One New Species and Two New Host Records of *Apiospora* from Bamboo and Maize in Northern Thailand with Thirteen New Combinations

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**Abstract:** The genus *Apiospora* is known as a cosmopolitan genus, found across various substrates. In this study, four *Apiospora* taxa were obtained from the decaying stems of bamboo and maize in northern Thailand. *Apiospora* collections were compared with known species based on the morphological characteristics and the DNA sequence data of internal transcribed spacer (ITS), the partial large subunit nuclear rDNA (LSU), the translation elongation factor 1-alpha gene (TEF1-α) and beta-tubulins (TUB2). *Apiospora chiangraiense* sp. nov. and two new host records (*Ap. intestini* and *Ap. raskravinandra*) are introduced here based on the morphological characteristics and multi-locus analyses. Additionally, thirteen species previously identified as *Arthrinium* are introduced as new combinations in *Apiospora*, viz., *Ap. acutiapica, Ap. bambusicola, Ap. biseriata, Ap. cordylines, Ap. cyclobalanopsidis, Ap. euphorbiae, Ap. gelatinosa, Ap. locuta-pollinis, Ap. minutispora, Ap. pseudoraskravinandrae, Ap. septate, Ap. setariae* and *Ap. sorghi*.

**Keywords:** one new species; new combinations; new host records; phylogeny; taxonomy

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1. **Introduction**

*Apiospora* was introduced by Saccardo with *Ap. montagnei* as the type species [1]. The genus was reported in both sexual and asexual morphs. The sexual morphs are characterized by multi-locular perithecial stromata with hyaline ascospores surrounded by a thick gelatinous sheath [2–4]. The asexual morph of *Apiospora* was characterized by basauxic conidiogenesis, with globose to subglobose conidia, which are usually lenticular in the side view, obvoid and pale brown to brown [2,5,6]. Species of *Apiospora* are similar in morphology, thus it is difficult to distinguish them without molecular phylogenetic data. The size, color and shape of conidia and the morphology of conidiophores (e.g., size, shape and septation) should be used together to better identify them. For example, conidiophores of some species reduce to conidiogenous cells (e.g., *Ap. bambusicola, Ap. acutiapicum*), while some species have semi-micronematous to macronematous conidiophores (e.g., *Ap. bambusicola, Ap. intestini*).

*Apiospora* species have a worldwide distribution and can be found from various hosts [3,7–9]. Most *Apiospora* species are associated with plants as endophytes, pathogens
or saprobes, especially on bamboo [2,3,10,11]. To date, more than 25 species have been found from bamboo [2,3,10,11]. *Apiospora* species can cause leaf necrosis and twig dieback in the olive tree (*Olea europaea*), leaf edge spot of the peach (*Prunus persica*), blight disease of bamboo (*Schizostachyum*), leaf spot of rosemary (*Salvia rosmarinus*), kernel blight of barley (*Hordeum vulgare*) and brown culm streak of *Phyllostachys praecox* [11–17]. Some species have also been isolated from lichens, air, soil and animal tissues, and a few species are human pathogens which can cause cutaneous infections in humans [9,18–23].

The morphological relationships between *Arthrinium* and *Apiospora* have long been debated after Ellis [24], as the morphological characteristics of these two genera are similar and difficult to distinguish based on morphology alone. *Apiospora* was synonymized under *Arthrinium* by Crous et al. [3] as they found that *Apiospora* is the sexual morph of *Arthrinium* and phylogenetic analyses showed that the two genera formed a monophyletic clade. Meanwhile, the phylogenetic analyses results from Pintos et al. [25] showed *Arthrinium* forms a monophyletic clade that separates from all other sequences of *Apiospora* and suggested that *Arthrinium s. str.* could actually be phylogenetically different from *Apiospora*, but this is in need of clarification using the phylogeny of additional species before making a conclusive taxonomic decision on the issue. Recently, Pintos and Alvarado [4] showed that *Apiospora* and *Arthrinium* present independent lineages, thus they separate well into two genera.

Morphologically, the conidia of *Apiospora* are more or less rounded in the face view and lenticular in the side view and conidiophores sometimes develop forming acervuli. Whereas the conidia of *Arthrinium* are variously shaped (angular, curved, fusiform, globose, polygonal, navicular) and the conidiophores of some species have thick blackish septa [14]. Ecologically, *Apiospora* species are mostly reported on Poaceae, while *Arthrinium* species commonly occur on Cyperaceae and Juncaceae. Moreover, *Apiospora* has a worldwide distribution, and species in the genus can be found from tropical and subtropical areas to the Mediterranean, temperate and cold regions, while *Arthrinium* species are rarely found from tropical and subtropical habitats. Hence, Pintos and Alvarado [4] considered that genetic, morphological and ecological differences are sufficient to support the taxonomic separation of the two genera, and accordingly, 55 *Arthrinium* species were transferred to *Apiospora* based on the phylogenetic analyses. Presently, 117 records of *Apiospora* are listed in the Index Fungorum [26].

The aims of this study are to determine the phylogenetic placement of the genus *Apiospora* and describe the three taxa that were isolated from maize and bamboo in Chiang Rai province, Thailand. Based on the morphological characteristics and phylogenetic analyses of a combined dataset of the internal transcribed spacer (ITS), the partial large subunit nuclear rDNA (LSU), the translation elongation factor 1-alpha gene (TEF1-α) and beta-tubulins (TUB2), a new species, *Ap. chiangraiense*, as well as two new host records, *Ap. rasikravindrae* and *Ap. intestini*, are introduced. In addition, thirteen species of *Arthrinium* were synonymized under *Apiospora*.

### 2. Materials and Methods

#### 2.1. Sample Collection, Isolation and Morphological Characteristic Examination

Fresh specimens of bamboo and maize culms with fungal fruiting bodies were collected from Chiang Rai province, Thailand from September–October 2020. Specimens were brought to the laboratory in plastic Ziploc bags for observation. Senanayake et al. [27] were followed for the morphological observations and single-spore isolation. The morphological characteristics were examined under a stereomicroscope (Motic SMZ-171, Wetzlar, Germany). The conidiomata were observed and photographed using a Nikon ECLIPSE Ni-U compound microscope connected to a Nikon camera series DS-Ri2 (New York, United States). The germinating ascospores were transferred aseptically to fresh potato dextrose agar (PDA) media and incubated at room temperature (25 °C) for 2–4 weeks. The morphological characteristics of cultures were checked and recorded after 30–60 days.
The herbarium specimens have been deposited at the herbarium of Mae Fah Luang University (MFLU) and Kunming Institute of Botany (HKAS), while the living cultures have been deposited at Mae Fah Luang University Culture Collection (MFLUCC). The Faces of Fungi and the Index Fungorum numbers are registered as outlined in Jayasiri et al. [28], and the Index Fungorum [26].

