and LR5 [84], NS1 and NS4 [83], rRPB2-5F and rRPB2-7cR [85], EF1-983F and EF1-2218R [86], and T1 and BT2B [87,88] were used to amplify the PCR fragments of these genes, respectively. Components of the PCR reaction mixture and the PCR thermal cycle program for ITS, LSU, SSU, rpb2, and tef1-α genes followed the condition described in Jiang et al. [50]. The PCR thermal cycle program for tub2 was set up initially at 94 °C for 3 min, followed by 35 cycles of denaturation at 94 °C for 30 s, annealing at 52 °C for 40 s, elongation at 72 °C for 1 min, a final extension at 72 °C for 10 min, before being held at 4 °C. PCR products were sent to TsingKe Biological Technology (Beijing) Co., Ltd., Beijing, China for purification and sequencing. The quality of the Sanger DNA sequences and sequence consensus from forward and reverse directions were checked and compiled manually in BioEdit v. 7.2.3 [89].

2.3. Sequence Alignment and Phylogenetic Analyses

The generated ITS sequences of the new isolates were used to search the related fungal group via the nucleotide BLAST search tool in the NCBI website (https://blast.ncbi.nlm.nih.gov/Blast.cgi; accessed on 5 December 2021). The nucleotide BLAST searches of the ITS sequence showed that the newly generated sequences had the closest similarity with species in families Anastomitrabeculiaceae, Parabambusicolaceae, Pyrenochaetopsidaceae and Tetraploasphaeriaceae. Thus, sequences generated from this study were analyzed with representative taxa in Anastomitrabeculiaceae, Parabambusicolaceae, Pyrenochaetopsidaceae and Tetraploasphaeriaceae, which were retrieved from GenBank based on recent publications (Table 1). Individual gene alignments were performed and improved manually where necessary using MEGA 7 [90]. Ambiguous sites were excluded from the alignment. Improved individual gene alignments were prior analyzed by maximum likelihood (ML) analysis using RaxmlGUI version 7.3.0 [91]. After checking the tree topologies of every individual gene alignment for congruence, the combined gene dataset of each family was analyzed based on Bayesian inference (BI), maximum likelihood (ML) and maximum parsimony (MP) analyses.
Table 1. GenBank accession numbers used in the phylogenetic analyses. The ex-type cultures are indicated with superscript “^T”, and the newly generated sequences are indicated in bold.

| Taxon                        | Voucher/Strain No. | Family | ITS | LSU | SSU | rpb2 | tub2 | tefl-a |
|------------------------------|-------------------|--------|-----|-----|-----|------|------|--------|
| Anastomitrabeilia didymospora| MFLUCC 16-0412^T  | Anast  | NR  | MW  | NG  | n/a  | n/a  | MW     |
| Anastomitrabeilia didymospora| MFLUCC 16-0417    | Anast  | MW  | MW  | MW  | n/a  | n/a  | MW     |
| Anastomitrabeilia didymospora| MFLUCC 11-0197^T  | Anast  | ON  | ON  | ON  | n/a  | n/a  | ON     |
| Anastomitrabeilia didymospora| MFLUCC 11-0200    | Anast  | ON  | ON  | ON  | n/a  | n/a  | ON     |
| Aquastroma magniostiolata    | KT 2485/HHUF 30122^T | Parab  | NR  | NG  | NG  | n/a  | n/a  | AB     |
| Aquatisphaeria thailandica   | MFLUCC 21-0025^T  | Tetra  | MW  | MW  | MW  | n/a  | n/a  | n/a    |
| Aquatisphaeria thailandica   | DLUCC B151       | Tetra  | n/a | MW  | MW  | n/a  | n/a  | n/a    |
| Bambusicola loculata         | MFLUCC 13-0856^T  | Bambu  | NR  | NG  | NG  | KP   | n/a  | KP     |
| Bambusicola massarinia       | MFLUCC 11-0389^T  | Bambu  | NR  | NG  | NG  | KP   | n/a  | KP     |
| Brevicollum hyalosporum      | MFLUCC 17-0071    | Neohe  | MG  | MG  | MG  | n/a  | n/a  | MG     |
| Brevicollum hyalosporum      | MAF 243400^T      | Neohe  | NR  | NG  | NG  | LC   | n/a  | LC     |
| Brevicollum versicolor       | HHUF 30591^T     | Neohe  | NR  | NG  | NG  | LC   | n/a  | LC     |
| Camarographium koreanum      | CBS 117159^T      | Macro  | JQ  | JQ  | n/a | n/a  | n/a  | n/a    |
| Crassiparies quadririspinus  | KHI11/HHUF 30409^T | Neohe  | NR  | NG  | NG  | n/a  | n/a  | n/a    |
| Crassiparies quadririspinus  | KT 2986/HHUF 30590 | Neohe  | LC  | LC  | LC  | n/a  | n/a  | n/a    |
| Dendryphiella fasciculata    | MFLUCC 17-1074^T  | Dictyo | NR  | NG  | n/a | n/a  | n/a  | n/a    |
| Dictycheirospora aquatica    | KUMCC 15-0305^T  | Dictyo | NR  | KY  | n/a | n/a  | n/a  | n/a    |
| Dictyosporium elegans        | NBRC 32502        | Dictyo | DQ  | DQ  | n/a | n/a  | n/a  | n/a    |
| Didymocrea sadesianii        | CBS 438.65        | Didymo | MH  | DQ  | n/a | n/a  | n/a  | n/a    |
| Didymosphaeria rubi-ulmifolii| MFLUCC 14-0023^T  | Didymo | n/a | KJ  | n/a | KJ   | n/a  | KJ     |
| Ernakulamia cochinensis      | PRC 3992          | Tetra  | LT  | LT  | n/a | n/a  | n/a  | n/a    |
Table 1. Cont.

