

Taxonomic analysis of Amphisphaeriales in China: discovery of multiple novel taxa

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Abstract

Amphisphaeriales primarily contains saprobes, pathogens, and endophytes. This order of fungi is difficult to identify because of its taxonomic and morphological complexities. However, it has significant ecological and economic value and has recently become a major focus in fungal research. A total of 164 strains, isolated from decaying plant materials, diseased leaves, and healthy leaves, were used to explore the taxonomic diversity of Amphisphaeriales in China based on analyses of its morphology and multi-locus phylogenies (internal transcribed spacer [ITS], large subunit of ribosomal DNA [LSU], translation elongation factor 1- α [*tef1 α*], and beta tubulin [*tub2*]). The results of these analyses showed that all these collected strains belonged to 71 species, including Apiosporaceae (*Apiospora* and *Nigrospora*), Beltraniaceae (*Beltraniella*), and Sporocadaceae (*Neopestalotiopsis*, *Pestalotiopsis*, and *Pseudopestalotiopsis*). These analyses reveal three major findings: 38 new species, 33 known species (with *A. locuta-pollinis* (syn. *A. fuxianhuensis*) included among the known species. Through this study, we confirm a primary association of *Apiospora* with Poaceae in tropical and subtropical climates and documents multi-species co-infections. Our findings significantly contribute to the understanding of the placement of new taxa in Apiosporaceae, Beltraniaceae, and Sporocadaceae. Moreover, the results of this study contribute to the future taxonomic revisions and systematic studies of Amphisphaeriales.

Keywords: Amphisphaeriales, new species, Apiosporaceae, Beltraniaceae, Sporocadaceae, Phylogeny, Taxonomy

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Introduction

The order Amphisphaeriales was introduced by Eriksson and Hawksworth in 1986 and was taxonomically classified within the subclass Xylariomycetidae, class Sordariomycetes, and subphylum Pezizomycotina^[1]. Amphisphaeriales and Xylariales had historically been treated as closely related orders or even synonyms^[2,3], and were later formally considered synonymous^[4,5]. Amphisphaeriales was resurrected based on morphological and phylogenetic data^[6]. Previous studies have provided key evidence supporting the recognition of Amphisphaeriales and Xylariales as distinct orders, with divergence time serving as a critical criterion^[7–11]. The sexual morph of Amphisphaeriales is defined as follows: ascomata are predominantly solitary, globose to subglobose, coriaceous, and erumpent, occurring with or without stromatic tissues; asci are cylindrical or clavate with a J+ or J– apical ring; ascospores are ellipsoid, apiosporous, fusiform, or oval in shape, unicellular to trans-septate, variously colored, and possess either smooth or ornamented walls with or without appendages or mucilaginous sheaths^[6,11,12]. The asexual morph of Amphisphaeriales is characterized by acervular or pycnidial conidiomata with holoblastic, annellidic, ampulliform or lageniform conidiogenous cells; conidia range from aseptate to transeuseptate, come in various colors, and often bear appendages^[6,12]. Some species of Amphisphaeriales are mainly saprobes, pathogens or endophytes on plants^[6]. Some *Arthrimum* species, such as *Arthrimum phaeospermum*, were reported as human pathogens causing cutaneous mycosis^[13]. Members of Amphisphaeriales exhibit diverse bioactivities with practical applications;

for example, *Arthrimum arundinis* has been utilized as an antifungal agent in pharmaceuticals^[14]. Similarly, *Seiridium* species produce seiridins because of their phytotoxicity and antimicrobial potential^[15]. Currently, Amphisphaeriales comprises 16 families and two *incertae sedis* genera^[16]. In this study, we investigate three families (Apiosporaceae, Beltraniaceae, and Sporocadaceae) by refining their taxonomic boundaries and clarifying phylogenetic relationships. This study addresses the gaps in knowledge about this fungal group in China and establishes a robust classification framework, demonstrating significant academic value.

The family Apiosporaceae was established to accommodate fungal genera that was characterized by apiosporous hyaline ascospores and a basauxic, *Arthrimum*-like mode of conidiogenesis^[17]. Saccardo established the genus *Apiospora*, designating *A. montagnei* as its type species^[18]. The genus *Arthrimum* was established with *Arthrimum caricicola* as its type species by Schmidt and Kunze^[19] and validated by Fries^[20]. Based on the principles advocated by Hawksworth^[21], Crous and Groenewald^[22] synonymized the sexual genus *Apiospora* with *Arthrimum* and prioritized the use of the latter. Five genera were established in Apiosporaceae: *Appendicospora*, *Arthrimum*, *Dictyoarthrinium*, *Endocalyx*, and *Nigrospora*^[10]. Samarakoon and Konta have subsequently segregated the genera *Dictyoarthrinium*, *Endocalyx*, and *Appendicospora* from the Apiosporaceae based on a series of phylogenetic analyses^[11,23,24]. Pintos and Alvarado^[25] proposed the taxonomic separation of *Apiospora* and *Arthrimum* by integrating genetic fragments and morphological and ecological data. Thus, the family Apiosporaceae currently accommodates three genera: *Apiospora*,

Arthrinium, and *Nigrospora*. Notably, the *Apiospora* contains various species that are difficult to distinguish because of their highly similar morphological characteristics. However, *Apiospora* and *Arthrinium* can be distinguished based on three primary characteristics: 1) conidial morphology: *Apiospora* appears nearly spherical and lenticular with a pale equatorial slit, whereas *Arthrinium* exhibits an angular, curved, boat-shaped, fusiform, and polygonal morphology^[22,25–28]; 2) host preference: *Apiospora* predominantly colonizes Poaceae and other plants, while *Arthrinium* occurs mainly on Cyperaceae or Juncaceae^[28,29]; and 3) biogeography: *Apiospora* is common in tropical and subtropical regions, but *Arthrinium* is frequently reported from temperate, cold, or alpine habitats^[25,28,29].

The fungal tribe Beltraniaceae was established by a single genus *Beltrania*^[30]. Nannizzi^[31] later introduced the Beltraniaceae to accommodate *Beltrania* and its similar genera, thereby treating the earlier tribe as a synonym. Five genera, including *Beltrania*, *Beltraniella*, *Beltraniopsis*, *Parapleurotheciopsis*, and *Pseudobeltrania*, were emended to Beltraniaceae by Crous et al.^[32]. Then, Rajeshkumar et al. expanded the family Beltraniaceae^[33] by adding two other genera: *Hemibeltrania* and *Porobeltraniella*. Subsequently, four other *Beltrania*-like genera were proposed: *Pseudosubramaniomyces* was established by its type species, *Pseudosubramaniomyces fusisaprophyticus*^[34]; *Subsessila* was established by its type species *Subsessila turbinate*, collected from an unidentified decaying leaf in Thailand^[35]; *Anabeltraniomyces* and *Parabeltrania* were established with *Anabeltraniomyces maximus* as the type species from *Clusia* sp. and with *Parabeltrania persianiae* as the type species from indeterminate dead leaves, respectively, in Costa Rica in 2024^[36]. Liu et al.^[37] developed a dichotomous key to facilitate the identification of 11 genera within Beltraniaceae.

Sporocadaceae was originally established by Corda^[38] to accommodate the genera *Sporocadus*, *Pestalozzia* (currently *Pestalotia*), and *Prosthemia*. For a considerably long period, Sporocadaceae was synonymized with Amphisphaeriaceae^[39]. Sporocadaceae was resurrected by Jaklitsch et al.^[4]. Liu et al.^[40] established a relatively robust classification system for Sporocadaceae based on morphology and multi-gene phylogenetics. *Pestalotiopsis*, as an important taxon in Sporocadaceae, was established to accommodate species with 4-septate conidia^[41]. However, these pestalotioid taxa pose a challenge for accurate identification due to their high degree of morphological similarity, particularly in the absence of molecular data^[12]. Phylogenetic analysis of large subunit of ribosomal DNA (LSU) alignment, together with literature and morphological appraisal, defined the segregation of *Neopestalotiopsis* and *Pseudopestalotiopsis* from *Pestalotiopsis*^[42]. Liu et al.^[43] reported that the internal transcribed spacer (ITS) sequence lengths of *Neopestalotiopsis* was 480–484 bp, that of *Pestalotiopsis* was 489–495 bp, and that of *Pseudopestalotiopsis* was 536–540 bp. Razaghi et al. further revealed that whole-genome sizes of *Neopestalotiopsis* (49.73–53.78 Mbp) and *Pseudopestalotiopsis* (50.41–51.91 Mbp) are generally larger, but that of *Pestalotiopsis* is the smallest (< 50 Mbp)^[44].

In this study, we collected decaying plant materials, diseased leaves, and healthy leaves from eight provinces in China from 2022 to 2025. Through morphological comparisons and multi-gene phylogenetic analysis, a total of 71 species in the Amphisphaeriales were identified, comprising 38 new species and 33 known species, with *A. locuta-pollinis* (syn. *A. fuxianhuensis*) included among the known species. These findings significantly contribute to our understanding of taxa diversity in the Amphisphaeriales and help in refining its taxonomic framework.

Materials and methods

Sample collection, strain isolation, and morphological study

Between 2022 and 2025, plant specimens were collected from eight provinces across China. The distribution and predominant habitat types of samples were as follows: Fujian (1,230 specimens, natural forest and farmland), Guangdong (372 specimens, natural forest and farmland), Guangxi (500 specimens, natural forest and farmland), Guizhou (203 specimens, natural forest), Hainan (3,090 specimens, natural forest, farmland, riparian wetland, bamboo forest, and tea plantation), Shandong (345 specimens, natural forest, and farmland), Sichuan (183 specimens, alpine meadow, and bamboo forest), and Yunnan (304 specimens, natural forest, and alpine meadow). The time, geography, and host plant information were recorded for all these samples. Then, they were all preserved for further analysis. Pure colonies were isolated using the tissue method. The strains were deposited in 15% sterile glycerol at 4 °C. Typical specimens were preserved in the Herbarium of the Department of Plant Pathology, Shandong Agricultural University, Shandong, China (HSAUP). Living cultures were deposited in the Shandong Agricultural University Culture Collection (SAUCC) and China General Microbiological Culture Collection Center (CGMCC). After 7 or 14 days of growth on PDA, we recorded the morphological information of the isolates colony and photographed the plate surfaces (obverse and reverse) with a Canon G7X digital camera (Canon, Tokyo, Japan). Morphological features were described using two media: water agar (WA) with or without pine needles and potato dextrose agar (PDA) without pine needles. Fungal microstructures were observed using a stereomicroscope (Olympus SZ61, Olympus Corporation, Tokyo, Japan) and microscope (Olympus BX53, Olympus Corporation, Tokyo, Japan) with differential interference contrast (DIC), and subsequently captured using attached digital cameras (BioHD-A20c, FluoCa Scientific, Shanghai, China). We randomly measured the microstructures using Digimizer software v5.6.0 (www.digimizer.com) and calculated the average size (av.), with "n" indicating the total number of measurements.

The abbreviations of genera are as follows: *A.* = *Apiospora*, *B.* = *Beltraniella*, *Neo.* = *Neopestalotiopsis*, *Nig.* = *Nigrospora*, *P.* = *Pestalotiopsis*, and *Ps.* = *Pseudopestalotiopsis*. Newly introduced fungal species were registered with the Fungal Names database (<https://nmdc.cn/fungalnames/>)^[45].

DNA extraction, PCR amplification, and sequencing

Genomic DNA was extracted using the modified CTAB method^[46] or magnetic fungi DNA extraction kit (DC112-C7, VAMNE Magnetic Bacteria/Fungi DNA Extraction Kit [Prepackaged], Vazyme Biotech Co., Ltd). The respective primers and different conditions for the PCR are detailed in Table 1. The PCR amplification reactions were performed in a 25 µL mixture containing 12.5 µL of 2 × Hieff Canace Plus PCR Master Mix (AG12202, Accurate Biotechnology, Changsha, China), 1 µL each of forward and reverse primers (TsingKe, Qingdao, China), 1 µL of template genomic DNA, and nuclease-free water to adjust the final volume. The amplified products were separated by electrophoresis on a 1% agarose gel (Cat. Nos. RM02852, ABclonal Biotechnology Co., Ltd., Wuhan, China) stained with GelStain (GS101; TransGen Biotech, China) and then visualized under UV light. Target bands were excised from the gel, purified using a commercial gel extraction kit (DM1200, Beijing Solarbio Science & Technology Co., Ltd.), and subsequently sent for sequencing to Youkang Company Limited (Zhejiang, China).

Table 1. Molecular markers, and all PCR primers and programs used in this study.

Locs	PCR primers	Sequence (5'→3')	PCR cycles	Ref.
ITS	ITS5 ITS4	GGA AGT AAA AGT CGT AAC AAG G TCC TCC GCT TAT TGA TAT GC	95 °C 5 min; (95 °C 30 s, 55 °C 30 s, 72 °C 1 min) × 35 cycles	[47]
LSU	LROR LR5	GTA CCC GCT GAA CTT AAG C TCC TGA GGG AAA CTT CG	95 °C 5 min; (95 °C: 30 s, 52 °C: 30 s, 72 °C: 1 min) × 35 cycles	[48,49]
<i>tef1-α</i>	EF1-728F EF2	CAT CGA GAA GTT CGA GAA GG GGA RGT ACC AGT SAT CAT GTT	95 °C 5 min; (95 °C 30 s, 55 °C 60 s, 72 °C 1 min) × 30 cycles	[50,51]
<i>tub2</i>	Bt-2a Bt-2b	GGT AAC CAA ATC GGT GCT GCT TTC ACC CTC AGT GTA GTG ACC CTT GGC	95 °C 5 min; (95 °C: 30 s, 53 °C: 30 s, 72 °C: 1 min) × 35 cycles	[52]

Pairwise homoplasy index (PHI) test

PHI tests were conducted on concatenated multilocus datasets using SplitsTree software, with Φw values <0.05, indicating significant recombination^[53,54]. Phylogenetic relationships were visualized through split graphs generated via Log-Det transformation and split decomposition methods.

Sequence alignments and phylogenetic analysis

Species identity was confirmed for all assembled sequences through BLAST searches against the GenBank database^[55]. All sequences were aligned using MAFFT v.7 online service (<https://mafft.cbrc.jp/alignment/server/>) and then adjusted by MEGA v7.0^[56]. We deposited the nucleotide sequences in the NCBI's GenBank nucleotide database (www.ncbi.nlm.nih.gov). The newly-generated sequences (Supplementary Information 2) were aligned with related sequences (Supplementary Information 3–8). The phylogenetic trees were generated using maximum likelihood (RAxML-HPC2 on XSEDE v.8.2.12) and Bayesian inference (MrBayes v.3.2.7a, Linux)^[57]. In the phylogenetic trees, all tested isolates are highlighted in red. The phylogenetic tree visualizations were generated using ITOL (Interactive Tree of Life: <https://itol.embl.de/>)^[58] and final layout adjustments made in Adobe Illustrator CS6 (Adobe Systems Inc., USA).

Results

Phylogenetic analysis

The samples were collected from eight provinces of China and the collected strains majorly consisted of species belonging to Apiosporaceae (*Apiospora*, *Nigrospora*), Beltraniaceae (*Beltraniella*), and Sporocadaceae (*Neopestalotiopsis*, *Pestalotiopsis*, and *Pseudopestalotiopsis*). Consequently, 71 species are described (Table 2), representing six genera: *Apiospora*, *Nigrospora*, *Beltraniella*, *Neopestalotiopsis*, *Pestalotiopsis*, and *Pseudopestalotiopsis*. Details of known species are provided in Supplementary Information 1^[59–114].

Taxonomy

Amphisphaeriales D. Hawksw. & O.E. Erikss.

Notes: Amphisphaeriales was established within the subclass Xylariomycetidae^[1]. Sixteen families and two Amphisphaeriales genera *incertae sedis* are accepted^[16]. A dichotomous key for Amphisphaeriales is provided in Supplementary Information 9.

Apiosporaceae K.D. Hyde, J. Fröhl., Joanne E. Taylor & M.E. Barr

Notes: Apiosporaceae was established to accommodate genera with basauxic conidiogenesis^[17]. The family Apiosporaceae included *Apiospora*, *Arthrimum*, and *Nigrospora*^[16].

Apiospora Sacc.

Notes: Saccardo^[18] introduced the genus *Apiospora* with *Apiospora montagnei* as its type species. *Apiospora* conidia appear more or less rounded and lenticular^[115]. *Apiospora* species have a worldwide distribution and a broad host range, existing primarily as endophytes, pathogens, or saprobes on plants^[68,73]. Most of the species have been isolated from diverse sources such as air, lichens, soil, seaweeds, and animal tissues. A few species act as human pathogens, causing cutaneous infections^[64].

In the phylogenetic tree containing 384 *Apiospora* isolates, the strain *Arthrimum caricicola* (CBS 145127) acted as the outgroup. The alignment sequences have 2,898 concatenated nucleotide bases, viz. 1–868 (ITS), 869–1,704 (LSU), 1705–2,203 (*tub2*), and 2,204–2,898 (*tef1-α*). Among these sequences, 1,522 characters were constant, 170 characters were variable and parsimony-uninformative, and 1,206 characters were parsimony-informative. As the topologies were consistent in the ML and BI analyses, only the ML tree is shown in this study. The 383 tested strains were identified as belonging to 166 species based on the phylogenetic analysis of ITS, LSU, *tef1-α*, and *tub2* genes. BI analysis was conducted on 6,265,000 generations of 12,532 trees; 3/4 of the trees were used to compute the posterior probability using the majority-rule consensus tree method (Fig. 1; first value: Bayesian inference posterior probability [BIPP] ≥ 0.90 displayed).

Apiospora alpiniae Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. Fig. 2

Fungal names: FN 573274

Etymology: The epithet "*alpiniae*" indicates the host genus of the holotype, specifically *Alpinia zerumbet*.

On PDA. Asexual morph: *hyphae* 1.53–3.60 μm diameter, hyaline, branched, thick-walled, septate, guttulate. *Conidiophores* are reduced to conidiogenous cells. *Conidiogenous cells* 5.97–19.43 × 3.05–5.35 μm (av. = 13.48 ± 4.68 × 4.10 ± 0.82 μm, *n* = 18) are produced from hyphae, and are holoblastic, hyaline, cylindrical, straight, aseptate, smooth-walled, and guttulate. *Conidia* 6.18–19.48 × 3.77–7.83 μm (av. = 9.57 ± 3.71 × 5.81 ± 0.89 μm, *n* = 24) from hyphae, and are globose, subglobose to cylindric-clavate, aseptate, dark brown, smooth to slightly rough, and guttulate, with a pale equatorial slit.

Culture characteristics – The colony surfaces are white, flat, and floccose, with abundant aerial mycelia, colony margin entire and reverse red in the center, and white at the margin on the PDA medium. The diameter of the colony was 90 mm after culturing for 7 days at 25 °C.

Material examined – China, Hainan Province, Diaoluoshan National Forest Park (18.6786181 N, 109.9481903 E, 150.6 m), on diseased *Alpinia zerumbet* leaves, 27 March 2024, Q.Y. Liu (HSAUP 7430-1, holotype), ex-type culture CGMCC 3.29207 = SAUCC 7430-1; *ibid.*, Ledong Li Autonomous County, Jianfengling National Forest Park (18.700142 N, 108.812270, 126 m), on diseased leaves of *Bambusa ventricosa*, 4 December 2024, Q.Y. Liu (HSAUP 14447-3), living cultures SAUCC 14447-3.

Table 2. Content of fungal species in this study.

Phylum: Ascomycota	
Subphylum: Pezizomycotina	
Class: Sordariomycetes O.E. Erikss. & Winka	
Order: Amphisphaeriales D. Hawksw. & O.E. Erikss.	
Family: Apiosporaceae K.D. Hyde, J. Fröhl., Joanne E. Taylor & M.E. Barr	
Genus: <i>Apiospora</i> Sacc.	
1.	<i>Apiospora adinandrae</i> X.Y. Liu, Z.X. Zhang and X.G. Zhang, Journal of Fungi 10 (1, no. 74): 6 (2024) (new host record)
2.	<i>Apiospora alpiniae</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
3.	<i>Apiospora areacearum</i> L.S. Dissan., K.D. Hyde & J.C. Kang, Mycosphere 15 (1): 1675–1793 (2024) (new host and geographical records)
4.	<i>Apiospora babylonica</i> H. Sheng, Z.X. Zhang & X.G. Zhang, Microorganisms 12: 1372 (2024) (new host and geographical records)
5.	<i>Apiospora baihualingensis</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
6.	<i>Apiospora bambusicaulis</i> K.M. Yu & Y.L. Jiang, MycoKeys 112: 233–252 (2025) (new geographical record)
7.	<i>Apiospora baotingensis</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
8.	<i>Apiospora yinggelingensis</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
9.	<i>Apiospora campsidis</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
10.	<i>Apiospora changjiangensis</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
11.	<i>Apiospora chiangraiense</i> X.G. Tian & Tibpromma S, Life 11: 1071 (2021) (new host and geographical records)
12.	<i>Apiospora clavata</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
13.	<i>Apiospora danzhouensis</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
14.	<i>Apiospora dematiacea</i> C.F. Liao & Doilom, Journal of Fungi 9 (no. 1087): 10 (2023) (new host and geographical records)
15.	<i>Apiospora diaoluoshanensis</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
16.	<i>Apiospora dryopteris</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
17.	<i>Apiospora elongata</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
18.	<i>Apiospora guangdongensis</i> J.Y. Zhang & Y.Z. Lu, Journal of Fungi 9 (no. 1096): 12 (2023) (new geographical record)
19.	<i>Apiospora guangzhouensis</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
20.	<i>Apiospora hainanensis</i> R.Y. Liu, J.W. Xia & X.G. Zhang, MycoKeys 95: 37 (2023)
21.	<i>Apiospora hydei</i> (Crous) Pintos & P. Alvarado, Fungal Systematics and Evolution 7: 207 (2021)
22.	<i>Apiospora hysterina</i> (Sacc.) Pintos & Alvarado, Fungal Systematics and Evolution 7:206P. (2021)
23.	<i>Apiospora intestini</i> (Kajale, Sonawane & Rohit Sharma) Pintos & P. Alvarado, Fungal Systematics and Evolution 7: 206 (2021) (new host and geographical records)
24.	<i>Apiospora pseudosae</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
25.	<i>Apiospora jiangxiensis</i> (Mei Wang & L. Cai) Pintos & P. Alvarado, Fungal Systematics and Evolution 7: 206 (2021) (new geographical record)
26.	<i>Apiospora lageniformis</i> S.L. Kwon & J.J. Kim, Mycobiology 50 (5): 302–316 (2022) (new host and geographical records)
27.	<i>Apiospora armeniaca</i> H. Sheng, Z.X. Zhang & X.G. Zhang, Microorganisms 2024, 12, 1372 (new host and geographical records)
28.	<i>Apiospora lingshuiensis</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
29.	<i>Apiospora locuta-pollinis</i> (F. Liu & L. Cai) Pintos & P. Alvarado, Fungal Systematics and Evolution 7: 207 (2021) (new host record)
30.	<i>Apiospora longistroma</i> (D.Q. Dai & K.D. Hyde) Pintos & P. Alvarado, Fungal Systematics and Evolution 7: 207 (2021) (new geographical record)
31.	<i>Apiospora multiplex</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
32.	<i>Apiospora pingtangensis</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
33.	<i>Apiospora pseudoparenchymatica</i> (M. Wang & L. Cai) Pintos & P. Alvarado, Fungal Systematics and Evolution 7: 207 (2021) (new geographical record)
34.	<i>Apiospora cyclobalanopsidis</i> (Yao Feng & Jian K. Liu) X.G. Tian & Tibpromma, in Tian, Karunarathna, Mapook, Promputtha, Xu, Bao & Tibpromma, Life 11 (no. 1071): 17 (2021) (new host and geographical records)
35.	<i>Apiospora qiongzongensis</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
36.	<i>Apiospora renhuaensis</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
37.	<i>Apiospora rutila</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
38.	<i>Apiospora shaoguanensis</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
39.	<i>Apiospora taianensis</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
40.	<i>Apiospora teapae</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
41.	<i>Apiospora ventricosa</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
42.	<i>Apiospora wuyishanensis</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
43.	<i>Apiospora xiangxiensis</i> X.Y. Chang & M.J. Chen, MycoKeys 116: 214 (2025) (new host and geographical records)
44.	<i>Apiospora zingiberis</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
Genus: <i>Nigrospora</i> Zimm.	
45.	<i>Nigrospora bambusae</i> Mei Wang & L. Cai, Persoonia 39: 127 (2017) (new geographical record)
46.	<i>Nigrospora brasiliensis</i> A.C.Q. Brito, C. Conforto, A.R. Machado, Persoonia 42: 439 (2019) (new host and geographical records)
47.	<i>Nigrospora buddlejiae</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
48.	<i>Nigrospora camelliae-sinensis</i> Mei Wang & L. Cai, Persoonia 39: 127 (2017) (new host record)
49.	<i>Nigrospora chinensis</i> Mei Wang & L. Cai, Persoonia 39: 129 (2017) (new host record)
50.	<i>Nigrospora helwingiae</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
51.	<i>Nigrospora lacticolonia</i> Mei Wang & L. Cai, Persoonia 39: 06 (2017) (new host record)
52.	<i>Nigrospora officinalis</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
53.	<i>Nigrospora oryzae</i> (Berk. & Broome) Petch (1924) (new host record)
54.	<i>Nigrospora penniseti</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
55.	<i>Nigrospora pseudosae</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
56.	<i>Nigrospora pyriformis</i> Mei Wang & L. Cai, Persoonia 39: 126 (2017) (new host record)
57.	<i>Nigrospora rubi</i> Mei Wang & L. Cai, Persoonia 39: 127 (2017) (new host and geographical records)
58.	<i>Nigrospora sacchari-officinarum</i> M. Raza & L. Cai, Fungal Diversity 99: 95 (2019) (new host record)