2.2. DNA Extraction, PCR Amplification and Sequencing

The genomic DNA was extracted from living pure cultures using the Biospin Fungus Genomic DNA extraction Kit (BioFlux, P.R. China) following the manufacturer’s protocol. The internal transcribed spacer (ITS) with the primer pair of ITS4/ITS5 [29], the partial large subunit nuclear rDNA (LSU) with the primer pair of LR0R/LR5 [30], the translation elongation factor 1-alpha gene (TEF1-α) with the primers of EF1-728F/EF-2 [31,32] and the TUB2 with primers of bt2a.bt2b [33] were used to amplify the genes ITS, LSU, TEF1-α and TUB2. The polymerase chain reaction (PCR) was carried out under the following protocol: the final volume of 25 µL consisting of 2 µL of DNA template, 1 µL of each forward and reverse primers, 12.5 µL of 2× FastTaq Premix (mixture of Taq DNA polymerase, dNTPs, and a buffer) and 9.5 µL of deionized water. The PCR thermal cycle program was as follows: for ITS and LSU: initial denaturation at 95 °C for 5 min, then 35 cycles of denaturation at 94 °C for 30 s, annealing at 52 °C for 30 s and extension at 72 °C for 1 min and final extension at 72 °C for 10 min; for TEF1-α: initial denaturation at 94 °C for 5 min, then 35 cycles of denaturation at 94 °C for 1 min, annealing at 56 °C for 1 min and extension at 72 °C for 90 s and final extension at 72 °C for 10 min; for TUB2: initial denaturation at 95 °C for 5 min, then 35 cycles of denaturation at 94 °C for 45 s, annealing at 55 °C for 45 s and extension at 72 °C for 1 min and final extension at 72 °C for 10 min. The PCR products were checked in 1% agarose gels and sent to Tsing Ke Biological Technology (Kunming) Co., China for sequencing. The sequence quality was checked, and the sequences were condensed with SeqMan. The sequences derived in this study were deposited in the GenBank, and the accession numbers were obtained (Table 1).
Table 1. Taxa names, strain numbers, host, countries and corresponding GenBank accession numbers of the taxa used in the phylogenetic analyses of this study.

