Morphology and Phylogeny Reveal *Vamsapriyaceae* fam. nov. (*Xylariales, Sordariomycetes*) with Two Novel *Vamsapriya* Species

Ya-Ru Sun 1,2,3, Ning-Guo Liu 2,4, Milan C. Samarakoon 2, Ruvishika S. Jayawardena 2,3,5, Kevin D. Hyde 2,3,5 and Yong Wang 1,*

Abstract: Phylogenetic analyses of combined LSU, rpb2, tub2 and ITS sequence data of representative *Xylariales* taxa indicated that *Diabolocovidia, Didymobotryum* and *Vamsapriya* cluster together and form a distinct clade in *Xylariales*. Morphological comparison also shows their distinctiveness from other families of *Xylariales*. Therefore, we introduce it as a novel family, *Vamsapriyaceae*. Based on morphological characteristics, *Podosporium* and *Tretophragmia*, which were previously classified in *Ascomycota* genera *incertae sedis*, are now included in the *Vamsapriyaceae*. In addition, three *Vamsapriya* species, *V. chiangmaensis* sp. nov, *V. uniseptata* sp. nov, and *V. indica* are described and illustrated in this paper.

Keywords: three new taxa; *Ascomycota* genera *incertae sedis*; multi-gene phylogeny; new family; taxonomy

1. Introduction

*Xylariales* is a large order with both conspicuous and inconspicuous fruiting bodies, and unitunicate, perithecial ascomycetes [1,2]. Many species of *Xylariales* are saprobes and endophytes [3,4]. Some *Xylariales* species can produce secondary metabolites which are especially important for the pharmaceutical chemical industry [3,5,6].

*Xylariales* was established by Nannfeldt [7] to accommodate the type family *Xylariaceae*, along with *Diatrypaceae, Hypocreaceae, Hyponecctiaeae, Lasiosphaeriaceae* and *Polystigmataceae*. The previous classification of *Xylariales* was mainly based on morphology [8–13]. With the development of molecular technology, the classification basis of *Xylariales* was gradually diversified [2,14–16]. Smith et al. [2] performed the first multigene analysis to find the familial relationships within *Xylariales* and treated the order with seven families. Lumbsch and Huhndorf [17] listed six families in *Xylariales*, while Senanayake et al. [18] revised *Xylariales* and accepted 11 families. Hyde et al. [19] redefined the families of *Sordariomycetes* and accepted 15 families in *Xylariales* based on morphology and multigene analysis, viz. *Barlmaeiaceae, Cainiaceae, Clypeosphaeriaceae, Conioceissiaceae, Diatrypaceae, Graphostromataceae, Hansfordiaceae, Hypoxylaceae, Induratiaceae, Lopadostomataceae, Microdochiaeae, Polystigmataceae, Requieniellaceae, Xylariaeaceae* and *Zygosporiaceae*. Hyde et al. [20] introduced *Fasciatisporaceae* to accommodate *Fasciatispora* in *Xylariales*. However, the taxonomic position of many taxa...
in Xylariales are still uncertain, and they are treated as genera *incertae sedis* [20,21]. This may probably be due to monospecific genera with either sexual or asexual morph, with no additional collections and lack of molecular data, and sometimes due to the polyphyletic nature of some genera (such as *Anthostomella* and *Xylaria*) [22–25].

*Vamsapriya* was introduced by Gawas and Bhat [26] based on abundant asexual morphs of the genus, which is characterized by erect, cylindrical, dark brown, synnematos conidiophores, monotretic, clavate to cylindrical conidiogenous cells, and cylindrical or broadly fusiform or obclavate, brown to dark brown conidia [26–33]. The first sexual morph of *Vamsapriya* was described by Dai et al. [28], which has solitary, immersed ascomata visible as black dots, 8spored, unitunicate asci, and hyaline, fusiform apiospores. They linked the sexual morph of *V. bambusicola* (MFLUCC 11-0637) to the asexual morph of *V. bambusicola* (MFLUCC 11-0477) using ITS phylogenies [27,28]. The phylogenetic placement of *Vamsapriya* has been confusing. Dai et al. [27,28] and Jiang et al. [31] accepted *Vamsapriya* into the *Xylariaceae*. However, phylogenetic analyses using broader taxon sampling indicated that *Vamsapriya* was distant from *Xylariaceae* [19,34].

This study aims to resolve the phylogenetic position of *Vamsapriya*. Three *Vamsapriya* collections (*V. chiangmaiensis* sp. nov, *V. uniseptata* sp. nov, and *V. indica*) on bamboo from China and Thailand are described and illustrated herein. *Vamsapriya*, along with *Diabolocovidia* and *Didymobotryum*, formed a distinct monophyletic clade in the combined LSU, rpb2, tub2 and ITS phylogenetic analyses. A new family, *Vamsapriyaceae*, is thus established. *Podosporium* and *Tretophragmia* are also accepted in *Vamsapriyaceae* based on their morphology of hyphomycetous asexual morph.

### 2. Materials and Methods

#### 2.1. Collection, Examination, Isolation and Conservation

Fresh specimens were collected from bamboo in terrestrial habitats in China and Thailand between August 2019 and September 2020. Sample collections and observations were followed by the method described in Senanayake et al. [35]. The samples were stored in envelopes and taken to the laboratory for examination. Morphological observations were done using a stereo microscope (LEICA M125 C, Wetzlar, Germany). The fungal structures were captured using a Nikon ECLIPSE Ni compound microscope (Nikon, Tokyo, Japan) fitted with a NikonDS-Ri2 digital camera (Nikon, Tokyo, Japan). The Tarosoft (R) Image Frame Work software was used to take the measurements. Adobe Photoshop CS6 software (Adobe Systems, San Jose, CA, USA) was used to do photo-plates.

Single spore isolation was carried out to obtain pure cultures following the method described in Senanayake et al. [35]. Germinated spores were transferred to pure potato dextrose agar (PDA) and cultivated under normal light at 26 °C for four weeks. Herbarium specimens were deposited in the Fungarium of Mae Fah Luang University (MFLU), Chiang Rai, Thailand, and the herbarium of the Guizhou Academy of Agriculture Sciences (GZAAS), Guiyang, China. Pure cultures were deposited in the Mae Fah Luang University Culture Collection (MFLUCC) and the Guizhou Culture Collection (GZCC). FacesOfFungi (FoF) and Index Fungorum numbers were obtained as described in Jayasiri et al. [36] and Index Fungorum [37].

#### 2.2. DNA Extraction, PCR Amplification and Sequencing

Genomic DNA was extracted from fresh fungal mycelia using the Genomic DNA Extraction Kit (GD2416 BIOMIGA, San Diego, CA, USA). Polymerase chain reactions (PCR) were carried out using a BIO-RAD T100 Thermal Cycler in a 20 µL reaction volume which contained 10 µL 2x PCR Master Mix, 7 µL ddH2O, 1 µL of each primer, and 1 µL template DNA. The PCR thermal cycle program and primers are given in Table 1. The PCR products were sent for sequencing to SinoGenoMax, Beijing, China.
Table 1. Primers and PCR protocol used in this study.

| Locus   | Primers | PCR Procedure                                                                 | Reference |
|---------|---------|-------------------------------------------------------------------------------|-----------|
| LSU     | LR0R    | 94 °C 3 min; 35 cycles of 94 °C 30 s, 52 °C 30 s, 72 °C 1 min; 72 °C 8 min; 4 °C on hold | [38,39]  |
|         | LR5     |                                                                                |           |
| ITS     | ITS5    |                                                                                |           |
|         | ITS4    |                                                                                |           |

2.3. Phylogenetic Analyses

The sequences used in this study (Table 2) were downloaded from GenBank according to the results of blast searches and previous studies [27–33]. Alignments for each locus were carried out in MAFFT v7.212 [40]. AliView [41] was used for checking the alignments and changing the format. Terminal ends and ambiguous regions of the alignment were deleted manually. Four single gene alignments were combined using the Sequence Matrix [42].