(to be continued)

Table 2. (continued)

59.	<i>Nigrospora vesicularifera</i> M. Raza & L. Cai, Fungal Diversity 99: 96 (2019) (new host record) Family: Beltraniaceae Nann. Genus: <i>Beltraniella</i> Subram.
60.	<i>Beltraniella obovata</i> D.H. Li, J.W. Xia & X.G. Zhang, sp. nov. Family: Sporocadaceae Corda Genus: <i>Neopestalotiopsis</i> Maharachch., K.D. Hyde & Crous
61.	<i>Neopestalotiopsis bamboensis</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
62.	<i>Neopestalotiopsis mianyangensis</i> W.L. Li & Jian K. Liu, Journal of Fungi 8: 10 (2022) (new host record) Genus: <i>Pestalotiopsis</i> Steyaert
63.	<i>Pestalotiopsis castanopsis</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
64.	<i>Pestalotiopsis dracaenae</i> Yong Wang bis, Y. Song, K. Geng & K.D. Hyde, Fungal Diversity 75: 164 (2015) (new host record)
65.	<i>Pestalotiopsis hydei</i> Huanraluek & Jayaward, Phytotaxa 479 (1): 023–043 (2021) (new host and geographical records)
66.	<i>Pestalotiopsis nanpingensis</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
67.	<i>Pestalotiopsis rhizomaticola</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
68.	<i>Pestalotiopsis rostrata</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
69.	<i>Pestalotiopsis smilacicola</i> Y.R. Sun & Yong Wang bis, Microbiology Spectrum 11(1): e03987-22, 15 (2023) (new host and geographical records)
70.	<i>Pestalotiopsis yuxiensis</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. Genus: <i>Pseudopestalotiopsis</i> Maharachch., K.D. Hyde & Crous
71.	<i>Pseudopestalotiopsis xishuangbannaensis</i> Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.

Distribution – China, Hainan Province.

Ecology – Associated with diseased leaves of *Alpinia zerumbet* and *Bambusa ventricosa*.

Notes – The phylogenetic analysis showed that our isolates are genetically similar to *A. cannae* (ZHKUCC 22-0127, ex-type) and *A. sacchari* (CBS 372.67, ex-type), forming a distinct subclade. *Apiospora alpiniae* and *A. cannae* (ZHKUCC 22-0127, ex-type) showed nucleotide differences in the ITS (2/489 bp), LSU (2/788 bp), *tef1-α* (4/387 bp), and *tub2* (5/419 bp) gene regions. *Apiospora alpiniae* and *A. sacchari* (CBS 372.67, ex-type) showed nucleotide differences in the ITS (6/518 bp), *tef1-α* (3/387 bp), and *tub2* (7/419 bp) gene regions. Morphologically, *Apiospora alpiniae* has large conidiogenous cells and conidia than *A. sacchari* (5.97–19.43 × 3.05–5.35 vs. 5–12 × 2.5–4 μm; 6.18–19.48 vs. 6–8 μm)^[22]. *Apiospora alpiniae* has shorter conidiogenous cells than *A. cannae* (5.97–19.43 vs. 20–25 μm)^[83]. Thus, *Apiospora alpiniae* was established as a new species.

Apiospora baihualingensis Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. Fig. 3
Fungal names: FN 573275

Etymology – The epithet "*baihualingensis*" indicates the geographical location of the holotype, specifically Baihualing Tropical Rainforest Cultural Tourism Zone, Hainan Province.

On PDA. Asexual morph: *hyphae* 2.32–5.36 μm diameter, hyaline, branched, thick-walled, septate, guttulate. *Conidiophores* 34.37–95.12 × 3.16–3.34 μm (av. = 64.75 ± 42.95 × 3.25 ± 0.13 μm, *n* = 2), hyaline to pale brown, unbranched, straight or flexuous, smooth, guttulate, aseptate. *Conidiophores* are occasionally reduced to conidiogenous cells. *Conidiogenous cells* 4.97–12.82 × 3.35–5.85 μm (av. = 8.76 ± 3.17 × 4.13 ± 0.86 μm, *n* = 18), from hyphae or conidiophores, holoblastic or polyblastic, hyaline to pale brown, cylindrical to ampulliform, straight, aseptate, smooth-walled, guttulate. *Conidia* 7.36–13.88 × 5.44–8.07 μm (av. = 9.23 ± 1.83 × 7.13 ± 0.76 μm, *n* = 23), globose to subglobose, aseptate, pale brown to dark brown from immature to mature, smooth to slightly rough, guttulate, without the pale equatorial slit.

Culture characteristics – Colonies on PDA mycelium moderate, margin entire, surface white, and reverse side is light brown in the center and white at the edges. The diameter of the colony was 90 mm after culturing for 7 days at 25 °C.

Material examined – China, Hainan Province, Qiongzong Li and Miao Autonomous County, Baihualing Tropical Rainforest Tourism and Culture Zone (19.005802 N, 109.825167 E, 392 m), on diseased

bamboo leaves (Poaceae sp.), 3 December 2023, Q.Y. Liu (HSAUP 14296-2A, holotype), ex-type culture CGMCC 3.29212 = SAUCC 14296-2A; *ibid.*, HSAUP 14296-2B, living culture SAUCC 14296-2B.

Distribution – China, Hainan Province.

Ecology – Associated with diseased bamboo leaves (Poaceae sp.).

Notes – *Apiospora baihualingensis* belongs to the large clade, where it shows a relationship with *A. diaoluoshanensis*. *Apiospora baihualingensis* differs from *A. diaoluoshanensis* (SAUCC 7508-4A, ex-type) by having larger conidia (7.36–13.88 × 5.44–8.07 vs. 5.71–10.10 × 3.75–7.15 μm), longer conidiogenous cells (4.97–12.82 × 3.35–5.85 vs. 1.83–9.29 × 1.72–3.70 μm), and the presence of 12 distinct nucleotide positions (2/520 bp [99.6%] in ITS, 9/424 bp [97.9%] in *tef1-α*, 1/368 bp [99.7%] in *tub2*). Thus, *Apiospora baihualingensis* as a new species. For details, see [Supplementary Information 11](#).

Apiospora baotingensis Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. Fig. 4
Fungal names: FN 573276

Etymology – The epithet "*baotingensis*" refers to the location where the type was collected, Baoting County, Hainan Province.

On diseased bamboo leaves. Asexual morph: *hyphae* 1.3–2.5 μm diameter, hyaline, branched, thick-walled, septate. *Conidiophores* are reduced to conidiogenous cells. *Conidiogenous cells* 8.1–18.0 × 1.7–2.7 μm (av. = 12.1 ± 2.9 × 2.2 ± 0.3 μm, *n* = 19), holoblastic or polyblastic, hyaline, cylindrical, straight, aseptate, smooth-walled. *Conidia* 6.2–7.7 × 4.4–7.5 μm (av. = 6.9 ± 0.5 × 6.1 ± 0.9 μm, *n* = 20), globose to subglobose, aseptate, smooth, dark brown, with a pale equatorial slit.

Culture characteristics – Colonies on PDA mycelium abundant, filiform, margin undulate, surface white and reverse yellowish white. The diameter of the colony was 52 mm after culturing for 7 days at 25 °C.

Material examined – China, Hainan Province, Baoting County, Diaoluoshan National Forest Park (18.4452181 N, 109.451703 E, 850 m), on diseased leaves of bamboo (Poaceae sp.), 27 March 2024, Y.X. Shang (HSAUP 7464-1A, holotype), ex-type culture CGMCC 3.29222 = SAUCC 7464-1A; *ibid.*, HSAUP 7464-1B, living culture SAUCC 7464-1B.

Distribution – China, Hainan Province.

Ecology – Associated with diseased bamboo leaves (Poaceae sp.).

Notes – Based on phylogenetic analysis, the two isolates of the new species *A. baotingensis* cluster with *A. changjiangensis*. Two species showed nucleotide differences in the ITS (3/520 bp), LSU (1/735 bp), *tef1-α* (15/417 bp), and *tub2* (15/384 bp) gene regions.