| Taxa Names                  | Strain Numbers | Substrates Lag | Countries Lag | GenBank Accession Numbers                  |
|-----------------------------|----------------|----------------|---------------|--------------------------------------------|
|                             |                |                |               | ITS            | LSU            | TUB2            | TEF 1-α          |
| Apiospora acutipica         | KUMCC 20-0210  | Bambusa bambos | China         | MT946343       | MT946339       | MT947366        | MT947360         |
| Apiospora aquaticum         | S-642          | Submerged wood  | China         | MK828608       | MK835806       | -               | -               |
| Apiospora arundinis         | CBS 133509     | Aspergillus flavus sclerotium | USA | KF144886       | KF144930       | KF144976        | KF145018         |
| Apiospora arundinis         | CBS 449.92     | Bamboo          | Canada        | KF144887       | KF144931       | KF144977        | KF145019         |
| Apiospora aurea             | CBS 244.83     |                | Japan         | AB200251       | KF144935       | KF144981        | KF145023         |
| Apiospora balearica         | CBS 145129     | Underdetermined poaceae | Spain | MK014869       | MK014836       | MK017975        | MK017946         |
| Apiospora bambusae          | ICPM 6889      | Bamboo          | New Zealand   | MK014874       | MK014841       | MK017980        | MK017951         |
| Apiospora bambusae          | CBS 145133     | Phyllostachys aurea | Spain | MK014875       | MK014842       | MK017981        | MK017952         |
| Apiospora bambusicolor      | MFLUCC20-0144  | Schizostachyum brachycladum | Thailand | MW173030       | MW173087       | -               | MW183262         |
| Apiospora biserialis        | CGMCC 3.20135  | Bamboo          | China         | MW481708       | MW478885       | MW522955        | MW522938         |
| Apiospora biserialis        | GZCC 20_0099   | Bamboo          | China         | MW481709       | MW478886       | MW522956        | MW522939         |
| Apiospora biserialis        | GZCC 20_0100   | Bamboo          | China         | MW481710       | MW478887       | MW522957        | MW522940         |
| Apiospora camelliae-sinensis | LC 5007     | Camellia sinensis | China   | KY494704       | KY494780       | KY705173        | KY705103         |
| Apiospora camelliae-sinensis | LC 8181     | Brassica rapa  | Thailand      | KY494761       | KY494837       | KY705229        | KY705157         |
| Apiospora chromolaenae      | MFLUCC17-1505  | Chromolaena odorata | Thailand | MT214342       | MT214436       | -               | MT235802         |
| Apiospora chiangraiense     | MFLUCC21-0053  | Dead culms of bamboo | Thailand | MZ542520       | MZ542524       | MZ546409        | -               |
| Apiospora cordylinae        | GUCC 10026     | Cordyline fruticosa | China | MT040105       | MT040147       | MT040126        | -               |
| Apiospora cyclobalanopsidis | CGMCC 3.20136  | Cyclobalanopsidis gauca | China | MW481713       | MW478892       | MW522962        | MW522945         |
| Apiospora cyclobalanopsidis | CGMCC 20_0103  | Cyclobalanopsidis gauca | China | MW481714       | MW478893       | MW522963        | MW522946         |
| Apiospora descalsii         | CBS 145130     | Ampelodesmos mauritianicus | Spain | MK014870       | MK014837       | MK017976        | MK017947         |
| Apiospora dichotomanthi     | LC 4950        | Dicotomanthes tristimpanicarpa | China | KY494697       | KY494773       | KY705167        | KY705086         |
| Apiospora dichotomanthi     | LC 8175        | Dicotomanthes tristimpanicarpa | China | KY494755       | KY494831       | KY705223        | KY705151         |
| Apiospora esporleinsensis   | CBS 145136     | Phyllostachys aurea | Spain | MK014878       | MK014845       | MK017983        | MK017954         |
| Apiospora euphorbiae        | IMI 285638b    | Bambusa sp.    | Bangladesh    | AB220241       | AB220335       | AB220288        | -               |
| Apiospora gaoyouensis       | CFCC 52301     | Phragmites australis | China | MH197124       | -              | MH236789        | MH236793         |
| Apiospora gaoyouensis       | CFCC 52302     | Phragmites australis | China | MH197125       | -              | MH236790        | MH236794         |
| Apiospora garethienses      | KUMCC 16-0202  | Dead culms of bamboo | China | KY356086       | KY356091       | -              | -               |
| Apiospora gelatinosa        | KHAS 11962     | Bamboo          | China         | MW481706       | MW478888       | MW522958        | MW522941         |
| Apiospora gelatinosa        | GZASAS 20-0107 | Bamboo          | China         | MW481707       | MW478889       | MW522959        | MW522942         |
| Apiospora guizhouensis      | LC 5318        | Air in karst cave | China | KY494708       | KY494784       | KY705177        | KY705107         |
| Apiospora guizhouensis      | LC 5322        | Air in karst cave | China | KY494709       | KY494785       | KY705178        | KY705108         |
| Apiospora hispanica         | IMI 326877     | Beach sand      | Spain         | AB220242       | AB220336       | AB220289        | -               |
| Taxa Names                      | Strain Numbers | Substrates               | Countries | GenBank Accession Numbers |
|--------------------------------|----------------|--------------------------|-----------|--------------------------|
|                                |                |                          |           | ITS                      |
| Apiospora hydei                | CBS 114990     | Bambusa tuloides         | China     | KF144890 KF144936 KF144982 KF145024 |
| Apiospora hydei                | KUMCC 16-0204  | Dead culms of bamboo     | China     | KY356087 KY356092 - -    |
| Apiospora hypophodii            | MFLUCC15-0003  | Bambusa tuloides         | China     | KRO69110 - - -           |
| Apiospora hypophodii            | KUMCC 16-0201  | Culms of bamboo          | China     | KY356088 KY356093 - -    |
| Apiospora iberica              | CBS 145137     | Arundo donax             | Portugal  | MK014879 MK014846 MK017984 MK017955 |
| Apiospora intestini             | CBS 135835     | Gut of a grasshopper     | India     | KR011352 MIH87777 KR011350 KR011351 |
| Apiospora intestini             | MFLUCC 21-0052 | Dead culms of bamboo     | Thailand  | MZ542521 MZ542525 MZ546410 MZ546406 |
| Apiospora italica              | CBS 145138     | Arundo donax             | Italy     | MK014880 MK014847 MK017985 MK017956 |
| Apiospora italica              | CBS 145139     | Phragmites australis     | Spain     | MK014881 MK014848 MK017986 - |
| Apiospora jatrophae            | AMH-9557       | Jatropha podagrica       | India     | JQ246355 - - -           |
| Apiospora jatrophae            | AMH-9556       | Jatropha podagrica       | India     | HE981191 - - -           |
| Apiospora jiangxiensis         | LC 4494        | Phyllostachys sp.        | China     | KY494690 KY494766 KY705160 KY705089 |
| Apiospora jiangxiensis         | LC 4577        | Maesa sp.                | China     | KY494693 KY494769 KY705163 KY705092 |
| Apiospora kogelbergensis       | CBS 113332     | Cannomois virgata        | South Africa | KF144891 KF144937 KF144983 KF145025 |
| Apiospora kogelbergensis       | CBS 113333     | Dead culms of Restionaceae | South Africa | KF144892 KF144938 KF144984 KF145026 |
| Apiospora locuta-pollinis      | LC 11688       | Bee bread                | China     | MF939596 MF939623 MF939618 |
| Apiospora locuta-pollinis      | LC 11683       | Brassica campestris      | China     | MF939595 MF939622 MF939616 |
| Apiospora longistroma          | MFLUCC 11-0479 | Dead culms of bamboo     | Thailand  | KU940142 KU863130 - -    |
| Apiospora longistroma          | MFLUCC 11-0481 | Dead culms of bamboo     | Thailand  | KU940141 KU863129 - -    |
| Apiospora malayasiensis        | CBS 102053     | Macaranga hululletii     | Malaysia  | KF144896 KF144942 KF144988 KF145030 |
|                                |                |                          |           | AB220252 KF144947 KF144993 KF145035 |
| Apiospora marii                | CBS 497.90     | Beach sands              | Spain     | AB220243 AB220337 AB220290 - |
| Apiospora marii                | DiSSPA_A1      | Oleaeuropaea             | Italy     | MK602320 - - -           |
| Apiospora mediterranea         | IMI 326875     | Air                      | Spain     | AB220243 AB220337 AB220290 - |
| Apiospora minutispora          | I.70E-41       | Mountain soil            | Korea     | LCS17882 - - -           |
| Apiospora mytilomorpha         | DAOM 214595    | Andropogon sp.           | India     | KY494685 - - -           |
| Apiospora neobambusae          | LC 7106        | Leaves of bamboo         | China     | KY494718 KY494794 KY705186 KY806204 |
| Apiospora neobambusae          | LC 7124        | Leaves of bamboo         | China     | KY494727 KY494803 KY705195 KY806206 |
| Apiospora neochinensis         | CFCC 53036     | Fargesia sinlingensis    | China     | MK819291 MK818547 MK818548 MK818546 |
| Apiospora neochinensis         | CFCC 5307      | Fargesia sinlingensis    | China     | MK819292 MK818547 MK818548 MK818546 |
| Apiospora neogarethjonesii     | DQD 2019a      | Bamboo                   | China     | MK070897 MK070898 - -    |
| Apiospora neosubglobosa        | JHB 006        | Bamboo                   | China     | KY356089 KY356094 - -    |
| Apiospora neosubglobosa        | KUMCC 16-0203  | Bamboo                   | China     | KY356090 KY356095 - -    |
| Taxa Names                        | Strain Numbers | Substrates                  | Countries   | GenBank Accession Numbers |
|----------------------------------|----------------|------------------------------|-------------|---------------------------|
|                                  |                |                              |             |                           |
| Apiospora obovata                | LC 4940        | Lithocarpus sp.              | China       | KY494696 KY494772 KY705166 KY705095 |
| Apiospora obovata                | LC 8177        | Lithocarpus sp.              | China       | KY494757 KY494833 KY705225 KY705153 |
| Apiospora ovata                  | CBS 115042     | Arundinaria hindsii          | China       | KF144903 KF144950 KF144995 KF145037 |
| Apiospora paraphaeosperma        | MFLUCC13-0644  | Dead culms of bamboo         | Thailand    | KX822128 KX822124 - - |
| Apiospora phragmitis             | CPC 18900      | Phragmites australis         | Italy       | KF144909 KF144956 KF145001 KF145043 |
| Apiospora phyllostachydys        | MFLUCC18-1101  | Phyllostachys heteroclada    | China       | MK351842 MH368077 MK291949 MK340918 |
| Apiospora piptatheri             | CBS 145149     | Piptatherum miliaceum        | Spain       | MK014893 MK014860 - MK017969 |
| Apiospora pseudomarii            | GUCC 10228     | Aristolochia debilis         | China       | MT040124 - MT040166 MT040145 |
| Apiospora pseudoparenchymatica   | LC 7234        | Leaves of bamboo             | China       | KY494743 KY494819 KY705211 KY705139 |
| Apiospora pseudoparenchymatica   | LC 8173        | Leaves of bamboo             | China       | KY494753 KY494829 KY705221 KY705149 |
| Apiospora pseudorakravindrae     | KUMCC 20-0208  | Bambusa dolichoclada         | Thailand    | MT946344 - MT947367 MT947361 |
| Apiospora pseudosinensis         | CPC 21546      | Leaves of bamboo             | Netherlands | KF144910 KF144957 - KF145044 |
| Apiospora pseudospegazzinii      | CBS 102052     | Macaranga hulletii           | Malaysia    | KF144911 KF144958 KF145002 KF145045 |
| Apiospora pterosperma            | CBS 123185     | Machaerina sinclatii         | New Zealand | KF144912 KF144959 KF145003 - |
| Apiospora pterosperma            | CPC 20193      | Lepidosperma gladiatum       | Australia   | KF144913 KF144960 KF145004 KF145046 |
| Apiospora qinlingensis           | CFCC 52303     | Fargesia qinlingensis        | China       | MH1197120 - MH236791 MH236795 |
| Apiospora qinlingensis           | CFCC 52304     | Fargesia qinlingensis        | China       | MH1197121 - MH236792 MH236796 |
| Apiospora rasikravindrae         | LC 8179        | Brassica rapa                | China       | KY494759 KY494835 KY705227 KY705155 |
| Apiospora rasikravindrae         | NFCCI 2144     | Soil                        | Norway      | JF326454 - - - - |
| Apiospora rasikravindrae         | MFLUCC 21-0051 | Dead culms of bamboo         | Thailand    | MZ524253 MZ524257 MZ546412 MZ546408 |
| Apiospora rasikravindrae         | MFLUCC 21-0054 | Dead culms of Maize          | Thailand    | MZ524252 MZ524256 MZ546411 MZ546407 |
| Apiospora sacchari               | CBS 372.67     | Air                         | -           | KF144918 KF144964 KF145007 KF145049 |
| Apiospora sacchari               | CBS 664.74     | Soil under Calluna vulgaris  | Netherlands | KF144919 KF144965 KF145008 KF145050 |
| Apiospora saccharola             | CBS 191.73     | Air                         | Netherlands | KF144920 KF144966 KF145009 KF145051 |
| Apiospora saccharola             | CBS 831.71     | -                           | Netherlands | KF144922 KF144969 KF145012 KF145054 |
| Apiospora septata                | CGMCC 3.20134  | bamboo                      | China       | MW481717 MW478890 MW522960 MW522943 |
| Apiospora septata                | GZCC 20_0109   | bamboo                      | China       | MW481712 MW478891 MW522961 MW522944 |
| Apiospora serenensis             | IMI 326869     | bamboo, pharmaceutical       | Spain       | AB220250 AB220344 AB220297 - |
| Apiospora setariae               | MT492005       | Setaria viridis             | China       | MT492005 - MT497467 MW118457 |
| Apiospora setostroma             | KUMCC 19-0217  | Dead branches of bamboo      | China       | MN528012 MN528011 - MN527357 |
| Taxa Names                  | Strain Numbers | Substrates                  | Countries     | GenBank Accession Numbers |
|----------------------------|----------------|-----------------------------|---------------|----------------------------|
|                            |                |rts                               |               |                            |
| Apiospora sorghi           | URM 93000      | Sorghum bicolor              | Brazil        | MK371706                   |
| Apiospora subglobosa       | MFLUCC11-0397  | Dead culms of bamboo         | Thailand      | K069112 - K069113          |
| Apiospora subrosea         | LC 7291        | Leaves of bamboo             | China         | KY494751 - KY494827        |
| Apiospora subrosea         | LC 7292        | Leaves of bamboo             | China         | KY494752 - KY494828        |
| Apiospora thailandica      | MFLUCC 15-0199 | Dead culms of bamboo         | Thailand      | KU940146 - KU863134        |
| Apiospora thailandica      | MFLUCC15-0202  | Dead culms of bamboo         | Thailand      | KU940145 - KU863133        |
| Apiospora vietnaminensis   | IMI 99670      | Citrus sinensis              | Vietnam       | KX986096 - KX986111        |
| Apiospora xenocordella     | CBS 478.86     | Soil from roadway            | Zimbabwe      | KF144925 - KF145013        |
| Apiospora yunnana          | CBS 595.66     | Soil                         | Austria       | KF144926 - KF144971        |
| Apiospora yunnana          | DDQ 00281      | Phyllostachys nigra          | China         | KU940148 - KU863136        |
| Arthrinium austriacum      | GZU 345004     | Carex pendula                | Austria       | MW208928 - MW208860        |
| Arthrinium austriacum      | GZU 345006     | Carex pendula                | Austria       | MW208929 - MW208860        |
| Arthrinium cf. sporophleoides | GZU 345102   | Carex firma                  | Austria       | MW208944 - MW208866        |
| Arthrinium caricola        | CBS 145127     | Carex ericetorum             | China         | MK048178 - MK014838        |
| Arthrinium crenatum        | AG 19066       | Poaceae, Carex               | France        | MW208931 - MW208861        |
| Arthrinium curvatum        | AP 25418       | Leaves of Carex sp.          | China         | MK048172 - MK014839        |
| Arthrinium japonicum       | IFO 30500      | -                            | Japan         | AB220262 - AB220356        |
| Arthrinium japonicum       | IFO 31098      | Leaves of Carex despalata    | Japan         | AB220264 - AB220358        |
| Arthrinium luzulae         | AP7619-3       | Luzula sylvestra             | Spain         | MW208937 - MW208863        |
| Arthrinium morthieri       | GZU 345043     | Cyperaceae carex             | Austria       | MW208938 - MW208864        |
| Arthrinium puccinioides    | CBS 14317      | Leaves of Hordeum vulgare    | Iran          | KF144906 - KF144953        |
| Arthrinium phaeospermum    | CBS 14318      | Leaves of Hordeum vulgare    | Iran          | KF144907 - KF144954        |
| Arthrinium spinaferrioides | CBS 549.86     | Lepidossperma gladiatum      | Germany       | AB220253 - AB220347        |
| Arthrinium sphaerosperrum  | AP25619/CBS 146355 | Poaceae                | Norway        | AB220241 - AB220347        |
| Arthrinium sporophleum     | CBS 145135     | Dead leaves of juncus sp.    | Spain         | MK014898 - MK014865        |
| Arthrinium trachycarpum    | CFCC 53038     | Trachycarpus fortune         | China         | KF144908 - KF144954        |
| Arthrinium urticae         | IMI 326344     | Trachycarpus fortune         | China         | KF144909 - KF144954        |
| Arthrinium trachycarpum    | CFCC 53039     | Trachycarpus fortune         | China         | KF144909 - KF144954        |
| Nigrospora aurantica       | CGMCC 3.18130  | Nelumbo sp.                  | China         | KX986064 - KX986098        |
| Nigrospora camelliae-sinensis | CGMCC 3.18125 | Camellia sinensis           | China         | KX985986 - KX986103        |
| Nigrospora chinensis       | CGMCC 3.18127  | Machilus breviflora          | China         | KX986023 - KX986107        |
Table 1. Cont.