Table 2. Taxa names, strain numbers and corresponding sequences used for the molecular phylogenetic analyses.

| Taxa               | Strain Numbers | ITS              | LSU              | rpb2                  | tub2        |
|--------------------|----------------|------------------|------------------|-----------------------|-------------|
| Amphirosellinia fushanensis | HAST 9111209   | GU339496         | N/A              | GQ848339              | GQ495950    |
| Amphirosellinia nigrospora    | HAST 91092308  | GU322457         | N/A              | GQ848340              | GQ495951    |
| Amphisphaeria sorbi          | MFLUCC 13-0721 | NR_153531        | KP74475          | N/A                   | N/A         |
| Amphisphaeria thailandica   | MFLU 18-0794   | NR_168783        | NG_068588        | MK033640              | MK033639    |
| Anthostomella obesa         | MFLUCC 14-0171 | KP297410         | KP340544         | KP340531              | KP406164    |
| Anthostomella krabbiensis   | MFLUCC 15-0678 | KX305927         | KX305928         | KX305929              | N/A         |
| Barrmaelia rhamnicola      | CBS 142772     | NR_153497        | N/A              | MF488999              | MF490018    |
| Barrmaelia rappazii        | CBS 142771     | NR_153496        | N/A              | MF488998              | MF490017    |
| Barrmaelia macrospora      | CBS 142768     | NR_167684        | N/A              | MF488995              | MF490014    |
| Biscogniauxia arima        | WSP 122        | NR_167683        | N/A              | GQ304736              | AY951672    |
| Biscogniauxia mangiferae   | MFLU 18-0827   | MN337232         | MN336236         | MN366247              | MN509782    |
| Biscogniauxia nummularia   | MUCL 51395     | NR_153649        | NG_066378        | KY624236              | KX271241    |
| Biscogniauxia repanda      | ATCC 62606     | KY610383         | KY610428         | N/A                   | KX271242    |
| Brunneiperidium gracilicentum | MFLUCC 14-0011 | KP297400         | KP340542         | KP340528              | KP406611    |
| Brunneiperidium involucratum | MFLUCC 14-0009 | KP297399         | KP340541         | KP340527              | KP406610    |
| Cainia anthoxanthis        | MFLUCC 15-0539 | NR_138407        | NG_070382        | N/A                   | N/A         |
| Cainia graminis            | MFLUCC 15-0540 | KR092793         | KR092781         | N/A                   | N/A         |
| Cainia desmazeri           | CBS 137.62     | MH858124         | MH869702         | N/A                   | N/A         |
| Clypeosphaeria mammillana  | CBS 140735     | N/A              | NG_067338        | MF489001              | MH706437    |
| Colloidoscila bambusae      | GZUH 102       | KP054279         | KP054280         | KP276675              | N/A         |
| Colloidoscila japonica     | CBS 124266     | JF440974         | JF440974         | KY624273              | KY624316    |
| Colloidoscila fangjingshanensis | GZUH 10109    | KR002590         | KR002591         | KR002592              | KR002589    |
| Collodiscula leigongshanensis | GZUH10107    | KP054281         | KP054282         | KR002588              | KR002587    |
| Conioceiopsis anandra      | CBS 125766     | MH863747         | MH875215         | N/A                   | N/A         |
| Conioceiopsis maxima       | CBS 593.74     | NR_137751        | NG_070051        | N/A                   | N/A         |
| Conioceiopsis cruciformis  | CBS 126674     | MH864206         | MH875663         | N/A                   | N/A         |
| Conioiella limonispora     | CBS 283.64     | KF719198         | KF719210         | N/A                   | N/A         |
| Conioiella gamsii          | CBS 114379     | GU553325         | GU553329         | N/A                   | N/A         |
| Daldinia macaronesca       | CBS 113049     | JX658504         | KYI610477        | KY624294              | KX271266    |
| Daldinia loculatoides      | CBS 113459     | NR_150406        | NG_069531        | N/A                   | MG334557    |
| Diabolocorticium claudi    | CBS 146630     | MT373367         | MT373350         | N/A                   | N/A         |
| Diatrypella heveae         | MFLUCC 17-0368 | NR_150406        | NG_069531        | N/A                   | MG334557    |
| Diatrypella tectonae       | MFLUCC 12-0172 | NR_150406        | NG_069423        | N/A                   | KY421043    |
| Didymobryotremus rigidum   | JCM 8837       | LC228650         | LC228707         | N/A                   | N/A         |
| Entosordaria quercina      | CBS 142774     | NR_153499        | N/A              | MF489004              | MF489022    |
| Entosordaria perfidiosa    | CBS 142773     | NR_153498        | N/A              | MF489003              | MF489021    |
| Eutypa linearis           | MFLUCC 11-0503 | KU940150         | KU863138         | N/A                   | N/A         |
Table 2. Cont.

| Taxa                      | Strain Numbers | ITS    | LSU    | rpb2 | tub2 |
|---------------------------|----------------|--------|--------|------|------|
| Fasciatispora arengae     | MFLUCC 15-0326b | MK120301 | MK120276 | N/A  | N/A  |
| Fasciatispora arengae     | MFLUCC 15-0326c | MK120302 | MK120277 | N/A  | N/A  |
| Graphostroma platystomum  | CBS 270.87     | JX658535 | N/A    | N/A  | HG934108 |
| Hansfordia pulvinata      | CBS 254.59     | KF893288 | MH869394 | N/A  | N/A  |
| Hansfordia pulvinata      | CBS 144422     | MK442587 | MK442527 | N/A  | N/A  |
| Hansfordia pruni          | CBS 125767     | MH863748 | MH875216 | N/A  | N/A  |
| Hansfordia pruni          | CBS 276.51     | MH868654 | MH868374 | N/A  | N/A  |
| Hypoxylon fragiforme      | MFLUCC 15-0326b | MK120301 | MK120276 | N/A  | N/A  |
| Hypoxylon fragiforme      | MFLUCC 15-0326c | MK120302 | MK120277 | N/A  | N/A  |
| Hypoxylon neosublenormandii | CBS 270.87     | JX658535 | N/A    | N/A  | HG934108 |

Abbreviations: ATCC: American Type Culture Collection, Virginia, USA; CBS: Centraalbureau voor Schimmelcultures, Utrecht, Netherlands; CPC: Culture collection of Pedro Crous, housed at CBS; GZCC: Guizhou Culture Collection, Guiyang, China; GZUH: The herbarium of Guizhou University, Guiyang, China; JDR: Herbarium of Jack D. Rogers; KUMCC: The Kunming Institute of Botany Collection, Kunming, China; MFLU: The Fungarium of Mae Fah Luang University, Chiang Rai, Thailand; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Rai, Thailand; MUCL: Mycothèque de l’Université Catholique de Louvain, Belgium; WSP: Washington State University, U.S.A. The newly generated sequences are indicated in red. Ex-type strains are in bold.
Single gene analyses were done to compare the topologies and clade stabilities, respectively. Single and combined phylogenies were subjected to Bayesian posterior probability (BYPP), maximum likelihood (ML) and maximum parsimony (MP) analyses. The BYPP analysis was performed in MrBayes v. 3.2.6 [43]. MrModeltest v. 2.3 [44] was used to estimate the best model. GTR+I+G model was chosen for LSU and rpb2; SYM+I+G (Xylariales analysis) and GTR+G (Vamsapriya analysis) models were chosen for ITS; HKY+I+G model was chosen for tub2. Six chains were run and trees were sampled every 1000th generation, the temperature value of the heated chain was set at 0.15. The first 25% sampled trees were discarded as “burn-in”, and the remaining trees were used for calculating BYPP in the majority rule consensus tree. The ML analyses were carried out using IQ-TREE [45] on the IQ-TREE web server (http://iqtree.cibiv.univie.ac.at, 6 September 2021) under partitioned models. The best-fit substitution models were determined by W-IQ-TREE [45]: TIM3e+I+G4 for LSU; TIM3+F+I+G4 for rpb2; TIM2+F+I+G4 for tub2; SYM+I+G4 for ITS. Ultrafast bootstrap analysis was implemented with 1000 replicates. The MP analyses were carried out with a heuristic search in PAUP v. 4.0 b10 [46]. Bootstrap analysis was used to estimate clade stability, including 1,000 replicates, each with 10 replicates of random stepwise addition of taxa [47].

Phylogenetic trees were viewed using FigTree v1.4.4 [48] and modified in Adobe Illustrator CS6 software (Adobe Systems, USA). The sequences generated from our collections were deposited in GenBank.