Fig. 1 to be continued

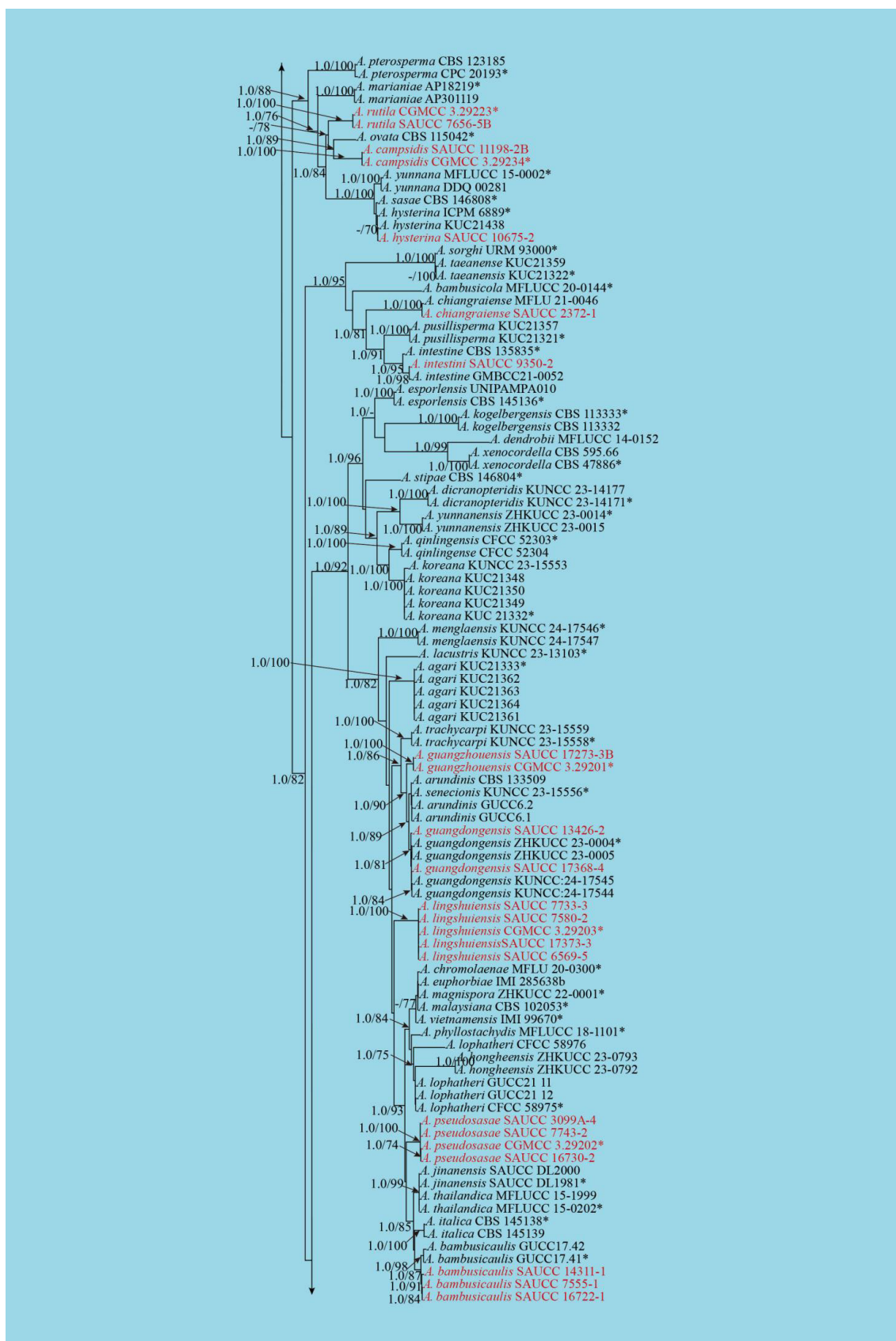


Fig. 1 to be continued

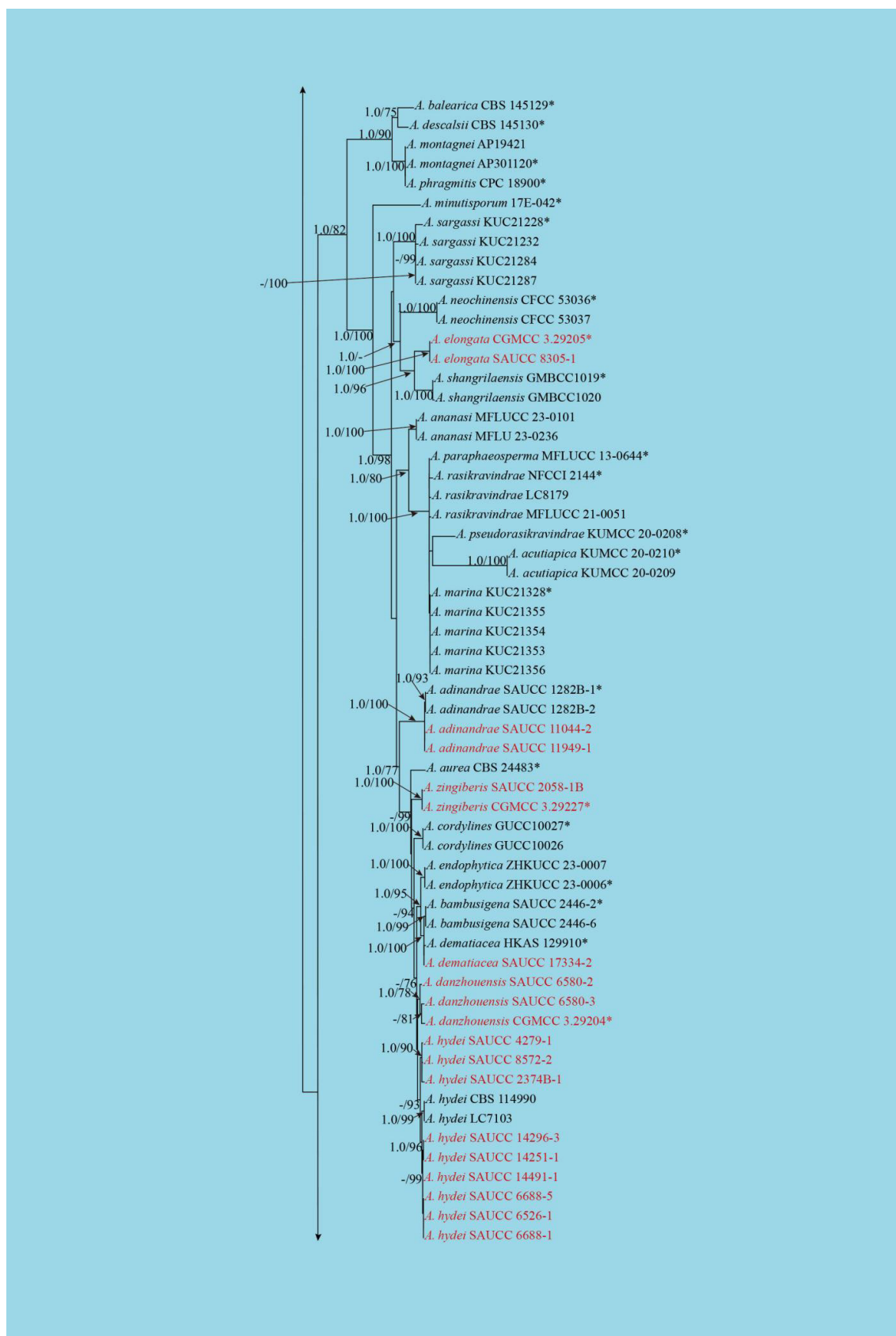


Fig. 1 to be continued

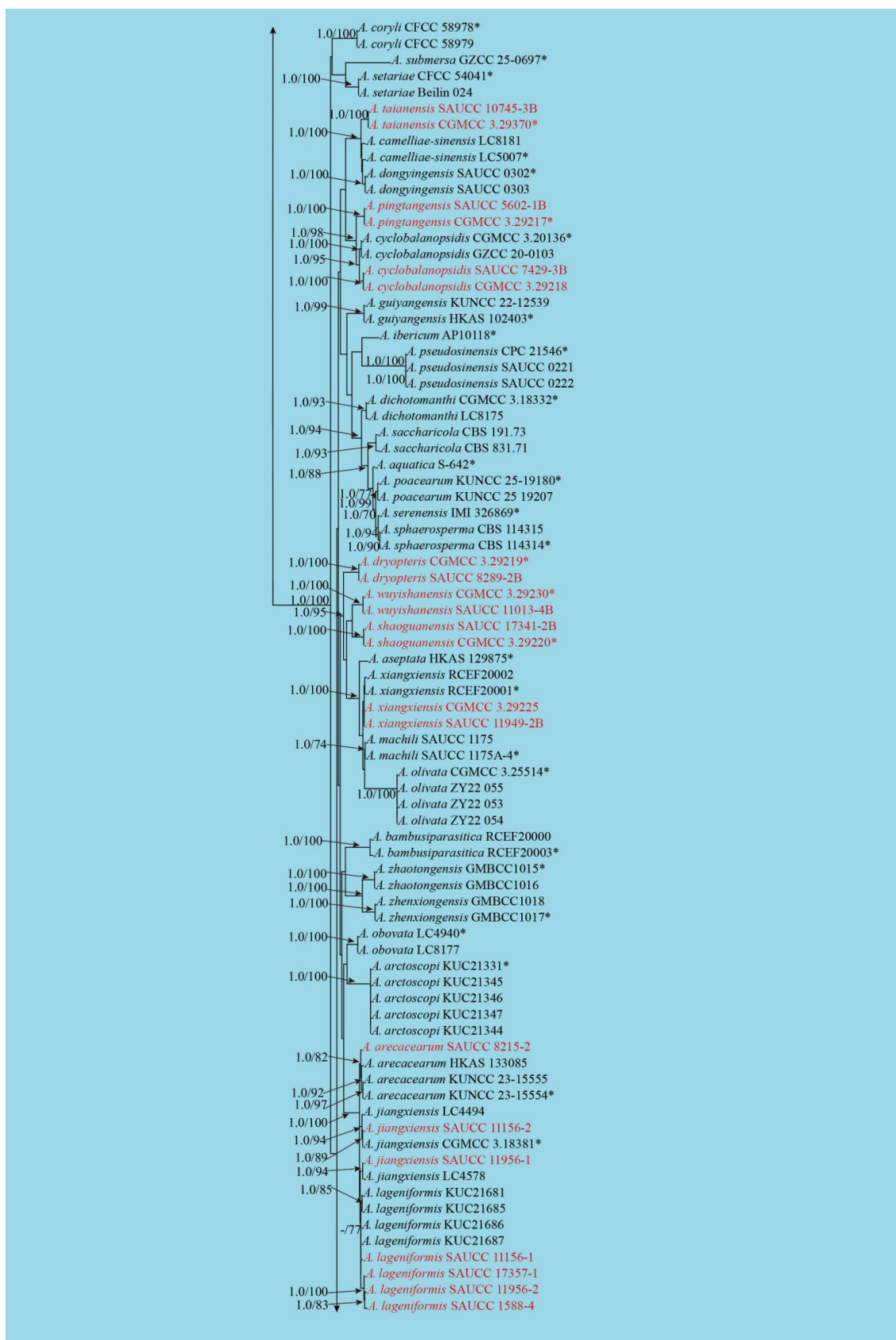


Fig. 1 to be continued

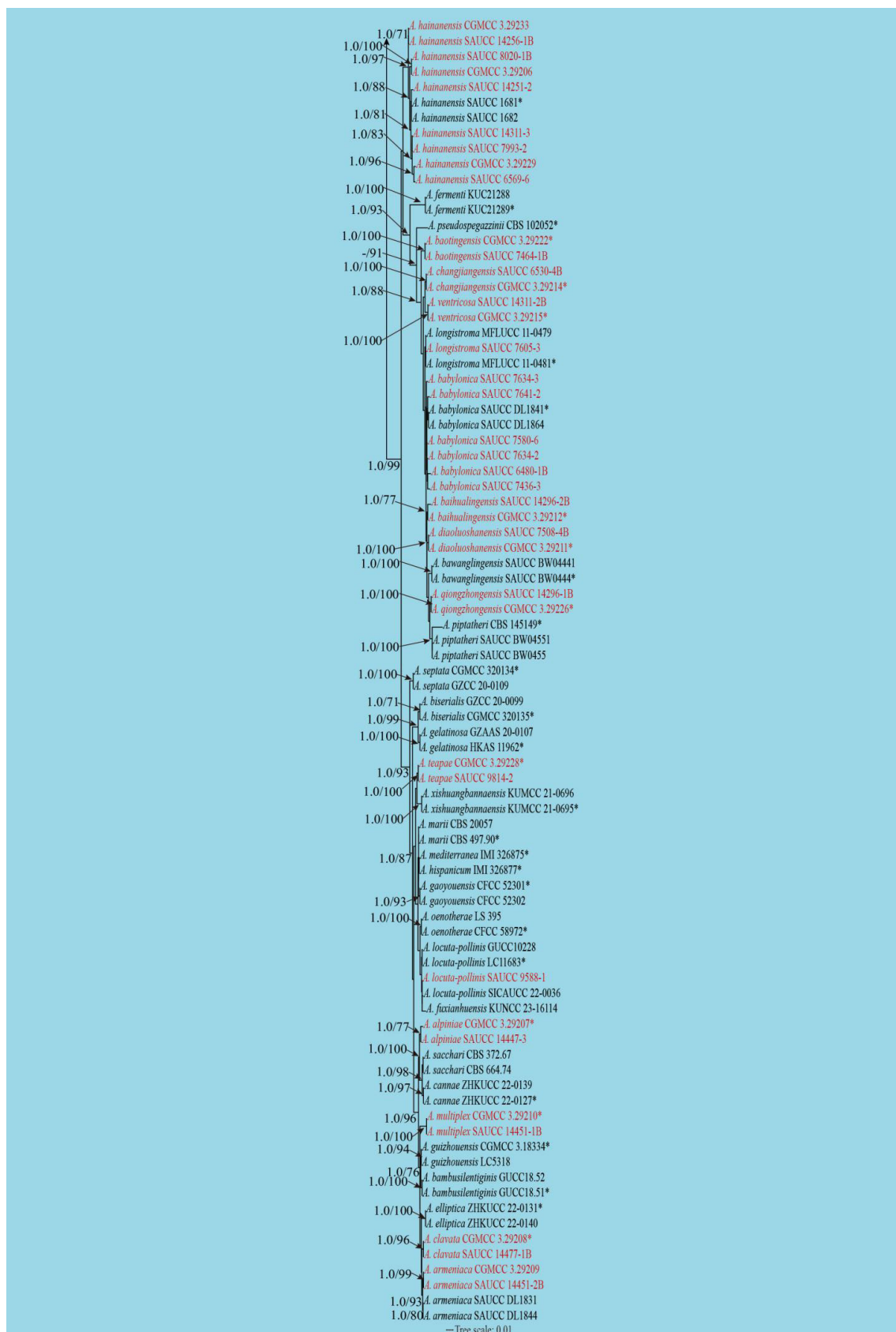


Fig. 1 Phylogenetic tree of the genus *Apiospora* based on the alignment of ITS, LSU, *tef1-α*, and *tub2* sequences, with *Arthrinium caricicola* serving as the outgroup. The Bayesian inference posterior probability (left, BIPP ≥ 0.90) and the maximum likelihood bootstrap value (right, MLBV ≥ 70%) are shown as BIPP/MLBV above the nodes. Strains marked "*" in the tree are represented as ex-type or ex-epitype. Strains in this study are highlighted in red. The scale bar at the bottom indicates 0.01 substitutions per site. Furthermore, four single-gene trees were evaluated for *Apiospora* (Supplementary Information 10).

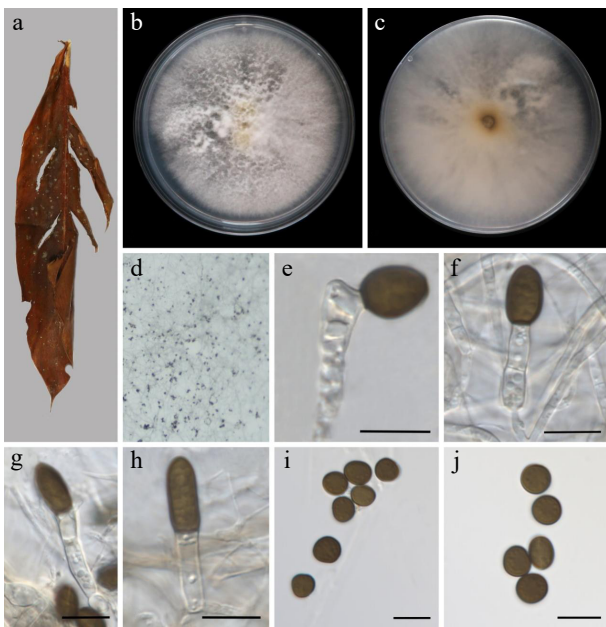


Fig. 2 *Apiospora alpiniae* (CGMCC 3.29207, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; top view (b) and bottom view (c). (d) Conidiomata formed in culture. (e–h) Conidia developed from conidiogenous cells. (i, j) Conidia. Scale bars: 10 µm (e–j).

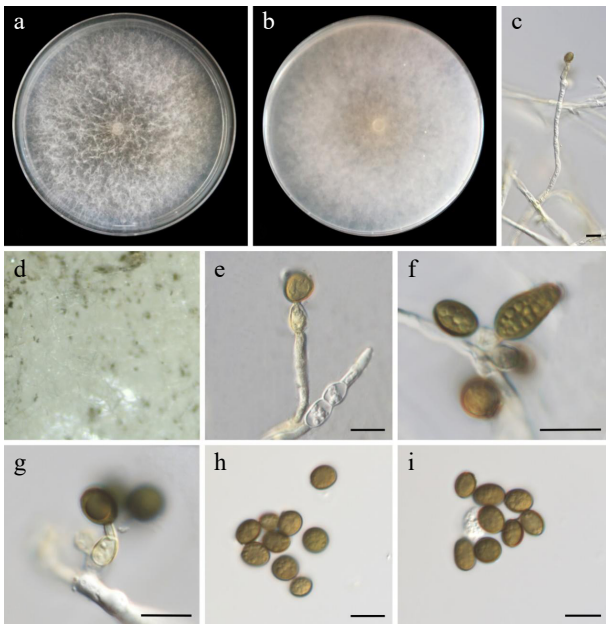


Fig. 3 *Apiospora baihualingensis* (CGMCC 3.29212, ex-type culture). (a, b) Colonies after incubation on PDA for 7 days; top view (a) and bottom view (b). (d) Conidiomata formed in culture. (c, e) Conidiophores and conidiogenous cells giving rise to conidia. (f, g) Conidia developed from conidiogenous cells. (h, i) Conidia. Scale bars: 10 µm (e–i).

Morphologically, *A. baotingensis* differs significantly from *A. changjiangensis* in having longer conidiogenous cells ($8.1\text{--}18.0 \times 1.7\text{--}2.7$ vs. $3.66\text{--}12.53 \times 1.23\text{--}4.75$ µm), and *A. baotingensis* possesses sterile cells. Thus, we described *A. baotingensis* as a new species.

Apiospora yinggelingensis Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. **Fig. 5**
Fungal names: FN 573277

Etymology – The epithet “yinggelingensis” refers to the location where the type was collected, Yinggeling National Forest Park, Hainan Province.

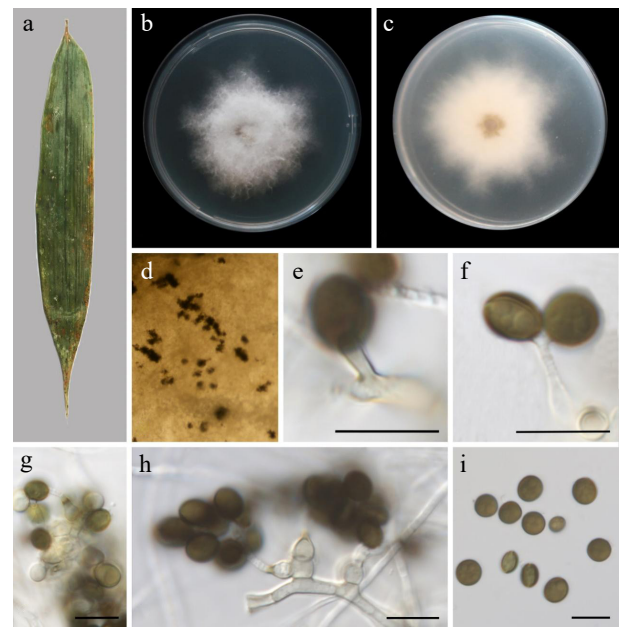


Fig. 4 *Apiospora baotingensis* (CGMCC 3.29222, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; top view (b) and bottom view (c). (d) Conidiomata formed in culture. (e–h) Conidia developed from conidiogenous cells. (i) Conidia. Scale bars: 10 µm (e–i).

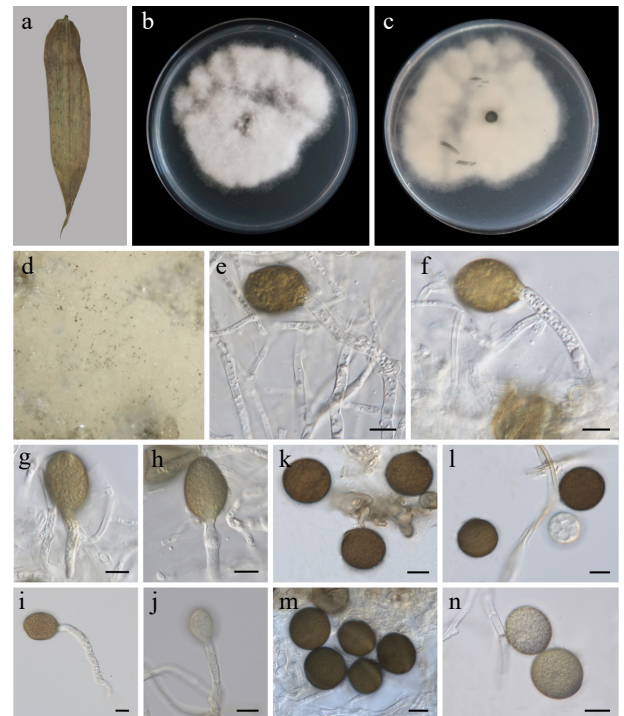


Fig. 5 *Apiospora yinggelingensis* (CGMCC 3.29235, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; top view (b) and bottom view (c). (d) Conidiomata formed in culture. (e–j) Conidia developed from conidiogenous cells. (k–n) Conidia. Scale bars: 10 µm (e–n).

On diseased bamboo leaves. Asexual morph: *hyphae* $1.9\text{--}5.7$ µm diameter, micronematous, hyaline, branched, thick-walled, septate, guttulate. *Conidiophores* are cylindrical, septate, verrucose and flexuous, and are occasionally reduced to conidiogenous cells. *Conidiogenous cells* $3.2\text{--}7.8$ µm diameter (av. = 4.85 ± 1.46 , $n = 19$),

arise from hyphae; they are holoblastic, monoblastic, hyaline, cylindrical, straight, aseptate and smooth-walled. *Conidia* $13.5\text{--}21.3 \times 15.5\text{--}23.9 \mu\text{m}$ diameter (av. = $19.0 \pm 1.9 \times 20.1 \pm 1.8 \mu\text{m}$, $n = 35$), globose to subglobose, aseptate, smooth, hyaline to dark brown from immature to mature, with a pale equatorial slit.

Culture characteristics – The colony surfaces are white, flat, spreading, filiform, with abundant aerial mycelia and reverse pale yellow on the PDA medium. The diameter of the colony was 64.5 mm after culturing for 7 days at 25 °C.

Material examined – China, Hainan Province, Changjiang Li Autonomous County, Yinggeling National Forest Park (19.117621 N, 109.150697 E, 650.05 m), on diseased bamboo leaves (Poaceae sp.), 11 April 2023, J. Zhang (HSAUP 3634-2A, holotype), ex-type culture CGMCC 3.29235 = SAUCC 3634-2A; *ibid.*, HSAUP 3634-2B, living culture SAUCC 3634-2B.

Distribution – China, Hainan Province.

Ecology – Associated with diseased leaves of bamboo (Poaceae sp.).

Notes – Phylogenetic analysis indicated that the two strains of *A. bawanglingensis* sp. nov. were clustered in a separate clade, exhibiting a close relationship with *A. hyphopodii*. The nucleotide differences in the ITS gene regions between our strains and *A. hyphopodii* (MFLUCC 15-0003, ex-type) are 8/507 bp. Morphologically, our isolates differ significantly from *A. hyphopodii* (MFLUCC 15-0003, ex-type) in possessing wider conidiogenous cells ($3.2\text{--}7.8$ vs. $2\text{--}3.5 \mu\text{m}$) and larger conidia ($13.5\text{--}21.3 \times 15.5\text{--}23.9$ vs. $5\text{--}10 \times 4\text{--}8 \mu\text{m}$). Mature conidia of *A. yinggelingensis* exhibit a color spectrum ranging from hyaline to dark brown. *Arthrinium hyphopodii* was originally identified in the bamboo of Yunnan Province, China^[6]. It was subsequently synonymized under *A. hyphopodii* based on phylogenetic evidence^[25]. Thus, we described *A. yinggelingensis* as a new species.

Apiospora campsidis Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. Fig. 6

Fungal names: FN 573278

Etymology – The epithet "*campsidis*" refers to the host of the holotype, specifically *Campsis radicans*.

On diseased *Campsis radicans* leaves. Asexual morph: *hyphae* $1.6\text{--}3.9 \mu\text{m}$ diameter, micronematous, hyaline to pale brown, branched, thick-walled, septate. *Conidiophores* $13.98\text{--}39.36 \times 2.37\text{--}4.50 \mu\text{m}$ (av. = $24.49 \pm 8.59 \times 3.50 \pm 0.62 \mu\text{m}$, $n = 10$), hyaline, septate, smooth, and thin-walled. *Conidiophores* are reduced to conidiogenous cells. *Conidiogenous cells* $7.41\text{--}16.49 \times 2.97\text{--}5.96 \mu\text{m}$ (av. = $10.47 \pm 3.43 \times 4.30 \pm 0.77 \mu\text{m}$, $n = 14$) arising from hyphae, holoblastic or polyblastic, hyaline to pale brown, cylindrical, straight, smooth-walled. *Conidia* $14.26\text{--}21.12 \times 8.96\text{--}17.29 \mu\text{m}$ (av. = $16.31 \pm 2.03 \times 17.29 \pm 2.21 \mu\text{m}$, $n = 18$), globose, ellipsoidal to cylindrical, aseptate, hyaline to dark brown from immature to mature, smooth, guttulate, without the pale equatorial slit.

Culture characteristics – Colonies on PDA mycelium moderate, spreading, margin irregular, surface and reverse white to pale brown. The diameter of the colony was 44.2–57.2 mm after culturing for 7 days at 25 °C.

Material examined – China, Fujian Province, Wuyishan City (27.644737 N, 117.883815 E, 239.5 m), on diseased *Campsis radicans* leaves (Bignoniaceae sp.), 20 October 2024, Q.Y. Liu (HSAUP 11198-2A, holotype), ex-type culture CGMCC 3.29234 = SAUCC 11198-2A; *ibid.*, HSAUP 11198-2B, living culture SAUCC 11198-2B.

Distribution – China, Fujian Province.

Ecology – Associated with diseased leaves of *Campsis radicans*.

Notes – *Apiospora campsidis* (SAUCC 11198-2A, ex-type) was found to be phylogenetically related to *A. ovata* (CBS 115042, ex-type). Two species showed nucleotide differences in the ITS (19/479 bp), LSU (2/750 bp), *tef1-α* (64/428 bp), and *tub2* (34/396 bp) gene regions. Morphologically, *A. campsidis* can be distinguished from *A.*

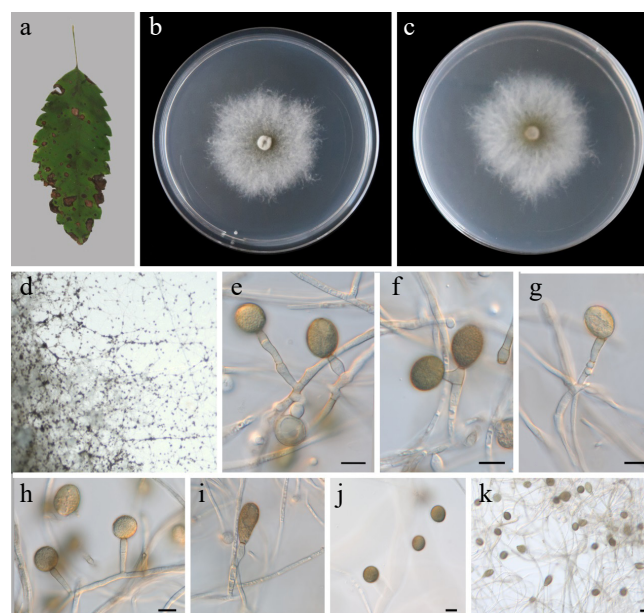


Fig. 6 *Apiospora campsidis* (CGMCC 3.29234, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; top view (b) and top view (c). (d) Conidiomata formed in culture. (e–g, i) Conidiophores and conidiogenous cells giving rise to conidia. (h) Conidia developed from conidiogenous cells. (j) Conidia. (k) Hyphae and conidia. Scale bars: 10 μm (e–k).

ovata by its smaller conidiophores ($13.98\text{--}39.36 \times 2.37\text{--}4.50$ vs. $60 \times 5\text{--}7 \mu\text{m}$). Additionally, the difference between *A. campsidis* and *A. ovata* lies in the fact that the conidial morphologies of *A. campsidis* range from globose, ellipsoidal to cylindrical, while those of *A. ovata* range from oval to broadly ellipsoid. *Apiospora ovata* produces sterile cells and medium brown conidia, whereas *A. campsidis* lacks sterile cells and develops hyaline to dark brown conidia at maturity. *Arthrinium ovatum* was originally identified by Crous and Groenewald^[22] from *Arundinaria hindsii* in Hong Kong, China. It was subsequently synonymized under *A. ovata* based on phylogenetic evidence^[25]. Thus, we described this fungus as a new species.

Apiospora changjiangensis Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. Fig. 7
Fungal names: FN 573279

Etymology – The epithet "*changjiangensis*" refers to the geographical location of the holotype, specifically Changjiang Li Autonomous County.

On PDA. Asexual morph: *hyphae* $1.17\text{--}3.31 \mu\text{m}$ diameter, hyaline, branched, thick-walled, septate, guttulate. *Conidiophores* are reduced to conidiogenous cells. *Conidiogenous cells* $3.66\text{--}12.53 \times 1.23\text{--}4.75 \mu\text{m}$ (av. = $6.97 \pm 2.64 \times 2.57 \pm 1.07 \mu\text{m}$, $n = 22$), holoblastic, hyaline, ampulliform or cylindrical, straight or pale curved, aseptate, smooth-walled. *Conidia* $5.39\text{--}7.79 \times 4.04\text{--}6.96 \mu\text{m}$ (av. = $6.67 \pm 0.57 \times 5.66 \pm 0.78 \mu\text{m}$, $n = 37$), globose to subglobose, aseptate, brown, smooth to slightly rough, with a pale equatorial slit.

Culture characteristics – Colonies on PDA mycelium moderate, margin undulate, surface and reverse white to pale orange. The diameter of the colony was 59.16–75.00 mm after culturing for 7 days at 25 °C.

Material examined – China, Hainan Province, Changjiang Li Autonomous County, Bawangling National Forest Park (19.0859333 N, 109.122752 E, 462 m), on diseased leaves of bamboo (Poaceae sp.), 14 October 2023, Q.Y. Liu (HSAUP 6530-4A, holotype), ex-type culture CGMCC 3.29214 = SAUCC 6530-4A; *ibid.*, HSAUP 6530-4B, living culture SAUCC 6530-4B.

Distribution – China, Hainan Province.

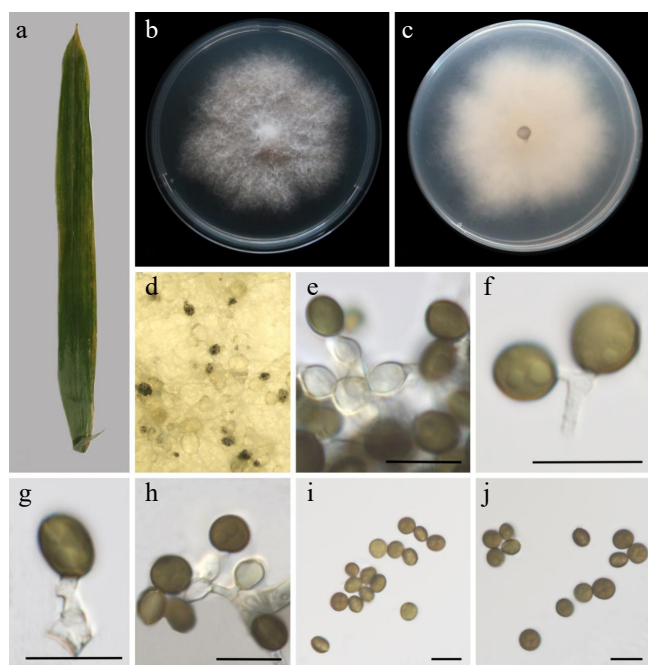


Fig. 7 *Apiospora changjiangensis* (CGMCC 3.29214, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; top view (b) and bottom view (c). (d) Conidiomata formed in culture. (e–h) Conidia developed from conidiogenous cells. (i, j) Conidia. Scale bars: 10 µm (e–j).

Ecology – Associated with diseased bamboo leaves (Poaceae sp.).

Notes – *Apiospora changjiangensis* (SAUCC 6530-4A, ex-type) was found to be phylogenetically related to *A. ventricosa* (SAUCC 14311-2A, ex-type). Two species showed nucleotide differences in the ITS (2/520 bp), LSU (2/744 bp), *tef1-α* (11/423 bp), and *tub2* (2/386 bp) gene regions. Morphologically, *A. changjiangensis* differs significantly from *A. ventricosa* (SAUCC 14311-2A, ex-type) in possessing larger conidiogenous cells ($3.66\text{--}12.53 \times 1.23\text{--}4.75$ vs. $2.65\text{--}5.06 \times 2.55\text{--}3.61$ µm), and *A. changjiangensis* has conidiophores, which are reduced to conidiogenous cells. Thus, *Apiospora changjiangensis* was described as a new species.

Apiospora clavata Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. **Fig. 8**

Fungal names: FN 573280

Etymology – the epithet "*clavata*" refers to the clavate conidia.