| Taxa Names                  | Strain Numbers | Substrates          | Countries | GenBank Accession Numbers            |
|-----------------------------|----------------|---------------------|-----------|--------------------------------------|
| **Nigrospora gorlenkoana**  | CBS 480.73     | Vitis vinifera      | Kazakhstan| KX986048 KX986109 KY019456 KY019420  |
| **Nigrospora guiliniensis** | CGMCC 3.18124  | Camellia sinensis   | China     | KX985983 KX986113 KY019459 KY019292  |
| **Nigrospora hainanensis**  | CGMCC 3.18129  | Musa paradisiaca    | China     | KX986091 KX986112 KY019464 KY019415  |
| **Nigrospora lacticolonia** | CGMCC 3.18123  | Camellia sinensis   | China     | KX983978 KX986105 KY019458 KY019291  |
| **Nigrospora musae**        | CBS 319.34     | Musa sp.            | Australia | MH855545 KX986110 KY019455 KY019419  |
| **Nigrospora oryzae**       | LC2693         | Neolitsea sp.       | China     | KX986044 KX986101 KY019471 KY019299  |
| **Nigrospora osmanthi**     | CGMCC 3.18126  | Hedera nepalensis   | China     | KX986010 KX986106 KY019461 KY019421  |
| **Nigrospora pyriformis**   | CGMCC 3.18122  | Citrus sinensis     | China     | KX985940 KX986100 KY019457 KY019290  |
| **Nigrospora rubi**         | LC2698         | Rubus sp.           | China     | KX985948 KX986102 KY019475 KY019302  |
| **Nigrospora sphaerica**    | LC7298         | Nelumbo sp.         | China     | KX985937 KX986097 KY019606 KY019401  |
| **Nigrospora vesicularis**  | CGMCC 3.18128  | Musa paradisiaca    | China     | KX986088 KX986099 KY019463 KY019294  |
| **Sporocadus trimorphus**   | CBS 114203     | Rosa canina         | Sweden    | MH553977 MH554196 MH554636 MH554395  |

Notes: Newly generated sequences are indicated by ▲ after the species name. Ex-type strains are in bold. - = information not available. Abbreviations: AMH: Ajrekar Mycological Herbarium, Pune, Maharashtra, India; CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, Netherlands; CFCC: China Forestry Culture Collection Center, Beijing, China; CPC: Culture collection of Pedro Crous, housed at the Westerdijk Fungal Biodiversity Institute; DAOM: Canadian Collection of Fungal Cultures, Ottawa, Canada; DDQ: D.Q. Dai; GUCC: Guizhou University Culture Collection, Guizhou, China; ICMP: International Collection of Microorganisms from Plants, New Zealand; IFO: Institute for Fermentation, Osaka, Japan; IMI: Culture collection of CABI Europe UK Centre, Egham, UK; JHB: H.B. Jiang; KUMCC: Culture collection of Kunming Institute of Botany, Yunnan, China; LC: Personal culture collection of Lei Cai, housed in the Institute of Microbiology, Chinese Academy of Sciences, China; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Rai, Thailand; NFCCI: National Fungal Culture Collection of India.
2.3. Phylogenetic Analyses

The sequences generated in this study were subjected to a basic local alignment search tool (BLAST) search in the GenBank to identify closely related *Apiospora* taxa to the taxa obtained in this study. The sequences of *Apiospora* were also obtained from recently published data [4,18,34–39]. Consensus sequences were assembled and aligned using BioEdit and MAFFT v.7.110 online program, respectively (http://mafft.cbrc.jp/alignment/server, accessed on 12 August 2021) [40], and manually edited using BioEdit v7.2.3 [41].

The construction of the combined phylogenetic trees was completed using maximum likelihood (ML) and Bayesian inference posterior probabilities (BYPP), with *Sporocadus trimorphus* (CBS 114203) as the outgroup taxon. The models were selected as GTRGAMMA for maximum likelihood, while the best-fit models were selected as GTR + I + G for ITS, LSU and HKY + I + G for TUB2, and TEF1-α for the Bayesian posterior probability analysis. The maximum likelihood (ML) analysis was performed using RAxML-HPC v.8 [42,43] on the XSEDE TeraGrid of the CIPRES Science Gateway (https://www.phylo.org, accessed on 12 August 2021) [44] with a rapid bootstrap analysis, followed by 1000 bootstrap replicates. The final tree was selected amongst the suboptimal trees from each run by comparing the likelihood scores under the GTRGAMMA substitution model. The Bayesian analyses were performed by MrBayes v. 3.2 [45]. Markov chain Monte Carlo (MCMC) was run for 5,000,000 generations, and the trees were sampled every 100th generation. The first 10% of the trees that represented the burn-in phase were discarded, and only the remaining 90% of the trees were used for calculating the posterior probabilities (PP) for the majority rule consensus tree. Phylogenetic trees were visualized with FigTree v. 1.4.2 [46] and modified in Adobe Illustrator CS5 software (Adobe Systems, USA). The newly obtained sequences in this study were deposited in the GenBank.