| Taxon                        | Voucher/Strain No. | Family | GenBank Accession Number |
|------------------------------|-------------------|--------|--------------------------|
| Ernakulamia cochinensis      | MFLUCC 18-1237    | Tetra  | MT627670               |
|                              |                   |        | MN913716               |
| Ernakulamia krabensis        | KUMCC 18-0235 T   | Tetra  | NR_163341             |
|                              |                   |        | NG_066314             |
|                              |                   |        | NG_065780             |
|                              |                   |        | MK434872               |
| Ernakulamia tanakaii         | NFCCI 4617        | Tetra  | MN937228               |
|                              |                   |        | MN937210               |
|                              |                   |        | n/a                    |
|                              |                   |        | MN938311               |
| Ernakulamia tanakaii         | NFCCI 4615 T      | Tetra  | MN937229               |
|                              |                   |        | MN937211               |
|                              |                   |        | n/a                    |
|                              |                   |        | MN938312               |
| Ernakulamia xishuangbannaen-| KUMCC 17-0187 T   | Tetra  | MH275080               |
| sis                         |                   |        | MH260314               |
| Falciformispora lignatilis   | BCC 21117         | Trema  | KF432942               |
|                              |                   |        | GU371826               |
|                              |                   |        | GU371834               |
|                              |                   |        | n/a                    |
|                              |                   |        | GU371819               |
| Halojulella avicenniae       | BCC 20173         | Haloj  | n/a                    |
|                              |                   |        | GU371822               |
|                              |                   |        | GU371830               |
|                              |                   |        | GU371786               |
|                              |                   |        | n/a                    |
|                              |                   |        | GU371815               |
| Halojulella avicenniae       | BCC 18422         | Haloj  | n/a                    |
|                              |                   |        | GU371823               |
|                              |                   |        | GU371831               |
|                              |                   |        | GU371787               |
|                              |                   |        | n/a                    |
|                              |                   |        | GU371816               |
| Halojulella avicenniae       | PUFDS542          | Haloj  | MK028713               |
|                              |                   |        | MK026757               |
|                              |                   |        | MK026754               |
|                              |                   |        | MN532682               |
|                              |                   |        | n/a                    |
|                              |                   |        | n/a                    |
| Helminthosporium aquaticum   | MFLUCC 15-0357 T  | Massa  | NR_155170              |
|                              |                   |        | NG_059656              |
|                              |                   |        | NG_063601              |
|                              |                   |        | n/a                    |
|                              |                   |        | n/a                    |
| Katumotoa bambusicola        | KT 1517a/HHUF 28661 T | Lenti | NR_154103              |
|                              |                   |        | NG_059386              |
|                              |                   |        | NG_060989              |
|                              |                   |        | AB539095               |
|                              |                   |        | n/a                    |
|                              |                   |        | AB539108               |
| Lonicericola fuyuanensis     | MFLU 19-2850 T    | Parab  | NR_172419              |
|                              |                   |        | NG_073809              |
|                              |                   |        | NG_070329              |
|                              |                   |        | n/a                    |
|                              |                   |        | n/a                    |
|                              |                   |        | MN938324               |
| Lonicericola hyaloseptispora | KUMCC 18-0149 T   | Parab  | NR_164294              |
|                              |                   |        | NG_066434              |
|                              |                   |        | NG_067680              |
|                              |                   |        | n/a                    |
|                              |                   |        | n/a                    |
| Lonicericola hyaloseptispora | KUMCC 18-0150    | Parab  | MK098194               |
|                              |                   |        | MK098200               |
|                              |                   |        | MK098206               |
|                              |                   |        | n/a                    |
|                              |                   |        | n/a                    |
|                              |                   |        | MK098210               |
| Macrodiplodiopsis desmazieri | CBS 140062 T     | Macro  | NR_132924              |
|                              |                   |        | NG_058182              |
|                              |                   |        | n/a                    |
|                              |                   |        | n/a                    |
|                              |                   |        | n/a                    |
| Magnicamarosporium iriomotense | KT 2822/HHUF 30125 T | Sulca | NR_153445              |
|                              |                   |        | NG_059389              |
|                              |                   |        | NG_060999              |
|                              |                   |        | n/a                    |
|                              |                   |        | n/a                    |
| Massarina eburnea            | CBS 473.64        | Massa  | OM337528               |
|                              |                   |        | MH877786               |
|                              |                   |        | GU296170               |
|                              |                   |        | GU371732               |
|                              |                   |        | n/a                    |
|                              |                   |        | GU349040               |
| Medicopsis romeroi           | CBS 252.60 T     | Neohe  | NR_130697              |
|                              |                   |        | NG_057800              |
|                              |                   |        | NG_061069              |
|                              |                   |        | KF015708               |
|                              |                   |        | n/a                    |
|                              |                   |        | KF015678               |
| Medicopsis romeroi           | CBS 132878       | Neohe  | KF015658               |
|                              |                   |        | KF015622               |
|                              |                   |        | KF015648               |
|                              |                   |        | KF015709               |
|                              |                   |        | n/a                    |
|                              |                   |        | KF015682               |
| Medicopsis romeroi           | CBS 122784       | Neohe  | KF366447               |
|                              |                   |        | EU754208               |
|                              |                   |        | EU754109               |
|                              |                   |        | KF015707               |
|                              |                   |        | n/a                    |
|                              |                   |        | KF015679               |
| Melanomma pulvis-pyrius      | CBS 124080       | Melan  | MH863349               |
|                              |                   |        | MH874873               |
|                              |                   |        | GU456302               |
|                              |                   |        | GU456350               |
|                              |                   |        | n/a                    |
|                              |                   |        | GU456265               |
| Monodictys sp.               | JO 10            | Parab  | AB807552               |
|                              |                   |        | AB797262               |
|                              |                   |        | n/a                    |
|                              |                   |        | n/a                    |
|                              |                   |        | AB808528               |
| Taxon                  | Voucher/Strain No. | Family | GenBank Accession Number |
|-----------------------|--------------------|--------|--------------------------|
|                       |                    |        | ITS          | LSU          | SSU          | rpb2         | tub2         | tef1-α        |
| Monodictys sp.        | KH 331            | Parab  | n/a          | AB807553    | AB797263     | n/a          | n/a          | AB808529     |
| Multilocularia bambusae | MFLUCC 11-0180 T  | Parab  | NR_148099    | NG_059654   | NG_061229    | n/a          | n/a          | KU705656     |
| Multiseptospora thailandica | MFLUCC 11-0183 T | Parab  | NR_148080    | NG_059554   | KP753955     | n/a          | n/a          | KU705657     |
| Multiseptospora thailandica | MFLUCC 11-0204 | Parab  | KU693447     | KU693440    | KU693444     | n/a          | n/a          | KU705659     |
| Multiseptospora thailandica | MFLUCC 12-0006 | Parab  | KU693448     | KU693441    | KU693445     | n/a          | n/a          | KU705660     |
| Multiseptospora thailandica | MFLUCC 11-0202 T | Parab  | n/a          | NG_059655   | NG_063600    | n/a          | n/a          | KU705658     |
| Multiseptospora thailandica | MFLUCC 17-2551 T | Testu  | MG602224    | MG602248    | MG602249     | MG602250     | n/a          | MG602251     |
| Neoaquastroma bauhiniae | MFLUCC 16-0398 T  | Parab  | NR_165217    | NG_067814   | NG_070696    | MH028251     | n/a          | MH028247     |
| Neoaquastroma bauhiniae | MFLUCC 17-2205    | Parab  | MH025953     | MH023320    | MH023316     | MH028252     | n/a          | MH028248     |
| Neoaquastroma guttulatum | MFLUCC 14-0917 T | Parab  | KX949739     | KX949740    | KX949741     | n/a          | n/a          | KX949742     |
| Neohendersonia kickxii | CBS 138869 T      | Sulca  | NR_137945    | NG_058125   | n/a          | n/a          | n/a          | MG076037     |
| Neohendersonia kickxii | CBS 112403 T      | Neohe  | NR_154248    | NG_058264   | n/a          | n/a          | n/a          | n/a          |
| Neohendersonia kickxii | CBS 122938        | Neohe  | KX820257     | KX820268    | n/a          | n/a          | n/a          | n/a          |
| Neohendersonia kickxii | CPC 24865         | Neohe  | KX820259     | KX820270    | n/a          | n/a          | n/a          | n/a          |
| Neomultiseptospora yunnanensis | KUMCC 21-0411 T | Parab  | OL898884     | OL898892    | OL898890     | n/a          | n/a          | OL964282     |
| Neomultiseptospora yunnanensis | KUN-HKAS 122240 T | Parab  | OL898885     | OL898886    | OL898891     | n/a          | n/a          | OL964283     |
| Neopyrenochaetopsis hominis | CBS 143033 T | Pyren  | LN880536     | LN880537    | n/a          | LT593073     | LN880539     | n/a          |
| Palmiascoma gregariascomum | MFLUCC 11-0175 T | Bambu  | NR_154316    | NG_059557   | KP753958     | KP998466     | n/a          | n/a          |
| Parabambusicola aquatica | MFLUCC 18-1140 T | Parab  | NR_171877    | NG_073791   | n/a          | n/a          | n/a          | n/a          |
| Parabambusicola bambusina | H 4321/MAFF 239462 | Parab  | LC014578     | AB807536    | AB797246     | n/a          | n/a          | AB808511     |
| Parabambusicola bambusina | KH 139/MAFF 243823 | Parab  | LC014579     | AB807537    | AB797247     | n/a          | n/a          | AB808512     |
| Parabambusicola bambusina | KT 2637/MAFF 243822 | Parab  | LC014580     | AB807538    | AB797248     | n/a          | n/a          | AB808513     |
| Taxon                    | Voucher/Strain No.          | Family   | GenBank Accession Number | ITS     | LSU     | SSU     | rpb2   | tub2   | tef1-α |
|-------------------------|----------------------------|----------|--------------------------|---------|---------|---------|--------|--------|--------|
| **Parabambusicola**     |                            |          |                          |         |         |         |        |        |        |
| hongheensis             | KUMCC 21-0410 T            | Parab    | OL898880 OL898921 OL898886 n/a n/a n/a |         |         |         |        |        |        |
| thysanolaenae           | KUMCC 18-0147 T            | Parab    | NR_164044 NG_066435 NG_067681 n/a n/a MK098209 |         |         |         |        |        |        |
| **Paraconiothyrium**    |                            |          |                          |         |         |         |        |        |        |
| estuarinum              | CBS 109850 T               | Didym    | NR_166007 MH874432 AY642522 LT854937 JX496355 n/a |         |         |         |        |        |        |
| **Paramonodictys**      |                            |          |                          |         |         |         |        |        |        |
| hongheensis             | KUMCC 21-0343 T            | Parab    | OL436229 OL436227 OL436232 n/a n/a OL505582 |         |         |         |        |        |        |
| **Paramonodictys**      |                            |          |                          |         |         |         |        |        |        |
| thysanolaenae           | KUMCC 21-0346              | Parab    | OL436235 OL436224 OL436225 n/a n/a OLS05583 |         |         |         |        |        |        |
| **Paramonodictys**      |                            |          |                          |         |         |         |        |        |        |
| solitarius              | GZCC 20-0007 T             | Parab    | MN901115 MN987935 MN901118 MT023015 n/a MT023012 |         |         |         |        |        |        |
| **Paramonodictys**      |                            |          |                          |         |         |         |        |        |        |
| solitarius              | MFLUCC 17-2333             | Parab    | MT627707 MN913703 MT864299 n/a n/a MT5954397 |         |         |         |        |        |        |
| **Paramulitisep-**      |                            |          |                          |         |         |         |        |        |        |
| tospora bambusae        | KUN-HKAS 122241A T         | Parab    | ON077075 ON077064 ON077070 n/a n/a ON075058 |         |         |         |        |        |        |
| **Paramulitisep-**      |                            |          |                          |         |         |         |        |        |        |
| tospora bambusae        | KUN-HKAS 122241B           | Parab    | ON077076 ON077065 ON077071 n/a n/a ON075059 |         |         |         |        |        |        |
| **Paraphaeosphaeria**   |                            |          |                          |         |         |         |        |        |        |
| michotii                | MFLUCC 13-0349 T           | Didym    | NR_155640 NG_059522 KJ939285 KP998465 n/a n/a n/a |         |         |         |        |        |        |
| **Paratrimmatostroma**  |                            |          |                          |         |         |         |        |        |        |
| kunmingensis            | KUN-HKAS 102224A T         | Parab    | MK098192 MK098196 MK098204 n/a n/a MK098208 |         |         |         |        |        |        |
| **Paratrimmatostroma**  |                            |          |                          |         |         |         |        |        |        |
| kunmingensis            | KUN-HKAS 102224B           | Parab    | MK098195 MK098201 MK098207 n/a n/a n/a n/a |         |         |         |        |        |        |
| **Peacescomata**        |                            |          |                          |         |         |         |        |        |        |
| helicoides              | MFLUCC 11-0136 T           | Lenti    | NR_154317 NG_059565 NG_061205 PK998460 n/a KP998461 |         |         |         |        |        |        |
| **Polyplosphaeria**     |                            |          |                          |         |         |         |        |        |        |
| fusca                   | KT 1043 Tetra              | AB524788 AB524603 AB524642 n/a AB524850 AB524819 |         |         |         |        |        |        |
| fusca                   | KT 1640 Tetra              | AB524790 AB524605 AB524646 n/a AB524852 AB524821 |         |         |         |        |        |        |
| fusca                   | KT 1616 T Tetra            | AB524789 AB524604 AB524663 n/a AB524851 AB524820 |         |         |         |        |        |        |
| fusca                   | KT 1686 Tetra              | AB524606 AB52465 n/a n/a n/a n/a n/a |         |         |         |        |        |        |
| fusca                   | KT 2124 Tetra              | AB524791 AB524607 AB524666 n/a AB524853 AB524822 |         |         |         |        |        |        |
| nabanheensis            | KUMCC 16-0151 T            | Tetra    | MH275078 MH260312 MH260352 n/a MH412745 n/a |         |         |         |        |        |        |
| Taxon                                      | Voucher/Strain No. | Family | GenBank Accession Number | ITS      | LSU      | SSU      | rpb2 | tub2 | tef1-α |
|--------------------------------------------|-------------------|--------|--------------------------|----------|----------|----------|------|------|--------|
| Polyplosphaeria pandanicola              | KUMCC 17-0180     | Tetra  | T                        | MH275079 | MH260313 | MH260353 | n/a  | n/a  | n/a    |
| Polyplosphaeria thailandica              | MFLUCC 15-0840    | Tetra  | T                        | KU248766 | KU248767 | n/a      | n/a  | n/a  | n/a    |
| Pseudochaetosphaeromorpha larensense     | CBS 640.73        | Macro  | T                        | NG_057978 | NG_061147 | KF015706 | n/a  | KF015684 |
| Pseudocoleophoma calamagrostidis         | KT 3284/HHUF 30450 | Dicty | T                        | NR_154375 | NG_059804 | NG_061264 | n/a  | n/a  | LCO14614 |
| Pseudomonodictys tectona                 | MFLUCC 12-0552    | Parab  | T                        | n/a      | NG_059590 | NG_061213 | KT285572 | n/a  | KT285571 |
| Pseudotetraploa curviappendiculata       | HHUF 28582        | Tetra  | T                        | AB524792 | AB524608 | AB524467 | n/a  | AB524854 | AB524823 |
| Pseudotetraploa curviappendiculata       | KT 2558           | Tetra  | T                        | AB524794 | AB524610 | AB524469 | n/a  | AB524856 | AB524825 |
| Pseudotetraploa curviappendiculata       | HHUF 28590        | Tetra  | T                        | AB524793 | AB524609 | AB524468 | n/a  | AB524855 | AB524824 |
| Pseudotetraploa javanica                 | HHUF 28596        | Tetra  | T                        | AB524795 | AB524611 | AB524470 | n/a  | AB524857 | AB524826 |
| Pseudotetraploa longissima               | HHUF 28580        | Tetra  | T                        | AB524796 | AB524612 | AB524471 | n/a  | AB524858 | AB524827 |
| Pseudotetraploa rajmachiensis           | NFCCI 4619        | Tetra  | T                        | MN937222 | MN937204 | n/a      | n/a  | MN938305 |
| Pseudotetraploa rajmachiensis           | NFCCI 4618        | Tetra  | T                        | MN937221 | MN937203 | n/a      | n/a  | MN938304 |
| Pseudotetraploa rajmachiensis           | NFCCI 4620        | Tetra  | T                        | MN937223 | MN937205 | n/a      | n/a  | MN938306 |
| Pyrenochaetopsis americana               | FMR 1375          | Pyren  | T                        | LT592912 | LN907368 | n/a      | LT593050 | LT592981 |
| Pyrenochaetopsis yunnanensis            | KUMCC 21-0843     | Pyren  | T                        | ON077077 | ON077066 | ON077072 | ON075066 | ON075064 | ON075060 |
| Pyrenochaetopsis botulispora             | UTHSC:DI 16-289   | Pyren  | T                        | LT592941 | LN907432 | n/a      | LT593080 | LT593010 |
| Pyrenochaetopsis botulispora             | UTHSC:DI 16-297   | Pyren  | T                        | LT592945 | LN907440 | n/a      | LT593084 | LT593014 |
| Pyrenochaetopsis botulispora             | CBS 142458        | Pyren  | T                        | LT592946 | LN907441 | n/a      | LT593085 | LT593015 |
| Pyrenochaetopsis chromolaenae           | MFLUCC 17-1440    | Pyren  | T                        | MT214378 | MT214472 | NG_070172 | MT235827 | n/a  | MT235790 |
| Pyrenochaetopsis confuens                | CBS 142459        | Pyren  | T                        | LT592950 | LN907446 | n/a      | LT593089 | LT593019 |
| Pyrenochaetopsis decipiens              | CBS 343.85        | Pyren  | T                        | LT623223 | GQ387624 | NG_065569 | LT623280 | LT623240 |
Table 1. Cont.