On PDA. Asexual morph: *hyphae* $1.53\text{--}3.75$ µm diameter, hyaline to pale yellow, branched, thick-walled, guttulate, septate. *Conidiophores* $18.53\text{--}126.98 \times 2.09\text{--}4.66$ µm (av. = $65.73 \pm 40.47 \times 2.98 \pm 0.96$ µm, $n = 16$), hyaline, unbranched, straight or flexuous, verrucose, septate. *Conidiogenous cells* $3.35\text{--}12.57 \times 1.93\text{--}5.02$ µm (av. = $7.85 \pm 3.09 \times 3.62 \pm 0.84$ µm, $n = 16$), polyblastic, hyaline, cylindrical-clavate, straight, aseptate, smooth-walled. *Conidia* $5.82\text{--}21.11 \times 3.41\text{--}7.99$ µm (av. = $8.09 \pm 3.01 \times 6.23 \pm 0.99$ µm, $n = 42$), globose, subglobose to clavate, aseptate, dark brown, smooth to slightly rough, guttulate, without the pale equatorial slit.

Culture characteristics – The colony surfaces are white, flat, with abundant aerial mycelia and reverse white on the PDA medium. The diameter of the colony was 90 mm after culturing at 7 days at 25 °C.

Material examined – China, Hainan Province, Ledong Li Autonomous County, Jianfengling National Forest Park (18.700142 N, 108.812270 E, 126 m), on diseased leaves of *Bambusa multiplex* f. *livida*, 4 December 2024, Q.Y. Liu (HSAUP 14477-1A), ex-type culture CGMCC 3.29208 = SAUCC 14477-1A; *ibid.*, HSAUP 14477-1B, living culture SAUCC 14477-1B.

Distribution – China, Hainan Province.

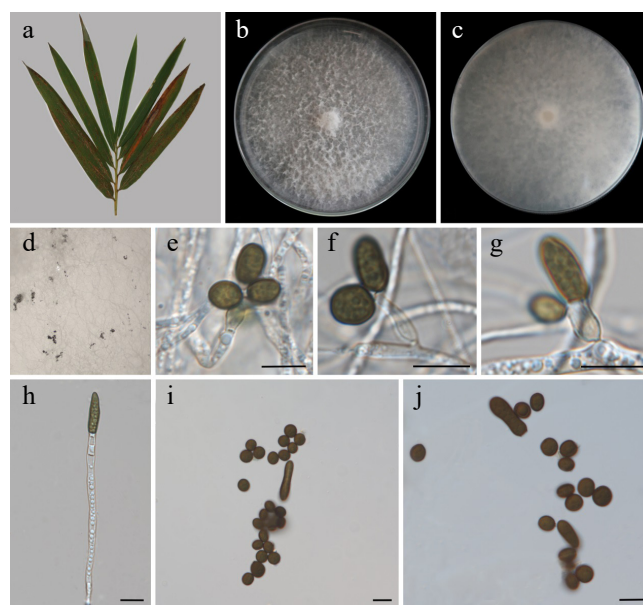


Fig. 8 *Apiospora clavata* (CGMCC 3.29208, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; top view (b) and bottom view (c). (d) Conidiomata formed in culture. (e–g) Conidia developed from conidiogenous cells. (h) Conidia developed from conidiophores. (i, j) Conidia. Scale bars: 10 µm (e–j).

Ecology – Associated with diseased leaves of *Bambusa multiplex* f. *livida*.

Notes – *Apiospora clavata* belongs to the large clade, and it shows a relationship with *A. armeniaca*. *Apiospora clavata* differs from *A. armeniaca* (SAUCC DL1831, ex-type) in having differently shaped (globose, subglobose to clavate vs. globose to subglobose to lenticular) and larger conidia ($5.82\text{--}21.11 \times 3.41\text{--}7.99$ vs. $6.2\text{--}7.3 \times 4.8\text{--}6.1$ µm), longer conidiogenous cells ($3.35\text{--}12.57 \times 1.93\text{--}5.02$ vs. $5.3\text{--}6.8 \times 4.1\text{--}5.6$ µm), and 8 fixed nucleotide differences in the *tef1-α* gene (8/383 bp)^[62]. Therefore, we introduced *A. clavata* as a new species.

Apiospora danzhouensis Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. **Fig. 9**

Fungal names: FN 573281

Etymology – The epithet "*danzhouensis*" refers to the geographical origin of the strains, namely, Danzhou City, Hainan Province.

On diseased bamboo leaves. Asexual morph: *hyphae* $1.23\text{--}6.39$ µm diameter, hyaline, branched, thick-walled, septate or aseptate. *Conidiophores* are reduced to conidiogenous cells. *Conidiogenous cells* $6.31\text{--}23.81 \times 1.16\text{--}4.07$ µm (av. = $13.63 \pm 5.48 \times 2.57 \pm 0.79$ µm, $n = 20$) aggregated in clusters on hyphae, holoblastic, hyaline or medium brown, cylindrical, straight or curved, aseptate, smooth-walled. *Conidia* $12.13\text{--}20.72 \times 6.97\text{--}15.80$ µm (av. = $15.64 \pm 1.91 \times 12.81 \pm 1.56$ µm, $n = 38$), globose to cylindric-clavate, aseptate, dark brown, smooth to slightly rough, guttulate, hyaline, transitioning to pale brown and becoming dark brown when fully mature, without a central scar.

Culture characteristics – The colony surfaces are white, woolly, flat, spreading, filiform, with abundant aerial mycelia, margin lightly sparse and reverse yellowish white on the PDA medium. The diameter of the colony was 74.85–77.32 mm after culturing at 7 days at 25 °C.

Material examined – China, Hainan Province, Danzhou City, Hainan Tropical Botanical Garden (19.511933 N, 109.500840 E, 108 m), on diseased bamboo leaves (Poaceae sp.), 15 October 2023, H.D. Li (HSAUP 6688-4, holotype), ex-type culture CGMCC 3.29204 = SAUCC 6688-4; China, Hainan Province, Changjiang Li Autonomous County, Bawangling National Forest Park (19.085933 N, 109.122752

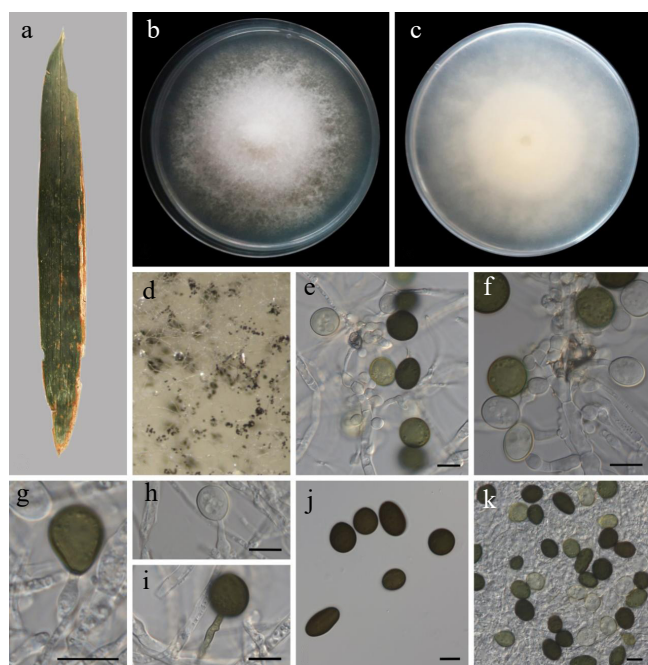


Fig. 9 *Apiospora danzhouensis* (CGMCC 3.29204, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; top view (b) and bottom view (c). (d) Conidiomata formed in culture. (e–i) Conidia developed from conidiogenous cells. (j, k) Conidia. Scale bars: 10 µm (e–k).

E, 462.68 m), on diseased bamboo leaves (Poaceae sp.), 14 October 2023, W.W. Liu, HSAUP 6580-3, living culture SAUCC 6580-3; *ibid.*, HSAUP 6580-2, living culture SAUCC 6580-2.

Distribution – China, Hainan Province.

Ecology – Associated with diseased bamboo leaves (Poaceae sp.).

Notes – *Apiospora danzhouensis* (SAUCC 6688-4, ex-type) was found to be phylogenetically related to *A. hydei* (CBS 114990, ex-type). The two species showed nucleotide differences in the *tef1-α* (13/405 bp) and *tub2* (3/379 bp) gene regions. Morphologically, *A. danzhouensis* differs from *A. hydei* in having wider hyphae (1.23–6.39 µm, hyaline vs. 2–3 µm, hyaline to pale brown), longer conidiogenous cells (6.31–23.81 × 1.16–4.07 vs. 5–8 × 4–5 µm), and bigger conidia (12.13–20.72 × 6.97–15.80 µm, without a central scar vs. (15–)17–19(–22) µm diameter in surface view and (10–)11–12(–14) µm diameter in side view, with a central scar)^[22]. Thus, we described this fungus as a new species.

Apiospora diaoluoshanensis Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. Fig. 10

Fungal Names: FN 573282

Etymology – The epithet "*diaoluoshanensis*" refers to the geographical location of the holotype, specifically Diaoluoshan National Forest Park, Hainan Province.

On PDA. Asexual morph: *hyphae* 2.15–3.42 µm diameter, hyaline, branched, thick-walled, septate, guttulate. *Conidiophores* 44.77–79.38 × 2.77–4.20 µm (av. = 58.68 ± 18.27 × 3.65 ± 0.76 µm, *n* = 8), hyaline, branched or unbranched, straight or flexuous, smooth, guttulate, aseptate. *Conidiophores* are occasionally reduced to conidiogenous cells. *Conidiogenous cells* 1.83–9.29 × 1.72–3.70 µm (av. = 6.11 ± 2.77 × 3.12 ± 0.82 µm, *n* = 15), sometimes from hyphae, holoblastic, hyaline, cylindrical, straight, aseptate, smooth-walled, guttulate. *Conidia* 5.71–10.10 × 3.75–7.15 µm (av. = 6.64 ± 0.93 × 5.48 ± 0.87 µm, *n* = 21), globose, subglobose to lenticular, aseptate, hyaline, pale brown to dark brown, immature to mature, smooth to slightly rough, guttulate, with a pale equatorial slit.

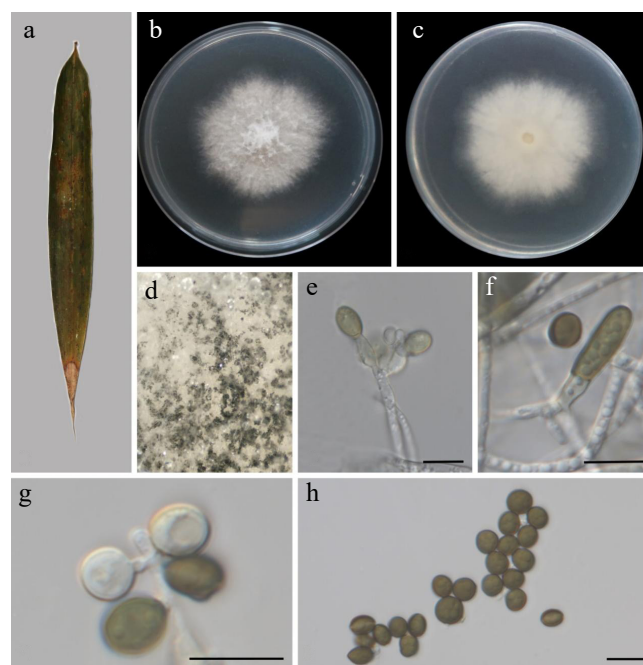


Fig. 10 *Apiospora diaoluoshanensis* (CGMCC 3.29211, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; top view (b) and bottom view (c). (d) Conidiomata formed in culture. (e) Conidiophores and conidiogenous cells giving rise to conidia. (f, g) Conidia developed from conidiogenous cells. (h) Conidia. Scale bars: 10 µm (e–h).

Culture characteristics – Colonies on PDA mycelium moderate, margin entire, surface and reverse white. The diameter of the colony was 44.2–57.2 mm after culturing at 7 days at 25 °C.

Material examined – China, Hainan Province, Diaoluoshan National Forest Park (18.660546 N, 109.936445 E, 94 m), on diseased leaves of bamboo (Poaceae sp.), 27 March 2024, M.Y. Zhang (HSAUP 7508-4A, holotype), ex-type culture CGMCC 3.29211 = SAUCC 7508-4A; *ibid.*, HSAUP 7508-4B, living culture SAUCC 7508-4B.

Distribution – China, Hainan Province.

Ecology – Associated with diseased bamboo leaves (Poaceae sp.).

Notes – See the notes of *Apiospora baihualingensis*.

Apiospora dryopteris Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. Fig. 11
Fungal names: FN 573283

Etymology – The epithet "*dryopteris*" refers to the host of the holotype, specifically *Dryopteris fuscipes*.

On diseased leaves of *Dryopteris fuscipes*. Asexual morph: *hyphae* 1.8–3.2 µm diameter, hyaline, branched, thick-walled, septate. *Conidiophores* 20.65–42.75 × 1.72–4.65 µm (av. = 29.09 ± 8.11 × 3.83 ± 0.91 µm, *n* = 10), hyaline, flexuous, branched, aseptate, smooth and thin-walled. *Conidiogenous cells* 4.27–19.07 × 2.52–5.89 µm (av. = 11.04 ± 3.44 × 4.10 ± 1.09 µm, *n* = 23), holoblastic or polyblastic, hyaline to pale brown, cylindrical or ampulliform, straight or flexuous, smooth-walled. *Conidia* 9.57–23.32 × 5.57–10.11 µm (av. = 12.25 ± 3.11 × 7.97 ± 1.47 µm, *n* = 27), globose to cylindric-clavate, aseptate, pale brown to dark brown from immature to mature, smooth, guttulate, with a pale equatorial slit.

Culture characteristics – Colonies on PDA mycelium abundant, margin entire, floccose, surface white, and reverse pale yellow. The diameter of the colony was 90 mm after culturing at 7 days at 25 °C.

Material examined – China, Yunnan Province, Yuxi City, Yulongma Mountain Scenic Area (24.418646 N, 102.606913 E, 2270 m), on diseased leaves of *Dryopteris fuscipes*, 12 May 2024, Q.Y. Liu (HSAUP 8289-2A, holotype), ex-type culture CGMCC 3.29219 = SAUCC 8289-2A; *ibid.*, HSAUP 8289-2B, living culture SAUCC 8289-2B.

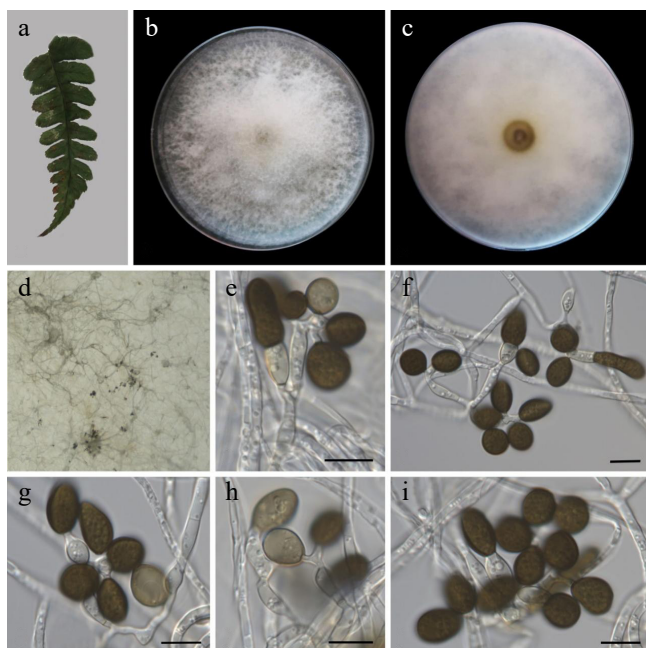


Fig. 11 *Apiospora dryopteris* (CGMCC 3.29219, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days from above (b) and below (c). (d) Conidiomata formed in culture. (e–i) Conidia developed from conidiophores and conidiogenous cells. Scale bars: 10 μ m (e–i).

Distribution – China, Yunnan Province.

Ecology – Associated with diseased leaves of *Dryopteris fuscipes*.

Notes – *Apiospora dryopteris* (SAUCC 8289-2A, ex-type) was found to be phylogenetically related to *A. wuyishanensis* (SAUCC 11013-4A, ex-type). *Apiospora dryopteris* differs from *A. wuyishanensis* (SAUCC 11013-4A, ex-type) in its production of significant conidia (globose to cylindric-clavate, $9.57\text{--}23.32 \times 5.57\text{--}10.11 \mu\text{m}$ vs. globose to ellipsoid, $8.32\text{--}10.75 \times 6.17\text{--}10.13 \mu\text{m}$). Two species showed nucleotide differences in the ITS (7/498 bp), LSU (1/737 bp), *tef1- α* (30/409), and *tub2* (24/395) gene regions. Thus, we described this fungus as a new species.

Apiospora elongata Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. **Fig. 12**

Fungal names: FN 573284

Etymology – The specific epithet refers to the elongated conidia.

On diseased bamboo leaves. Asexual morph: *hyphae* $2.2\text{--}4.4 \mu\text{m}$ diameter, hyaline, branched, thick-walled, septate or aseptate, guttulate. *Conidiophores* $57.03\text{--}82.42 \times 2.36\text{--}4.52 \mu\text{m}$ (av. = $73.34 \pm 7.93 \times 3.41 \pm 0.69 \mu\text{m}$, $n = 20$), hyaline, unbranched, straight or flexuous, smooth, guttulate, aseptate. *Conidiophores* are occasionally reduced to conidiogenous cells. *Conidiogenous cells* $9.92\text{--}25.92 \times 3.02\text{--}4.44 \mu\text{m}$ (av. = $15.35 \pm 4.95 \times 3.82 \pm 0.54 \mu\text{m}$, $n = 19$), holoblastic, hyaline, cylindrical, straight or flexuous, septate or aseptate, smooth-walled, guttulate. *Conidia* $10.77\text{--}28.09 \times 4.98\text{--}11.84 \mu\text{m}$ (av. = $18.32 \pm 5.37 \times 9.23 \pm 1.74 \mu\text{m}$, $n = 28$), obglobose to elongated, aseptate, pale brown to dark brown from immature to mature, slightly rough, guttulate, without a central scar.

Culture characteristics – The colony surfaces are white, flat, spreading, floccose, with abundant aerial mycelia, colony margin entire and reverse white on the PDA medium. The diameter of the colony was 90 mm after culturing for 7 days at 25°C .

Material examined – China, Yunnan Province, Yuxi City, Longma Mountain Scenic Area (24.418646 N, 102.606913 E, 2270 m), on diseased leaves of bamboo (Poaceae sp.), 12 May 2024, Q.Y. Liu (HSAUP 8305-4, holotype), ex-type culture CGMCC 3.29205 = SAUCC 8305-4; *ibid.*, HSAUP 8305-1, living culture SAUCC 8305-1.

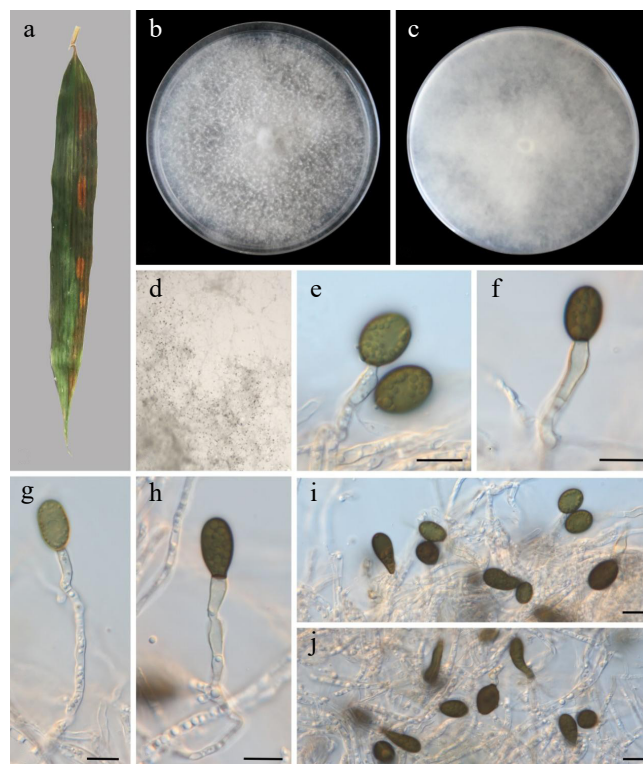


Fig. 12 *Apiospora elongata* (CGMCC 3.29205, ex-type culture). (a) Leaf of host plant. (b, c) Colonies after incubation on PDA for 7 days from above (b) and below (c). (d) Conidiomata formed in culture. (e, f) Conidia developed from conidiogenous cells. (g, h) Conidiophores, conidiogenous cells with conidia. (i, j) Conidia. Scale bars: 10 μ m (e–j).

Distribution – China, Yunnan Province.

Ecology – Associated with diseased bamboo leaves (Poaceae sp.).

Notes – *Apiospora elongata* (SAUCC 8305-4, ex-type) was found to be phylogenetically related to *A. shangrilaensis* (GMBC1019, ex-type). Two species showed nucleotide differences in the ITS (18/548 bp), LSU (4/733 bp), *tef1- α* (12/417 bp), and *tub2* (14/379 bp) gene regions. Morphologically, *A. shangrilaensis* has a confirmed sexual morph, but its asexual morph remains undetected^[116]. Thus, we introduced *A. elongata* as a new species.

Apiospora guangzhouensis Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. **Fig. 13**

Fungal names: FN 573285

Etymology – The specific epithet is derived from the Guangzhou City, Guangdong Province, China, where the holotype was collected.

On diseased bamboo leaves. Asexual morph: *hyphae* $1.67\text{--}3.43 \mu\text{m}$ diameter, hyaline, branched, thick-walled, septate, guttulate. *Conidiophores* $17.51\text{--}33.75 \times 1.51\text{--}3.72 \mu\text{m}$ (av. = $26.68 \pm 6.20 \times 2.84 \pm 0.6 \mu\text{m}$, $n = 17$), hyaline, macronematous, branched, straight or flexuous, smooth and thin-walled, hyaline. *Conidiophores* are occasionally reduced to conidiogenous cells. *Conidiogenous cells* $4.80\text{--}12.72 \times 2.20\text{--}3.86 \mu\text{m}$ (av. = $7.97 \pm 2.72 \times 2.74 \pm 0.53 \mu\text{m}$, $n = 18$), holoblastic, hyaline, cylindrical, straight, aseptate, smooth-walled. *Conidia* $5.41\text{--}10.94 \times 3.47\text{--}6.71 \mu\text{m}$ (av. = $6.71 \pm 1.29 \times 5.41 \pm 0.86 \mu\text{m}$, $n = 44$), globose to cylindric-clavate, aseptate, dark brown, smooth to slightly rough, without the pale equatorial slit.

Culture characteristics – The colony surfaces are pale brown, flat, spreading, filiform with thin aerial mycelium and reverse pale yellow on the PDA medium. The diameter of colony was 60 mm after culturing for 7 days at 25°C .