3. Results

3.1. Phylogeny

The combined ITS, LSU, TEF1-α and TUB2 dataset comprised 138 strains, including four newly sequenced strains, with *Sporocadus trimorphus* (CBS 114203) as the outgroup taxon. Multi-locus sequences were concatenated, which comprised 2820 nucleotide characters, including gaps (ITS: 1–637, LSU: 638–1518, TEF1-α: 1519–1971 and TUB2: 1972–2799). The phylogenic tree from the RAxML analysis had similar topology to the Bayesian analysis. The RAxML analysis of the combined dataset yielded the best scoring tree (Figure 1) with a final ML optimization likelihood value of −27840.652840. The matrix had 1446 distinct alignment patterns, with 27.45% undetermined characters or gaps. The estimated base frequencies were as follows: A = 0.238477, C = 0.253732, G = 0.254209, T = 0.253582; substitution rates AC = 1.244445, AG = 3.021293, AT = 1.211434, CG = 1.060781, CT = 4.719948, GT = 1.000000; gamma distribution shape parameter α = 0.298987.

The phylogenetic trees generated by maximum likelihood and Bayesian show the taxonomic placements of our total strains belong to *Apiospora*. The strains MFLUCC 21-0051 and MFLUCC 21-0054 clustered together with members of *Apiospora* and grouped with *Ap. rasikravindrae* (NFCCCL 2144 and LC 8179). The strain MFLUCC 21-0052 presented as a distinct lineage and sister to *Ap. intestine* (CBS 135835) with significant statistical support (ML/BI = 100/1.00). The strain MFLUCC 21-0053 clustered with *Ap. intestine* (CBS 135835), but in a distinct clade with high support (ML/BI = 100/1.00).
Figure 1. Cont.
3.2. Taxon Treatment

**Apiospora chiangraiense** X.G. Tian and Tibpromma S., sp. nov. (Figure 2).

Index Fungorum number: IF558492; Faces of Fungi number: FoF 09905.

Etymology: Referring to Chiang Rai Province, Thailand, where the fungus was collected.
Figure 2. *Apiospora chiangraiense* (MFLU 21-0046, holotype). (a–c) Appearance of the fungus on dead culms of bamboo. (d–i) Conidia with conidiophores. (j–l) Conidiogenous cells bearing conidia. (n,o,q) Conidia. (p) Conidia with germ-slit. (m) Germinated conidium. (r,s) Colonies on PDA media (r forward, s reversed). Scale bars: a = 4000 μm, b = 1000 μm, c = 200 μm and d–q = 10 μm.

*Saprobic* on dead culms of bamboo. **Sexual morph**: undetermined. **Asexual morph**: Colonies on natural substrate are dry, dark brown to black, velvety, dull, consisting of a sterile mycelial outer zone and a round, glistening, abundantly sporulating center, with conidia readily liberated when disturbed. **Mycelium** is superficial, branched, hyaline to dark
brown, septate, smooth-walled and hyphae. **Conidiophores** are reduced to conidiogenous cells, grouped together to form sporodochia. **Conidiogenous cells** are 4–7.5 μm high × 3–4 μm diam. \( \bar{x} = 6 \times 3.5 \mu m^2, n = 30 \), monoblastic or polyblastic, aggregated in clusters on hyphae, hyaline to light brown, smooth and cylindrical to subcylindrical. **Conidia** are aseptate, pale brown to dark brown, in the surface view 6.5–8 × 6–8 μm\(^2\) \( \bar{x} = 7.5 \times 7 \mu m^2, n = 50 \), in the lateral view 6–7.5 × 4–5.5 μm\(^2\) \( \bar{x} = 7 \times 5 \mu m^2, n = 50 \), with a central scar, globose in the surface view, a lenticular inside view, with straight germ slit spore length.

**Culture characteristics**: Conidia germinating on PDA within 24 h at room temperature (25 °C). On the PDA, the colonies’ surfaces are white, lightly yellow, wooly, flat, spreading, filiform, with abundant aerial mycelia and reverse off-white to yellow.

Material examined: THAILAND, Chiang Rai Province, Muang District, on dead culms of bamboo, 23 October 2020, X.G. Tian bb-4-5, (MFLU 21-0046, holotype); ex-type culture, MFLUCC 21-0053.

**Notes**: In the phylogenetic analyses, **Apiospora chiangraiense** formed a distinct clade sister to **Ap. intestini** with strong bootstrap support values (ML/BI = 100/1.00). Morphologically, **Ap. chiangraiense** is distinct from **Ap. intestini** by conidiogenous cells, conidiophores and conidia. The conidiophores of **Ap. intestini** are usually hyaline, macronematous, mononematous and transversely septate, while **Ap. chiangraiense** has reduced conidiophores and conidiogenous cells grouped together to form sporodochia. Additionally, **Ap. chiangraiense** has larger conidia compared to **Ap. intestini** (surface view 6.5–8 × 6–8 μm\(^2\), lateral view 6–7.5 × 4–5.5 μm versus surface view 4.5–5.5 (–6) μm diam, side view (2–) 4 (–6) μm diam). Based on pairwise nucleotide comparisons, **Ap. chiangraiense** is different from **Ap. intestini** (CBS 135835) in 27/583 bp (4.63/) of the ITS, 9/814 (1.1%) of the LSU and 61/696 bp (8.76%) of TUB2, but we were unable to compare TEF-α pairwise nucleotides as the amplification of TEF-α was not successful for this species. However, both the phylogenetic analyses and morphological characteristics supported our species as a distinct new species.

**Apiospora intestini** (Kajale, Sonawane and Rohit Sharma) Pintos and P. Alvarado, Fungal Systematics and Evolution 7: 206 (2021) (Figure 3).

Index Fungorum number: IF 837744.

**Saprobic** on dead culms of bamboo. **Sexual morph**: undetermined. **Asexual morph**: Colonies are on natural substrate surface, gregarious, powdery, dark brown to black, dull with conidia readily liberated when disturbed. **Conidiophores** are 1.5–2 μm wide (\( \bar{x} = 2 \mu m, n = 40 \) ) hyaline, macronematous, mononematous, transversely septate, thick-walled, brown. **Conidiogenous cells** are 6–9.5 × 1.5–2 μm\(^2\) \( \bar{x} = 7.5 \times 2 \mu m^2, n = 30 \), intercalary, cylindrical, hyaline. **Conidia** are 6.5–5 × 6–10 μm\(^2\) \( \bar{x} = 7 \times 5.5 \mu m^2, n = 50 \), borne as bunches on conidiophores, lateral, pale brown to brown, smooth-walled, globose to subglobose or irregularly round, aseptate, with a central scar and without germ slit.

**Culture characteristics**: Conidia germinating on PDA within 24 h at room temperature. The colonies’ surfaces are white, cottony, flat, spreading, filiform, mycelia not tightly attached to the surface and the reverse lightly pigmented.

Material examined: THAILAND, Chiang Rai Province, Muang District, on dead culms of bamboo, 23 October 2020, X.G. Tian bb-4-2 (MFLU 21-0045, living culture, MFLUCC 21-0052).