| Taxon                  | Voucher/Strain No. | Family | GenBank Accession Number | ITS  | LSU  | SSU  | rpb2 | tub2 | tef1-α |
|------------------------|--------------------|--------|--------------------------|------|------|------|------|------|---------|
| *Pyrenochaetopsis*      |                    |        |                          |      |      |      |      |      |         |
| *globosa*               | CBS 143034         | Pyren  | LT592934                 | LN907418 | n/a | LT593072 | LT593003 | n/a |
| *indica*                | CBS 124454         | Pyren  | LT623224                 | GQ387626 | GQ387565 | LT623281 | LT623241 | n/a |
| *kuksensis*             | CBS 146534/MeND-F-57 | Pyren  | MT371092                 | MT371397 | n/a | MT372656 | MT372662 | n/a |
| *kuksensis*             | MeND-F-58          | Pyren  | MT371093                 | MT371398 | n/a | MT372657 | MT372663 | n/a |
| *leptospora*            | CBS 101635         | Pyren  | LT623225                 | EU754151 | n/a | LT623283 | LT623243 | n/a |
| *leptospora*            | CBS 122787         | Pyren  | LT592899                 | LN907341 | NG_065571 | LT593037 | LT592968 | n/a |
| *microspora*            | CBS 102876         | Pyren  | LT592897                 | LN907336 | n/a | LT593035 | LT592966 | n/a |
| *paucisetosa*           | CBS 142460         | Pyren  | KJ869117                 | KJ869175 | n/a | LT623286 | KJ869243 | n/a |
| *poae*                  | CBS 146846         | Pyren  | MT853115                 | MT853182 | n/a | MT857727 | MT857726 | MT857725 |
| *rajhradensis*          | CBS 119739         | Pyren  | LT623227                 | GQ387632 | n/a | LT623285 | LT623245 | n/a |
| *setiosissima*          | CGMCC 3.19296      | Pyren  | MK348586                 | MK348581 | n/a | MK35077 | MK348221 | n/a |
| *sinensis*              | CBS 139506/IBRC:M30051 | Pyren  | KF730241                 | KF803343 | NG_065034 | n/a | KX789523 | n/a |
| *tabarestanensis*       | HGUP 1802          | Pyren  | MH697394                 | MH697393 | n/a | MH697395 | MH697392 | n/a |
| *terricola*             | CBS 142461/FMR 13769 | Pyren  | LT592935                 | LN907420 | n/a | LT593074 | LT593004 | n/a |
| *uberiformis*           | CBS 125427         | Tetra  | AB524797                 | AB524613 | AB524472 | n/a | AB524859 | AB524828 |
| *bicorns*               | KT 2607            | Tetra  | AB524798                 | AB524614 | AB524473 | n/a | AB524860 | AB524829 |
| *meridionalis*          | KT 920             | Tetra  | AB524801                 | AB524617 | AB524476 | n/a | AB524863 | AB524832 |
| *setpentrientalis*      | CBS 125429         | Tetra  | AB524799                 | AB524615 | AB524474 | n/a | AB524861 | AB524830 |
| *setpentrientalis*      | CBS 125431         | Tetra  | AB524802                 | AB524618 | AB524477 | n/a | AB524864 | AB524833 |
| *setpentrientalis*      | CBS 125432         | Tetra  | AB524803                 | AB524619 | AB524478 | n/a | AB524865 | AB524834 |
| *setpentrientalis*      | CBS 125433         | Tetra  | AB524804                 | AB524620 | AB524479 | n/a | AB524866 | AB524835 |
Table 1. Cont.

| Taxon                          | Voucher/Strain No. | Family   | GenBank Accession Number |
|-------------------------------|--------------------|----------|----------------------------|
|                               |                    |          | ITS | LSU | SSU | rpb2 | tub2 | tef1-α |
| **Quadricrura septentrionalis** | CBS 125430 T       | Tetra    | AB524800 | AB524616 | AB524475 | n/a | AB524862 | AB524831 |
| **Scolecohyalosporium submersum** | KUMCC 21-0412 T  | Parab    | OL898883 | OL898924 | OL898889 | n/a | n/a | OL964281 |
| **Scolecohyalosporium submersum** | KUMCC 21-0413     | Parab    | OL898881 | OL898922 | OL898887 | n/a | n/a | OL964279 |
| **Scolecohyalosporium submersum** | KUN-HKAS 122242   | Parab    | OL898882 | OL898923 | OL898888 | n/a | n/a | OL964280 |
| **Setoseptoria phragmitis**   | CBS 114802 T       | Lenti    | KT376474 | KT376472 | KT376471 | n/a | n/a | n/a |
| **Shrungabeeja longiappendiculata** | BCC 76463 T      | Tetra    | KT376475 | KT376473 | n/a | n/a | n/a | n/a |
| **Shrungabeeja longiappendiculata** | BCC 76464       | Tetra    | MT627681 | MN913685 | n/a | n/a | n/a | n/a |
| **Spegazzinia tesserithra**   | SH 287             | Didym    | n/a | AB807584 | AB797294 | n/a | n/a | AB808560 |
| **Sulcatispora acerina**      | KT 2982 T          | Sulca    | LC014597 | LC014610 | LC014605 | n/a | n/a | LC014615 |
| **Sulcatispora berchienia**   | KT 1607 / HHUF 29097 T | Tetra | NR_153444 | NG_059390 | NG_064843 | n/a | n/a | AB808509 |
| **Tetraploa aquatica**        | MFLU 19-0995 T     | Tetra    | MT530448 | MT530452 | n/a | n/a | n/a | n/a |
| **Tetraploa aquatica**        | MFLU 19-0996       | Tetra    | MT530449 | MT530453 | MT530454 | n/a | n/a | n/a |
| **Tetraploa aristata**        | CBS 996.70         | Tetra    | AB524805 | AB524627 | AB52486 | n/a | n/a | AB524836 |
| **Tetraploa bambusae**        | KUMCC 21-0844      | Tetra    | ON077078 | ON077067 | ON077073 | n/a | ON075065 | ON075061 |
| **Tetraploa cylindrica**      | KUMCC 20-0205 T    | Tetra    | MT893205 | MT893204 | MT893203 | n/a | MT899418 | MT899417 |
| **Tetraploa dashaoensis**     | KUMCC 21-0010 T    | Tetra    | OL473549 | OL473555 | OL473556 | n/a | OL505601 | OL505599 |
| **Tetraploa dwibahubeeja**    | NFCCI 4621 T       | Tetra    | MN937225 | MN937207 | n/a | n/a | MN938308 | n/a |
| **Tetraploa dwibahubeeja**    | NFCCI 4622         | Tetra    | MN937224 | MN937206 | n/a | n/a | MN938307 | n/a |
| **Tetraploa dwibahubeeja**    | NFCCI 4623         | Tetra    | MN937226 | MN937208 | n/a | n/a | MN938309 | n/a |
| **Tetraploa endophytica**     | CBS 147114 T       | Tetra    | n/a | MW659165 | KT270279 | n/a | n/a | MW659821 |
| **Tetraploa nagasakienensis** | KUMCC 18-0109      | Tetra    | MK079890 | MK079891 | MK079888 | n/a | n/a | n/a |
| **Tetraploa nagasakienensis** | KT 1682 T          | Tetra    | AB524806 | AB524630 | AB52489 | n/a | AB524868 | AB524837 |
| **Tetraploa obpyriformis**    | KUMCC 21-0011 T    | Tetra    | OL473558 | OL473554 | OL473557 | n/a | OL505600 | OL505598 |
| Taxon                | Voucher/Strain No. | Family       | GenBank Accession Number |
|---------------------|--------------------|--------------|--------------------------|
|                     |                    | ITs          | LSU          | SSU | rpb2 | tub2 | tef1-α |
| Tetraploa pseudoaristata | NFCCI 4624 T      | Tetra        | MN937232     | MN937214 | n/a   | n/a   | MN938315 | n/a   |
| Tetraploa pseudoaristata | NFCCI 4625      | Tetra        | MN937230     | MN937212 | n/a   | n/a   | MN938313  | n/a   |
| Tetraploa pseudoaristata | NFCCI 4626      | Tetra        | MN937231     | MN937213 | n/a   | n/a   | MN938314  | n/a   |
| Tetraploa puzheheiensis | MFLUCC 20-0151 T | Tetra        | MT627744     | MT627655 | n/a   | n/a   | n/a       | n/a   |
| Tetraploa sascola    | FU31019           | Tetra        | MN937236     | MN937218 | n/a   | n/a   | n/a       | n/a   |
| Tetraploa sascola    | KT 563 T          | Tetra        | AB524807     | AB524631 | AB524490 | n/a   | AB524869  | AB524838 |
| Tetraploa sp.        | KT 1684           | Tetra        | n/a          | AB524628 | AB524487 | n/a   | n/a       | n/a   |
| Tetraploa sp.        | KT 2578           | Tetra        | AB524629     | AB524488 | n/a   | n/a   | n/a       | n/a   |
| Tetraploa sp.        | CY112             | Tetra        | HQ607964     | n/a     | n/a   | n/a   | n/a       | n/a   |
| Tetraploa thrajabahuboeja | NFCCI 4627 T     | Tetra        | MN937235     | MN937217 | n/a   | n/a   | MN938318  | n/a   |
| Tetraploa thrajabahuboeja | NFCCI 4628  | Tetra        | MN937233     | MN937215 | n/a   | n/a   | MN938316  | n/a   |
| Tetraploa thrajabahuboeja | NFCCI 4629  | Tetra        | MN937234     | MN937216 | n/a   | n/a   | MN938317  | n/a   |
| Tetraploa yakushimensis | KT 1906/HHUF 29652 T | Tetra   | NR_119405 | NG_042330 | NG_064836 | n/a   | AB524870  | AB524839 |
| Tetraploa yunnanensis | MFLUCC 19-0319 T | Tetra        | MT627743     | MN913735 | MT864341 | MT878451 | n/a       | n/a   |
| Trematosphaeria grisea | CBS 332.50 T | Trema        | NR_132039 | NG_057979 | NG_062930 | KP015720 | n/a       | KP015698 |
| Trematosphaeria pertusa | CBS 122368 T | Trema        | NR_132040 | NG_057809 | n/a     | n/a     | n/a       | n/a   |
| Tingoldiago graminicola | KH 68 T          | Lenti        | LC014598     | AB521743 | AB521726 | n/a     | n/a       | AB808561 |
| Triplosphaeria acuta  | KT 1170 T         | Tetra        | AB524809     | AB524633 | AB524492 | n/a     | AB524871  | AB524840 |
| Triplosphaeria cylindrica | KT 1800       | Tetra        | AB524810     | AB524635 | AB524494 | n/a     | AB524872  | AB524841 |
| Triplosphaeria cylindrica | KT 2550       | Tetra        | AB524811     | AB524636 | AB524495 | n/a     | AB524873  | AB524842 |
| Triplosphaeria maxima | KT 870/HHUF 29390 T | Tetra  | AB524812 | AB524637 | AB524496 | n/a     | AB524874  | AB524843 |
| Triplosphaeria sp.    | HHUF 27481        | Tetra        | AB524815     | AB524640 | AB524499 | n/a     | AB524877  | AB524846 |
| Triplosphaeria sp.    | KT 2546           | Tetra        | AB524816     | AB524641 | AB524500 | n/a     | AB524878  | AB524847 |
| Triplosphaeria yezoensis | KT 1715 T       | Tetra        | AB524813     | AB524638 | AB524497 | n/a     | AB524875  | AB524844 |
| Triplosphaeria yezoensis | KT 1732          | Tetra        | AB524814     | AB524639 | AB524498 | n/a     | AB524876  | AB524845 |
### Table 1. Cont.