3. Results
3.1. Phylogenetic Analyses

In Xylariales phylogenetic analyses, the final combined dataset of Xylariales consists of 84 strains representing fifteen families along with the outgroup Amphisphaeria sorbi (MFLUCC 13-0721) and A. thailandica (MFLU 18-0794) in Amphisphaeriales. The aligned sequence matrix comprises LSU (1–829), rpb2 (830–1875), tub2 (1876–3579) and ITS (3580–4305), sequence data for a total of 4305 characters, including coded alignment gaps. Among them, 1894 characters were constant, 374 variable characters were parsimony-uninformative and 2037 characters were parsimony informative. The matrix had 2693 distinct alignment patterns. The BYPP, ML, and MP analyses based on combined sequence data provided similar tree topology. For BYPP, the standard deviation of split frequencies was reached at 0.0099 after 2,980,000 generations. The most likely tree (−ln = 66,531.894) is presented (Figure 1). The MP analysis resulted in two trees with TL = 15,668, CI = 0.302, RI = 0.524, RC = 0.158, HI = 0.698.

The single locus trees (Supplemental Figures S1–S4) and the multi-locus (LSU, rpb2, tub2 and ITS) tree (Figure 1) showed similar tree topology. In multigene analyses, Vamsapriya species clustered with Diabolocovidia claustri and Didymbotryum rigidum, and they formed an internal distinct clade with maximum support (ML-bs = 100%, MP-bs = 100%, BYPP = 1.00). Xylariaceae, Induratiaeaceae and Clypeosphaeriaceae clustered together, which is a sister to Vamsapriyaceae without significant support. Moreover, V. chiangmaiensis (MFLUCC 21-0065) formed a sister clade to V. yunnana; however, the support for this relationship in Figure 1 is extremely poor and does not exist in Figure 2, and V. uniseptata (GZCC 21-0892) is sister to V. indica. Our isolate MFLUCC 21-0066 grouped in V. indica clade with MFLUCC 12-0544 and DLUCC:2062, indicating they are phylogenetically the same species. Two Anthostomella (Xylariaceae) species, A. formosa (MFLUCC 14-0170) and A. obesa (MFLUCC 14-0171) formed a distinct clade and is sister to Cainiaceae.
Figure 1. Maximum likelihood (RAxML) tree, based on analysis of a combined dataset of LSU, rpb2, tub2 and ITS sequence data. The tree is rooted with Amphisphaeria sorbi (MFLUCC 13-0721) and A. thailandica (MFLUCC 18-0794). Bootstrap support values for ML and MP greater than 50% and Bayesian posterior probabilities greater than 0.95 are given near nodes, respectively. Ex-type strains are in bold, the new isolates are in red.

The ITS based on Vamsapriya analyses contained 12 taxa and rooted with Diabolocovidia claustra (CBS 146630) and Didymobotryum rigidum (JCM-8837). The manually adjusted ITS alignment contained 563 characters. The best scoring RAxML tree with a final likelihood value of $-1737.963458$ is presented (Figure 2). Maximum parsimony analysis comprised 563 characters, of which 446 were constant, 54 were parsimony-informative, and 63 were parsimony-uninformative; the tree length is 184, CI = 0.739, RI = 0.597, RC = 0.441, HI = 0.261. The results showed our strain MFLUCC 21-0066 clustered together with V. indica (MFLUCC 13-0721) and A. thailandica (MFLUCC 18-0794). Bootstrap support values for ML and MP greater than 50% and Bayesian posterior probabilities greater than 0.95 are given near nodes, respectively. Ex-type strains are in bold, the new isolates are in red.
3.2. Taxonomy

_Vamsapriyaceae_ Y.R. Sun, Yong Wang bis & K.D. Hyde, fam. nov.

Index Fungorum number: IF558620; Facesoffungi number: FoF09926

Etymology: Name reflects the type genus

Type genus: _Vamsapriya_ Gawas & Bhat

Saprobic on dead wood. Sexual morph: _Ascomata_ solitary, scattered, immersed, sub-globose, black, ostiolate. Peridium thin-walled, brown. _Paraphyses_ hyaline, septate. _Asci_ 8-spored, unitunicate, cylindrical, short pedicellate, with a J+ apical ring. _Ascospores_ apiosporous, fusiform to broad fusiform, hyaline. Asexual morph: Hyphomycetous.

_Colonies_ on natural substrate effuse, black, velvety. _Mycelium_ immersed, septate, branched. _Synnemata_ present or absent; when present (_Didymobotryum, Podosporium, Tretophragmia, Vamsapriya_), _synnemata_ erect, rigid, dark brown, composed of compact parallel conidiophores. _Conidiophores_ erect, straight or curved, cylindrical, dark brown, septate. _Conidigenous cells_ mono- or polytretic, integrated, terminal, clavate to cylindrical, brown. _Conidia_ catenate or solitary, acrogenous, simple, pigmented, multi-shaped, septate; when absent (_Diabolocovidia_, adapted from Crous et al. [49]), _conidiophores_ micronematous, flexuous, mostly reduced to a terminal conidigenous cell. _Conidigenous cells_ monoblastic, subcylindrical to clavate, pale brown, smooth. _Conidia_ catenate, acrogenous, brown, ellipsoid to obovoid, thin-walled, aseptate.

Notes: A new family, _Vamsapriyaceae_, is introduced to accommodate _Diabolocovidia, Didymobotryum, Podosporium, Tretophragmia_, and _Vamsapriya_. Their phylogenetic position, which is distinct from other families, supports the establishment of the new family within _Xylariales_. Although the phylogeny of _Podosporium_ and _Tretophragmia_ could not be inferred due to the lack of molecular data, their morphological characters resemble _Didymobotryum_ and _Vamsapriya_ in having brown to dark, simple, straight synnemata, mononectic conidigenous cells and solitary, obclavate, multi-septate, dark brown conidia [50–53]. We thus temporarily accept _Podosporium_ and _Tretophragmia_ in _Vamsapriyaceae_ based on morphology. Sequence data are needed to resolve their phylogenetic affinities.

_Vamsapriya_ Gawas & Bhat, Mycotaxon 94: 150 (2006) [2005]
Index Fungorum number: IF29041; Facesoffungi number: FoF00372
Type species: Vamsapriya indica Gawas & Bhat, Mycotaxon 94: 150 (2006) [2005]
Saprobic on dead wood. Sexual morph: Ascomata solitary, scattered, immersed, sub-globose, black, ostiolate. Peridium thin-walled, brown. Paraphyses hyaline, septate. Asci 8-spored, unitunicate, cylindrical, straight, short pedicellate, with a J+ apical ring. Ascospores uniseriate or overlapping uniseriate, fusiform to broad fusiform, apiosporous, hyaline, pointed at both ends, surrounded by a mucilaginous sheath. Asexual morph: Hyphomycetous. Colonies on natural substrate effuse, black, velvety. Mycelium immersed, septate, branched. Conidiophores macronematous, syncnematous, erect, straight or curved, dark brown, cylindrical, septate. Synnemata erect, rigid, dark brown, composed of compact parallel conidiophores. Conidiogenous cells monotropic, integrated, terminal, clavate to cylindrical. Conidia catenate or solitary, acrogenous, cylindrical, oblong, fusiform or obclavate, brown to dark brown, septate, verruculose.

Notes: Vamsapriya species are reported from tropical and subtropical regions, and most species are found in terrestrial as saprobes [26–31]. Nine species are accepted in the Vamsapriya, of which six have molecular data. Vamsapriya is the only holomorphic genus in Vamsapriyaceae, and V. bambusicola is the only species with a sexual-asexual connection in Vamsapriya. Bamboo seems to be the host preference for Vamsapriya species [26–33].