**Notes**: **Apiospora intestini** was introduced by Crous et al. [19] based on the morphology of asexual morph and the phylogenetic analyses. In this paper, our new isolate (MFLUCC 21-0052) clustered with the ex-type strain of **Ap. intestini** with relatively high support (ML/BI = 100/1.00). Morphologically, the conidia of the new isolate (MFLUCC 21-0052) are similar to the holotype **Ap. intestini** (CBS 135835) in having similar size of conidiophores that are borne as bunches, intercalary and terminal, brown, smooth, aseptate and globose to subglobose. Based on nucleotide comparisons, **Ap. intestini** (MFLUCC 21-0052) is slightly different from **Ap. intestini** in 12/580 bp (2.07%) of the ITS, 2/814 (0.24%) of the LSU,
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2/684 bp (0.29%) of TUB2 and 2/610 bp (0.32%) of TEF1-α. Based on both phylogeny and morphology, the new isolate (MFLUCC 21-0052) is identified as Ap. intestini. This is the first report of Ap. intestini (MFLUCC 21-0052) isolated from dead culms of bamboo in Thailand, which was originally isolated from a grasshopper’s gut in India.

Figure 3. Apiospora intestini (MFLU 21-0045). (a–c) Appearance of the fungus on dead culms of bamboo. (d–g) Conidia with conidiophores. (h–j, l, m) Conidiogenous cells bearing conidia. (n–s) Conidia. (k) Germinated conidium. (t, u) Colonies on PDA media (t forward, u reversed). Scale bars: a = 4000 μm, b = 1000 μm, c = 200 μm, d–g = 20 μm, h–m = 10 μm and n–s = 5 μm.

Apiospora rasikravindrae (Shiv M. Singh, L.S. Yadav, P.N. Singh, Rahul Sharma and S.K. Singh) Pintos and P. Alvarado, Fungal Systematics and Evolution 7: 207 (2021) (Figure 4).

Index Fungorum number: IF 837716; Faces of Fungi number: FoF 01994.

Saprobic on dead culms of bamboo. Colonies appear as spotty patches on natural substrate surface. Conidiomata are immersed, pycnidial, scattered, globose to slightly conical, ostiolar, black, coriaceous. Conidiophores are 9–26 × 1–2.5 μm² (x = 17.5 × 2 μm², n = 15), arising mostly from swollen basal cells, micro to semi-macronematous, mononematous, unbranched, straight or flexuous, smooth and thin-walled, hyaline. Conidiogenous cells are basauxic, discrete, hyaline, smooth-walled. Conidia in surface view are 9–11 × 9–10.5 μm² (x = 10 × 10 μm², n = 50), in lateral view 10–11 × 6.5–8 μm² (x = 10.5 × 7.5 μm², n = 20), lenticular, globose to ovoid, occasionally elongated to ellipsoidal, brown to dark brown, smooth-walled, with a longitudinal, thin-walled, with a pale equatorial slit.

Material examined: THAILAND, Chiang Rai Province, Muang District, isolated as Saprobic on dead culms of bamboo, 23 October 2020, X. G. Tian, bb-4-1 (MFLU 21-0044),
living culture, MFLUCC 21-0051; *ibid* decaying maize culms, 11 November 2020, X. G. Tian, corn-1-1 (HKAS 115764), living culture, MFLUCC 21-0054

**Figure 4.** *Apiospora rasikravindrae* (MFLU 21-0045). (a–c) Appearance of the fungus on dead culms of bamboo. (d–i) Conidia with conidiophores. (j,k,t,u) Conidiogenous cells bearing conidia. (l,m) Conidia with germ-slit. (p–r) Conidia. (n) Germinated conidium. (o,s) Colonies on PDA media (o forward, s reversed). Scale bars: a = 4000 µm, b = 2000 µm, c = 200 µm and d–s = 10 µm.
Notes: The National Center for Biotechnology Information (NCBI) BLAST results of ITS, LSU, TUB2 and TEF1-α sequences of our new isolate (MFLUCC 21-0054) showed high similarities with *Apiospora rasikravindrae* (LC 8179) (100%, 100%, 98.90% and 98.97%, respectively), while the new isolate (MFLUCC 21-0051) also showed high similarities with *Apiospora rasikravindrae* (LC 8179) (99.83%, 100%, 99.61% and 99.51%, respectively). Our phylogenetic analyses showed that the two new isolates clustered with the ex-type strain of *Ap. rasikravindrae* (NFCCI 2144) and *Ap. rasikravindrae* (LC 8179). Morphologically, our new isolate is closely related to the holotype of *Ap. rasikravindrae* in having lenticular, globose to ovoid, occasionally elongated to ellipsoidal, brown to dark brown, smooth-walled, germ-slit conidia and micro-semi-macronematous, mononematous, unbranched, straight or flexuous, smooth and thin-walled and hyaline conidiophores. Hence, the two new isolates are identified as *Ap. rasikravindrae*.

*Apiospora rasikravindrae* was originally isolated from soil in Norway [47]. *Apiospora rasikravindrae* occurred on *Capsicum*, *Kappaphycus alvarezii*, *Pinus*, *Platanus acerifolia*, rice, *Sargassum thunbergia* and *Triticum aestivum* from Brazil, China, India, Japan, Netherlands, Svalbard and Thailand [3,48]. Dai et al. [3] describe and illustrate both sexual and asexual morphs for *Ap. rasikravindrae* and it was collected on the stems of bamboo. In this study, the isolate MFLUCC 21-0051 was newly collected from bamboo, while the isolate MFLUCC 21-0054 was newly recorded from maize.

### 3.3. New Combinations

*Apiospora acutiapica* (Senan. and Cheew) X.G. Tian and Tibpromma S., comb. nov.

Index Fungorum number: IF558499.

Basionym: *Arthrinium acutiapicum* Senan. and Cheew, Frontiers in Microbiology 11. 2020.

Notes: *Arthrinium acutiapicum* was introduced by Senanayake et al. [34] and was collected on dead twigs of *Bambusa bambos* in China. Senanayake et al. [34] mentioned that this species is distinct from *Ar. pseudorasikravindrae*, which is a sister to *Ar. acutiapicum*, by the reduction of conidiophores to conidiogenous cells, cylindrical to ampulliform, pale brown conidiogenous cells with pointed, hyaline apex and brown to dark brown and smooth-walled conidia with a dark equatorial slit [34].

In our phylogenetic analysis based on combined LSU, ITS, TEF1-α and TUB2 sequence data, *Arthrinium acutiapicum* clustered with *Apiospora pseudorasikravindrae (=*Ar. pseudorasikravindrae*) with high support (ML/BI = 95/-). Thus, we propose the transfer of *Ar. acutiapicum* under the new combination *Ap. acutiapica*, based on the morphological and phylogenetic analyses.

*Apiospora bambusicola* (X. Tang, K.D. Hyde and J.C. Kang) X.G. Tian and Tibpromma S., comb. nov.

Index Fungorum number: IF558493; Faces of Fungi number: FoF 09162.

Basionym: *Arthrinium bambusicola* X. Tang, K.D. Hyde and J.C. Kang, Biodiversity Data Journal 8 (e58755): 11 2020.

Notes: *Arthrinium bambusicola* was introduced by Tang et al. [18] and was collected on dead culms of *Schizostachyum brachycladum* in Thailand. Tang et al. [18] mentioned that *Ar. bambusicola* were retrieved as a sister taxon of *Ar. gutiae* with high support (ML/BI = 83/0.99), but differs from *Ar. gutiae* in having larger conidia and irregularly rounded, guttulate to roughened conidia. Pintos and Alvarado [4] transferred *Ar. gutiae* to *Apiospora* based on the phylogenetic analyses and morphological characters.

In our phylogenetic analyses based on combined LSU, ITS, TEF1-α and TUB2 sequence data, *Arthrinium bambusicola* is a sister to the newly introduced species *Ap. chiangraiense* with high support (ML/BI = 80/0.99). Thus, we propose the transfer of *Ar. bambusicola* under the new combination *Ap. bambusicola*, based on the morphological and phylogenetic analyses.