| Taxon                  | Voucher/Strain No. | Family  | GenBank Accession Number | ITS     | LSU     | SSU     | rpbd    | tub2    | tef1-α |
|-----------------------|--------------------|---------|--------------------------|---------|---------|---------|---------|---------|---------|
| Trematosphaeria grisea| CBS 332.50 T       | Trema   |                          | NR_132039 | NG_057979 | NG_062930 | KF015720 | n/a     | KF015698 |
| Trematosphaeria pertusa| CBS 122368 T      | Trema   |                          | NR_132040 | NG_057809 | n/a     | n/a     | n/a     | n/a     |
| Xenopyrenochaetopsis pratorum | CBS 445.81/FMR 14878 T | Pyren  |                          | JF740263 | GU238136 | NG_062792 | KT389671 | KT389846 | n/a     |

Abbreviations: BCC: BIOTEC Culture Collection, Bangkok, Thailand; BCRC: FU: Bioresource Collection and Research Center Collection, Taiwan; CBS: the Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands; CGMCC: China General Microbiological Culture Collection Center; CPC: Collection of Pedro Crous housed at CBS; DLUCC: Dali University Culture Collection, Yunnan, China; PMR: Facultad de Medicina, Universitat Rovira i Virgili, Reus, Spain; GZCC: Guizhou Culture Collection, Guizhou, China; H: University of Helsinki, Helsinki, Finland; HGUP: Herbarium of Department of Plant Pathology, Guizhou University, Guizhou, China; HUF: the Herbarium of Hiroaki University Fungi, Aomori, Japan; IBRC: M: Herbarium of the Plant bank, Iranian Biological Resource Center; KH: K. Hirayama; KT: Kazuaki Tanaka, Japan; KUMCC: Kunming Institute of Botany Culture Collection, Yunnan, China; KUN-HKAS: Herbarium of Cryptogams Kunning Institute of Botany Academia Sinica, Yunnan, China; MeND-F: Fungal Collection of Mendeleum—Institute of Genetics, Mendel University, Czech Republic; MAFF: the National Institute of Agrobiological Sciences, Japan; MFLU: the Herbarium of Mae Fah Luang University Chiang Rai, Thailand; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Rai, Thailand; NBRC: Biological Resource Center, National Institute of Technology and Evaluation, Chiba, Japan; NFCC: National Fungal Culture Collection of India, Maharashtra, India; PRC: the Herbarium of the Charles University, Prague, Czech Republic; PPUF: Culture Collection at Pondicherry University, Puducherry, India; SH: S. Hughes; UTHSC: Fungas Testing Laboratory at the University of Texas Health Science Center, San Antonio, Texas, USA. Abbreviations of families: Anast: Anastomitrabeculiaceae; Bambu: Bambusicolaceae; Dicty: Dictyosporiaceae; Didym: Didymosphaeraceae; Haloj: Halojulellaceae; Lent: Lentitheciaceae; Macro: Macrodiplodiopsidaceae; Massa: Massarinaeae; Melan: Melanommataeae; Neohe: Neohendersoniaceae; Parab: Parabambusicolaceae; Pyren: Pyrenochnetopsisidae; Sulca: Sulcatisporaceae; Testu: Testudinaceae; Tetra: Tetraploasphaeraceae; Trem: Trematosphaeriaceae.

The evolutionary model of nucleotide substitution analysis was selected independently for each locus using MrModeltest 2.3 [92]. The best-fit model under the Akaike Information Criterion (AIC) of each locus was shown in Table 2. Bayesian inference (BI) was analyzed using MrBayes on XSEDE v. 3.2.7a via the CIPRES Science Gateway v. 3.3 [93]. Posterior probabilities (PP) [94,95] were determined by Markov Chain Monte Carlo sampling (MCMC). Two parallel runs with six simultaneous Markov chains were run for 1–2 million generations and stopped automatically when the average standard deviation of split frequencies reached below 0.01. Trees were sampled every 100th generation. The MCMC heated chain was set with a “temperature” value of 0.15. All sampled topologies beneath the asymptote (25%) were discarded as part of the burn-in procedure, and the remaining trees were used for calculating posterior probabilities in the majority rule consensus tree. Maximum likelihood (ML) was analyzed in RaxmlGUI version 7.3.0 [91] using the default algorithm of the program from a random starting tree for each run that was adjusted by setting up the GTR + GAMMA1 model of nucleotide substitution with 1000 rapid bootstrap replicates. Maximum parsimony was analyzed by PAUP v. 4.0b10 [96] using the heuristic search function with 1000 random stepwise addition replicates and tree bisection-reconnection (TBR) as the branch-swapping algorithm. Maxtrees were set up to 1000, and a zero of maximum branch length was collapsed. All characters were unordered and of equal weight, and gaps were treated as missing data. Significant parsimonious trees were determined by Kishino–Hasegawa tests (KHT) [97]. All equally parsimonious trees were saved. Clade stability was estimated by bootstrap (BS) support values with 1000 replicates, each with 10 replicates of random stepwise addition of taxa [98]. Descriptive tree statistics viz. tree length (TL), consistency index (CI), retention index (RI), relative consistency index (RC) and homoplasy index (HI) were calculated.
Table 2. The best nucleotide substitution model for each locus based on the Akaike Information Criterion (AIC) generated by MrModeltest v. 2.3.

| Phylogenetic Analyses | Nucleotide Substitution Models |
|-----------------------|--------------------------------|
|                       | ITS   | LSU   | SSU   | rpb2  | tefl-α | tub2  |
| A1: Anastomitrabeculiaceae | SYM+G | GTR+I+G | GTR+I | n/a   | GTR+I+G | n/a   |
| A2: Parabambusicolaceae  | GTR+I+G | GTR+I+G | HKY+I+G | n/a   | GTR+I+G | n/a   |
| A3: Pyrenochaetopsidaceae | SYM+G | GTR+I | n/a   | SYM+I+G | GTR+G | n/a   |
| A4: Tetraploasphaeriaceae | GTR+I+G | GTR+I+G | GTR+I+G | n/a   | HKY+I+G | GTR+I+G |

Phylograms were visualized on FigTree v. 1.4.0 [99], and layouts of trees were drawn in Microsoft Office PowerPoint 2016 (Microsoft Inc., Redmond, WA, USA). The newly generated sequences in this study are deposited in GenBank (Table 1). The final alignment and tree were submitted in TreeBASE (https://www.treebase.org; accessed on 25 March 2022) under submission ID: 29589 (A1: Anastomitrabeculiaceae), 29590 (A2: Parabambusicolaceae), 29592 (A3: Pyrenochaetopsidaceae), and 29593 (A4: Tetraploasphaeriaceae).

3. Results

3.1. Phylogeny

Four phylogenetic analyses were conducted to resolve phylogenetic relationships of taxa in Anastomitrabeculiaceae (Analysis 1), Parabambusicolaceae (Analysis 2), Pyrenochaetopsidaceae (Analysis 3), and Tetraploasphaeriaceae (Analysis 4) as follows:

Analysis 1: Taxa in Anastomitrabeculiaceae were analyzed with related taxa in families Halojulaceae and Neohendersoniaceae based on a combined LSU, SSU, ITS, and tefl-α DNA sequence dataset. The Data matrix comprised 20 taxa, of which two species in Massarinaceae (*Helminthosporium aquaticum* MFLUCC 15-0357, and *Massarina eburnea* CBS 473.643) were selected as the outgroup taxa. The dataset consists of 3471 total characters, including gaps (LSU: 1–870 bp, SSU: 871–1900 bp, ITS: 1901–2499 bp, tefl-α: 2500–3471 bp). The best scoring RAxML tree is presented in Figure 1 with a final ML optimization likelihood value of $-10679.529226$ (ln). RAxML analysis yielded 750 distinct alignment patterns, and the proportion of gaps and completely undetermined characters in this alignment was 21.29%. The proportion of invariable sites $I = 0.402038$ and the gamma distribution shape parameter $\alpha = 0.46716$. The Tree-Length was $0.871849$ with estimated base frequencies were as follows: $A = 0.242670$, $C = 0.243741$, $G = 0.248897$, $T = 0.244693$, and substitution rates $AC = 1.181725$, $AG = 2.821009$, $AT = 1.536446$, $CG = 0.754762$, $CT = 7.660341$, $GT = 1.000000$. The maximum parsimonious dataset consisted of 3471 characters, with 2722 characters being constant (proportion $= 0.784212$), 212 variable characters being parsimony-uninformative and 537 characters being parsimony-informative. The parsimonious analysis yielded six parsimonious trees, of which the first parsimonious tree was selected as the best tree for the Kishino–Hasegawa test ($TL = 1178$, $CI = 0.778$, $RI = 0.845$, $RC = 0.657$, $HI = 0.222$). Bayesian analysis yielded 10,001 trees from one million runs, of which 7501 were sampled. Bayesian posterior probabilities (BPP) from MCMC were evaluated with the final average standard deviation of split frequencies $= 0.004119$.

The phylogenetic results based on maximum likelihood (ML), maximum parsimony (MP) and Bayesian inference analyses (Figure 1) showed overall similar tree topologies. Two new strains of *Anastomitrabeculia didymospora* (MFLUCC 11-0197, MFLUCC 11-0200) shared the same branch length with 72% ML support and grouped with the type strains of *A. didymospora* (MFLUCC 16-0412, MFLUCC 16-0416) with high support (100% ML, 100% MP, 1.00 PP) in Anastomitrabeculiaceae.
Analysis 1: Taxa in Anastomitrabeculiaceae were analyzed with related representative genera in Parabambusicolaceae and other related families, including Bambusicolaceae, Didymosphaeriaceae, Lentitheciaceae, Macrodiplodiopsidaceae, Sulcatisporaceae, and Trematosphaeriaceae based on a combined ITS, LSU, SSU, and tef1-α sequence dataset. The data matrix comprised 65 taxa with Melanomma pulvispyrus CBS 124080 (Melanommataceae) being the outgroup taxon. The dataset consists of 3828 total characters, including gaps (ITS: 1–601 bp, LSU: 602–1487 bp, SSU: 1488–2891 bp, tef1-α: 2892–3828 bp). The best scoring RAxML tree is presented in Figure 2 with a final ML optimization likelihood value of −25582.174441 (ln). RAxML analysis yielded 1375 distinct alignment patterns, and the proportion of gaps and completely undetermined characters in this alignment was 27.28%. The gamma distribution shape parameter alpha = 0.193883 and the Tree-Length = 2.813374. Estimated base frequencies were as follows: A = 0.236013, C = 0.254062, G = 0.272236, T = 0.237689, with substitution rates AC = 1.230009, AG = 2.581111, AT = 1.427698, CG = 1.028329, CT = 5.964523, GT = 1.000000. Bayesian analysis yielded 20,001 trees from two million runs, of which 15001 were sampled. Bayesian posterior probabilities (BYPP) from MCMC were evaluated with the final average standard deviation of split frequencies = 0.005045.

The phylogenetic results based on maximum likelihood (ML) and Bayesian inference analyses (Figure 2) showed overall similar tree topologies. A novel genus, Paramultisep-tospora formed a stable subclade, clustered with the genera Multisep-tospora, Neomultisep-tospora, and Scolecohyalosporium with low support. These four genera formed a well-resolved clade (100% ML, 1.00 PP) within Parabambusicolaceae.