Material examined – China, Guangdong Province, Guangzhou City, Conghua District (19.005802 N, 109.825167 E, 392 m), on

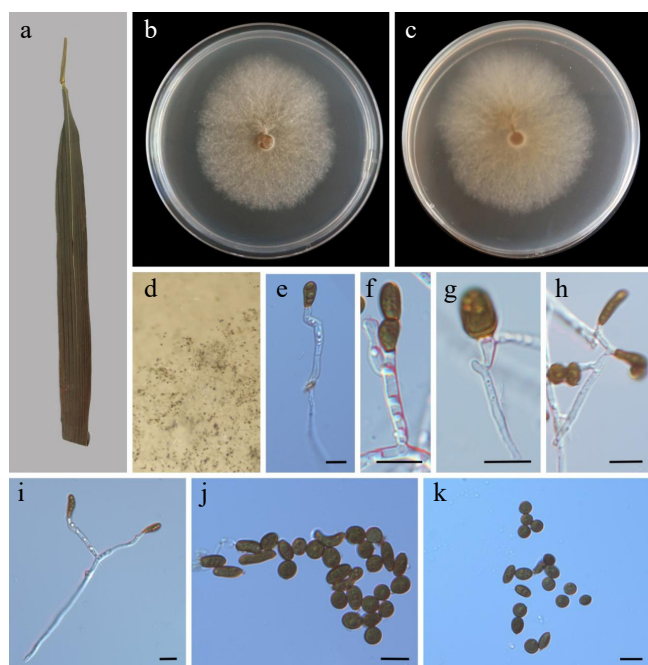


Fig. 13 *Apiospora guangzhouensis* (CGMCC 3.29201, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; top view (b) and bottom view (c). (d) Conidiomata formed in culture. (e, g, h) Conidiophores with conidiogenous cells and conidia. (f) Conidia masses developed from conidiogenous cells. (i) Conidiophores with conidia. j-k Conidia. Scale bars: 10 µm (e-k).

diseased bamboo leaves (*Poaceae* sp.), 1 March 2025, Q.Y. Liu (HSAUP 17273-3A, holotype), ex-type culture CGMCC 3.29201 = SAUCC 17273-3A; *ibid.*, HSAUP 17273-3B, living culture SAUCC 17273-3B.

Distribution – China, Guangdong Province.

Ecology – Associated with diseased leaves of bamboo (*Poaceae* sp.).

Notes – *Apiospora guangzhouensis* belongs to the large clade, where it shows relationships with *A. arundinis*, *A. guangdongensis*, and *A. senecionis*. *Apiospora guangzhouensis* and *A. arundinis* (GUCC6.1) showed nucleotide differences in the ITS (4/469 bp), *tef1-α* (18/406 bp), and *tub2* (8/341 bp) gene regions^[63]. *Apiospora guangzhouensis* differs from *A. guangdongensis* (ZHKUCC 23-0004, ex-type) in its production of significant conidiophores (branched, 17.51–33.75 × 1.51–3.72 µm vs. unbranched, 45–53 × 2–4 µm) and nucleotide differences in the ITS (4/469 bp), *tef1-α* (20/406 bp), and *tub2* (9/341 bp) gene regions^[66]. *Apiospora guangzhouensis* is distinct from *A. senecionis* (HKAS 127245, ex-type) in producing narrower conidiogenous cells (2.20–3.86 vs. 6–7 µm), smaller conidia (dark brown, 5.41–10.94 × 3.47–6.71 µm vs. golden yellow to light brown from immature to mature, 8–17 µm diameter), and nucleotide differences in the ITS (1/539 bp), LSU (1/320 bp), and *tub2* (28/796 bp) gene regions^[61]. Thus, we described this fungus as a new species.

Apiospora pseudosasa Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. **Fig. 14**
Fungal names: FN 573287

Etymology – The epithet "*pseudosasa*" refers to the host of the holotype, specifically *Pseudosasa japonica*.

On diseased *Pseudosasa japonica* leaves. Asexual morph: *hyphae* 1.34–3.1 µm diameter, micronematous, hyaline, branched, thick-walled, septate or aseptate. *Conidiophores* 20.57–57.27 × 1.51–2.77 µm (av. = 37.04 ± 15.41 × 2.25 ± 0.62 µm, *n* = 9), hyaline, straight or flexuous, smooth and thin-walled, hyaline. *Conidiophores* are occasionally reduced to conidiogenous cells. *Conidiogenous cells*

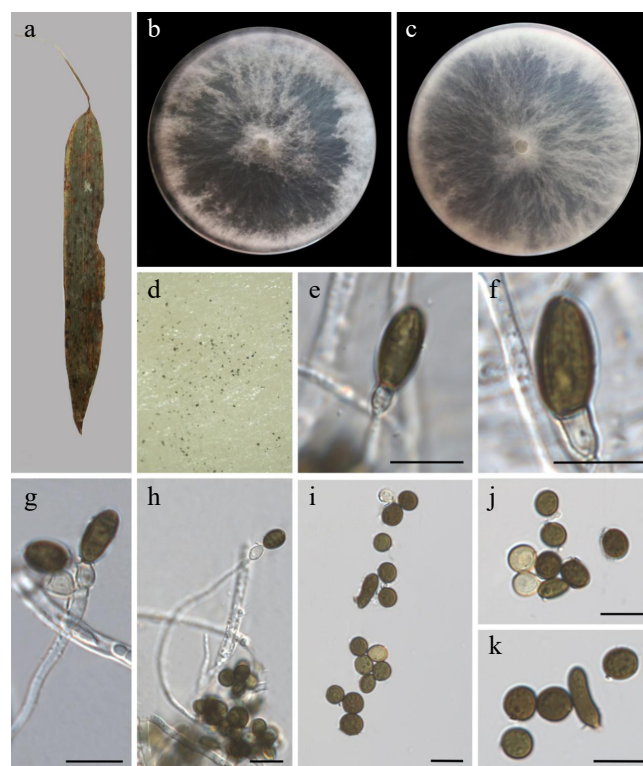


Fig. 14 *Apiospora pseudosasa* (CGMCC 3.29202, ex-type culture). a Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; top view (b) and bottom view (c). (d) Conidiomata formed in culture. (e, f) Conidia developed from conidiogenous cells. (g, h) Conidiophores with conidiogenous cells. (i–k) Conidia. Scale bars: 10 µm (e–k).

3.63–5.73 × 2.18–4.04 µm (av. = 4.67 ± 0.92 × 3.28 ± 0.61 µm, *n* = 11), holoblastic, hyaline, cylindrical, curved, aseptate, smooth-walled. *Conidia* 5.64–11.53 × 4.39–7.30 µm (av. = 6.88 ± 1.33 × 5.81 ± 0.73 µm, *n* = 28), globose to cylindric-clavate, aseptate, dark brown, smooth to slightly rough, guttulate, pale brown to dark brown from immature to mature with an equatorial germ slit.

Culture characteristics – On the PDA, dense, entire margin, aerial mycelium white, crateriform, and reverse white. The diameter of colony was 90 mm after culturing for 7 days at 25 °C.

Material examined – China, Hainan Province, Diaoluoshan National Forest Park (18.678618 N, 109.948190 E, 150.62 m), on diseased *Pseudosasa japonica* leaves (*Poaceae* sp.), 27 March 2024, Q.Y. Liu (HSAUP 7654-2, holotype), ex-type culture CGMCC 3.29202 = SAUCC 7654-2; *ibid.*, on diseased leaves of bamboo (*Poaceae* sp.), 27 March 2024, Z.X. Dong, HSAUP 7743-2, living culture SAUCC 7743-2; *ibid.*, Lingshui Li Autonomous County, Benhao Town (18.727155 N, 109.866009 E, 944 m), on diseased leaves of bamboo (*Poaceae* sp.), 09 April 2023, J. Zhang, HSAUP 3099A-4, living culture SAUCC 3099A-4; *ibid.*, Diaoluoshan National Forest Park (18.678618 N, 109.948190 E, 150.62 m), on diseased leaves of bamboo (*Poaceae* sp.), 06 March 2025, Q.Y. Liu, HSAUP 16730-2, living culture SAUCC 16730-2.

Distribution – China, Hainan Province.

Ecology – Associated with diseased leaves of bamboo (*Poaceae* sp.).

Notes – *Apiospora pseudosasa* belongs to the large clade, where it shows a relationship with *A. bambusicaulis*, *A. jinanensis*, *A. italica*, and *A. thailandica*. *Apiospora pseudosasa* is distinct from *A. bambusicaulis* (GUCC17.41, ex-type) in producing longer conidiogenous cells (3.63–5.73 vs. 1.5–3.5 µm), having bigger conidia (5.64–11.53 × 4.39–7.30 vs. 4.5–6 × 5–6 µm), and in 57 nucleotide

differences (8/499 bp in ITS, 1/766 bp in LSU, 21/422 bp in *tef1-α*, 27/391 bp in *tub2*)^[63]. *Apiospora pseudosasa* differs from *A. jinanensis* (SAUCC DL1981, ex-type) in producing shorter and narrower conidiogenous cells ($3.63\text{--}5.73 \times 2.18\text{--}4.04$ vs. $5.6\text{--}7.9 \times 4.2\text{--}6.6$ μm) and in 52 nucleotide differences (9/500 bp in ITS, 1/766 bp in LSU, 21/423 bp in *tef1-α*, 21/392 bp in *tub2*) in the gene regions^[62]. *Apiospora pseudosasa* differs from *A. italica* (CBS 145138, ex-type) in its production of significantly larger conidia size ($5.64\text{--}11.53 \times 4.39\text{--}7.30$ vs. $4\text{--}6 \times 3\text{--}4$ μm) and the presence of nucleotide differences (25/422 bp in *tef1-α*, 29/392 bp in *tub2*)^[72]. *Apiospora pseudosasa* differs from *A. thailandica* (MFLUCC 15-0202, ex-type) in producing shorter and wider conidiogenous cells ($3.63\text{--}5.73 \times 2.18\text{--}4.04$ vs. $11.5\text{--}39 \times 2\text{--}3.5$ μm) and in the presence of nucleotide differences (9/499 bp in ITS). Sequence data for *tef1-α* and *tub2* genes were not available from strain MFLUCC 15-0202^[81]. Thus, we described this fungus as a new species.

Apiospora lingshuiensis Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. Fig. 15

Fungal names: FN 573289

Etymology – "*lingshuiensis*" refers to the place Lingshui, from where the holotype was collected.

On diseased leaves of bamboo. Asexual morph: *hyphae* 1.4–4.8 μm diameter, hyaline, branched, thick-walled, septate or aseptate, guttulate. *Conidiophores* $51.32\text{--}55.89 \times 1.55\text{--}3.76$ μm (av. = $53.60 \pm 3.23 \times 2.67 \pm 1.57$ μm, $n = 12$), hyaline, unbranched, straight or flexuous, smooth, aseptate, and are occasionally reduced to conidiogenous cells. *Conidiogenous cells* $1.37\text{--}31.59 \times 1.65\text{--}4.20$ μm (av. = $7.69 \pm 6.63 \times 2.82 \pm 0.71$ μm, $n = 22$), holoblastic or polyblastic, hyaline, cylindrical or doliiform, straight or flexuous, aseptate, smooth-walled. *Conidia* $6.71\text{--}14.69 \times 4.05\text{--}7.55$ μm (av. = $8.52 \pm 2.37 \times 5.79 \pm 1.04$ μm, $n = 21$), obglobose to cylindric-clavate, aseptate, pale brown to dark brown from immature to mature, slightly rough, with a central scar.

Culture characteristics – Colonies on PDA mycelium abundant, floccose, margin undulate, surface white and reverse white. The diameter of the colony was 70 mm after culturing for 7 days at 25 °C.

Material examined – China, Hainan Province, Lingshui Li Autonomous County, Diaoluoshan National Forest Park (18.7275498 N, 109.8640066 E, 972.81 m), on diseased leaves of bamboo (*Poaceae* sp.), 9 April 2023, X.Y. Liu (HSAUP 2919-2, holotype), ex-type culture CGMCC 3.29203 = SAUCC 2919-2; *ibid.*, 27 March 2024, M.Y. Zhang, HSAUP 7580-2, living culture SAUCC 7580-2; *ibid.*, 6 March 2024, Z.X. Dong, HSAUP 7733-3, living culture SAUCC 7733-3; *ibid.*, Y.L. Wang, HSAUP 17373-3, living culture SAUCC 17373-3; *ibid.*, Changjiang Li Autonomous County, Bawangling National Forest Park (19.0859333 N, 109.122752 E, 462.68 m), on diseased leaves of bamboo (*Poaceae* sp.), 14 October 2023, Q.Y. Liu, HSAUP 6569-5, living culture SAUCC 6569-5.

Distribution – China, Hainan Province.

Ecology – Associated with diseased leaves of bamboo (*Poaceae* sp.).

Notes – *Apiospora lingshuiensis* belongs to the large clade, where it shows a relationship with *A. chromolaenae*. *Apiospora lingshuiensis* differs from *A. chromolaenae* (MFLU 20-0300, ex-type) in its production of significant conidia ($6.71\text{--}14.69 \times 4.05\text{--}7.55$ vs. $4\text{--}6 \times 4.5\text{--}6.5$ μm), conidiogenous cells ($1.37\text{--}31.59 \times 1.65\text{--}4.20$ vs. $6.5\text{--}12 \times 1\text{--}2$ μm), and the presence of nucleotide differences (47/512 bp in ITS, 2/742 bp in LSU)^[117]. Thus, we described *A. lingshuiensis* as a new species.

Apiospora locuta-pollinis (F. Liu & L. Cai) Pintos & P. Alvarado, Fungal Systematics and Evolution 7: 207 (2021)

Synonym. *Apiospora fuxianhuensis* H.W. Shen & Z.L. Luo

Description. See Zhao et al.^[75] and Shen et al.^[80].

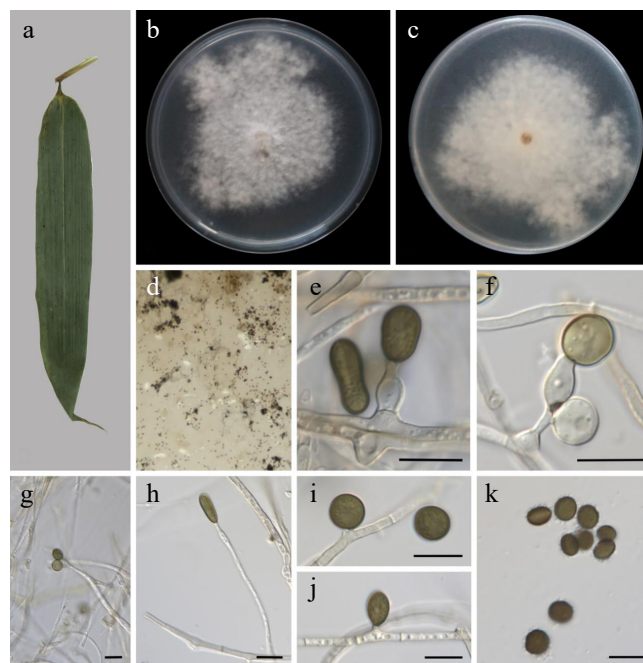


Fig. 15 *Apiospora lingshuiensis* (CGMCC 3.29203, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; top view (b) and bottom view (c). (d) Conidiomata formed in culture. (e, f, i, j) Conidia developed from conidiogenous cells. (g, h) Conidiophores and conidiogenous cells with conidia. (k) Conidia. Scale bars: 10 μm (e–k).

Notes – *Apiospora locuta-pollinis* was first described from Hubei Province, China. The strain of this species was isolated from *Brassica campestris*^[75]. Subsequently, *A. fuxianhuensis* was obtained from submerged decaying wood in Yunnan, China^[80]. Notably, they exhibit only minor sequence and morphology variations. *Apiospora fuxianhuensis* is designated as a synonym of *A. locuta-pollinis*.

Apiospora multiplex Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. Fig. 16

Fungal names: FN 573290

Etymology – The epithet "*multiplex*" refers to the host of the holotype, specifically *Bambusa multiplex*.

On diseased leaves of *Bambusa multiplex*. On PDA. Asexual morph: *hyphae* 1.77–4.67 μm diameter, hyaline, branched or unbranched, thick-walled, septate. *Conidiophores* mononematous, unbranched, straight or flexuous, smooth and thin-walled, septate, hyaline, and are occasionally reduced to conidiogenous cells. *Conidiogenous cells* $4.56\text{--}14.68 \times 2.63\text{--}7.65$ μm (av. = $9.90 \pm 3.31 \times 4.82 \pm 1.53$ μm, $n = 19$) from hyphae, holoblastic, hyaline, ampulliform or doliiform, straight, aseptate, smooth-walled. *Conidia* $5.17\text{--}9.09 \times 4.08\text{--}6.59$ μm (av. = $6.45 \pm 0.87 \times 5.28 \pm 0.60$ μm, $n = 28$), globose, subglobose to fusoid, aseptate, hyaline to dark brown from immature to mature, smooth to slightly rough, guttulate with a pale equatorial slit.

Culture characteristics – The colony surfaces are white, convex center and flat margins, floccose with abundant aerial mycelia, and reverse white on the PDA medium. The diameter of the colony was 90 mm after culturing for 7 days at 25 °C.

Material examined – China, Hainan Province, Ledong Li Autonomous County, Jianfengling National Forest Park (18.700142 N, 108.812270 E, 127 m), on diseased *Bambusa multiplex* leaves (*Poaceae* sp.), 4 December 2024, Q.Y. Liu (HSAUP 14451-1A, holotype), ex-type culture CGMCC 3.29210 = SAUCC 14451-1A; *ibid.*, HSAUP 14451-1B, living culture SAUCC 14451-1B.

Distribution – China, Hainan Province.



Fig. 16 *Apiospora multiplex* (CGMCC 3.29210, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; top view (b) and bottom view (c). (d) Conidiomata formed in culture. (e–g) Conidiogenous cells giving rise to conidia. (h) Conidia developed from conidiogenous cells. (i) Hyphae and conidia. (j) Conidia. Scale bars: 10 µm (e–j).

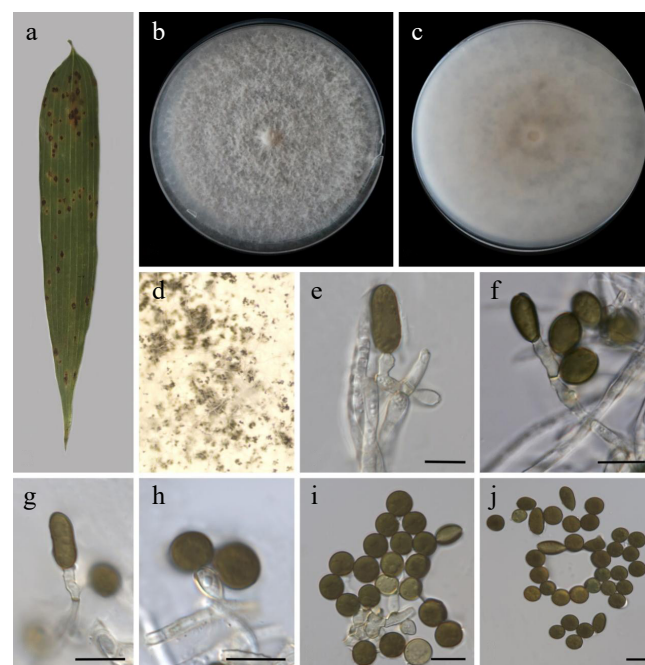


Fig. 17 *Apiospora pingtangensis* (CGMCC 3.29217, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; top view (b) and bottom view (c). (d) Conidiomata formed in culture. (e–h) Conidiophores and conidiogenous cells giving rise to conidia. (i) Conidia developed from conidiogenous cells. (j) Conidia. Scale bars: 10 µm (e–j).

Ecology – Associated with diseased leaves of *Bambusa multiplex* (Poaceae sp.).

Notes – *Apiospora multiplex* belongs to the large clade, where it shows a relationship with *A. guizhouensis*. Two species showed nucleotide differences in the ITS (1/518 bp), *tef1-α* (6/341 bp), and *tub2* (10/368 bp) gene regions. Morphologically, our isolates differ significantly from the ex-type strain of *A. guizhouensis* (LC5322, ex-type) in possessing larger conidiogenous cells ($4.56\text{--}14.68 \times 2.63\text{--}7.65$ vs. $3.5\text{--}8.0 \times 3.0\text{--}4.5$ µm)^[68]. *Arthrinium guizhouense* was originally identified from the air in karst cave in Guizhou Province^[68]. It was subsequently synonymized under *A. guizhouensis* based on phylogenetic evidence^[25]. Thus, we described *A. multiplex* as a new species.

Apiospora pingtangensis Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. **Fig. 17**
Fungal names: FN 573292

Etymology – The epithet "*pingtangensis*" refers to the location where the type was collected, Pingtang County.

On PDA. Asexual morph: *hyphae* 1.94–4.22 µm diameter, hyaline, branched, thick-walled, septate. *Conidiophores* 30.18–33.46 × 3.19–4.54 µm (av. = $31.82 \pm 2.32 \times 3.87 \pm 0.95$ µm, $n = 3$), hyaline, smooth, septate or aseptate, guttulate. *Conidiogenous cells* 3.13–13.13 × 2.24–3.81 µm (av. = $7.32 \pm 3.39 \times 2.95 \pm 0.60$ µm, $n = 16$), aggregated on hyphae or from conidiophores, holoblastic, hyaline, cylindrical, straight, aseptate, smooth-walled. *Conidia* 7.50–12.74 × 6.23–9.01 µm (av. = $8.86 \pm 1.42 \times 7.64 \pm 0.66$ µm, $n = 30$), globose to oblong elliptical, aseptate, pale brown to brown from immature to mature, smooth with a pale equatorial slit.

Culture characteristics – Colonies on PDA mycelium abundant, floccose, margin entire, surface white and reverse white to pale brown. The diameter of the colony was 90 mm after culturing for 7 days at 25 °C.

Material examined – China, Guizhou Province, Qiannan Buyi and Miao Autonomous Prefecture, Pingtang County, Kapu Maonan

Town (25.79510 N, 107.38631 E, 745 m), on diseased leaves of bamboo (Poaceae sp.), 23 August 2023, D.H. Li (HSAUP 5602-1A, holotype), ex-type culture CGMCC 3.29217 = SAUCC 5602-1A; *ibid.*, HSAUP 5602-1B, living culture SAUCC 5602-1B.

Distribution – China, Guizhou Province.

Ecology – Associated with diseased leaves of bamboo (Poaceae sp.).

Notes – *Apiospora pingtangensis* belongs to the large clade, where it shows a relationship with *A. cyclobalanopsidis*. *Apiospora pingtangensis* differs from *A. cyclobalanopsidis* (CGMCC 3.20136, ex-type) in its production of significant conidia ($7.50\text{--}12.74 \times 6.23\text{--}9.01$ vs. $8\text{--}12$ µm, $10\text{--}14$ µm) and conidiogenous cells ($3.13\text{--}13.13 \times 2.24\text{--}3.81$ vs. $6.0\text{--}19.0 \times 2.5\text{--}7.0$ µm) and the presence of 21 distinct nucleotide positions (12/412 bp in *tef1-α*, 9/392 bp in *tub2*)^[69]. *Arthrinium cyclobalanopsidis* was originally identified from *Cyclobalanopsidis glauca* in Guizhou Province, China^[69]. Subsequently, it was synonymized under *A. cyclobalanopsidis* after a phylogenetic analysis^[64]. Thus, *Apiospora pingtangensis* was described as a new species.