*Apiospora biserialis* (Y. Feng and Z.Y. Liu) X.G. Tian and Tibpromma S., comb. nov.
Index Fungorum number: IF558502; Faces of Fungi number: FoF 09569.  
**Basionym:** Arthrinium biseriale Y. Feng, J.K. Liu, C.G. Lin, Y.Y. Chen, M.M. Xiang and Z.Y. Liu, Frontiers in Microbiology 12. 2021.

**Notes:** Arthrinium biseriale was introduced by Feng et al. [49] from dead culms of bamboo in China. The phylogenetic analysis of Feng et al. [49] showed that Ar. biseriale is closely related to Ar. gelatinosum, but they are phylogenetically distinct and can be recognized as two different species. Morphologically, Ar. biseriale has smaller stromata and the spores of Ar. biseriale are more curved than those of Ar. gelatinosum [49].

In our phylogenetic analyses based on combined LSU, ITS, TEF1-α and TUB2 sequence data, Arthrinium biseriale clustered with Apiospora gelatinosa with high support (ML/BI = 90/0.99). Thus, we propose the transfer of Ar. biseriale under the new combination *Ap. biserialis*, based on the morphological and phylogenetic analyses.

**Apiospora cordylines** (T.Z. Chen, Yong Wang bis and K.D. Hyde) X.G. Tian and Tibpromma S., comb. nov.

Index Fungorum number: IF558494.  
**Basionym:** Arthrinium cordylines T.Z. Chen, Yong Wang bis and K.D. Hyde, Mycotaxon 136(1): 189 2021.

**Notes:** Arthrinium cordylines was introduced by Chen et al. [39] from the leaves of Cordyline fruticosa in China. Chen et al. [39] mentioned that Ar. cordylinae formed a well-supported branch with type strains of Ar. aureum (CBS 244.83) and Ar. hydei (CBS 114990). Meanwhile, a base difference comparison also confirmed Ar. cordylinae is a distinct species.

In our phylogenetic analyses, Arthrinium cordylines is a sister to *Ap. hydei* with high support (ML/BI = 96/0.99). Thus, we propose the transfer of Ar. cordylines under the new combination *Ap. cordylines*.

**Apiospora cyclobalanopsidis** (Y. Feng and Z.Y. Liu) X.G. Tian and Tibpromma S., comb. nov.

Index Fungorum number: IF558503; Faces of Fungi number: FoF 09572.  
**Basionym:** Arthrinium cyclobalanopsidis Y. Feng, J.K. Liu, C.G. Lin, Y.Y. Chen, M.M. Xiang and Z.Y. Liu, Frontiers in Microbiology 12. 2021.

**Notes:** Arthrinium cyclobalanopsidis was introduced by Feng et al. [49] from a leaf of Cyclobalanopsidis glauca Oerst in China. Feng et al. [49] showed that Ar. cyclobalanopsidis clustered with *Ar. camelliae-sinensis*, but can be distinguished from *Ar. camelliae-sinensis* by conidiogenous cells. Pintos and Alvarado [4] transferred *Ar. camelliae-sinensis* to *Apiospora camelliae-sinensis*, based on the phylogenetic analyses and morphological characteristics.

In our phylogenetic analyses based on combined LSU, ITS, TEF1-α and TUB2 sequence data, Arthrinium cyclobalanopsidis clustered with *Ap. camelliae-sinensis* with high support (ML/BI = 78/1.00). Thus, we propose the transfer of Ar. cyclobalanopsidis under the new combination *Ap. cyclobalanopsidis*, based on the morphological and phylogenetic analyses.

**Apiospora euphorbiae** (M.B. Ellis) X.G. Tian and Tibpromma S., comb. nov.

Index Fungorum number: IF558495.  
**Basionym:** Arthrinium euphorbiae M.B. Ellis, Mycol. Pap. 103: 6 1965.

**Notes:** Arthrinium euphorbiae was introduced by Ellis et al. [24] from the dead stems of Euphorbia in Zambia. Tang et al. [18] showed that Ar. euphorbiae is phylogenetically closely related to Ar. malaysianum, Ar. vietnamensis, and Ar. chromolaenae [4,18].

In our phylogenetic analyses, Ar. euphorbiae is a sister to *Ap. malaysiana (=Ar. malaysianum) with strong bootstrap support values (ML/PP = 94/0.99). Thus, we propose the transfer of Ar. euphorbiae under the new combination *Ap. euphorbiae*.

**Apiospora gelatinosa** (Y. Feng and Z.Y. Liu) X.G. Tian and Tibpromma S., comb. nov.

Index Fungorum number: IF558504; Faces of Fungi number: FoF 09570.  
**Basionym:** Arthrinium gelatinosum Y. Feng, J.K. Liu, C.G. Lin, Y.Y. Chen, M.M. Xiang and Z.Y. Liu, Frontiers in Microbiology 12. 2021.
Notes: *Arthrinium gelatinosum* was introduced by Feng et al. [49] from dead culms of bamboo in China. Feng et al. [49] mentioned that *Ar. gelatinosum* is a sister to *Ar. biseriale* with a well-supported lineage (ML/MP/BI = 93/98/1.00) [49].

In our phylogenetic analyses, *Arthrinium gelatinosum* clustered with *Apiospora biserialis* with high support (ML/BI = 90/0.99). Thus, we propose the transfer of *Ar. gelatinosum* under the new combination *Ap. gelatinosa*.

*Apiospora locuta-pollinis* (F. Liu and L. Cai) Pintos and P. Alvarado, X.G. Tian and Tibpromma S., comb. nov.

Index Fungorum number: 834523; Faces of Fungi number: FoF05221.

*Synonyms*: *Arthrinium pseudomarii* T.Z. Chen, Yong Wang bis and K.D. Hyde, Mycotaxon 136(1): 189. 2021.

*Basionym*: *Arthrinium locutum-pollinis* F. Liu and L. Cai (as ‘locuta- pollinis’), Mycosphere 9: 1094. 2018.

Notes: *Arthrinium pseudomarii* was introduced by Chen et al. [39] from the leaves of *Aristolochia debilis* in China. Chen et al. [39] mentioned that *Ar. pseudomarii* differs from *Ar. hispanicum*, *Ar. marii* and *Ar. mediterranei* by larger, subglobose to ellipsoid conidia and showed a close relationship with three species with high bootstrap support values (ML/MP = 95/93) [39].

In our phylogenetic analyses, *Ar. pseudomarii* (GUCC 10228) is a sister to *Ap. locuta-pollinis* (= *Ar. locuta-pollinis*) with high support of 95% ML. Based on the nucleotide comparisons, *Ar. pseudomarii* is slightly different from *Ap. locuta-pollinis* in 10/582 bp (1.72%) of ITS, but no base pair differences were observed in TUB2 and TEF1-α. Morphologically, the conidia of *Ar. pseudomarii* are similar to the holotype *Ap. locuta-pollinis* (LC 11683) in having similar size, brown with a hyaline equatorial rim, smooth, subglobose to ellipsoid conidia and hyaline to pale brown, smooth, ampulliform to doliiform conidiogenous cells aggregated into clusters on the hyphae. Thus, we identified that they are the same species, and we synonymize *Ar. pseudomarii* under the *Ap. locuta-pollinis*, based on the morphological and phylogenetic analyses.

*Apiospora minutispora* (K. Das, S.Y. Lee and H.Y. Jung) X.G. Tian and Tibpromma S., comb. nov.

Index Fungorum number: IF558497.

*Basionym*: *Arthrinium minutisporum* K. Das, S.Y. Lee and H.Y. Jung, Mycobiology 48(6): 453 2020.