Vamsapriya indica Gawas & Bhat, Mycotaxon 94: 150 (2006) [2005]
Index Fungorum number: IF550801; Facesoffungi number: FoF00374, Figure 3
Saprobic on dead bamboo culms. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. Colonies effuse, dark brown, hairy. Conidiophores macronematous, synnematous, single, erect, cylindrical, straight or slightly flexuous, dark brown, smooth-walled. Synnemata erect, straight or slightly flexuous, dark brown, rigid, with cylindrical to clavate apical fertile part, composed of compactly arranged conidiophores, 1300–1900 µm long, 80–150 µm wide at the base, 30–40 µm wide in the middle, 60–140 µm wide at the apical fertile region, with basal portion immersed. Conidiogenous cells monotropic, integrated, terminal, brown, cylindrical to clavate, apically rounded, smooth-walled, 4.5–8.5 × 3–4.5 µm (T = 6.5 × 4 µm, n = 30). Conidia catenate, acrogenous, cylindrical, rounded at the apex, taper and subtruncate at the base, olivaceous brown to brown, 2–8-septate, slightly constricted at the septa, smooth, 20–48 × 4.5–6.5 µm (T = 32 × 5.5 µm, n = 20).

Cultural characters: Conidia germinated on PDA within 12 h, germ tubes produced from both ends. Colonies reached 20 mm diam. within four weeks at 26 °C, cottony, flat, circular, edge entire, white from above, white to yellow from the below.

Material examined: Thailand, Chiang Mai Province, Mae Taeng District, Pa Pae, Mushroom Research Center, on bamboo culms, 10 September 2020, H.W. Shen, M38 (MFLU 21-0088; living culture, MFLUCC 21-0066).

Notes: Vamsapriya indica is the type species of Vamsapriya [26]. Dai et al. [27] collected V. indica from Thailand and provided the culture characters and sequences data. Bao et al. [32] reported it from a bamboo plant in a freshwater habitat in China. Including our collection, all of these four isolates are recorded from bamboo. Morphological comparison is shown in Table 3. Our collection has longer synnemata than those of the three isolates.
Figure 3. Vamsapriya indica (MFLU 21-0088) (a,b) Colonies on natural substrate. (c) Conidiophore and conidia. (d–f) Conidiogenous cells and developing conidia. (g–k) Conidia. (l) Germinated conidium. Scale bars: a = 2000 µm, b = 1000 µm, c = 200 µm, d–l = 20 µm.
## Table 3. Synopsis of characters of *Vamsapriya indica* collections.

| Taxon            | Host       | Habitat/Location       | Synnemata                                                                 | Conidiogenous Cells                                                                 | Conidia                                                                 |
|------------------|------------|------------------------|---------------------------------------------------------------------------|-------------------------------------------------------------------------------------|-------------------------------------------------------------------------|
| *V. indica* (M 393674) | Bamboo     | Terrestrial/India       | 700–1100 µm long, 60–160 µm wide at the base, 30–60 µm wide in the middle, 30–80 µm wide at the apical fertile region | Monotretic, clavate, dark brown, 4–9 × 2.5–4.5 µm                                | Catenate, acrogenous, brown, cylindrical, vermiform, 10–80 × 4–6 µm, 2–12-septate |
| *V. indica* (MFLU 13-0370) | Bamboo     | Terrestrial/Thailand    | 700–1100 µm long, 60–160 µm wide at the base, 30–60 µm wide in the middle, 30–80 µm wide at the apical fertile region | Monotretic, ellipsoidal, brown to dark brown, 4–9 × 2.5–4.5 µm (µ = 6.5 × 3.7 µm, n = 20) | Catenate, cylindrical, pale brown to dark brown 35–290 × 4–6.5 µm (µ = 66.6 × 5.6 µm, n = 20), 1–3-septate when young, more than 20–septate at maturity |
| *V. indica* (HKAS 115803) | Bamboo     | Freshwater/China        | 1145–1475 µm long, 105–235 µm wide at the base, 50–80 µm wide in the middle, 70–155 µm wide at the apical fertile region | Monotretic, clavate, dark brown 5–9 × 3–5 µm (µ = 20 × 5 µm, n = 30)               | Catenate, brown to dark brown, cylindrical to obclavate, 15–30 × 4–6.5 µm (µ = 20 × 5 µm, n = 30), 1–4-septate |
| *V. indica* (MFLU 21-0088) | Bamboo     | Terrestrial/Thailand    | 1300–1900 µm long, 80–150 µm wide at the base, 30–40 µm wide in the middle, 60–140 µm wide at the apical fertile region | Cylindrical to clavate, brown, 4.5–8.5 × 3–4.5 µm (µ = 6.5 × 4 µm, n = 30)         | Catenate, olivaceous brown to brown, cylindrical, 20–48 × 4.5–6.5 µm (µ = 32 × 5.5 µm, n = 20), 2–8-septate |
Vamsapriya chiangmaiensis Y.R. Sun, Yong Wang bis & K.D. Hyde, sp. nov.
Index Fungorum number: IF558618; Facesoffungi number: FoF09927, Figure 4

Figure 4. Vamsapriya chiangmaiensis (MFLU 21-0087, holotype) (a,b) Appearance of ascomata on host substrate. (c) Vertical section of ascoma. (d–f) Asci. (g) Paraphyses. (h) Apical ring of asci. (i–m) Ascospores. (n) Germinated ascospore. (o) Ascospore stained in Indian ink. (p,q) Colonies on PDA. Scale bars: c = 200 μm, d–g = 20 μm, f,h–o = 10 μm.
Etymology: Name reflects the collected site.
Holotype: MFLU 21-0087

Saprobic on dead bamboo culms. Sexual morph: Ascomata 650–1000 × 650–850 μm, solitary scattered, immersed within the host cortex, visible as black, circular dots, in cross section globose to subglobose. Ostiole raised, centric, periphysate ostiolar canal. Peridium composed of hyaline inner layer and dark brown to dark outer layer. Paraphyses long, hyaline, unbranched, septate, 1.5–4 μm wide (T = 2 μm, n = 15). Asci 8-spored, unitec, straight or slightly curved, cylindrical, short pedicellate, with apical ring, 140–190 × 6.5–12 μm (T = 160 × 9 μm, n = 15). Ascospores uniseriate, fusiform, 17–26 × 5.8–8 μm (T = 20.5 × 6.5 μm, n = 30), constricted apiosporous with a large cell 12.5–22 μm length, guttulate; basal cell 3.5–6.5 μm length, hyaline, smooth-walled, surrounded a gelatinous mucilaginous sheath. Asexual morph: Undetermined.

Culture characters: Ascospores germinated on PDA within 12 h, germ tubes produced from one end. Colonies reached 45 mm diam. within four weeks at 26 °C, flat, circular, cottony. White from above; brown to dark brown in the center, white to pale brown around from below.

Material examined: Thailand, Chiang Mai Province, Mae Taeng District, Mushroom Research Center, on bamboo culms, 15 July 2020, Y.R. Sun, M35 (MFLU 21-0087, holotype; ex-type living culture, MFLUCC 21-0065).

Notes: Vamsapriya chiangmaiensis is the second species that has a sexual morph in Vamsapriya. It is similar to V. bambusicola in having solitary, subglobose ascomata, 8-spored, uniseriate, cylindrical asci and fusiform hyaline ascospores. It can be distinguished by the longer asci (140–190 μm vs. 115–140 μm). In addition, polymorphic nucleotides from the ITS region showed 37 base differences, and the details are given in Table 4. Therefore, we identified V. chiangmaiensis as a new species following the suggestions for species delineation [54].

Table 4. Nucleotide differences in the ITS regions of V. bambusicola and V. chiangmaiensis. Numbers are in reference to the nucleotide position of DNA sequences (V. bambusicola) submitted in GenBank.

| Species                      | ITS                                                                 |
|------------------------------|---------------------------------------------------------------------|
| V. bambusicola (MFLUCC 11-0477) | C T C G T T A A C C C G C C T C T A A                                    |
| V. chiangmaiensis (MFLUCC 21-0065) | 216 221 229 232 235 239 241 432 446 447 451 461 465 557 558     |
| V. bambusicola (MFLUCC 11-0477) | T A A C T T G T C T C T C T G T T                                    |
| V. chiangmaiensis (MFLUCC 21-0065) | A G T T C C A C T C T G T T                                 |

Vamsapriya uniseptata N.G. Liu & K.D. Hyde, sp. nov.

Index Fungorum number: IF558619; Facesoffungi number: FoF09928, Figure 5.

Etymology: Name reflects the 1-septate conidia.