Apiospora qiongzongensis Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. **Fig. 18**

Fungal names: FN 573293

Etymology – The epithet "*qiongzongensis*" refers to the location where the type was collected, Qiongzong County.

Asexual morph: On PDA, *hyphae* 2.4–5.9 µm diameter, microne-matous, hyaline, smooth, branched, thick-walled, guttulate. *Conidio-phores* are occasionally reduced to conidiogenous cells. *Conidio-genous cells* 10.00–12.81 × 2.21–3.81 µm (av. = $11.52 \pm 1.16 \times 2.81 \pm 0.62$ µm), arising from hyphae, hyaline, cylindrical, straight or slightly flexuous, guttulate. *Conidia* 6.51–9.94 × 5.39–6.99 µm (av. = $7.81 \pm 1.12 \times 6.36 \pm 0.54$ µm, $n = 24$), smooth, pale brown to tanned, subglobose, ellipsoidal, aseptate, guttulate, smooth to slightly rough, with a thin germ slit.

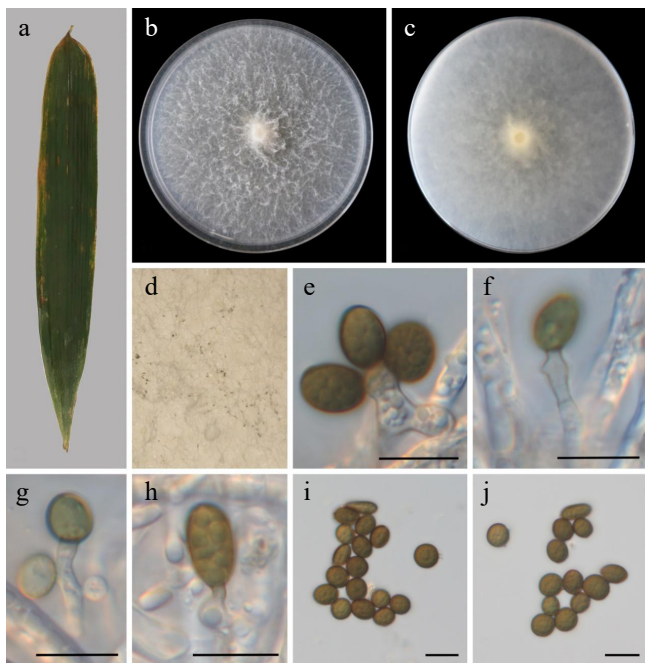


Fig. 18 *Apiospora qiongzhongensis* (CGMCC 3.29226, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; (b) top view and (c) bottom view. (d) Conidiomata formed in culture. (e–h) Conidia developed from conidiogenous cells. (i, j) Conidia. Scale bars: 10 µm (e–j).

Culture characteristics – The colony surfaces are white, flat, cottony, spreading, with filamentous margin, reverse similar in colour on the PDA medium. The diameter colony was 90 mm after culturing for 7 days at 25 °C.

Material examined – China, Hainan Province, Qiongzong Li and Miao Autonomous County, Baihualing Tropical Rainforest Tourism and Culture Zone (19.005802 N, 109.825167 E, 392 m), on diseased bamboo leaves (*Poaceae* sp.), 3 December 2024, Q.Y. Liu (HSAUP 14296-1A, holotype), ex-type culture CGMCC 3.29226 = SAUCC 14296-1A; *ibid.*, HSAUP 14296-1B, living culture SAUCC 14296-1B.

Distribution – China, Hainan Province.

Ecology – Associated with diseased leaves of bamboo (*Poaceae* sp.).

Notes – Based on phylogenetic analysis, the two isolates of the new species *A. qiongzhongensis* form an independent phylogenetic clade, which is closely related to *A. piptatheri*. *Apiospora qiongzhongensis* (SAUCC 14296-1A, ex-type) and *A. piptatheri* (CBS 145149, ex-type) showed nucleotide differences in the ITS (3/520 bp) and LSU (7/788 bp) gene regions. Morphologically, *A. qiongzhongensis* differs significantly from *A. piptatheri* in having shorter conidiogenous cells ($10.00\text{--}12.81 \times 2.21\text{--}3.81$ vs. $6\text{--}27 \times 2\text{--}5$ µm) and bigger conidia ($6.51\text{--}9.94 \times 5.39\text{--}6.99$ vs. $6\text{--}8 \times 3\text{--}5$ µm). No sterile cells were observed in *A. qiongzhongensis*. *Arthrinium piptatheri* was originally identified from *Piptatherum miliaceum* in Spain^[72]. It was subsequently synonymized under *A. piptatheri* based on phylogenetic evidence^[25]. Thus, we described *A. qiongzhongensis* as a new species. For details, see [Supplementary Information 11](#).

Apiospora renhuaensis Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. **Fig. 19**

Fungal names: FN 573294

Etymology – The epithet "*renhuaensis*" refers to the location where the type was collected, Renhua County.

On diseased leaves of bamboo. Asexual morph: *hyphae* 1.7–4.2 µm diameter, hyaline to pale brown, branched, thick-walled, septate. *Conidiophores* cylindrical, aseptate, flexuous, and are occasionally reduced to conidiogenous cells. *Conidiogenous cells*

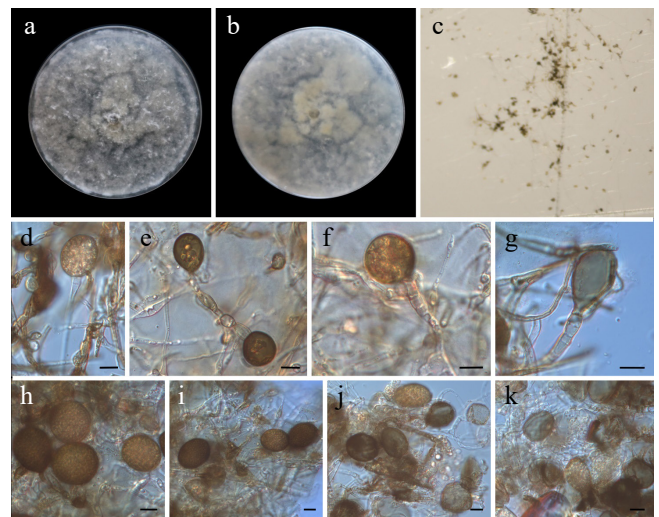


Fig. 19 *Apiospora renhuaensis* (CGMCC 3.29221, ex-type culture). (a, b) Colonies after incubation on PDA for 7 days; (a) top view and (b) bottom view. (c) Conidiomata formed in culture. (d–g) Conidiogenous cells with conidia and sterile cells. (h, i) Conidia. (j, k) Sterile cells. Scale bars: 10 µm (d–k).

$13.3\text{--}37.3 \times 3.7\text{--}6.5$ µm (av. = $21.7 \pm 7.5 \times 4.7 \pm 0.9$ µm, $n = 20$), holoblastic, hyaline to pale brown, cylindrical, straight, aseptate, smooth-walled. *Conidia* $18.4\text{--}30.6 \times 15.5\text{--}25.9$ µm diameter (av. = $25.3 \pm 3.4 \times 22.0 \pm 3.1$ µm, $n = 16$), globose to subglobose, aseptate, smooth, pale brown to dark brown from immature to mature, without the pale equatorial slit. *Sterile cells* pale brown, elongated ellipsoidal, $18\text{--}32 \times 15\text{--}22$ µm.

Culture characteristics – The colony surfaces are cream-colored, flat, floccose, aerial mycelia scant and reverse pale yellow on the PDA medium. The diameter of the colony was 90 mm after culturing for 7 days at 25 °C.

Material examined – China, Guangdong Province, Shaoguan City, Renhua County (25.087103 N, 113.743706 E, 106.2 m), on diseased bamboo leaves (*Poaceae* sp.), 11 April 2023, Y.L. Wang (HSAUP 17293-1A, holotype), ex-type culture CGMCC 3.29221 = SAUCC 17293-1A; *ibid.*, HSAUP 17293-1B, living culture SAUCC 17293-1B.

Distribution – China, Guangdong Province.

Ecology – Associated with diseased leaves of bamboo (*Poaceae* sp.).

Notes – Two isolates of the new species *A. renhuaensis* form an independent clade based on phylogenetic analysis, which is closely related to *A. anshunensis*. The two species showed nucleotide differences in the ITS (13/528 bp), LSU (2/760 bp), and *tub2* (18/384 bp) gene regions. Morphologically, *A. renhuaensis* differs significantly from *A. anshunensis* in its possession of sterile cells^[118]. Thus, we described *A. renhuaensis* as a new species.

Apiospora rutila Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. **Fig. 20**

Fungal names: FN 573295

Etymology – The epithet "*rutila*" refers to the host of the holotype, specifically *Bambusa rutila*.

On diseased leaves of *Bambusa rutila*. Asexual morph: *hyphae* 1.3–2.6 µm diameter, micronematous, hyaline to pale brown, branched, thick-walled, septate or aseptate. *Conidiophores* $20.57\text{--}57.27 \times 1.51\text{--}2.77$ µm (av. = $37.04 \pm 15.41 \times 2.25 \pm 0.62$ µm, $n = 9$), hyaline, straight or flexuous, septate, smooth and thin-walled, and are occasionally reduced to conidiogenous cells. *Conidiogenous cells* $4.39\text{--}13.76 \times 2.37\text{--}7.43$ µm (av. = $11.05 \pm 3.77 \times 3.64 \pm 2.13$ µm, $n = 17$), arising from hyphae, holoblastic, hyaline, cylindrical, curved, septate or aseptate, smooth-walled. *Conidia* $10.53\text{--}19.52 \times$

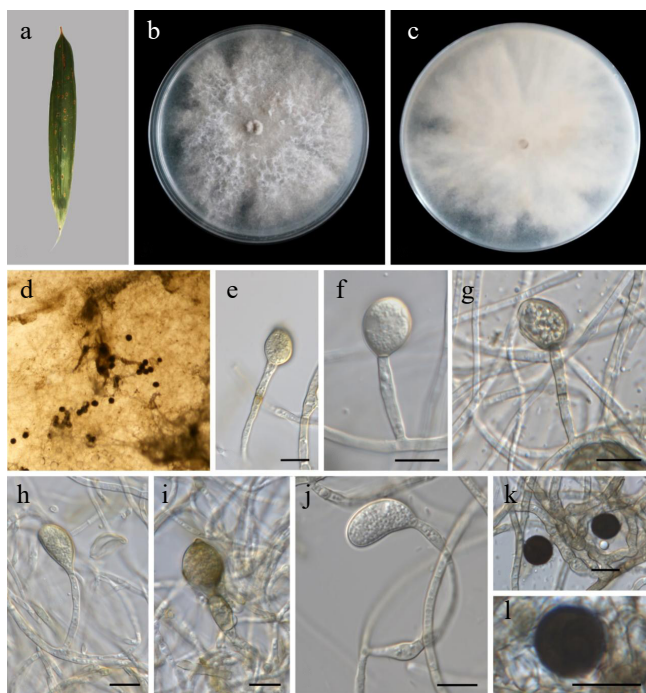


Fig. 20 *Apiospora rutila* (CGMCC 3.29223, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; top view (b) and bottom view (c). (d) Conidiomata formed in culture. (e–h) Conidiophore with conidium. (i, j) Conidia developed from conidiogenous cells. (k, l) Conidia. Scale bars: 10 µm (e–l).

9.29–14.20 µm (av. = $14.63 \pm 2.61 \times 10.89 \pm 1.41$ µm, $n = 16$), globose to ellipsoidal, aseptate, hyaline to dark brown from immature to mature, smooth, guttulate.

Culture characteristics – The colony is dense, with an undulate and irregular margin, a surface featuring patches of white aerial mycelia, and a cream-colored reverse on the PDA medium. The diameter of the colony was 76.8–86.6 mm after culturing for 7 days at 25 °C.

Material examined – China, Hainan Province, Diaoluoshan National Forest Park (18.678618 N, 109.948190 E, 150.62 m), on diseased *Bambusa rutila* leaves (Poaceae sp.), 12 March 2024, Q.Y. Liu (HSAUP 7656-5A, holotype), ex-type culture CGMCC 3.29223 = SAUCC 7656-5A; *ibid.*, HSAUP 7656-5B, living culture SAUCC 7656-5B.

Distribution – China, Hainan Province.

Ecology – Associated with diseased leaves of *Bambusa rutila* leaves (Poaceae sp.).

Notes – *Apiospora rutila* was described from the leaves of *Bambusa rutila* in China. The new species formed an independent clade that differed from *A. ovata* and *A. campsidis* in the phylogenetic analysis. *Apiospora rutila* and *A. ovata* (CBS 115042, ex-type) showed nucleotide differences in the ITS (37/501 bp), *tef1-α* (55/428 bp), and *tub2* (44/400 bp) gene regions. *Apiospora rutila* and *A. campsidis* (CBS 11198-2A, ex-type) showed nucleotide differences in the ITS (35/501 bp), *tef1-α* (51/428 bp), and *tub2* (41/400 bp) gene regions. In morphology, *A. ovata* has numerous sterile cells, whereas no sterile cells have been observed in *A. rutila*^[22]. The conidiophores of *A. rutila* are longer than those of *A. campsidis* ($20.57\text{--}57.27 \times 1.51\text{--}2.77$ vs. $13.98\text{--}39.36 \times 2.37\text{--}4.50$ µm). Thus, we described *A. rutila* as a new species.

Apiospora shaoguanensis Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. Fig. 21

Fungal names: FN 573297

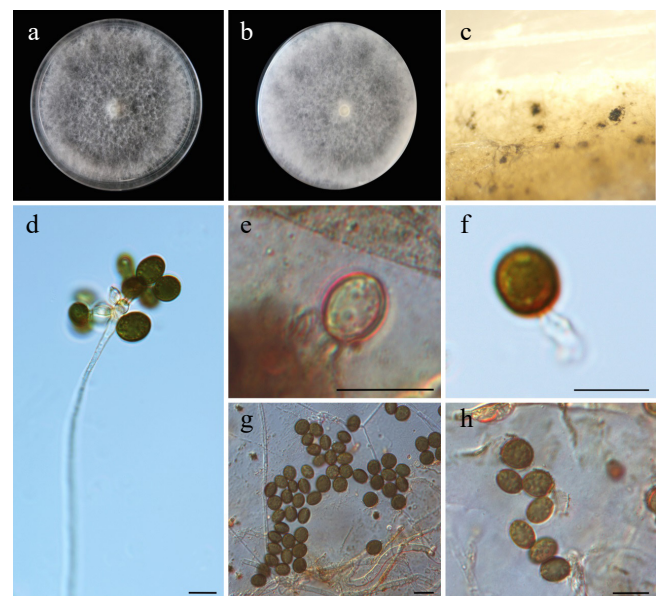


Fig. 21 *Apiospora shaoguanensis* (CGMCC 3.29220, ex-type culture). (a, b) Colonies after incubation on PDA for 7 days; top view (a) and bottom view (b). (c) Conidiomata formed in culture. (d) Conidiophores and conidiogenous cells giving rise to conidia. (e, f) Conidia developed from conidiogenous cells. (g, h) Conidia. Scale bars: 10 µm (d–h).

Etymology – The epithet "*shaoguanensis*" refers to the holotype collected from the shaoguan city, Guangdong Province.

On diseased bamboo leaves. Asexual morph: *hyphae* 1.3–4.9 µm diameter, hyaline to pale brown, branched, thick-walled, septate. *Conidiophores* $66.7\text{--}138.6 \times 2.26\text{--}4.88$ µm (av. = $94.14 \pm 38.9 \times 3.44 \pm 1.32$ µm, $n = 7$), hyaline, flexuous, aseptate, thin-walled, and are occasionally reduced to conidiogenous cells. *Conidiogenous cells* $3.34\text{--}9.57 \times 1.99\text{--}4.45$ µm (av. = $7.01 \pm 2.13 \times 3.32 \pm 0.93$ µm, $n = 16$), holoblastic or polyblastic, hyaline to pale brown, cylindrical, straight, smooth-walled. *Conidia* $7.06\text{--}9.84 \times 6.17\text{--}8.25$ µm (av. = $7.96 \pm 0.59 \times 7.36 \pm 0.53$ µm, $n = 23$), globose to ellipsoidal, aseptate, dark brown, smooth, guttulate with a pale equatorial slit.

Culture characteristics – Colonies on PDA mycelium abundant, margin entire, surface and reverse white. The diameter of the colony was 90 mm after culturing for 7 days at 25 °C.

Material examined – China, Guangdong Province, Shaoguan City, Danxia Mountain (25.004042 N, 113.676879 E, 90 m), on diseased leaves of bamboo leaves (Poaceae sp.), 3 March 2025, Y.L. Wang (HSAUP 17341-2A, holotype), ex-type culture CGMCC 3.29220 = SAUCC 17341-2A; *ibid.*, HSAUP 17341-2B, living culture SAUCC 17341-2B.

Distribution – China, Guangdong Province.

Ecology – Associated with diseased leaves of *Bambusa rutila* (Poaceae sp.).

Notes – *Apiospora shaoguanensis* (SAUCC 17341-2A, ex-type) was found to be phylogenetically related to *A. wuyishanensis* (SAUCC 11013-4A, ex-type). The two species showed nucleotide differences in the ITS (1/498 bp), *tef1-α* (24/409 bp), and *tub2* (16/391 bp) gene regions. Morphologically, *A. shaoguanensis* differs significantly from *A. wuyishanensis* (SAUCC 11013-4A, ex-type) in having longer conidiophores (94.14×3.44 vs. 23.1×2.58 µm) and smaller conidiogenous cells ($3.34\text{--}9.57 \times 1.99\text{--}4.45$ vs. $5.71\text{--}17.15 \times 3.71\text{--}5.38$ µm). Thus, we described *A. shaoguanensis* as a new species.

Apiospora taianensis Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. Fig. 22

Fungal names: FN 573298

Etymology – The epithet "*taianensis*" refers to the location where the type was collected: Tai'an City, Shandong Province.

On diseased bamboo leaves. Asexual morph: *hyphae* 1.8–6.7 μm diameter, hyaline to pale brown, branched, thick-walled, septate, guttulate. *Conidiophores* $34.26\text{--}88.94 \times 2.14\text{--}3.26 \mu\text{m}$ (av. = $67.05 \pm 26.01 \times 2.75 \pm 0.46 \mu\text{m}$, $n = 14$), hyaline, unbranched, straight or flexuous, smooth, aseptate, and are occasionally reduced to conidiogenous cells. *Conidiogenous cells* $6.4\text{--}20.1 \times 3.0\text{--}5.0 \mu\text{m}$ (av. = $15.1 \pm 5.5 \times 3.8 \pm 0.9 \mu\text{m}$, $n = 18$), holoblastic or polyblastic, hyaline, cylindrical, straight, aseptate, smooth-walled. *Conidia* $8.4\text{--}25.4 \times 3.4\text{--}9.6 \mu\text{m}$ (av. = $14.0 \pm 5.0 \times 7.6 \pm 1.5 \mu\text{m}$, $n = 27$), subglobose to cylindrical-clavate, aseptate, smooth, dark brown without the pale equatorial slit. Sterile cells are crescent-shaped.

Culture characteristics – The colony surfaces are flat, floccose, with moderate aerial mycelia, surfaces and reverse white on the PDA medium. The diameter of the colony was 90 mm after culturing for 7 days at 25 °C.

Material examined – China, Shandong Province, Tai'an City, Tian-waicun, Longtan Park (36.196715 N, 117.115043 E, 159.6 m), on diseased bamboo leaves (*Poaceae* sp.), 19 October 2024, Q.Y. Liu (HSAUP 10745-3A, holotype), ex-type culture CGMCC 3.29370 = SAUCC 10745-3A; *ibid.*, HSAUP 10745-3B, living culture SAUCC 10745-3B.

Distribution – China, Shandong Province.

Ecology – Associated with diseased leaves of bamboo (*Poaceae* sp.).

Notes – Based on phylogenetic analyses, the two isolates of the new species *Apiospora taianensis* form an independent clade, which is closely related to *A. dongyingensis* and *A. camelliae-sinensis*. *Apiospora taianensis* and *A. dongyingensis* (SAUCC 0302, ex-type) show nucleotide differences in the ITS (12/499 bp), LSU (1/751 bp), *tef1- α* (9/414 bp), and *tub2* (12/388 bp) gene regions. Morphologically, *A. taianensis* differs significantly from *A. dongyingensis* in having longer conidiogenous cells ($6.4\text{--}20.1 \times 3.0\text{--}5.0$ vs. $8.2\text{--}13.9 \times 4.2\text{--}8.2 \mu\text{m}$) and bigger conidia ($8.4\text{--}25.4 \times 3.4\text{--}9.6$ vs. $8.0\text{--}16.5 \times$

$5.5\text{--}9.0 \mu\text{m}$)^[29]. *Apiospora taianensis* and *A. camelliae-sinensis* (LC5007, ex-type) showed nucleotide differences of 1/499 bp, 1/751 bp, 4/414 bp, and 12/388 bp across four gene regions (ITS, LSU, *tef1- α* , and *tub2*, respectively). Morphologically, *A. taianensis* differs significantly from *A. camelliae-sinensis* in having longer conidiogenous cells ($6.4\text{--}20.1 \times 3.0\text{--}5.0$ vs. $4.0\text{--}9.5 \times 3.0\text{--}6.0 \mu\text{m}$) and bigger conidia ($8.4\text{--}25.4 \times 3.4\text{--}9.6$ vs. $9.0\text{--}13.5 \times 7.0\text{--}12.0 \mu\text{m}$)^[68]. *Arthrinium camelliae-sinensis* was originally identified from *Camellia sinensis* in Jiangxi Province, China^[68]. It was subsequently synonymized under *A. camelliae-sinensis* based on phylogenetic evidence^[25]. Thus, we described *A. taianensis* as a new species.

Apiospora teapae Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. Fig. 23

Fungal names: FN 573299

Etymology – The epithet "*teapae*" refers to the host of the holotype, specifically tea leaves.

On PDA. Asexual morph: *hyphae* 1.22–3.58 μm diameter, hyaline, branched, thick-walled, septate, guttulate. *Conidiophores* $35.38\text{--}60.66 \times 1.65\text{--}3.39 \mu\text{m}$ (av. = $46.94 \pm 9.78 \times 2.28 \pm 0.69 \mu\text{m}$, $n = 15$), hyaline, straight or flexuous, smooth and thin-walled, hyaline, septate, unbranched, guttulate, and are occasionally reduced to conidiogenous cells. *Conidiogenous cells* $8.00\text{--}19.19 \times 1.96\text{--}4.25 \mu\text{m}$ (av. = $12.01 \pm 3.85 \times 3.23 \pm 0.74 \mu\text{m}$, $n = 18$) from hyphae, holoblastic or polyblastic, hyaline, cylindrical or ampulliform, straight or flexuous, aseptate, smooth-walled, guttulate. *Conidia* $6.74\text{--}10.46 \times 6.00\text{--}8.14 \mu\text{m}$ (av. = $8.21 \pm 0.93 \times 6.92 \pm 0.63 \mu\text{m}$, $n = 19$), globose to ellipsoidal, aseptate, pale brown to dark brown, smooth to slightly rough, guttulate.