Figure 1. Phylogram generated from RAxML analysis of a concatenated LSU-SSU-ITS-tef1-α sequence dataset to represent the phylogenetic relationships of taxa in Anastomitrabeculiaceae, Halojulellaceae, and Neohendersoniaceae. Bootstrap support values for ML and MP equal to or greater than 70% and the Bayesian posterior probabilities equal to or higher than 0.95 PP are indicated above the nodes as ML/MP/PP. Support values lower than 70% ML/MP and 0.95 PP are indicated by a hyphen (-). Ex-type strains are in bold and the newly generated sequences are indicated in blue.
Figure 2. Phylogram generated from RAxML analysis of a concatenated ITS-LSU-SSU-tef1-α sequence dataset to represent the phylogenetic relationships of novel taxa in Parabambusicolaceae with other related families in Pleosporales. Bootstrap support values for ML equal to or greater than 70% and the Bayesian posterior probabilities equal to or higher than 0.95 PP are indicated above the nodes as ML/PP. Support values lower than 70% ML and 0.95 PP are indicated by a hyphen (-). Ex-type strains are in bold, and the new species is indicated in blue. The arrow in the figure is indicated the support value at the node.

Analysis 3: A new species, Pyrenochaetopsis yunnanensis, was analyzed with taxa in Pyrenochaetopsidaceae based on a combined LSU, ITS, rpb2 and tub2 DNA sequence dataset. The data matrix comprised 25 taxa, with Neopyrenochaetopsis hominis CBS 143033 being the outgroup taxon. The dataset consists of 2819 total characters, including gaps (LSU: 1–908 bp, ITS: 909–1468 bp, rpb2: 1469–2437 bp, tub2: 2438–2819 bp). The best scoring RAxML tree is presented in Figure 3 with a final ML optimization likelihood value of -12390.524384 (ln). RAxML analysis yielded 814 distinct alignment patterns, and the proportion of gaps and completely undetermined characters in this alignment was 7.92%. The proportion of invariable sites I = 0.518277 and the gamma distribution shape parameter alpha = 0.456186. The Tree-Length = 2.561446 with estimated base frequencies
were as follows: \( A = 0.244976, \ C = 0.246101, \ G = 0.270141, \ T = 0.238781 \), and substitution rates \( AC = 2.182690, \ AG = 6.088919, \ AT = 2.687456, \ CG = 1.526108, \ CT = 12.069267, \) \( GT = 1.000000 \). The maximum parsimonious dataset consisted of 2819 characters, with 2067 characters being constant (proportion = 0.733239), 267 variable characters being parsimony-uninformative and 485 characters being parsimony-informative. The parsimonious analysis yielded eight parsimonious trees, of which the first parsimonious tree was selected as the best tree for the Kishino–Hasegawa test (TL = 1836, CI = 0.583, RI = 0.594, RC = 0.346, HI = 0.417). Bayesian analysis yielded 10,001 trees from one million runs, of which 7501 were sampled. Bayesian posterior probabilities (BYPP) from MCMC were evaluated with the final average standard deviation of split frequencies = 0.006366.

Phylograms generated from maximum likelihood (ML), maximum parsimony (MP) and Bayesian inference analyses (Figure 3) were overall similar tree topologies. A new species, *Pyrenochaetopsis yunnanensis* (KUMCC 21-0843), has a close relationship with *P. terricola* (HGUP 1802) with high support (100% ML, 100% MP, 1.00 PP) and formed a well-resolved clade basal on *P. confluens* (CBS 142459), *P. decipiens* (CBS 343.85) and *P. indica* (CBS 124454) within Pyrenoachetopsidaceae.

Figure 3. Phylogram generated from RAxML analysis of a concatenated LSU-ITS*-tef1*-tub2* sequence dataset to represent the phylogenetic relationships of a novel taxon in Pyrenoachetopsidaceae. Bootstrap support values for ML and MP equal to or greater than 70% and the Bayesian posterior probabilities equal to or higher than 0.95 PP are indicated above the nodes as ML/MP/PP. Support values lower than 70% ML/MP and 0.95 PP are indicated by a hyphen (−). Ex-type strains are in bold, and the new species is indicated in blue. The arrow is indicated the support value at the node.

Analysis 4: A new species, *Tetraploa bambusae*, was analyzed with other representative taxa in Tetraploaasphaeriaceae based on a combined LSU, ITS, SSU, *tub2* and *tef1*-α DNA sequence dataset. The data matrix comprised 71 taxa, with *Muritestudina chiangraensis* (MFLUCC 17-2551) being the outgroup taxon. The dataset consists of 3397 total characters, including gaps (LSU: 1–853 bp, ITS: 854–1427 bp, SSU: 1428–2421 bp, *tub2*: 2422–3078 bp, *tef1*-α: 3079–3397 bp). The best scoring RAxML tree is presented in Figure 4 with a final ML optimization likelihood value of \(-18736.220881\) (ln). RAxML analysis yielded 1138 distinct alignment patterns, and the proportion of gaps and completely undetermined characters in this alignment was 27.96%. The proportion of invariable sites \( I = 0.573772 \) and the gamma distribution shape parameter alpha = 0.671292. The Tree-Length = 3.408354, and the estimated base frequencies were as follows: \( A = 0.239956, \ C = 0.252519, \ G = 0.274658, \)
T = 0.232866, and substitution rates AC = 2.302918, AG = 3.658670, AT = 1.691247, CG = 1.425389, CT = 8.553285, GT = 1.000000. The maximum parsimonious dataset consisted of 3397 characters, with 2452 characters being constant (proportion = 0.721813), 177 variable characters being parsimony-uninformative and 768 characters being parsimony-informative. The parsimonious analysis yielded 1000 parsimonious trees, of which the first parsimonious tree was selected as the best tree for the Kishino–Hasegawa test (TL = 2787, CI = 0.532, RI = 0.832, RC = 0.443, HI = 0.468). Bayesian analysis yielded 10,001 trees from one million runs, of which 7501 were sampled. Bayesian posterior probabilities (BYPP) from MCMC were evaluated with the final average standard deviation of split frequencies = 0.007021.

Phylograms generated from maximum likelihood (ML), maximum parsimony (MP) and Bayesian inference analyses (Figure 4) were overall similar tree topologies. A new species, Tetraploa bambusae (KUMCC 21-0844) formed a low support subclade (63% ML, 37% MP, 0.83 PP) with Tetraploa sp. (KT 1684) and clustered with T. endophytica (CBS 147114) and T. obpyriformis (KUMCC 21-0011) with high support (99% ML, 98% MP, 1.00 PP).

Figure 4. Phylogram generated from RAxML analysis of a concatenated LSU-ITS-SSU-tub2-tef1-α sequence dataset to represent the phylogenetic relationships of the novel taxon in Tetraploasphaeriaceae. Bootstrap support values for ML and MP equal to or greater than 70% and the Bayesian posterior probabilities equal to or higher than 0.95 PP are indicated above the nodes as ML/MP/PP. Support values lower than 70% ML/MP and 0.95 PP are indicated by a hyphen (-). Ex-type strains are in bold, and the new species is indicated in blue.
3.2. Taxonomy

**Anastomitrabeculiaceae** Bhunjun, Phukhams. and K.D. Hyde

Bhunjun et al. [71] introduced the novel family Anastomitrabeculiaceae to accommodate a monotypic genus *Anastomitrabeculia* based on morphological characteristics and phylogenetic analyses of a combined LSU, SSU and *tef1-a* dataset coupled with divergence time estimates using molecular clock methodologies. The novel taxa were isolated from bamboo culms submerged in freshwater in southern Thailand. The genus is characterized by gregarious, uni-loculate, globose to subglobose, coriaceous ascomata, immersed under a clypeus to semi-immersed, with short, carbonaceous ostiolar neck, bitunicate, fissitunicate, cylindric-clavate asci, embedded in a hyaline, trabeculate pseudoparaphyses, and hyaline, fusiform, septate ascospores with longitudinally striate wall ornamentation, surrounded by a distinct, mucilaginous sheath [71]. According to Bhunjun et al. [71], Anastomitrabeculiaceae has a close phylogenetic relationship with Halojulellaceae. However, Halojulellaceae can be distinguished from Anastomitrabeculiaceae in having cellular pseudoparaphyses and pigmented ascospores. In this study, we collected *Anastomitrabeculia didymospora* from bamboo branches in terrestrial habitats in northern Thailand reported for the first time.

**Anastomitrabeculia didymospora** Bhunjun, Phukhams. and K.D. Hyde, in Bhunjun, Phukhamsakda, Jeewon, Promputtha and Hyde, Journal of Fungi 7(2, no. 94): 12 (2021)

Index Fungorum number: IF 556559, Figure 5

Holotype information: Thailand, Krabi Province (8.1° N, 98.9° E), on dead bamboo culms submerged in freshwater, 15 December 2015, C. Phukhamsakda, KR001 (MFLU 20-0694), ex-type living culture = MFLUCC 16-0412.

Saprobic on dead branches of bamboo, visible as raised, black spots, with spike-like on the host surface. Sexual morph: Ascomata 200–320 μm high, 580–730 μm diam (excluding neck), gregarious, scattered to clustered, immersed under the clypeus to erumpent through host tissue by an ostiolar neck, ampulliform to subconical or hemispherical, uni-loculate, dark brown to black. Ostiolar neck 70–170 μm high, 130–200 μm diam, black, short, central, carbonaceous, papillate, protruding through host tissue. Peridium 30–100 μm wide at the sides, 6–15 μm wide at the base, unequally thick, poorly developed at the base, composed of fungal tissues intermixed with host tissues, of dark brown to black pseudoparenchymatous cells, arranged in a textura angularis. Hamathecium 1–2 μm wide, composed of dense, septate, branched, anastomosed, trabeculate pseudoparaphyses, embedded in a gelatinous matrix. Ascii (100–)120–140–(170) × 16–20(–24) μm (x = 131.6 × 19.2 μm, n = 20), eight-spored, bitunicate, fissitunicate, cylindric-clavate, with a short pedicel, apically rounded with an ocular chamber. Ascospores (22–)25–30 × (6–)8–10 μm (x = 27.1 × 8.2 μm, n = 20), overlapping 1–2-seriate, hyaline, fusiform, straight to curved, 1(–3)-septate, wider in the upper part, rough-walled, with longitudinal furrows on the surface, surrounded by a distinct mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics: Ascospores germinated on PDA within 12 h. Colonies on PDA reaching 29–33 mm diam after 2 weeks at room temperature (30–35 °C). Colonies medium dense, irregular in shape, flat to slightly raised, surface smooth with an undulate edge, floccose to fluffy; colonies from above white at the margin, pale gray at the middle, with white hyphal turfs at the center; from below white to cream at the margin, yellowish-brown at the middle, dark greenish-gray to black at the center, slightly radiating inwards colony; not producing pigment on PDA.

Material examined: Thailand, Chiang Rai Province, Phan District, Mae Yen Subdistrict, Pu Khang Waterfall, on dead branches of bamboo, 13 January 2011, N.N. Wijayawardene, RP0113 (MFLU 11-0233), living culture: MFLUCC 11-0197; Chiang Mai Province, Mae Rim District, Mae Sa Waterfall, on dead branches of bamboo, 12 March 2011, R. Phookamsak, RP0116 (MFLU11-0236), living culture: MFLUCC 11-0200.

Known distribution: Krabi Province, southern Thailand [71], Chiang Mai and Chiang Rai Provinces, northern Thailand (this study).