Holotype: GZAAS 21-0378

Saprobic on submerged decaying wood in terrestrial habitat. Colonies on natural substrate effuse, black, velvety. Asexual morph: Hyphomycetous. Mycelium mostly immersed, composed of septate, branched, hyaline to brown hyphae. Conidiophores macronematous, synnematous, erect, straight or broadly curved, dark brown, cylindrical, septate. Synnemata erect, rigid, dark brown, composed of compact parallel conidiophores, up to 1300 μm long, 30–50 μm wide in the middle. Conidiogenous cells monomorphic, integrated, terminal, clavate, brown to dark brown. Conidia catenate, acrogenous, olivaceous brown, smooth, oblong, rounded at the apex, taper and subtruncate at the base, 1-septate at the middle, septa thickened and darkened, slightly constricted at the septa, with a large globose in each cell, 14–19 × 3.5–4.5 μm (T = 16.5 × 5 μm, n = 30). Sexual morph: Unknown.
Cultural characters: Conidia germinated on PDA within 12 h and germ tubes produced from both ends. Colonies reached 30 mm within four weeks at 26 °C, flat, circular, cottony, white from above, from below brown to dark brown in the center, white to pale brown around.

Material examined: China, Guizhou Province, Xingyi City, Qingshuihe Town, 8 August 2019, N.G. Liu, Q1 (GZAAS 21-0378, holotype; ex-type living culture, GZCC 21-0892).

Notes: *Vamsapriya uniseptata* is distinguishable by having smaller, 1-septate conidia, while other *Vamsapriya* species have elongated phragmoconidia. In the BLASTn search, the closest match of the ITS sequence of *V. uniseptata* is *V. khunkonensis* (MFLUCC 13-0497, MFLUCC 11-0475 (93.4%)), followed by *V. indica* (MFLUCC 12-0544 (91.7%)). The LSU sequence of *V. uniseptata* is *V. indica* (DLUCC:2062 (99.8%)) and *V. khunkonensis* (MFLUCC 11-0475 (99.7%)). *Vamsapriya uniseptata* can be distinguished from *V. khunkonensis* in the multigene phylogenetic analyses. The ITS region of *V. indica* (MFLUCC 13-0497) differs by 23 base pairs (527 bp without gaps). Based on distinct morphology and phylogeny, *V. uniseptata* is introduced as a novel taxon.

![Figure 5](image-url). *Vamsapriya uniseptata* (GZAAS:21-0378, holotype) (a,b) Colonies on natural substrate. (c) Conidiophores and conidia. (d-f) Conidiogenous cells and developing conidia. (g-k) Conidia. (l) Germinated conidium. Scale bars: c = 100 μm, d,e,g,h = 5 μm, f = 10 μm.
3.3. Other Accepted Genera in Vamsapriyaceae

**Diabolocovidia** Crous, Persoonia 44: 331 (2020)

Parasitic on leaves in terrestrial habitats. Mycelium composed of septate, branched, hyaline to pale brown hyphae. Asexual morph: Hyphomycetous. Conidiophores solitary, flexuous, mostly reduced to a terminal conidiogenous cell. Conidiogenous cells monoblastic, terminal, subcylindrical to clavate, pale brown, smooth. Conidia catenate, acrogenous, brown, ellipsoid to obvoid, thin-walled, un-septate, verruculose [49]. Sexual morph: Unknown.

Type species: *Diabolocovidia claustri* Crous

Notes: *Diabolocovidia* is a monotypic genus introduced by Crous et al. [49] to accommodate *Diabolocovidia claustri*, which was isolated from leaves of *Serenoa repens* in the U.S.A. *Diabolocovidia claustri* is characterized by mononematous, micronematous conidiophores in *Xylariaceae*. In their phylogenetic analyses, *Diabolocovidia* is basal to *Vamsapriya* [49]. *Diabolocovidia* is the only genus without synnemata in *Vamsapriyaceae*.

**Didymobotryum** Sacc., Syll. fung. (Abellini) 4: 626 (1886)

Parasitic on decaying plants materials in terrestrial habitats. Colonies on natural substrate effuse, olivaceous to dark brown, velvety. Mycelium mostly immersed, composed of septate, branched, thick-walled, subhyaline hyphae. Asexual morph: Hyphomycetous. Conidiophores macronematous, synnematous, erect, straight or broadly curved, dark brown, cylindrical, septate. Synnemata erect, rigid, dark brown, composed of compact parallel conidiophores. Conidiogenous cells monotretic, integrated, integrated or discrete, cylindrical to clavate, olivaceous brown to dark brown. Conidia solitary, acrogenous, cylindrical, verrucose, 1-septate, slightly constricted at the septa, olivaceous brown to brown. Sexual morph: Unknown.

Type species: *Didymobotryum rigidum* (Berk. & Broome) Sacc.

Notes: *Didymobotryum* was introduced by Saccardo [55] typified by *D. rigidum*. *Didymobotryum* species have a worldwide distribution [56–59]. Six species are accepted in the Index Fungorum [37] but only *D. rigidum* has molecular data (ITS: LC228650, LSU: LC228707).

**Podosporium** Schwein., Trans. Am. phil. Soc., New Series 4(2): 278 (1832) [1834]

Parasitic on decaying plants materials in terrestrial habitats. Colonies on natural substrate effuse, olivaceous to dark brown, velvety. Mycelium mostly immersed, composed of septate, branched, thick-walled, subhyaline hyphae. Asexual morph: Hyphomycetous. Conidiophores macronematous, synnematous, erect, straight or broadly curved, dark brown, cylindrical, septate. Synnemata erect, rigid, dark brown, composed of compact parallel conidiophores. Conidiogenous cells monotretic, integrated, integrated or discrete, cylindrical to clavate, olivaceous brown to dark brown. Conidia solitary, obclavate or bacilliform, multi-septate, brown to dark brown. Sexual morph: Unknown.

Type species: *Podosporium rigidum* Schwein.

Notes: *Podosporium* was introduced by Schweinitz [60] with *P. rigidum* as the type species. Since then, many *Podosporium* species have been discovered worldwide [60–63]. Most of them are saprobes in terrestrial habitats [60–63]. There are 67 species listed in the Index Fungorum [37] but no sequence data are available.

**Tretophragmia** Subram. & Natarajan, Proc. Natl. Inst. Sci. India, B, Biol. Sci. 39: 550 (1974) [1973]

Saprobic on plants materials in terrestrial habitats. Colonies on natural substrate effuse, dark, velvety. Asexual morph: Hyphomycetous. Conidiophores macronematous, synnematous, brown, septate, erect, straight or broadly curved. Synnemata rigid, brown to dark, simple, erect, straight, consisting of a stalk and a capitata, broadened, fertile head. Conidiogenous cells monotretic, subulate or cylindrical, darkly pigmented. Conidia solitary,
obclavate to fusiform or irregular in shape, straight, curved or bent, multi-septate, dark brown. Sexual morph: Unknown.

Type species: Tretophragmia nilgirensis (Subram.) Subram. & Natarajan

Notes: Tretophragmia was introduced in 1974. The asexual morph of Tretophragmia is similar to Didymobotryum, Podosporium and Vamsapriya, while no sexual morph is reported. Seifert et al. [53] treated Tretophragmia as a synonym of Podosporium. However, Tretophragmia is accepted in the Index Fungorum [37] and the MycoBank [64] as a separate genus. So far, only two species of Tretophragmia have been described [37] and no sequence data are available. Thus, based on morphology and until DNA sequences data are available, we regard this as a separate genus.

4. Discussion

In this study, three Vamsapriya species, V. chiangmaiensis, V. indica and V. uniseptata were collected from bamboo in terrestrial habitats. In our phylogenetic analyses of combined LSU, rpb2, tub2 and ITS sequence data, Diabolocovidia, Didymobotryum and Vamsapriya formed a distinct clade in Xylariales. Morphological comparison also shows their distinctiveness from other families in Xylariales. Therefore, we propose Vamsapriyaceae as a new family in Xylariales. The sexual morph of Vamsapriya differs from those of Xylariaceae in having hyaline asciopores [28,30]. It is noteworthy that the sexual morph of Vamsapriya is similar to Induratiaceae in having 8-spored asci with J+ apical ring and hyaline, asciopores, but Induratia (Induratiaceae) differs in having geniculosporium assexual morphs [34]. Apioclypea is morphologically similar to the sexual morph of Vamsapriya in having 8-spored, pedunculate, cylindrical asci and biseriate, fusiform, hyaline ascospores with a mucilaginous sheath, but its asexual morph is unknown [19,21].