Culture characteristics – The colony surfaces are pale orange, raised in the center and flat around the edges, filiform, with abundant aerial mycelia, colony margin undulate and reverse orange on the PDA medium. The diameter of the colony was 71.71–75.00 mm after culturing for 7 days at 25 °C.

Material examined – China, Yunnan Province, Meng Hai County, Meng Hai Town (21.991154 N, 100.489806 E, 1146 m), on tea leaves, 11 July 2024, Q.Y. Liu (HSAUP 9814-1, holotype), ex-type culture CGMCC 3.29228 = SAUCC 9814-1; *ibid.*, HSAUP 9814-2, living culture SAUCC 9814-2.

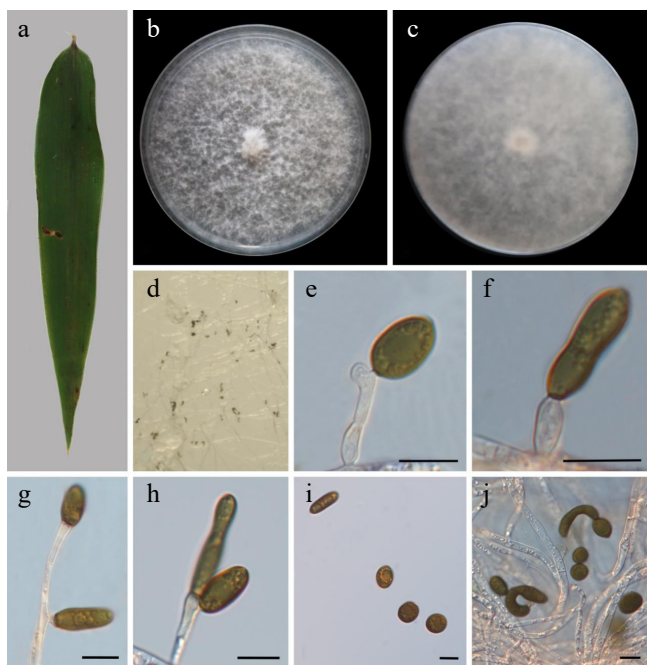


Fig. 22 *Apiospora taianensis* (CGMCC 3.29370, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; (b) top view and (c) bottom view. (d) Conidiomata formed in culture. (e, f, h) Conidia developed from conidiogenous cells. (g) Conidia produced from conidiophores and conidiogenous cells. (i) Conidia. (j) Conidia, conidia masses, sterile cells and hyphae. Scale bars: 10 μm (e–j).

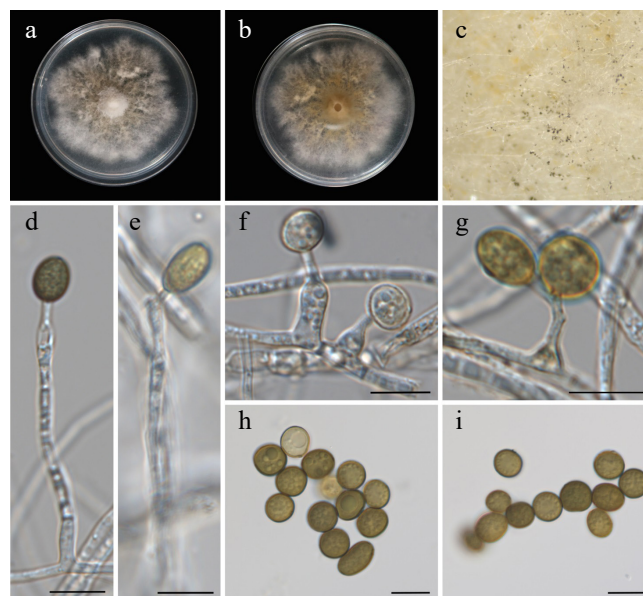


Fig. 23 *Apiospora teapae* (CGMCC 3.29228, ex-type culture). (a, b) Colonies after incubation on PDA for 7 days; (a) top view and (b) bottom view. (c) Conidiomata formed in culture. (d, e) Conidia developed from conidiophores. (f, g) Conidia developed from conidiogenous cells. (h, i) Conidia. Scale bars: 10 μm (d–i).

Distribution – China, Yunnan Province.

Ecology – Associated with tea leaves.

Notes – *Apiospora saprophytica* belongs to the large clade, where it shows a relationship with *A. xishuangbannaensis*. The two species showed nucleotide differences in the ITS (8/518 bp), *tef1-α* (9/414 bp), and *tub2* (8/387 bp) gene regions. Morphologically, our isolates differ significantly from *A. xishuangbannaensis* (KUMCC 21-0695, ex-type) in possessing shorter conidiogenous cells (8.00–19.19 × 1.96–4.25 vs. 6–37 × 1–5 μm) and narrower hyphae (1.22–3.58 vs. 1–6 μm)^[119]. Thus, we described *A. teapae* as a new species.

Apiospora ventricosa Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. Fig. 24

Fungal names: FN 573300

Etymology – The epithet "*ventricosa*" refers to the host of the holotype, specifically *Bambusa ventricosa*.

On PDA. Asexual morph: *hyphae* 2.12–5.38 μm diameter, hyaline to pale yellow, branched, thick-walled, septate. *Conidiophores* 7.39–26.35 × 1.85–3.20 μm (av. = 17.69 ± 8.00 × 2.57 ± 0.50 μm, *n* = 18), hyaline to pale yellow, branched or unbranched, straight or flexuous, smooth to pale verrucose, septate. *Conidiogenous cells* 2.65–5.06 × 2.55–3.61 μm (av. = 3.78 ± 0.93 × 3.03 ± 0.44 μm, *n* = 16), holoblastic or polyblastic, hyaline to pale yellow, cylindrical, straight, aseptate, smooth-walled. *Conidia* 4.69–7.59 × 3.76–6.79 μm (av. = 5.86 ± 0.69 × 5.20 ± 0.71 μm, *n* = 30), globose to subglobose, aseptate, dark brown, smooth to slightly rough, guttulate, with a pale equatorial slit.

Culture characteristics – The colony surfaces are pale yellow, flat, floccose, with abundant aerial mycelia, colony margin entire and reverse pale yellow on the PDA medium. The diameter of the colony was 90 mm after culturing for 7 days at 25 °C.

Material examined – China, Hainan Province, Qiongzong Li and Miao Autonomous County, Baihualing Tropical Rainforest Tourism and Cultural Zone (19.005802 N, 109.825167 E, 392 m), on diseased leaves of *Bambusa ventricosa*, 3 December 2024, Q.Y. Liu (HSAUP 14311-2A, holotype), ex-type culture CGMCC 3.29215 = SAUCC 14311-2A; *ibid.*, HSAUP 14311-2B, living culture SAUCC 14311-2B.

Distribution – China, Hainan Province.

Ecology – Associated with diseased leaves of *Bambusa ventricosa*.

Notes – See the notes of *Apiospora changjiangensis*.

Apiospora wuyishanensis Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. Fig. 25

Fungal names: FN 573301

Etymology – The epithet "*wuyishanensis*" refers to the holotype was collected from the wuyishan city, Fujian Province.

On diseased bamboo leaves. On WA. Asexual morph: *hyphae* 2.0–5.0 μm diameter, hyaline to pale brown, branched, thick-walled, septate. *Conidiophores* 21.1–26.5 × 2.1–2.9 μm (av. = 23.1 ± 3.0 × 2.58 ± 0.43 μm, *n* = 5), pale brown, flexuous, septate, thin-walled, and are occasionally reduced to conidiogenous cells. *Conidiogenous cells* 5.71–17.15 × 3.71–5.38 μm (av. = 9.22 ± 4.55 × 4.43 ± 0.62 μm, *n* = 5), holoblastic or polyblastic, brown, cylindrical or ampulliform, straight, smooth-walled. *Conidia* 8.32–10.75 × 6.17–10.13 μm (av. = 9.44 ± 0.62 × 7.97 ± 1.07 μm, *n* = 28), globose to ellipsoidal, aseptate, dark brown, smooth, guttulate with a pale equatorial slit.

Culture characteristics – Colonies on PDA mycelium abundant, margin entire, surface white, reverse pale yellow. The diameter of the colony was 90 mm after culturing for 7 days at 25 °C.

Material examined – China, Fujian Province, Wuyishan City (27.644737 N, 117.883815 E, 239.5 m), on diseased bamboo leaves (*Poaceae* sp.), 20 October 2024, Q.Y. Liu (HSAUP 11013-4A, holotype), ex-type culture CGMCC 3.29230 = SAUCC 11013-4A; *ibid.*, HSAUP 11013-4B, living culture SAUCC 11013-4B.

Distribution – China, Fujian Province.

Ecology – Associated with diseased leaves of bamboo (*Poaceae* sp.).

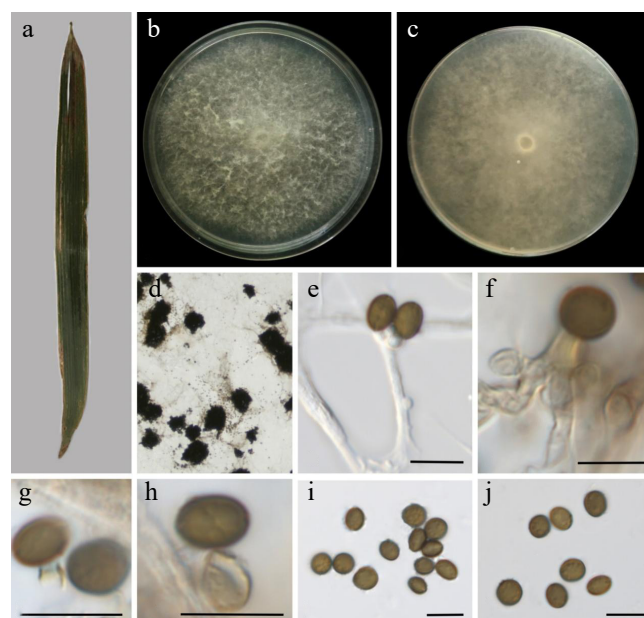


Fig. 24 *Apiospora ventricosa* (CGMCC 3.29215, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days from above (b) and below (c). (d) Conidiomata formed in culture. (e, f) Conidia developed from conidiophores and conidiogenous cells. (g, h) Conidia developed from conidiogenous cells. (i, j) Conidia. Scale bars: 10 μm (e–j).

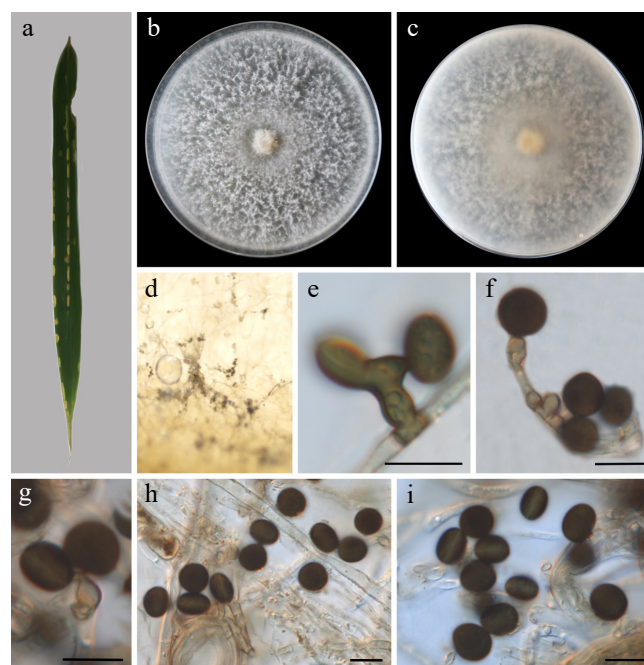


Fig. 25 *Apiospora wuyishanensis* (CGMCC 3.29230, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; top view (b) and bottom view (c). (d) Conidiomata formed in culture. (e, g) Conidia developed from conidiogenous cells. (f) Conidia developed from conidiophores and conidiogenous cells. (h, i) Conidia. Scale bars: 10 μm (e–i).

Notes – See the notes of *Apiospora shaoguanensis*.

Apiospora zingiberis Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. Fig. 26

Fungal names: FN 573302

Etymology – The epithet "*zingiberis*" refers to the host of the holotype, specifically *Zingiber zerumbet*.

On diseased leaves of *Zingiber zerumbet*. Asexual morph: *hyphae* 1.73–5.17 μm diameter, hyaline, branched, thick-walled, septate. *Conidiophores* 60.62–64.62 $\times$ 1.87–2.57 μm (av. = 62.62 $\pm$ 2.82 $\times$ 2.22 $\pm$ 0.49 μm , n = 2), hyaline, branched, straight or flexuous, smooth and thin-walled, hyaline, and are occasionally reduced to conidiogenous cells. *Conidiogenous cells* 8.41–41.30 $\times$ 1.64–4.30 μm (av. = 21.17 $\pm$ 10.71 $\times$ 2.86 $\pm$ 0.81 μm , n = 19), holoblastic, hyaline, cylindrical, straight or flexuous, aseptate or septate, smooth-walled. *Conidia* 10.32–18.44 $\times$ 9.41–15.88 μm (av. = 14.62 $\pm$ 2.16 $\times$ 12.95 $\pm$ 1.96 μm , n = 23), globose to cylindric-clavate, aseptate, hyaline, transitioning to pale brown and becoming dark brown when fully mature, smooth to slightly rough without a central scar.

Culture characteristics – The colony surfaces are white, medially raised, becoming thinner toward the edge, filiform, with abundant aerial mycelia and reverse yellowish white on the PDA medium. The diameter of the colony was 84.35–87.15 mm after culturing for 7 days at 25 $^{\circ}\text{C}$.

Material examined – China, Yunnan Province, Jinghong City, Xishuangbanna Primitive Forest Park (22.0312884 N, 100.8769031 E, 678 m), on diseased *Zingiber zerumbet* leaves, 17 March 2023, D.H. Li (HSAUP 2058-1A, holotype), ex-type culture CGMCC 3.29227 = SAUCC 2058-1A; *ibid.*, HSAUP 2058-1B, living culture SAUCC 2058-1B.

Distribution – China, Yunnan Province.

Ecology – Associated with diseased leaves of *Zingiber zerumbet*.

Notes – *Apiospora zingiberis* belongs to the large clade, where it shows a relationship with *A. bambusigena*, *A. cordylines*, *A. danzhouensis*, *A. dematiacea*, *A. endophytica*, and *A. hydei*. *Apiospora zingiberis* is distinct from *A. bambusigena* (SAUCC 2446-2, ex-type) in producing longer conidiophores (60.62–64.62 $\times$ 1.87–2.57 vs. 7.8–18.8 $\times$ 3.7–4.6 μm) and longer conidiogenous cells (8.41–41.30 $\times$ 1.64–4.30 vs. 5.2–8.8 $\times$ 3.0–4.6 μm), and showed nucleotide differences in the *tef1- α* (27/326 bp) and *tub2* (8/796 bp)^[120]. *Apiospora zingiberis* differs from *A. cordylines* (GUCC10027, ex-type) in its production of significantly wider hyphae (1.73–5.17 vs. 1.5–2.5 μm), longer conidiogenous cells (8.41–41.30 $\times$ 1.64–4.30 vs. (3–)5–10(–15) $\times$ 2.6–5.3 μm), and nucleotide differences in the *tef1- α* (19/409 bp) and *tub2* (9/379 bp)^[76]. *Apiospora zingiberis* differs from *A. danzhouensis* (SAUCC 6688-4, ex-type) in its production of significantly longer conidiogenous cells (8.41–41.30 $\times$ 1.64–4.30 vs. 6.31–23.81 $\times$ 1.16–4.07 μm), and nucleotide differences in the *tef1- α* (23/401 bp) and *tub2* (8/379 bp). *Apiospora zingiberis* is distinguished from *A. dematiacea* (HKAS 129910, ex-type) by its conidial morphology and sequence divergence. The conidia of *A. zingiberis* (globose to cylindric-clavate, 10.32–18.44 $\times$ 9.41–15.88 μm) differ from those of *A. dematiacea* based on the globose to ellipsoid structure with longitudinal striations in surface view (14.5–18(–20) μm) and lenticular to lageniform in side view (18.5–23(–25) $\times$ 10–13 μm), and showed nucleotide differences in the *tef1- α* (29/407 bp) and *tub2* (9/379 bp)^[65]. *Apiospora zingiberis* differs from *A. endophytica* (ZHKUCC 23-0006, ex-type) in its production of significant conidiophore cells (8.41–41.30 $\times$ 1.64–4.30 vs. 4–14 $\times$ 2–7 μm) and in its conidia not having a thick equatorial slit, with 32 nucleotide differences in *tef1- α* and *tub2* (23/402 bp in *tef1- α* , 9/379 bp in *tub2*)^[66]. *Apiospora zingiberis* differs from *A. hydei* (CBS 114990, ex-type) in its production of significantly longer conidiophores (60.62–64.62 $\times$ 1.87–2.57 vs. 20–40 $\times$ 3–5 μm) and longer conidiogenous cells (8.41–41.30 $\times$ 1.64–4.30 vs. 5–8 $\times$ 4–5 μm), its conidia lacking a distinct equatorial germ slit, and in having 31 nucleotide differences in the *tef1- α* and *tub2* loci (21/402 bp in *tef1- α* ; 10/379 bp in *tub2*)^[22]. Thus, we introduced *A. zingiberis* as a novel species.

***Nigrospora* Zimm.**

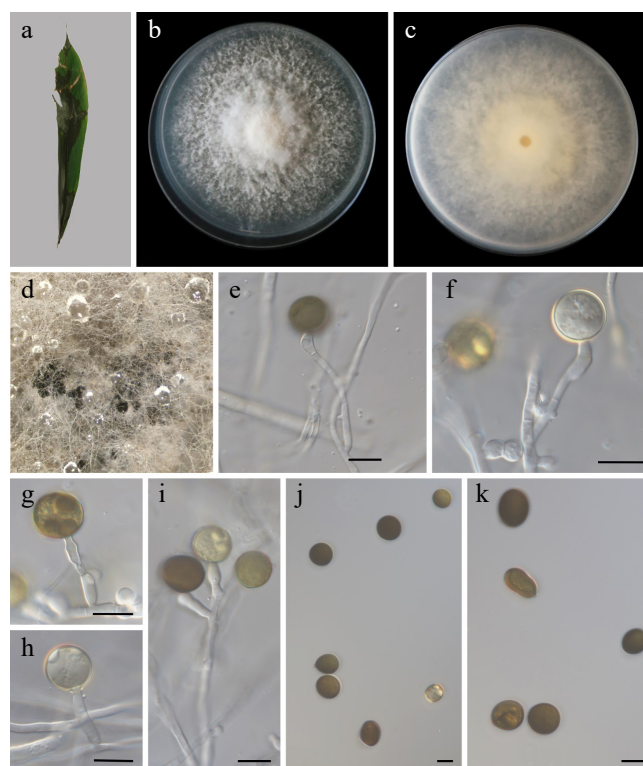


Fig. 26 *Apiospora zingiberis* (CGMCC 3.29227, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; top view (b) and bottom view (c). (d) Conidiomata formed in culture. (e–h) Conidia developed from conidiogenous cells. (i) Conidia developed from conidiophores and conidiogenous cells. (j, k) Conidia. Scale bars: 10 μm (e–k).

Notes – *Nigrospora* was proposed by Zimmerman^[121] with the type species *Nigrospora panici*. *Nigrospora* produces an asexual morph with branched, micronematous to semimacronematous conidiophores and monoblastic conidiogenous cells that bear black, shiny, aseptate conidia. It also forms a sexual morph consisting of perithecial ascomata with short-stalked, biseriate asci^[82,87,107].

In the phylogenetic tree comprising 126 *Nigrospora* isolates, the strain of *Apiospora pseudoparenchymatica* (LC7234) was classified as the outgroup. The alignment sequences contain 1,642 concatenated characters, viz. 1–547 (ITS), 548–1,094 (*tef1- α*), and 1,095–1,642 (*tub2*). Among these sequences, 1,013 characters were constant, 79 characters were variable and parsimony-uninformative, and 550 characters were parsimony-informative. The topologies were consistent from the ML and BI analyses; thus, the ML tree is reported in this study. All the tested 125 strains were identified to belong to 49 species upon analysis of ITS, *tef1- α* , and *tub2* gene sequences. BI analysis was performed over 2,555,000 generations in 5,112 trees; 3/4 of the trees were utilized to compute the posterior probability using the majority-rule consensus tree method (Fig. 27; first value: BIPP $\geq$ 0.90 displayed).

***Nigrospora buddlejae* Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.** Fig. 28

Fungal names: FN 573264

Etymology – The epithet "*buddlejae*" refers to the host of the holotype, specifically *Buddleja davidii*.

Asexual morph: *hyphae* smooth, pale brown, branched, septate, 2.6–5.3 μm diameter. *Conidiophores* are reduced to conidiogenous cells. *Conidiogenous cells* arising from hyphae, pale brown, subcylindrical, 7.82–10.22 $\times$ 5.45–9.27 μm (av. = 8.88 $\pm$ 0.96 $\times$ 6.84 $\pm$ 1.48, n = 15). *Conidia* solitary, elliptical or subglobose, black, shiny, smooth, aseptate, 16.61–22.24 $\times$ 15.14–17.67 μm (av. = 18.48 $\pm$ 1.69 $\times$ 16.38 $\pm$ 0.91, n = 21).

Culture characteristics – On the PDA medium, dense, entire margin, aerial mycelium black, and reverse brown. The diameter of the colony was 90 mm after culturing for 7 days at 25 °C.