Notes: *Arthrinium minutisporum* was introduced by Das et al. [37] from mountain soil in Korea. Morphologically, *Ar. minutisporum* is quite similar to *Ar. phragmites*, *Ar. aureum* and *Ar. Hydei*. However, the conidia of *Ar. minutisporum* are smaller than those of *Ar. phragmites*, *Ar. aureum* and *Ar. Hydei*, and *Ar. minutisporum* produce smaller conidiogenous cells than *Ar. phragmites* [39]. Pintos and Alvarado [4] transferred *Ar. phragmites*, *Ar. aureum* and *Ar. Hydei* to *Apiospora phragmites*, *Ap. aureum* and *Ap. Hydei*, based on the phylogenetic analyses and morphological characteristics. Whereas *Ar. minutisporum* was maintained in *Arthrinium*.

In our phylogenetic analyses, *Arthrinium minutisporum* forms a distinct subclade and is close to *Apiospora aurea*, *Ap. balearica* and *Ap. descalsii* with strong bootstrap support values (ML/PP = 99/1.00) within *Apiospora*. Thus, we propose the transfer of *Ar. minutisporum* under the new combination *Ap. minutispora*.

*Apiospora pseudorasikravindrae* (Senan. and Cheew) X.G. Tian and Tibpromma S., comb. nov.

Index Fungorum number: IF 558505.

*Basionym*: *Arthrinium pseudorasikravindrae* Senan. and Cheew, Frontiers in Microbiology 11. 2020.

Notes: *Arthrinium pseudorasikravindrae* was introduced by Senanayake et al. [34] from dead twigs of Bambusa bambos Voss. in China. *Arthrinium pseudorasikravindrae* is morphologically distinct from *Ar. chinense*, *Ar. paraphaeospermum* and *Ar.
rasikravindrae by its thick-walled, finely roughened conidia with a pale, equatorial slit and ampulliform, cylindrical or doliiform, basauxic conidiogenous cells [34]. Pintos and Alvarado [4] transferred Ar. chinense, Ar. paraphaeospermum and Ar. rasikravindrae to Apiospora and synonymized them under Apiospora chinense, Ap. paraphaeospermum and Ap rasikravindrae, respectively, based on the phylogenetic analyses and morphological characteristics.

Our phylogenetic analyses based on combined LSU, ITS, TEF1-α and TUB2 sequence data show Ar. pseudorasikravindrae is a sister to the new combinations Ap. acutiapica (=Ar. acutiapicum) with high support (ML/BI = 77/0.99). Thus, we propose the transfer of Ar. pseudorasikravindrae under the new combination Ap. pseudorasikravindrae.

**Apiospora septata** (Y. Feng and Jian K. Liu) X.G. Tian and Tibpromma S., comb. nov.

*Index Fungorum number: IF558506; Faces of Fungi number: FoF 09571.*
*Basiolym: Arthrinium septatum Y. Feng, J.K. Liu, C.G. Lin, Y.Y. Chen, M.M. Xiang and Z.Y. Liu, Frontiers in Microbiology 12. 2021.*

*Notes:* *Arthrinium septatum* was introduced by Feng et al. [49] from dead bamboo culms in China. Feng et al. [49] showed that *Arthrinium septatum* forms a well-supported clade and appears to be distinct from other *Arthrinium* species. *Arthrinium septatum* resembles *Ar. biseriale* in having a biseriate, broad fusiform to cylindrical ascospores and cylindrical, clavate asci. However, *Ar. septatum* differs from *Ar. biseriale* by having smaller stromata [49].

In our phylogenetic analyses, *Arthrinium septatum* groups in a well-supported clade with *Ap. pseudospegazzinii* and *Ap. gelatinosa*. Thus, we propose the transfer of *Ar. septatum* under the new combination *Ap. septata*, based on the morphological and phylogenetic analyses.

**Apiospora setariae** (Jiang, N.; Tian, C.M.) X.G. Tian and Tibpromma S., comb. nov.

*Index Fungorum number: IF835609.*
*Basiolym: Arthrinium setariae JIANG, N.; TIAN, C.M. Phytotaxa 483, 149-159. 2021.*

*Notes:* *Arthrinium setariae* was introduced by Jing et al. [38] from *Setaria viridis* in China. Jing et al. [38] mentioned that this species has larger conidia and is phylogenetically closely related to *Ar. jiangxiense*. Pintos and Alvarado [4] transferred *Ar. jiangxiense* to *Apiospora* and synonymized *Ap. jiangxiensis* based on the phylogenetic analyses and morphological characteristics.

In our phylogenetic analyses based on combined LSU, ITS, TEF1-α and TUB2 sequence data, *Arthrinium setariae* clustered with *Apiospora jiangxiense* with high support (ML/BI = 87/1.00). Thus, we propose the transfer of *Ar. setariae* under the new combination *Ap. setariae*, based on the morphological and phylogenetic analyses.

**Apiospora sorghi** (J.D.P. Bezerra, C.M Gonçalves and C.M. Souza-Motta) X.G. Tian and Tibpromma S., comb. nov.

*Index Fungorum number: IF558498; Faces of Fungi number: FoF 05762.*
*Basiolym: Arthrinium sorghi J.D.P. Bezerra, C.M Gonçalves and C.M. Souza-Motta, Fungal Diversity: 10.1007, 73 2020.*

*Notes:* *Arthrinium sorghi* was introduced as an endophyte by Bezerra et al. [36] from the leaves of *Sorghum bicolor* in Brazil. Bezerra et al. [36] mentioned that *Ar. sorghi* is treated as a unique lineage within *Arthrinium* based on ITS phylogenetic analysis. Morphologically, *Ar. sorghi* resembles *Ar. pseudosinense*, *Ar. ovatum* and *Ar. phaeospermum*, but differs from them by the culture characteristics, conidiophores and conidia size [36]. Pintos and Alvarado [4] transferred *Ar. pseudosinense*, *Ar. ovatum* and *Ar. phaeospermum* to *Apiospora pseudosinensis*, *Ap. ovata* and *Ap. phaeospermum* based on the phylogenetic analyses and morphological characteristics.

In our phylogenetic analyses based on combined LSU, ITS, TEF1-α and TUB2 sequence data, *Arthrinium sorghi* clustered with *Apiospora bambusucila* with high support (ML/BI = 78.0.99). Thus, we propose the transfer of *Ar. sorghi* under the new combination *Ap. sorghi*, based on the morphological and phylogenetic analyses.
4. Discussion

In this study, the new taxon *Apiospora chiangraiense* and two new host records, viz., *Ap. intestini* and *Ap. rasikravindrae*, are introduced based on the morphological and phylogenetic analyses. In addition, thirteen new combinations are proposed based on the phylogenetic analyses.

*Apiospora* was previously synonymized under *Arthrinium*, but Pintos et al. [14] re-evaluated the placements of these two genera and transferred 55 species to *Apiospora* based on a phylogenetic analysis. Currently, 117 species of *Apiospora* are listed in the Index Fungorum [33]. Among these 117 species, 55 species have been confirmed in *Apiospora* by phylogenetic analyses [4]; however, the remaining 62 species need to be confirmed, as the sequence data of these species are not available. The morphology of *Apiospora* and *Arthrinium* are quite similar, so it is difficult to distinguish *Apiospora* and *Arthrinium* based only on morphology.

In the phylogenetic analyses, two *Arthrinium* species, viz., *Arthrinium trachycarpum* and *Ar. urticae*, formed a distinct clade out of *Arthrinium*, and this result is consistent with previous studies [18]. However, the morphologies of these two species are not significantly different from *Arthrinium*; thus, more collections are required to clarify the placement of these two species [24,50]. In addition, our phylogenetic analyses showed that *Apiospora sorghi*, *Ap. bambusucila*, *Ap. chiangraiense* and *Ap. intestini* are not clustered together in *Apiospora* major clades (Figure 1). We also compared the LSU sequence of these four species with other *Apiospora* species, but a few base pair differences were found. Moreover, their morphologies fit well within the species concept of *Apiospora*. Thus, further phylogenetic analyses are necessary to confirm whether *Apiospora* is a species complex or not.

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