Clypeosphaeriaceae and Induratiaceae are two other families that are phylogenetically related to Vamsapriyaceae, but they are distinct in morphology. Apioclypea, Aquasphaeria, Brunniapiospora, Clypeosphaeria, Crassoascus, and Palmaria (Clypeosphaeriaceae) lack asexual morph descriptions and Diabolocovidia, Didymobotryum, Podosporium and Tretophragmia (Vamsapriyaceae) do not have sexual morph descriptions for the comparisons in Tables 5 and 6.

Diabolocovidia claustri was isolated on leaves of Serenoc repens by Crous et al. [49]. Although it has a close phylogenetic relationship with Vamsapriya, they are quite different in morphology. Diabolocovidia has micronematous rather than synnematous conidiophores, blastic rather than tretic conidiogenous cells, and ellipsoid to obvoid, aseptate conidia [49]. The phenomenon that Diabolocovidia mixes with synnematous and tretic genera like Didymobotryum and Vamsapriya reminds us of an example that Vanakripa with blastic conidiogenous resides in the phialidic genus Conioscypha [65]. These probably indicate the polyphyletic nature of some hyphomycetous groups. However, since D. claustri is the only species represented by one isolate in Diabolocovidia, we suggest using more collections to confirm its phylogenetic placement in the future.

When introducing Vamsapriya, Gawas and Bhat [26] pointed out Vamsapriya (conidia catenate, cylindrical to vermiciform, phragmosporous) exhibits a combination of morphological characters of Didymobotryum (conidia catenate, ellipsoidal-cylindrical, didymosporous) [51,53,54] and Podosporium (conidia solitary, obclavate, phragmosporous) [56,61,63]. However, as more species are added to these three genera, such generic concepts based on conidial morphology have been dispelled. For example, V. uniseptata resembles species of Didymobotryum in having catenate, oblong, and 1-septate conidia, but it clusters with the type species of Vamsapriya, V. indica. Vamsapriya breviconidiophora and V. yunnana resemble Podosporium species in having obclavate, solitary, and multi-septate conidia, but they are grouped with V. aquatica, which has catenate, cylindrical to obclavate, multi-septate conidia in the phylogenetic tree. Either the authors did not follow the generic concepts strictly when introducing species, or these three genera are probably congeneric. We tend to infer the latter; however, the conclusion requires a detailed re-examination of herbarium specimens and molecular data.
Table 5. Asexual morph comparison of the genera in Clypeosphaeriaceae, Induratiaceae and Vamsapriyaceae.

| Family    | Genus       | Asexual Morph | Synnemata | Conidiogenous Cells | Conidia                        |
|-----------|-------------|---------------|-----------|---------------------|--------------------------------|
| Vamsapriyaceae | Diabolocvidia | Absent      | Monoblastic, subcylindrical to clavate, pale brown | Catenate, acrogenous, brown, ellipsoid to obovoid, unseptate |
|          | Didymobotryum | Present     | Monotretic, integrated, terminal, clavate to cylindrical, pale brown to brown | Catenate, olivaceous brown to brown, cylindrical |
|          | Podosporium  | Present     | Mono- or polytretic, subulate or cylindrical, darkly pigmented | Solitary, obclavate or bacilliform, multi-septate, brown to dark brown |
|          | Tretophragmia | Present     | Monotretic, subulate or cylindrical, darkly pigmented | Solitary, obclavate to fusiform or irregular in shape, multi-septate, dark brown |
|          | Vamsapriya    | Present     | Monotretic, clavate to cylindrical | Catenate or solitary, acrogenous, cylindrical, oblong, fusiform or obclavate, brown to dark brown, septate |
| Induratiaceae | Emarcea      | Absent      | Integrated, terminal, pale brown, forming a rachis with numerous small, pimple-like denticles | Hyaline, smooth, falcate, granular, apex subobtuse, base truncate |
|          | Induratia    | Absent      | Terminal, solitary or sometimes two celled at the ends of branches, cylindrical, pale brown, bearing inconspicuous denticles | Narrowly ellipsoid to subglobose, hyaline |

Table 6. Sexual morph comparison of the genera in Clypeosphaeriaceae, Induratiaceae and Vamsapriyaceae.

| Family    | Genus       | Sexual Morph | Asci | Ascospores                        |
|-----------|-------------|--------------|------|-----------------------------------|
| Vamsapriyaceae | Vamsapriya    | 8-spored, uniloculate, cylindrical, short pedicellate, with J+ apical ring | Apiosporous, fusiform to broad fusiform, hyaline, with sheath |
| Induratiaceae | Emarcea      | 8-spored, uniloculate, cylindrical, pedicellate, with J+ ring | Overlapping uniseriate, long fusiform, hyaline, 2-celled |
|          | Induratia    | 8-spored, uniloculate, cylindrical, short pedicellate, with a J+ apical ring | Uniseriate, naviculate to ellipsoidal, mostly hyaline, constricted apiosporous |
| Clypeosphaeriaceae | Aquasphaeria   | 8-spored, uniloculate, cylindrical, with J- apical ring | Biseriate, cylindrical and ovoid, hyaline |
|          | Apioclypea   | 8-spored, pedunculate, cylindrical, fissitunicate | Biseriate, fusiform, hyaline, with sheath /
|          | Brunneiaipiospora | 8-spored, uniloculate, cylindrical, pedicellate with J+ or J- ascal ring | Hyaline to light brown apiospores with a mucilaginous sheath |
|          | Clypeosphaeria | 8-spored, uniloculate, cylindrical to broadly cylindrical, pedicellate, with J+ or J- ascal ring | Ellipsoidal to fusiform, unicellular to septate, hyaline to dark brown ascospores, sometimes with sheaths or appendages |
|          | Crassoascus  | 8-spored, uniloculate, cylindrical, short pedicellate, with J+ ring | Bright brown to dark brown, multiseptate, fusiform ascospores, with hyaline refractive cap-like appendages at each end |
|          | Palmaria     | Cylindric to clavate, with a J- subapical ring | Apiosporous, hyaline, 1-septate, obclavate, with a mucilaginous sheath |

Supplementary Materials: The following are available online at https://www.mdpi.com/article/10.3390/jof7110891/s1, Figure S1: Maximum likelihood (RAxML) tree based on ITS sequence data. The tree is rooted with Amphisphaeria sorbi (MFLUCC 13-0721) and A. thailandica (MFLU 18-0794). Figure S2: Maximum likelihood (RAxML) tree based on LSU sequence data. The tree is rooted with Amphisphaeria sorbi (MFLUCC 13-0721) and A. thailandica (MFLU 18-0794). Figure S3: Maximum likelihood (RAxML) tree based on tub2 sequence data. The tree is rooted with Amphisphaeria thailandica.
Figure S4: Maximum likelihood (RAxML) tree based on rpb2 sequence data. The tree is rooted with *Amphisphaeria thailandica* (MFLU 18-0794).

**Author Contributions:** Methodology, Y.-R.S.; Software, Y.-R.S.; Supervision, R.S.J., K.D.H. and Y.W.; Writing—original draft, Y.-R.S.; Writing—review & editing, N.-G.L., M.C.S., R.S.J., K.D.H. and Y.W. All authors have read and agreed to the published version of the manuscript.

**Funding:** The study was funded by Guizhou Science Technology Department International Cooperation Basic project [2018]5806), National Natural Science Foundation of China (No. 31972222, 31560489), Program of Introducing Talents of Discipline to Universities of China (111 Program, D20023), and Talent project of Guizhou Science and Technology Cooperation Platform [2017]5788-5, [2019]5641 and [2020]5001).

**Institutional Review Board Statement:** Not applicable.

**Data Availability Statement:** Not applicable.

**Acknowledgments:** We thank Shaun Pennycook for checking the nomenclature. We also thank the support of the Thailand Research Foundation. Ya-Ru Sun would like to thank Hong-Wei Shen for collecting the samples. Samantha C. Karunarathna is thanked for giving suggestions in this study. Kevin D. Hyde would like to thank the Thailand Research grant entitled “Impact of climate change on fungal diversity and biogeography in the Greater Mekong Subregion” (grant no: RDG6130001).