Known host and habitats: saprobic on bamboo in freshwater [71] and terrestrial environments (this study).
Notes: The nucleotide BLAST search of ITS, LSU and tef1-α sequences resulted in the two newly generated strains (MFLUCC 11-0197 and MFLUCC 11-0200) being similar to Anastomitrabeculia didymospora MFLU 20-0694 (100% similarity). A nucleotide pairwise comparison of ITS, LSU and tef1-α sequences also indicated that strains MFLUCC 11-0197 and MFLUCC 11-0200 are consistent (less than 1.5% different base pair) with A. didymospora MFLU 20-0694 (type strain). We, therefore, identified our strains as A. didymospora.

Morphologically, the new collection (MFLU 11-0233) is slightly larger in ascomata, asci, and ascospores than those of the type of A. didymospora [71]. The differences in the size range may be affected by environmental factors. Bhunjun et al. [71] mentioned that A. didymospora (MFLU 20-0694) has one-septate ascospores; however, we found that the species has 1(–3)-septate ascospores in this study. The host preference of A. didymospora is currently restricted to bamboo. However, the species is reported from terrestrial habitats for the first time.

Figure 5. Anastomitrabeculia didymospora (MFLU 11-0233). (a) The appearance of ascomata on the host surface; (b) Vertical section of ascoma with ostiolar neck; (c,d) Peridium; (e) Pseudoparaphyses stained in cotton blue; (f–h) Asci; (i–l) Ascospores; (m) Germinating ascospore; (n,o) Culture characteristics on PDA after two weeks ((n) = from above, (o) = from below). Scale bars: (b) = 100 µm, (c–h) = 20 µm, (i–m) = 10 µm.

Parabambusicolaceae Kaz. Tanaka and K. Hiray.

Parabambusicolaceae was introduced by Tanaka et al. [27] to accommodate the genera Aquastroma, Multiseptospora, Parabambusicola, and the other two “Monodictys sp.”. Later, a monotypic genus Multilocularia was included in this family by Li et al. [100], while Wansasinghe et al. [101] and Phukhamsakda et al. [102] addressed both sexual and coelomycetous
asexual species of Neoaquastroma in this family. Phukhamsakda et al. [102] also included Pseudomonodictys in Parabambusicolaceae. Subsequently, many genera were introduced in this family, including Lonicericola, Neomultiseptospora, Paramonodictys, Paratrimmatostroma, and Scolcohyalosporium [63,103,104]. Presently, 11 genera are accepted in this family based solely on the morpho-molecular approach. We follow the latest treatment of Xie et al. [104] and introduce the new genus Paramultiseptospora to accommodate a single species P. bambusae sp. nov. in this study.

Paramultiseptospora Phookamsak, H.B. Jiang and Chomnunti, gen. nov.
Index Fungorum number: IF 554966
Etymology: Referring to relations with phylogenetically close genus Multiseptospora.
Saprobic on dead stems of bamboo. Sexual morph: Ascomata gregarious, scattered to clustered, immersed in dark brown longitudinal clypeus, visible as raised, becoming superficial, lying along the host surface, uni-loculate, hemispherical to flattened ellipsoidal, or quadrilateral, glabrous, with apapillate ostiole. Peridium thin- to thick-walled, slightly thick at the sides, thinner at the apex, poorly developed at the base, composed of several layers of brown to dark brown, pseudoparenchymatous cells, paler brown to hyaline toward the inner layers, arranged in a textura angularis, outer layers intermixed with host tissues. Hamathecium composed of dense, branched, septate cellular pseudoparaphyses, anastomosed above the asci, embedded in a hyaline gelatinous matrix. Asci eight-spored, bitunicate, fissitunicate, cylindric-clavate to clavate, shortly pedicellate, with a well-developed ocular chamber. Ascospores overlapping one to three-seriate, hyaline, fusiform to oblong, with rounded ends, septate, constricted at the septa, smooth-walled, surrounded by a thick, mucilaginous sheath, with small guttules. Asexual morph: Undetermined.

Type species: Paramultiseptospora bambusae Phookamsak and H.B. Jiang, sp. nov.
Notes: A monotypic genus Paramultiseptospora is introduced herein due to the differences in morphological characteristics with the other related genera (viz. Multiseptospora, Neomultiseptospora and Scolcohyalosporium), although the phylogenetic affinity of the genus does not support in this study. Paramultiseptospora formed a stable clade, closely related to Multiseptospora and Scolcohyalosporium in both BI and ML analyses and clustered with Neomultiseptospora. These four genera formed a well-resolved clade (100% ML, 1.00 PP; Figure 2) within Parabambusicolaceae. Paramultiseptospora can be easily distinguished from Multiseptospora and Scolcohyalosporium in having hemispherical to flattened ellipsoidal, glabrous, ascomata, immersed in longitudinal clypeus, visible as raised, lying along the host surface, cylindric-clavate to clavate asci with short pedicel and fusiform to oblong ascospores, with rounded ends. Meanwhile, Multiseptospora has globose to subglobose ascomata, covered by dark, hair-like hyphae, broadly cylindrical, subsessile asci, and fusiform to verriform ascospore, with acute ends [33]. Scolcohyalosporium is different in having conical to ovoid, black, rough-walled ascomata, erumpent to superficial on the host, long cylindrical asci, with short pedicel and filiform ascospores [104]. Paramultiseptospora morphologically resembles Neomultiseptospora in having hemispherical to subconical, glabrous ascomata, immersed in the host, with apapillate ostiole, clavate asci, with short pedicel and fusiform or oblong, septate ascospores, surrounded by a thick mucilaginous sheath. However, these two genera are slightly different in the characteristics of ascomata on the host. Paramultiseptospora formed gregarious, scattered to clustered ascomata, immersed in dark brown longitudinal clypeus, lying along the host surface whereas Neomultiseptospora formed solitary, scattered, immersed, visible as raised, black dome-shaped on the host surface [104]. Phylogenetically, Paramultiseptospora always formed a separate branch from Neomultiseptospora. Therefore, we consider Paramultiseptospora as a distinct genus with Neomultiseptospora based on morphology coupled with the phylogenetic relationship.

Paramultiseptospora bambusae Phookamsak and H.B. Jiang, sp. nov.
Index Fungorum number: IF 554968, Figure 6
Etymology: Referring to the host, bamboo, of on which the species was collected.
Holotype: KUN-HKAS 122241
Saprobic on a dead stem of bamboo. Sexual morph: Ascomata 115–150 µm high, 340–470 µm diam, gregarious, scattered to clustered, immersed in dark brown longitudinal clypeus, visible as raised, becoming superficial, lying along the host surface, uni-loculate, hemispherical to flattened ellipsoidal, or quadrilateral, glabrous, indistinct apapillate ostiole. Peridium 30–90 µm wide at the sides toward the apex, 10–25 µm wide at the base, thin- to thick-walled, slightly thick at the sides, thinner at the apex, poorly developed at the base, composed of several layers of brown to dark brown, pseudoparenchymatous cells, paler brown to hyaline toward the inner layers, arranged in a textura angularis, outer layers intermixed with host tissues. Hamathecium composed of dense, 1–2.5 µm wide, branched, septate cellular pseudoparaphyses, anastomosed above the asci, embedded in a hyaline gelatinous matrix. Asci (70–)75–90(–95) × 16–20(–22) µm (x = 83.3 × 19.6 µm, n = 30), eight-spored, bitunicate, fissitunicate, cylindric-clavate to clavate, shortly pedicellate, apically rounded, with a well-developed ocular chamber. Ascospores (23–)25–28(–29) × 5–8 µm (x = 25.8 × 6.6 µm, n = 30), overlapping one to three-seriate, hyaline, fusiform to oblong, with rounded ends, narrower toward the end cells, enlarged at the third cell from above, slightly curved, six-septate, constricted at the septa, smooth-walled, surrounded by a thick, mucilaginous sheath, with small guttules. Asexual morph: Undetermined

Material examined: China, Yunnan Province, Honghe Autonomous Prefecture, Honghe County, Honghe Hani Rice Terraces (23°5′35″ N, 102°46′47″ E, 1432 + 6 msl), on dead stem of bamboo, 26 January 2021, R. Phookamsak, BN09F (KUN-HKAS 122241, holotype), ex-type strain: KUN-HKAS 122241A. Notes: DNA was extracted from fruit bodies. Known distribution: Yunnan Province, China. Known host and habitats: saprobic on a stem of bamboo in a terrestrial environment. Notes: The nucleotide BLAST search of ITS sequence indicated that Paramultiseptospora bambusae (KUN-HKAS 122241A) has the closest similarity with Multiseptospora thailandica strain MFLUCC 11-0183 (ex-type strain) with 95.58% similarity (Identities = 432/452, with no gap), strains MFLUCC 11-0204 and MFLUCC 12-0006 with 95.48% similarity (Identities = 444/465, with no gap) and is similar to “Pleosporales sp. strain 1192” (95.54% similarity, Identities = 407/426, with no gap). Paramultiseptospora bambusae (KUN-HKAS 122241A) also matches with Neomultiseptospora yunnanensis strain KUMCC 21-0411 (ex-type strain) with 92.84% similarity (Identities = 428/461, with no gap) and Scolecohyalosporium submersum strain KUMCC 21-0412 (ex-type strain) with 92.57% similarity (Identities = 436/471, with two gaps). The nucleotide BLAST search of LSU sequence indicated that P. bambusae (KUN-HKAS 122241A) is similar to S. submersum strains KUMCC 21-0412, KUMCC 21-0413 and KUN-HKAS 122242 with 98.57% similarity (Identities = 830/842, with two gaps), similar to M. thailandica strain MFLUCC 12-0006 (98.56% similarity, Identities = 830/843, with four gaps) and strain MFLUCC 11-0204 (98.46% similarity, Identities = 821/833, with three gaps), and is similar to N. yunnanensis strain KUMCC 21-0411 (97.59% similarity, Identities = 811/831, with one gap) and strain KUN-HKAS 122240 (97.23% similarity, Identities = 808/831, with one gap). Based on a nucleotide pairwise comparison, Paramultiseptospora bambusae (KUN-HKAS 122241A) differs from Multiseptospora thailandica (MFLUCC 11-0183, ex-type strain) in 88/570 bp of ITS (15.44%), 13/765 bp of LSU (1.7%), and 28/645 bp of tef1-α (4.34%). Paramultiseptospora bambusae (KUN-HKAS 122241A) differs from Scolecohyalosporium submersum (KUMCC 21-0412) in 85/595 bp of ITS (14.28%), 12/842 bp of LSU (1.42%), and 39/921 bp of tef1-α (4.23%). The species is also different from Neomultiseptospora yunnanensis strain KUMCC 21-0411 (ex-type strain) in 102/606 bp of ITS (16.83%), 21/832 bp of LSU (2.52%), and 52/979 bp of tef1-α (5.31%). Paramultiseptospora bambusae is morphologically similar to N. yunnanensis but differs in having fusiform to oblong, six-septate ascospores with rounded ends, narrower toward the end cells, and constricted at the septa, whereas N. yunnanensis has fusiform to ellipsoidal, or oblong, (four to) five-septate ascospores, with rounded ends, slightly constricted at the central septum, which are less constricted at the other septa [104].
(2.52%), and 52/979 bp of tef1-α (5.31%). Paramultiseptospora bambusae is morphologically similar to N. yunnanensis but differs in having fusiform to oblong, six-septate ascospores with rounded ends, narrower toward the end cells, and constricted at the septa, whereas N. yunnanensis has fusiform to ellipsoidal, or oblong, (four to) five-septate ascospores, with rounded ends, slightly constricted at the central septum, which are less constricted at the other septa [104].

**Figure 6.** Paramultiseptospora bambusae (KUN-HKAS 122241, holotype). (a) The appearance of ascomata on host substrate; (b) Vertical section of ascoma; (c) Peridium; (d) Asci embedded in cellular pseudoparaphyses; (e) Ascus; (f) Ascospores stained with Indian ink showing a thick mucilaginous sheath surrounded ascospores; (g–j) Ascospores. Scale bars: (b) = 100 µm, (c) = 50 µm, (d–f) = 20 µm, (g–j) = 10 µm.