**Conflicts of Interest:** The authors declare no conflict of interest.

**References**

1. Eriksson, O.E.; Winka, K. Supraordinal taxa of Ascomycota. *Mycotaxon* 1997, 1, 1–16.
2. Smith, G.J.D.; Liew, E.C.; Hyde, K.D. The Xylariales: A monophyletic order containing 7 families. *Fungal Diversity* 2003, 13, 185–218.
3. Stadler, M. Importance of secondary metabolites in the Xylariaeae as parameters for assessment of their taxonomy, phylogeny, and functional biodiversity. *Curr. Res. Environ. Appl. Mycol.* 2011, 1, 75–133. [CrossRef]
4. U’Ren, J.M.; Miadlikowska, J.; Zimmerman, N.B.; Lutzoni, F.; Stajich, J.E.; Arnold, A.E. Contributions of North American endophytes to the phylogeny, ecology, and taxonomy of Xylariaceae (Sordariomycetes, Ascomycota). *Mol. Phylogenet. Evol.* 2016, 98, 210–232. [CrossRef] [PubMed]
5. Helaly, S.E.; Thongbai, B.; Stadler, M. Diversity of biologically active secondary metabolites from endophytic and saprotrophic fungi of the ascomycete order Xylariales. *Nat. Product Rep.* 2018, 35, 992–1014. [CrossRef]
6. Becker, K.; Stadler, M. Recent progress in biodiversity research on the Xylariales and their secondary metabolism. *J. Antibiot.* 2021, 74, 1–23. [CrossRef]
7. Nannfeldt, J.A. Studien über die Morphologie und Systematik der nicht-lichenisierten inoperculalen Discomyceten. *Nova Acta Regiae Societatis Scientiarum Upsaliensis Ser. IV* 1932, 8, 1–368.
8. Munk, A. The system of the Pyrenomycetes. *Dansk Botanisk Arkt* 1953, 15, 1–163.
9. Müller, E.; von Arx, J.A. Die Gattungen der didymosporen Pyrenomyceten. *Beiträge Kryptogamflora Schweiz* 1962, 11, 1–922.
10. Muller, E. Pyrenomycetes: Meliolales, coronophorales, sphaeriales. In *The Fungi, an Advanced Treatise*; Academic Press: London, UK, 1973.
11. Wehmeyer, L.E. The Pyrenomycetous fungi. *Mycol. Mem.* 1975, 6, 1–250.
12. Barr, M.E. Prodromus to nonlichenized, pyrenomycetous members of class Hymenoascomycetes. *Mycotaxon* 1990, 39, 43–184.
13. Hawksworth, D.L.; Kirk, P.M.; Sutton, B.C.; Pegler, D.N. *Ainsworth and Bisby’s Dictionary of the Fungi*, 8th ed.; CAB International: Oxon, UK, 1995.
14. Kang, J.C.; Kong, R.Y.C.; Hyde, K.D. Studies on the Amphisphaeriales 1. *Amphisphaeriae* (sensu stricto) and its phylogenetic relationships inferred from 5.8S rDNA and ITS2 sequences. *Mol. Phylogenet. Evol.* 1998, 1, 147–157.
15. Kang, J.C.; Kong, R.Y.C.; Hyde, K.D. Phylogeny of *Amphisphaeriae* (sensu stricto) and related taxa revisited based on nrDNA sequences. *Mycotaxon* 2002, 81, 321–330.
16. Eriksson, O.E.; Baral, H.O.; Currath, R.S.; Hansen, K.; Kurtzman, C.P.; Rambold, G.; Lasessoa, T. Outline of Ascomycota—2003. *Myconet* 2003, 9, 1–89.
17. Lumbsch, H.T.; Huhndorf, S.M. Myconet volume 14 part one. Outline of ascomycota—2009. *Fieldiana Life Earth Sci.* 2010, 1, 1–22. [CrossRef]
18. Senanayake, I.C.; Maharachchikumbura, S.S.N.; Hyde, K.D.; Bhat, J.D.; Jones, E.B.G.; McKenzie, E.H.C.; Dai, D.Q.; Daranagama, D.A.; Dayarathe, M.C.; Goonasekara, I.D.; et al. Towards unraveling relationships in *Sordariomycetidae* (Sordariomycetes). *Fungal Divers.* 2015, 73, 73–144. [CrossRef]
19. Hyde, K.D.; Norphanphoun, C.; Maharachchikumbura, S.S.N.; Bhat, D.J.; Jones, E.B.G.; Bundhun, D.; Chen, Y.J.; Bao, D.F.; Boonmee, S.; Calabon, M.S.; et al. Refined families of Sordariomycetes. *Mycosphere* 2020, 11, 305–1059. [CrossRef]
20. Hyde, K.D.; Dong, Y.; Phookamsak, R.; Jeewon, R.; Bhat, D.J.; Jones, E.B.G.; Liu, N.G.; Abeywickrama, P.D.; Mapook, A.; Wei, D.P.; et al. Fungal diversity notes 1151–1276: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. Fungal Divers. 2020, 100, 5–277. [CrossRef]

21. Maharachchikumbura, S.S.N.; Hyde, K.D.; Jones, E.B.G.; McKenzie, E.H.C.; Bhat, J.D.; Dayaratne, M.C.; Huang, S.K.; Norphanphoun, C.; Senanayake, I.C.; Perera, R.H.; et al. Families of Sordariomycetes. Fungal Divers. 2016, 79, 1–317. [CrossRef]

22. Fröhlich, J.; Hyde, K.D. Palm Microfungi. Fungal Divers. Res. Ser. 2000, 3, 1–393.

23. Daranagama, D.A.; Camporesi, E.; Liu, X.Z.; Bhat, D.J.; Chamyuang, S.; Bahkali, A.H.; Studler, M.; Hyde, K.D. Tristriateripidium microsporum gen. et sp. nov. (Xylariales) on dead leaves of Arundo plinii. Mycol. Prog. 2015, 15, 1–8. [CrossRef]

24. Crous, P.W.; Wingfield, M.J.; Burgess, T.L.; Hardy, G.E.S.J.; Crane, C.; Barrett, S.; Cano-Lira, J.F.; le Roux, J.J.; Thangavel, R.; Guarro, J.; et al. Fungal Planet description sheets. 469–557. Persoonia 2016, 37, 218–403. [CrossRef]

25. Fiuza, P.O.; Silva, C.; Santos, T.A.B.; Raja, H.; Cañataeda-Ruiz, R.F.; Gusmão, L.F.P. Roselnygyc, a new asexual genus of the Xylariales (Ascomycota) from Brazil. Sydowia 2018, 70, 59–65.

26. Gaws, P; Bhat, D.J. Vamspriya indica gen. et sp. nov., a bambusicolous, synnematous fungus from India. Mycotaxon 2009, 94, 149–154.

27. Dai, D.Q.; Bahkali, A.H.; Li, Q.R.; Bhat, D.J.; Wijayawardene, N.N.; Li, W.J.; Chukeatbrote, E.; Zhao, R.L.; Xu, J.C.; Hyde, K.D. Vamspriya (Xylariaeaceae) redescribed, with two new species and molecular sequence data. Cryptogamie Mycologie 2014, 35, 339–357. [CrossRef]

28. Dai, D.Q.; Phookamsak, R.; Wijayawardene, N.N.; Li, W.J.; Bhat, D.J.; Xu, J.C.; Taylor, J.E.; Hyde, K.D.; Chukeatbrote, E. Bambusicolous fungi. Fungal Divers. 2017, 82, 1–105. [CrossRef]

29. Cañataeda-Ruiz, R.F.; Zhang, X.G.; Li, D.W.; Gusmão, L.F.P.; Pérez-Martinez, S.; Sosa, D. Notes on Vamspriya and V. camagueyensis comb. nov. Mycotaxon 2017, 132, 553–557. [CrossRef]

30. Hyde, K.D.; Norphanphoun, C.; Abreu, VP.; Bazzicalupo, A.; Thilini, C.K.W.; Clericuzio, M.; Dayaratne, M.C.; Dissanayake, A.J.; Ekanyaka, A.H.; He, M.Q.; et al. Fungal diversity notes 603–708: Taxonomic and phylogenetic notes on genera and species. Fungal Divers. 2017, 87, 1–235. [CrossRef]

31. Jiang, H.B.; Phookamsak, R.; Bhat, D.J.; Khan, S.; Bahkali, A.; Elgorban, A.M.; Hyde, K.D. Vamspriya yunnana, a new species of Vamspriya (Xylariaeaceae; Xylariales) associated with bamboo from Yunnan; China. Phyto taxa 2018, 356, 61–70. [CrossRef]

32. Bao, D.F.; Hyde, K.D.; McKenzie, E.H.; Jeewon, R.; Su, H.Y.; Naumpong, S.; Luo, Z.L. Biodiversity of Lignicolous Freshwater Hyphomycetes from China and Thailand and Description of Sixteen Species. J. Fungi 2021, 7, 669. [CrossRef]

33. Ling, Y.; Li, H.H.; Xia, J.W.; Zhang, X.G.; Li, Z. Vamspriya jinniuensis sp. nov.; and a first record of Garnaudia elegans from southern China. Mycotaxon 2018, 133, 367–372. [CrossRef]

34. Samarakoon, M.C.; Thongbai, B.; Hyde, K.D.; Brönstrup, M.; Beutling, U.; Lambert, C.; Miller, A.N.; Liu, J.K.; Promputtha, I.; Studler, M. Elucidation of the life cycle of the endophytic genus Muscodor and its transfer to Induratia in Induratiaceae fam. nov.; based on a polyphasic taxonomic approach. Fungal Divers. 2020, 101, 177–210. [CrossRef]

35. Senanayake, I.; Rathnayake, A.; Marasinghe, D.; Calabon, M.; Gentekaki, E.; Lee, H.B.; Hurdeal, V.G.; Ped, D.; Dissanayake, L.S.; Wijesinghe, S.N.; et al. Morphological approaches in studying fungi: Collection; Examination; Isolation; Sporulation and Preservation. Mycosphere 2020, 11, 2678–2754. [CrossRef]

36. Jayasiri, S.C.; Hyde, K.D.; Ariyawansa, H.A.; Bha, T.J.; Buyck, B.; Cai, L.; Dai, Y.C.; Abd-Elsalam, K.A.; Ertz, D.; Hidayat, I.; et al. Fungal Planet database: Fungal names linked with morphology; Phylogeny and human impacts. Fungal Divers. 2015, 74, 3–18. [CrossRef]

37. Index Fungorum. Available online: http://www.indexfungorum.org/Names/Names.asp (accessed on 6 September 2021).

38. Vilgalys, R.; Hester, M. Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several Cryptococcus species. J. Bacteriol. 1992, 174, 4238–4246. [CrossRef]

39. White, T.J.; Bruns, T.; Lee, S.; Taylor, J. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. PCR Protoc. Guide Methods Appl. 1990, 18, 315–322.

40. Kato, K.; Standley, D.M. MAFFT multiple sequence alignment software version 7: Improvements in performance and usability. Mol. Biol. Evol. 2013, 30, 772–780. [CrossRef]

41. Larsson, A. AllView: A fast and lightweight alignment viewer and editor for large datasets. Bioinformatics 2014, 30, 3276–3278. [CrossRef]

42. Vaidya, G.; Lohman, D.J.; Meier, R. SequenceMatrix: Concatenation software for the fast assembly of multi-genre datasets with character set and codon information. Cladistics 2011, 27, 171–180. [CrossRef]

43. Ronquist, F.; Teslenko, M.; van der Mark, P.; Ayres, D.L.; Darling, A.; Höhna, S.; Larget, B.; Liu, L.; Suchard, M.A.; Huelsenbeck, J.P. MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. Syst. Biol. 2012, 61, 539–542. [CrossRef]

44. Nylander, J. MrModeltest (Version 2.2); Evolutionary Biology Centre, Uppsala University: Uppsala, Sweden, 2004.

45. Trifinopoulos, J.; Nguyen, L.-T.; von Haeseler, A.; Minh, B.Q. W-IQ-TREE: A fast online phylogenetic tool for maximum likelihood analysis. Nucleic Acids Res. 2016, 44, W232–W235. [CrossRef]

46. Swofford, D.L. PAUP*: Phylogenetic Analysis Using Parsimony (*and Other Methods); Version 4.0b10; Sinauer Associates: Sunderland, MA, USA, 2002.

47. Hillis, D.M.; Bull, J.J. An empirical test of bootstrapping as a method for assessing confidence in phylogenetic analysis. Syst. Biol. 1993, 42, 182–192. [CrossRef]

48. Rambaut, A. FigTree. Version 1.4.2; University of Edinburgh: Edinburgh, UK, 2014.
49. Crous, P.W.; Wingfield, M.J.; Chooi, Y.H.; Gilchrist, C.L.; Lacey, E.; Pitt, J.I.; Roets, F.; Swart, W.J.; Cano-Lira, J.F.; Valenzuela-Lopez, N. Fungal Planet description sheets:1042–1111. Pers. Mol. Phylogeny Evol. Fungi 2020, 44, 301. [CrossRef]
50. Seifert, K. Contributions toward a mycobiota of Indonesia: Synnematous hyphomycetes. Mem. N. Y. Bot. Gard 1990, 59, 109–154.
51. Zhang, Y.D.; Ma, J.; Ma, L.G.; Zhang, X.G. A new species of Podosporium and a new record from southern China. Mycotaxon 2010, 114, 401–405. [CrossRef]
52. Wang, J.Y.; Zhang, K.; Yang, C.L.; Xia, J.W.; Ma, Y.R.; Gao, J.M.; Li, X.Y.; Zhang, X.G.; Cai, Y.M. Podosporium bacilliforme sp. nov. and a first record of Phaeoblastophora peckii from southern China. Mycotaxon 2016, 131, 841–846. [CrossRef]
53. Seifert, K.; Morgan-Jones, G.; Gams, W.; Kendrick, B. The Genera of Hyphomycetes; CBS-KNA W Fungal Biodiversity Centre: Utrecht, The Netherlands, 2011.
54. Jeewon, R.; Hyde, K.D. Establishing species boundaries and new taxa among fungi: Recommendations to resolve taxonomic ambiguities. Mycosphere 2016, 7, 1669–1677. [CrossRef]
55. Saccardo, P.A. Sylloge Hyphomycetum. Sylloge Fungorum 1886, 4, 807.
56. Berkeley, M.J.; Broome, C.E. Enumeration of the fungi of Ceylon. Part II; containing the remainder of the hymenomycetes; with the remaining established tribes of fungi. J. Linn. Soc. Bot. 1873, 14, 29–140. [CrossRef]
57. Ellis, M.B. Dematiaceous Hyphomycetes; Commonwealth Mycological Institute: Kew, UK, 1971.
58. Zhuang, W.Y. Higher Fungi of Tropical China; Mycotaxon Ltd.: Ithaca, NY, USA, 2001.
59. Wang, X.M.; Liu, G.N.; Chen, S.S.; Du, X.F. Records of Beltrania rhombica and Didymobotryum rigidum from China. Mycotaxon 2017, 132, 525–529. [CrossRef]
60. Von Schweinitz, L.D. Synopsis fungorum in America boreali media degentium. Trans. Am. Philos. Soc. 1832, 4, 141–316. [CrossRef]
61. Ciferri, R. Observations on meliolicolous hyphales from Santo Domingo. Sydowia 1955, 9, 302.
62. Mercado, S. Nuevos e interesantes hifomicetes enterblásticos de Cuba. Acta Bot. Cubi 1983, 16, 1–8.
63. Crous, P.W.; Wingfield, M.J.; Kendrick, W.B. Foliicolous dematiaceous hyphomycetes from Syzygium cordatum. Can. J. Bot. 1995, 73, 224–234. [CrossRef]
64. Mycobank. Available online: https://www.mycobank.org/ (accessed on 6 September 2021).
65. Yang, H.; Dong, W.; Yu, X.D.; Bhat, D.J.; Boonmee, S.; Zhang, H. Four freshwater dematiaceous hyphomycetes in Sordariomycetes with two new species of Parafuscosporella. Phytotaxa 2020, 44, 19–34. [CrossRef]