**Pyrenochaetopsidaceae** Valenzuela-Lopez et al.

Pyrenochaetopsidaceae was introduced by Valenzuela Lopez et al. [105] to accommodate the asexual genera Pyrenochaetopsis (type genus), Neopyrenochaetopsis and Xenopyrenochaetopsis. The family is characterized by pycnidial, pale brown to brown, solitary or confluent, glabrous or setose, subglobose to ovoid conidiomata, with apapillate or papillate ostiole, acropleurogenous conidiophores, phialidic, hyaline, discrete or integrated, septate conidiogenous cells, and aseptate, hyaline, smooth- and thin-walled, ovoid, cylindrical to allantoid ascospores [105]. Mapook et al. [106] introduced a novel species, *Pyrenochaetopsis chromolaenae* collected on *Chromolaena odorata* in Thailand and reported the sexual morph of *Pyrenochaetopsis* for the first time. The sexual morph is characterized by brown to dark brown solitary or scattered, globose ascomata, superficial on the host, with short papillate ostiole, with reddish-brown setae covering the papilla, thin-walled peridium, fissitunicate, cylindric-clavate asci, with a short, bulbous pedicel, and hyaline...
to pale brown or yellowish-brown, cylindrical to broadly fusiform, three to four-septate ascospores [106]. Species in Pyrenochaetopsidaceae have been isolated from various substrates as saprobes and also opportunistic pathogens on humans as well as on cysts of plant-parasitic nematodes. [81,105,106].

Pyrenochaetopsis was treated as the generic type of Pyrenochaetopsidaceae and is typified by P. leptospora. The genus was introduced by de Gruyter et al. [107] to accommodate phoma-like taxa. Recently, 19 species are accepted in this genus [108]. In this study, we introduce a holomorph species, P. yunnanensis, which occurred on bamboo in Yunnan, China.

**Pyrenochaetopsis yunnanensis** C.F. Liao, H.B. Jiang and Phookamsak, sp. nov.

Index Fungorum number: IF 554979, Figure 7

**Etymology:** Referring to the locality, Yunnan Province of China, of which the species was collected.

**Holotype:** KUN-HKAS 123172

Saprobic on dead stem of bamboo. Sexual morph: Ascomata 190–280 µm high, 270–460 µm diam, gregarious, scattered to clustered, immersed to semi-immersed under the clypeus, visible as raised, black, shiny, rough on host surface, uni- to tri-loculate, subglobose to subconical, or quadrilateral, glabrous, ostiole central with minute papillate, protruding through host tissue. Peridium 30–80 µm wide at sides toward the apex, 10–30 µm wide at the base, unequally thickness, poorly developed at the base, composed of several layers of dark brown pseudoparenchymatous cells, arranged in *textura angularis* to *textura prismatica*, outer layers intermixed with host cortex. Hamathecium composed of dense, 1.5–2.5 µm wide, filamentous, branched, septate, cellular pseudoparaphyses, anastomosed above the asci, embedded in a hyaline gelatinous matrix. Asci (58–)70–95(–110) × 11–14(–15.5) µm (*x* = 80.2 × 12.8 µm, *n* = 30), eight-spored, bitunicate, fissitunicate, clavate, with short pedicel, apically rounded, with a well-developed ocular chamber. Ascospores (18–)20–25(–28) × (4.5–)5–6.5(–8) µm (*x* = 23.4 × 5.8 µm, *n* = 30), overlapping one to three-seriate, hyaline, fusiform, with acute ends, slightly curved, one to three-septate, slightly constricted at the central septum, not constricted at the other septa, smooth-walled, lacking mucilaginous sheath. Asexual morph: Coelomycetous, sporulated on PDA after two months at room temperature (15–20 °C), visible as black dots, superficial or immersed in PDA. Conidiomata 50–100 µm high, 68–105 µm diam, pycnidial, black, solitary, or in a small group, immersed to superficial, globose to subglobose, uni- to multi-loculate, setose, with dark brown, septate setae (35–75 × 2–4 µm, *n* = 20), ostiole central, with pore-like opening or pimple-like. Peridial wall 7.5–20 µm wide, equally thin-walled, composed of one to two layers, of brown to dark brown pseudoparenchymatous cells, arranged in *textura angularis* to *textura prismatica*, or *textura globulosa*. Conidiophores reduced to conidiogenous cells. Conidiogenous cells 2–4 × (1.8–)2–3.5 µm (*x* = 3.5 × 2.8 µm, *n* = 30) phialidic, hyaline, discrete, aseptate, arising from the inner cavity of the pycnidial wall, difficult to distinguish from the pycnidial wall. Conidia (2.8–)3–4 × 1–2(–2.5) µm (*x* = 3.4 × 1.9 µm, *n* = 50) hyaline, subglobose to oblong, aseptate, with small guttules.

Culture characteristics: Ascospores germinated on PDA within 24 h. Cultures reach 25–28 mm diam after one week at room temperature (15–20 °C). Colonies medium dense, irregular in shape, flat to slightly raised, surface smooth with a lobate edge, floccose to cottony; colony from above pale gray to white-gray at the margin, white at the middle toward the center, sectored; from below white at the margin, pale yellowish-brown at middle toward the center; not producing pigmentation on PDA. Sporulation on PDA after two months.

Material examined: China, Yunnan Province, Honghe Autonomous Prefecture, Honghe County, Honghe Hani Rice Terraces (23°5’35” N, 102°46’47” E, 1432 + 6 msl), on dead stem of bamboo in a terrestrial environment, 26 January 2021, R. Phookamsak, BN09P (KUN-HKAS 123172, holotype), ex-type living culture: KUMCC 21-0843.
Known distribution: Yunnan Province, China.

Known host and habitats: saprobic on a stem of bamboo in a terrestrial environment.

Notes: The nucleotide BLAST search of ITS sequence indicated that *Pyrenochaetopsis yunnanensis* (KUMCC 21-0843) is similar to *Leptosphaeria* sp. (isolate NTOU5272 and R10) with 100% similarity (Identities = 521/521 and 490/490, with no gap), it is similar to *Pyrenochaetopsis terricola* strain HGUP1802 (ex-type strain) with 99.41% similarity (Identities = 506/509, with two gaps), and it is also identical to *Dokmaia* sp. isolate C126 (99.79% similarity, Identities = 485/486, with one gap). The nucleotide BLAST search of rpb2 sequence indicated that *P. yunnanensis* (KUMCC 21-0843) is similar to *P. terricola* strain HGUP1802 with 94.71% similarity (Identities = 948/1001, with no gap), and the nucleotide BLAST search of tub2 sequence also showed that *P. yunnanensis* (KUMCC 21-0843) is identical to *P. terricola* strain HGUP1802 with 98.61% similarity (Identities = 354/359, with three gaps) and is identical to *P. sinensis* strain LC12199 with 92.98% similarity (Identities = 265/285, with six gaps).

Based on a nucleotide pairwise comparison, *Pyrenochaetopsis yunnanensis* (KUMCC 21-0843) is consistent with *P. terricola* strain HGUP1802 in LSU nucleotide pairwise comparison but differs from *P. terricola* in 11/519 bp of ITS (2.12%), 53/1002 bp of rpb2 (5.29%), and 7/363 bp of tub2 (1.93%). *Pyrenochaetopsis yunnanensis* (KUMCC 21-0843) grouped with *P. terricola* strain HGUP1802 with high support (100% ML, 100% MP, 1.00 PP; Figure 3) in the present study. *Pyrenochaetopsis yunnanensis* (KUMCC 21-0843) morphological resembles *P. terricola* but the conidial size is slightly longer than *P. terricola* (2–3 × 1–2 µm) [109]. Wang et al. [109] isolated *P. terricola* from the soil in Guizhou Province, China and determined only the asexual morph sporulated on OA, while our novel species was found as a saprobe on bamboo and both sexual and asexual morph.

**Tetraplosphaeriaceae** Kaz. Tanaka and K. Hiray.

Tetraplosphaeriaceae was introduced by Tanaka et al. [12] to accommodate genera that mostly occurred on bamboo. Five genera that formed tetraploo-like asexual morph were initially introduced to this family, including *Polyplosphaeria*, *Pseudotetraploa*, *Quadricrura*, *Tetraplosphaeria* (generic type), and *Triplosphaeria* [12]. Later, *Tetraplosphaeria* was treated as a synonym of *Tetraploa* [72,110]. Recently, nine genera were accepted in this family viz. *Aquatisphaeria*, *Byssolophis*, *Ernakulamia*, *Polyplosphaeria*, *Pseudotetraploa*, *Quadricrura*, *Shrungabeeja*, *Tetraploa* (= *Tetraplosphaeria*), and *Triplosphaeria* [41,81,111–114]. Most species in *Tetraplosphaeriaceae* were reported as saprobes on bamboo, but some species were isolated from soil and water [81].

*Tetraploa* (= *Tetraplosphaeria*), generic type of *Tetraplosphaeriaceae*, was introduced by Berkeley and Broome [115] with *T. aristata* as the type species. The asexual morph of *Tetraploa* is characterized by lacking conidiophores, monoblastic conidiogenous cells, and brown, short-cylindrical, verrucose conidia, composed of four columns with four setose appendages at the apex [12,81]. The sexual morph is characterized by scattered to gregarious, immersed to erumpent, globose to subglobose, glabrous ascomata, with short-papillate to cylindrical ostiole, fissitunicate, cylindrical to clavate, short-pedicellate asci, and hyaline, narrowly fusiform, septate, smooth-walled ascospores, surrounded by a mucilaginous appendage-like sheath [12,81]. Species in *Tetraploa* mostly occurred on bamboos and other herbaceous plants or rotten wood as well as isolated from soil or raindrops [81]. In this study, the novel species, *T. bambusae*, isolated from bamboo in Yunnan, China is introduced based on morphological characteristics and multigene phylogenetic analyses.
Figure 7. *Pyrenochaetopsis yunnanensis* (KUN-HKAS 123172, holotype). (a) The appearance of ascomata on host substrate; (b) Vertical section of ascomata; (c) Peridium; (d) Pseudoparaphyses; (e) Asci; (f–h) Ascospores; (i) Ascospore stained with Indian ink; (j) Germinated ascospore; (k) Colony sporulated on PDA after two months; (l) Conidiomata immersed or superficial on PDA; (m) Squash mount of conidioma in water; (n) Section through pycnidial wall; (o) Vertical section of conidiomata; (p,q) Conidiogenous cells; (r) Conidia. Scale bars: (b) = 200 µm, (c,m) = 50 µm, (d,e,n,o) = 20 µm, (f–i,j,r) = 10 µm, (p,q) = 5 µm.

*Tetraploa bambusae* Phookamsak and H.B. Jiang, sp. nov.

Index Fungorum number: IF 554987, Figure 8

Etymology: Referring to the host, bamboo, of which the species was collected.

Holotype: KUN-HKAS 123174

Saprobic on dead twigs of bamboo. Sexual morph: Undetermined. Asexual morph: hyphomycetous. Colonies brown to brick orange, effuse to powdery, compact, with patch-like, superficial on the host substrate. Mycelia light brown to brown, branched, septate. Conidiophores up to 40–130 µm long, (1.5–)2–3.5 µm wide, macronematous, inconspicuous,
light brown, branched, septate. Conidiogenous cells monoblastic, discrete or integrated, determinate, cylindrical. Conidia \((21–23–30–33) \times (17–18–23–26) \mu m\) \((x = 24.1 \times 19.8 \mu m, n = 30)\), muriform, obovoid to turbinate, with obtuse end, brown to dark brown, composed of four columns of cells, four-septate in each column, coarsely verruculose, with four apical appendages, sometimes, a small piece of the denticle remains attached to the base of the conidium. Appendages 15–40 \mu m long, 2.5–4.5 \mu m wide at the base, widening to the base, tapering toward the apex, divergent, brown, one to three-septate, straight or slightly flexuous, smooth-walled.

Culture characteristics: Ascospores germinated on PDA within 24 h. Colonies on PDA reach 22–25 mm diam after two weeks at room temperature \((15–20 \degree C)\). Colonies dense, irregular in shape, raised to umbonate, surface smooth with an undulate edge, velvety; colony from above white–gray to pale gray at the margin, gray at the middle toward the center; from below white to cream at the margin, orange–brown at the middle, brown to dark brown at the center, slightly radiated outwards colony with concentric rings; not producing pigmentation on PDA.

Material examined: China, Yunnan Province, Kunming City, Kunming Institute of Botany, on dead twigs of bamboo, 31 January 2021, R. Phookamsak, KIB21-005 (KUN-HKAS 123174, holotype), ex-type living culture: KUMCC 21-0844. Known distribution: Yunnan Province, China. Known host and habitats: saprobic on twigs of bamboo in a terrestrial environment.

Notes: The nucleotide BLAST search of ITS sequence indicated that *Tetraploa bambusae* (KUMCC 21-0844) closest matches with “uncultured fungus” clone 035A11084, 109A74706, 036A17775, and 034A2039 with 96.30%, 96.05%, 95.80%, and 95.71% similarities, respectively. The species is similar to *Tetraplosphaeria* sp. strain WSF14_RG24_2 with 95.62% similarity (Identities = 502/525, with eight gaps), and it is similar to *Tetraploa yunnanensis* MFLUCC 19-0319 (ex-type strain) with 95.60% similarity (Identities = 521/545, with nine gaps). The nucleotide BLAST search of LSU sequence indicated that *T. bambusae* (KUMCC 21-0844) closest matches with *T. sasicola* strain MFLUCC 17-1387 with 99.88% similarity (Identities = 822/823, with no gap) and is similar to *Tetraploa obpyriformis* KUMCC 21-0011 with 99.64% similarity (Identities = 821/824, with one gap) and *Tetraploa* sp. KT 1684 with 99.51% similarity (Identities = 816/820, with one gap). The nucleotide BLAST search of *tub2* sequence also showed that *T. bambusae* (KUMCC 21-0844) closest matches with *Tetraplosphaeria sasicola* KT 563 with 88.51% similarity (Identities = 578/653, with 29 gaps) and is similar to *Tetraploa aristata* CBS 996.70 with 82.53% similarity (Identities = 529/641, with 27 gaps) and *Tetraplosphaeria yakushimensis* KT 1906 with 81.58% similarity (Identities = 536/657, with 38 gaps). Phylogenetic analyses based on a combined LSU-ITS-SSU-*tub2*-tef1-α sequence dataset demonstrated that *Tetraploa bambusae* (KUMCC 21-0844) is sister to *Tetraploa* sp. KT 1684 and clustered with *T. endophytica* CBS 147114 and *T. obpyriformis* KUMCC 21-0011 with high support (99% ML, 98% MP, 1.00 PP; Figure 4). Based on a nucleotide pairwise comparison, *T. bambusae* (KUMCC 21-0844) is consistent with *Tetraploa* sp. KT 1684 in LSU nucleotide pairwise comparison (differs in 1 bp), but it could not be compared for the other informative gene regions (viz. ITS, *tub2*, and tef1-α) due to the lack of sequence data of *Tetraploa* sp. KT 1684. Tanaka et al. [12] included *Tetraploa* sp. KT 1684 in their analyses when they introduced the new family Tetraplosphaeriaceae; however, the morphological characteristics of *Tetraploa* sp. KT 1684 were not described. Thus, we could not compare the morphology of the novel species with *Tetraploa* sp. KT 1684, while *T. obpyriformis* KUMCC 21-0011 is an unpublished species. *Tetraploa endophytica* CBS 147114 was isolated from the roots of *Microthlaspi perfoliatum* (Brassicaceae) as an endophyte. The strain did not sporulate in any of the different culture media [116]. Therefore, the species also could not compare their morphology.
**Figure 8.** *Tetraploa bambusae* (KUN-HKAS 123174, holotype). (a) The appearance of colony on host substrate; (b) Conidial mass; (c,d) Conidia attached with conidiophores; (e,f) Conidia; (g) Germinated conidium; (h) Culture characteristics on PDA after one week. Scale bars: (b) = 50 µm, (c–g) = 20 µm.

4. Discussion and Conclusions

Bambusicolous fungi are highly diverse and distributed in various families within Pleosporales. Since 2015, over 85 bambusicolous species have been introduced in Pleosporales [3,27,33,39,41,45,46,49,50,52,55,59,63,68,71,74,76–80,100,104,117–132]. Even though novel taxa have been continually introduced in recent years, studies into the diversity of bambusicolous fungi correlating with specific bamboo genera are still limited due to the lack of host species identification. Jiang [133] reported that 48% of pleosporalean taxa were associated with bamboos in Thailand, and 39% were discovered in Yunnan, China. However, documented species were restricted to some parts of Thailand (mainly found in northern) and Yunnan Province (e.g., Honghe, Kunming, and Xishuangbanna) as well as some provinces of China (e.g., Guangdong and Sichuan) and Japan, whereas other regions that show a high species richness of bamboos have received less attention. Hence, we believe that a huge number of novel taxa occurring on bamboo are waiting for discovery.
in other regions. In this study, we collected the ascomycetes on bamboo in Honghe and Kunming (Yunnan Province, China) and also included the collections from Chiang Mai and Chiang Rai Provinces (Thailand), which were collected in 2011. Based on morphological characteristics and multigene phylogenetic analyses, four novel taxa collected from Yunnan, China are introduced, including *Paramultiseptospora bambusae* sp. et gen. nov., *Pyrenochaetopsis yunnanensis* sp. nov., and *Tetraploa bambusae* sp. nov., whereas collections from Thailand are identified as *Anastomitrabeculia didymospora* and reported in terrestrial habitats for the first time.

*Anastomitrabeculia didymospora* is a putative species accommodated in *Anastomitrabeculaceae*. Bhunjun et al. [71] reported that the species that occurred on the bamboo host was submerged in freshwater. In this study, we also found the species occurring on a bamboo host in the terrestrial habitat near the waterfall. There are few studies concerning relationships between freshwater and terrestrial fungi [134–137]. Boonyuen et al. [136] mentioned that fungal species partially overlap between freshwater and terrestrial habitats, of which the submerged samples yielded the most fungal diversity. Boonyuen et al. [136] also suggested that the diversity of wood-inhabiting fungi depended on tree species, geography, and exposure period. There is no clear evidence to prove that terrestrial fungi will continue to thrive when submerged in water [137]. Kodseub et al. [137] attempted to investigate the differences in fungal communities that occurred in *Magnolia liliifera* wood from freshwater and terrestrial habitats. Kodseub et al. [137] mentioned that dominant fungi in the terrestrial environment were significantly different from fungi submerged in freshwater, and few species have been found in both freshwater and terrestrial habitats, suggesting that most fungi occurring on wood in terrestrial habitats did not thrive in freshwater habitats. According to Kodseub et al. [137], we hypothesized that *A. didymospora* is one of the few species that can survive in both freshwater and terrestrial habitats. The species may initially occur on a bamboo host in the terrestrial environment and continue to thrive in submerged freshwater.

Parabambusicolaceae shows to be heterogeneous, and it currently contains 12 genera, including the new genus introduced in this study. Even though most genera of *Parabambusicolaceae* contain a single species, they showed high genetic heterogeneity, which can be interpreted by their phylogenetic relationships. Most genera in Parabambusicolaceae are only represented by their sexual or asexual morph, except for *Neoaquastroma*. Hence, the morphology of some sexual and asexual genera could not be compared, which led to the generic status becoming questionable. More taxa sampling is required for a better understanding of each genus in Parabambusicolaceae.

*Pyrenochaetopsis* was introduced to accommodate phoma-like taxa that occurred on various host substrates [81,105,106,138]. The genus was previously treated in *Cucurbitariaceae* [72,107,139]. Later, Valenzuela-Lopez et al. [105] introduced the new family *Pyrenochaetopsidaceae* to accommodate this genus together with *Neopyrenochaetopsis* and *Xenopyrenochaetopsis*. Mapook et al. [106] determined the sexual morph of *Pyrenochaetopsis, P. chromolaenae*, for the first time. In the present study, the holomorph of *P. yunnanensis* sp. nov. is also determined. The sexual morph of *P. yunnanensis* can be distinguished from *P. chromolaenae* in having subglobose to subconical, or quadrilateral, glabrous ascomata and hyaline, fusiform, one to three-septate ascospores, whereas *P. chromolaenae* has globose ascomata with setose papilla and hyaline to pale brown or yellowish-brown, cylindrical to broadly fusiform, three to four-septate ascospores [106]. *Pyrenochaetopsis yunnanensis* is reported as a saprobe on bamboo host in Yunnan Province, China for the first time. Species of *Pyrenochaetopsis* are well-studied based on molecular analyses coupled with morphological characteristics of their asexual morph. Nevertheless, the sexual morph of this genus is still rarely detected.

In the present study, multigene phylogenetic analyses demonstrated that taxa in *Tetraploa* could be separated into two subclades. The main subclade (including the type species) comprises *T. aristata* (type species), *T. bambusae* sp. nov., *T. dwibahuberia*, *T. endophytica*, *T. obpyriformis*, *T. pseudoaristata*, *T. puzheheiensis*, *T. sasicola*, *T. thrayabahuberia*,
T. yakushimensis, T. yunnanensis, and Tetraploa spp. (CY 112, KT 1684). These species formed a well-resolved subclade within Tetraplosphaeriaceae (Figure 4). The second subclade comprises T. aquatica, T. cylindrica, T. nagasakiensis and Tetraploa sp. (KT 2578). Tetraploa aquatica, T. cylindrica, and T. nagasakiensis formed a well-resolved subclade, clustered with Tetraploa sp. KT 2578 with low support and constituted independently basal to the main subclade. Multigene phylogenetic analyses showed that T. aquatica, T. cylindrica, and T. nagasakiensis may be distinct genera with Tetraploa, but generic clarification insight into the morphology-based taxonomy is needed in the future study. Tetraploa sasicola (KT 563, ex-type strain) also formed a separate branch with T. sasicola (FU31019) in this study and also concurred with Liao et al. [140]. Tetraploa sasicola strain FU31019 may not be conspecific with T. sasicola (KT 563) pending further study.

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Data Availability Statement: All data availability was mentioned in the manuscript. The novel taxa were registered in Index Fungorum (http://www.indexfungorum.org/Names/Names.asp, accessed on 13 May 2022) including Index Fungorum numbers IF 554966, IF 554968, IF 554979 and IF 554987. Final alignment and phylogenetic tree were deposited in TreeBase (https://www.treebase.org/, accessed on 25 March 2022) with submission ID: 29589, 29590, 29592 and 29593) and the newly generated sequences were deposited in GenBank (https://www.ncbi.nlm.nih.gov/genbank/submit/, accessed on 28 March 2022) followed as ITS: ON077079, ON077080, ON077075, ON077076, ON077077, ON077078; LSU: ON077068, ON077069, ON077064, ON077065, ON077066, ON077067; SSU: ON077074, ON077070, ON077071, ON077072, ON077073; rpb2: ON075067, ON075066; tefl-α: ON075062, ON075063, ON075058, ON075059, ON075060, ON075061; tub2: ON075064, ON075065.

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