Material examined – China, Hainan Province, Wuzhishan City, Shuiman Township (18.907031 N, 109.672299 E, 716 m), on diseased leaves of *Buddleja davidii*, 10 April 2024, J. Zhang (HSAUP 3199-2A,

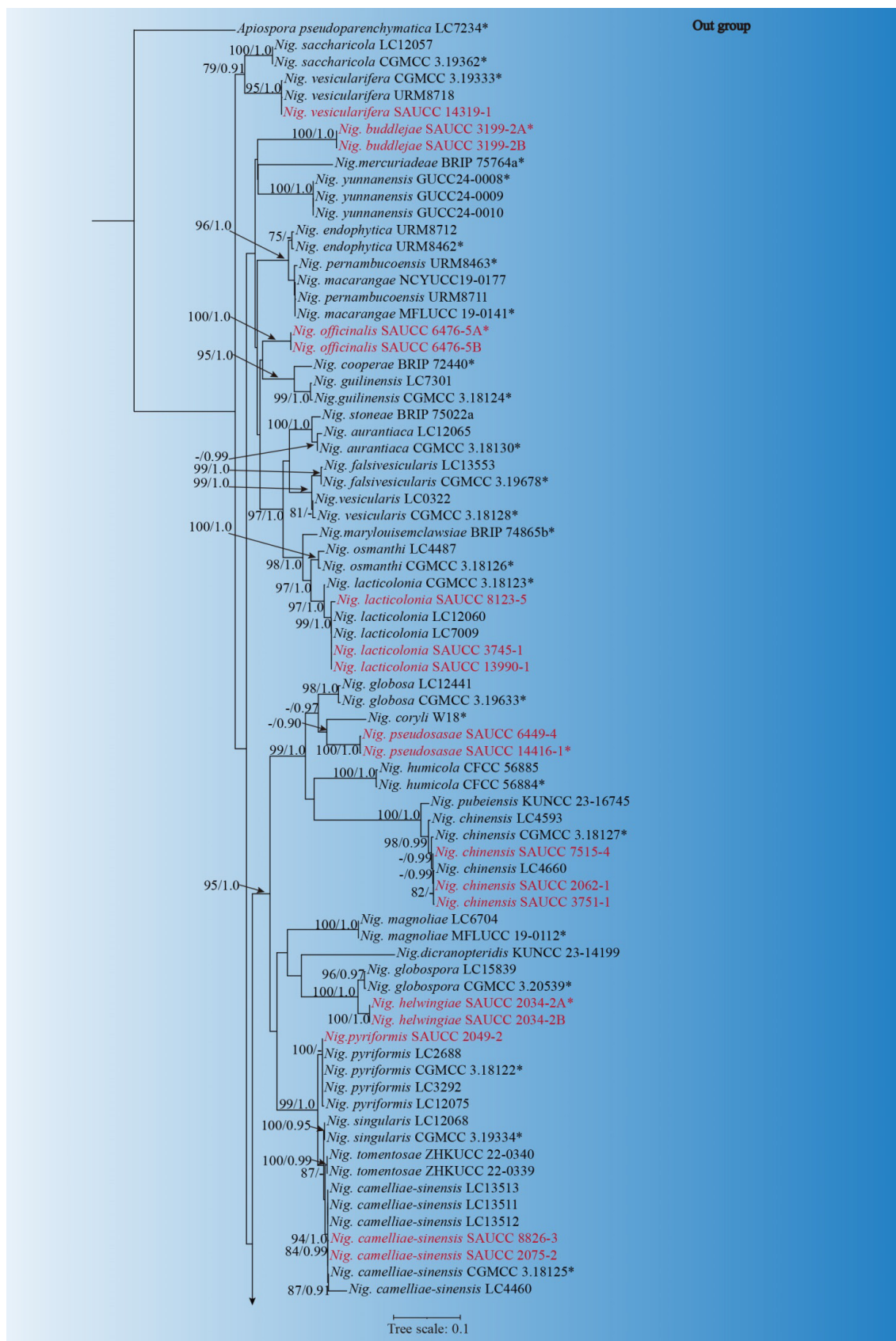


Fig. 27 to be continued

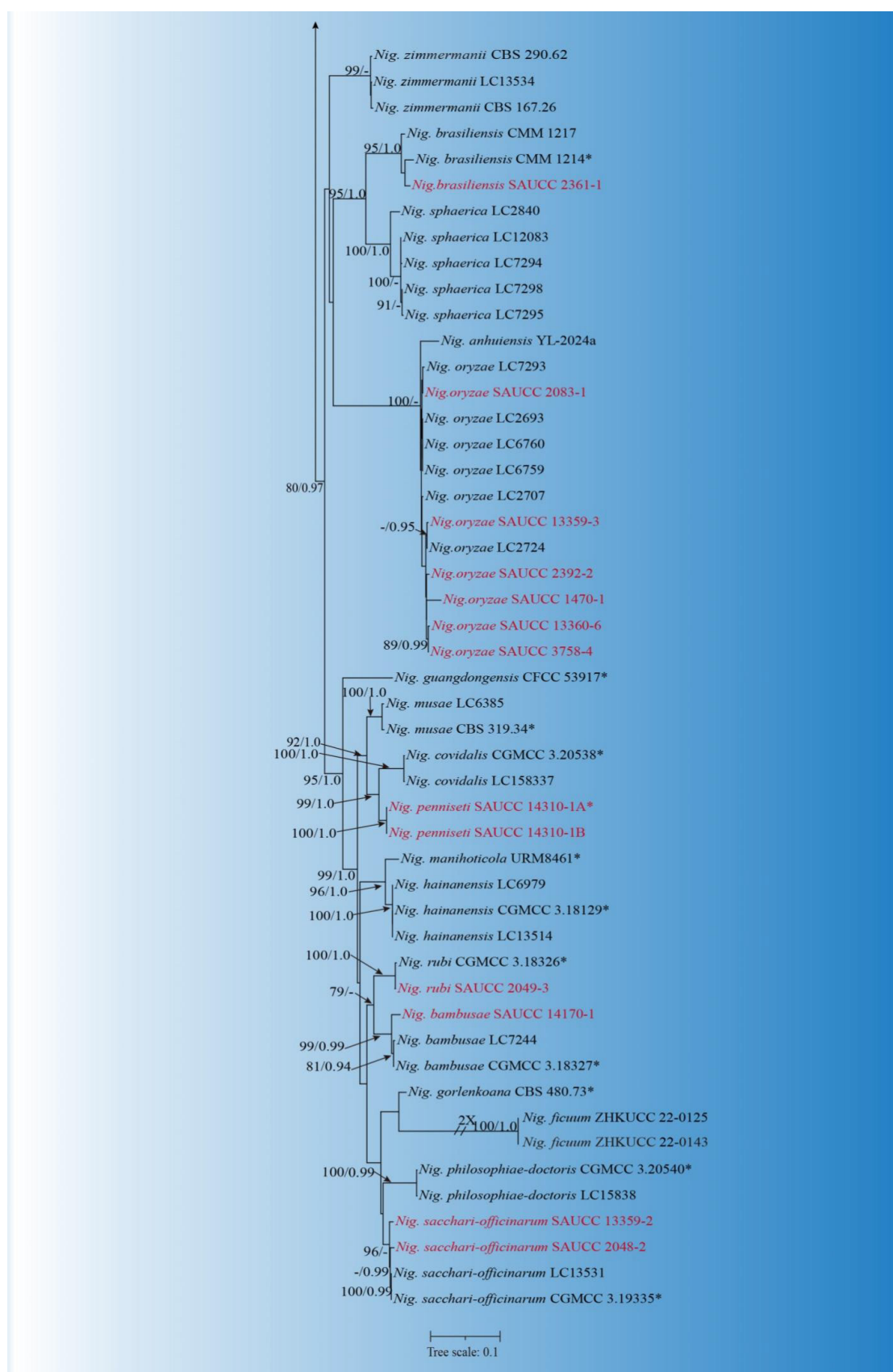


Fig. 27 Phylogenetic tree of the genus *Nigrospora* based on a concatenated ITS, *tef1-α*, and *tub2* sequences alignment, with *Apiospora pseudoparenchymatica* serving as the outgroup. The Bayesian inference posterior probability (right, BIPP ≥ 0.90) and the maximum likelihood bootstrap value (left, MLBV ≥ 75%) are shown as MLBV/BIPP above the nodes. Strains marked "*" in the tree are ex-type or ex-epitype. Strains isolated are highlighted in red. The scale bar at the bottom indicates 0.1 substitutions per site. To enhance the visual appeal of the evolutionary tree layout, certain branches are shortened by two diagonal lines ("//") with the number of times.

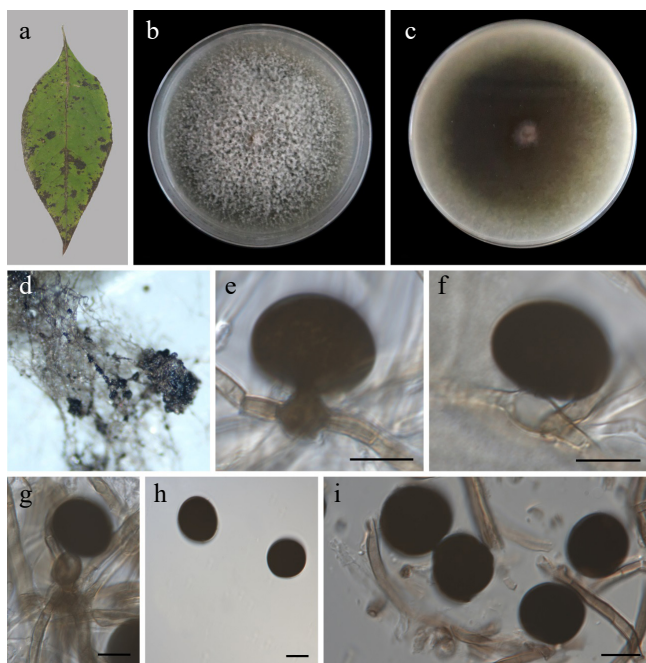


Fig. 28 *Nigrospora buddlejae* (CGMCC 3.29368, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; top view (b) and bottom view (c). (d) Conidiomata formed in culture. (e–g) Conidia developed from conidiogenous cells. (h, i) Conidia. Scale bars: 10 µm (e–i).

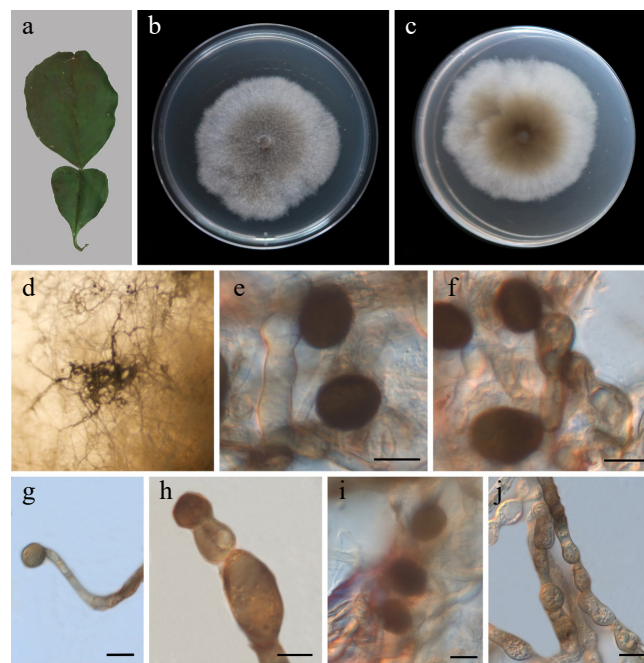


Fig. 29 *Nigrospora helwingiae* (CGMCC 3.29236, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; top view (b) and bottom view (c). (d) Conidiomata formed in culture. (e–h) Conidia developed from conidiogenous cells. (i) Conidia. (j) Hyphae. Scale bars: 10 µm (e–j).

holotype), ex-type culture CGMCC 3.29368 = SAUCC 3199-2A; *ibid.*, HSAUP 3199-2B, living culture 3199-2B.

Distribution – China, Hainan Province.

Ecology – Associated with diseased leaves of *Buddleja davidii*.

Notes – The strains of *Nigrospora buddlejae* are closed to *Nig. mercuriadeae* (ex-type BRIP 75764a; ITS: 35/451 bp, *tef1-α*: 41/258 bp, *tub2*: 43/346 bp) and *Nig. yunnanensis* (ex-type GUCC24-0008; ITS: 32/454 bp, *tef1-α*: 90/444 bp, *tub2*: 29/296). Morphologically, *Nig. buddlejae* can be differentiated from *Nig. yunnanensis* by its bigger conidia (16.61–22.24 × 15.14–17.67 vs. 14.5–18.5 × 11–17.5 µm)^[122]. *Nigrospora mercuriadeae* (BRIP 75764a, ex-type) was isolated from *Chromolaena odorata* in Australia, but its morphology was not described^[123]. Thus, we described *Nig. buddlejae* as a new species.

Nigrospora helwingiae Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. Fig. 29

Fungal names: FN 573265

Etymology – The epithet "*helwingiae*" refers to the host of the holotype, specifically *Helwingia japonica*.

Asexual morph: *hyphae* dense, guttulate, verrucose, hyaline to pale brown, branched, septate, 2.4–10.2 µm diameter. *Conidiophores* are reduced to conidiogenous cells. *Conidiogenous cells* pale brown, cylindrical, 12.92–27.56 × 3.21–10.63 µm (av. = 19.92 ± 8.07 × 6.78 ± 3.04, *n* = 4). *Conidia* solitary, elliptical or subglobose, pale brown to brown, shiny, slightly guttulate, aseptate, 9.03–18.78 × 8.88–14.19 µm (av. = 14.66 ± 2.49 × 12.17 ± 1.74, *n* = 21).

Culture characteristics – On the PDA medium, dense, entire margin. Both the surface and reverse of the aerial mycelium exhibit a brown center and a white periphery, crateriform. The diameter of the colony was 62.76 mm after culturing for 7 days at 25 °C.

Material examined – China, Yunnan Province, Jinghong City, Xishuangbanna Primitive Forest Park (22.0312884 N, 100.8769031 E, 678 m), on leaves of *Helwingia japonica*, 17 March 2023, D.H. Li (HSAUP 2034-2A, holotype), ex-type culture CGMCC 3.29236 = SAUCC 2034-2A; *ibid.*, HSAUP 2034-2B, living culture 2034-2B.

Distribution – China, Yunnan Province.

Ecology – Associated with leaves of *Helwingia japonica*.

Notes – Two strains representing *Nig. helwingiae* clustered in a well-supported clade and closely to *Nig. globospora* (CGMCC 3.20539, ex-type) (15/427 in *tef1-α*). Morphologically, *Nig. helwingiae* can be differentiated from *Nig. globospora* by its larger conidiogenous cells (12.92–27.56 × 3.21–10.63 vs. 8.5–9 × 3–4.5 µm) and bigger conidia (9.03–18.78 × 8.88–14.19 vs. 8.5–12 × 10.5–13.5 µm)^[124]. Thus, we described *Nig. helwingiae* as a new species.

Nigrospora officinalis Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. Fig. 30

Fungal names: FN 573266

Etymology – The epithet "*officinalis*" refers to the host of the holotype, specifically *Jasminum officinale*.

Asexual morph: *hyphae* smooth, pale brown, branched, septate, 2.0–3.8 µm diam. *Conidiophores* are reduced to conidiogenous cells. *Conidiogenous cells* arise from hyphae, and are pale brown, ellipsoidal, clavate to cylindrical, 6.48–11.48 × 5.46–6.51 µm (av. = 8.50 ± 1.88 × 6.00 ± 0.45, *n* = 18). *Conidia* globose or elliptical, pale brown to brown, shiny, slightly guttulate, aseptate, 13.32–17.40 × 10.37–15.64 µm (av. = 15.36 ± 1.33 × 13.25 ± 1.76, *n* = 19).

Culture characteristics – On the PDA medium, dense, colony margin undulate, aerial mycelium white to pale brown, crateriform, and reverse pale yellow. The diameter of the colony was 83 mm after culturing for 7 days at 25 °C.

Material examined – China, Hainan Province, Changjiang Li Autonomous County, Bawangling National Forest Park (19.0859333 N, 109.122752 E, 462 m), on diseased leaves of *Jasminum officinale*, 14 October 2023, W.W. Liu (HSAUP 6476-5A, holotype), ex-type culture CGMCC 3.29239 = SAUCC 6476-5A; *ibid.*, HSAUP 6476-5B, living culture 6476-5B.

Distribution – China, Hainan Province.

Ecology – Associated with diseased leaves of *Jasminum officinale*.

Notes – Strains representing *Nig. officinalis* and close to *Nig. cooperae* (BRIP 72440a, ex-type) (ITS 8/451 bp; *tef1-α* 72/444 bp;

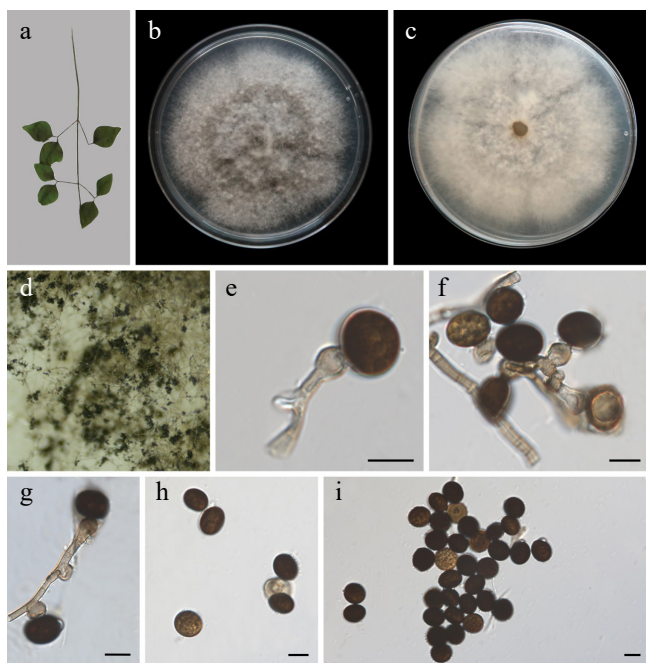


Fig. 30 *Nigrospora officinalis* (CGMCC 3.29239, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; top view (b) and bottom view (c). (d) Conidiomata formed in culture. (e–g) Conidia developed from conidiogenous cells. (h, i) Conidia. Scale bars: 10 µm (e–i).

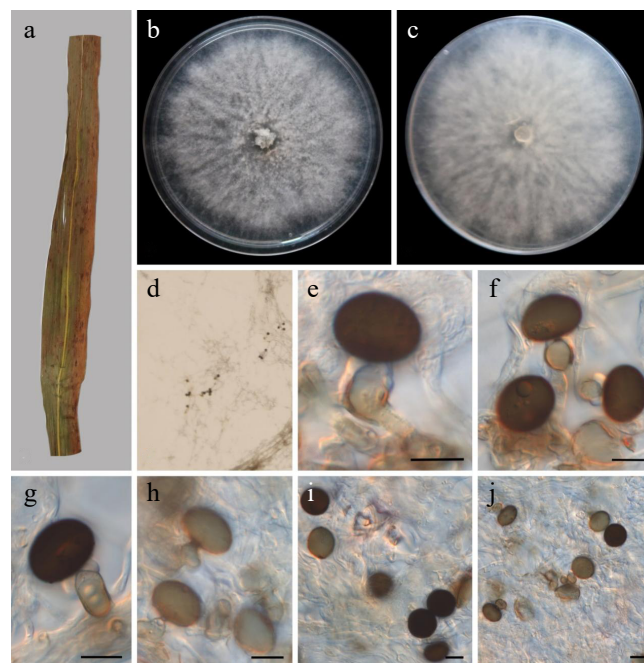


Fig. 31 *Nigrospora penniseti* (CGMCC 3.29237, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; top view (b) and bottom view (c). (d) Conidiomata formed in culture. (e–h) Conidia developed from conidiogenous cells. (i, j) Conidia. Scale bars: 10 µm (e–j).

tub2 30/337 bp) and *Nig. guilinensis* (CGMCC 3.18124, ex-type) (ITS 7/452 bp; *tef1-α* 73/443 bp; *tub2* 29/340 bp). Morphologically, *Nig. officinalis* can be differentiated from *Nig. cooperae* by its bigger conidia ($13.32\text{--}17.40 \times 10.37\text{--}15.64$ vs. $10\text{--}12.5 \times 8.5\text{--}10.5$ µm)^[125], and from *Nig. guilinensis* by its conidia (pale brown to brown, slightly guttulate, $13.32\text{--}17.40 \times 10.37\text{--}15.64$ vs. black, shiny, smooth, $11.5\text{--}15$ µm; ellipsoidal, $10.5\text{--}14 \times 8\text{--}12$ µm)^[82]. Based on comparison of morphology and phylogenetic trees, we described *Nig. officinalis* as a new species.

Nigrospora penniseti Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. Fig. 31

Fungal names: FN 573267

Etymology – The epithet "*penniseti*" refers to the host of the holotype, specifically *Pennisetum purpureum*.

Asexual morph: *hyphae* dense, smooth, hyaline to pale brown, branched, septate, $3.2\text{--}5.7$ µm diameter. *Conidiophores* are reduced to conidiogenous cells. *Conidiogenous cells* are aggregated in clusters on hyphae, and are pale brown, ellipsoidal to cylindrical, $6.72\text{--}15.46 \times 6.01\text{--}9.36$ µm (av. = $9.96 \pm 3.08 \times 7.36 \pm 1.10$, $n = 23$). *Conidia* solitary, elliptical or subglobose, pale brown to brown, shiny, slightly guttulate, aseptate, $14.73\text{--}19.35 \times 9.92\text{--}16.92$ µm (av. = $17.10 \pm 1.25 \times 13.85 \pm 2.47$, $n = 24$).

Culture characteristics – On the PDA medium, dense, entire margin, aerial mycelium white, and reverse white. The diameter of the colony was 90 mm after culturing for 7 days at 25 °C.

Material examined – China, Hainan Province, Qiongzong, Baihualing Tropical Rainforest (19.005802 N, 109.825167 E, 392 m), on diseased leaves of *Pennisetum purpureum*, 3 December 2024, Q.Y. Liu (HSAUP 14310-1A, holotype), ex-type culture CGMCC 3.29237 = SAUCC 14310-1A; *ibid.*, HSAUP 14310-1B, living culture 14310-1B.

Distribution – China, Hainan Province.

Ecology – Associated with diseased leaves of *Pennisetum purpureum*.

Notes – Two strains, representing *Nig. penniseti* clustered in a well-supported clade, and are close to *Nig. covidalis* (CGMCC

3.20538, ex-type) (ITS 2/454 bp; *tef1-α* 39/459 bp; *tub2* 6/327 bp). Morphologically, *Nig. penniseti* can be differentiated from *Nig. covidalis* by its larger conidiogenous cells ($6.72\text{--}15.46 \times 6.01\text{--}9.36$ vs. $5\text{--}8.5 \times 4.5\text{--}7$ µm) and bigger conidia ($14.73\text{--}19.35 \times 9.92\text{--}16.92$ vs. $9\text{--}14$ µm diameter)^[124]. Thus, we described *Nig. penniseti* as a new species.

Nigrospora pseudosasa Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. Fig. 32

Fungal names: FN 573268

Etymology – The epithet "*pseudosasa*" refers to the host of the holotype, specifically *Pseudosasa japonica*.

Asexual morph: *hyphae* smooth, hyaline to pale brown, branched, septate, verrucose, $1.6\text{--}3.4$ µm diameter. *Conidiophores* are reduced to conidiogenous cells. *Conidiogenous cells* arise from hyphae, hyaline to pale brown, ellipsoidal, clavate to cylindrical, $6.96\text{--}12.70 \times 3.85\text{--}6.71$ µm (av. = $10.18 \pm 2.19 \times 5.11 \pm 1.00$, $n = 17$). *Conidia* globose or elliptical, brown, shiny, aseptate, $10.81\text{--}13.67 \times 7.91\text{--}11.71$ µm (av. = $12.63 \pm 0.89 \times 10.31 \pm 1.12$, $n = 19$).

Culture characteristics – On the PDA medium, dense, entire margin, aerial mycelium white, crateriform, and reverse white. The diameter of the colony was 61 mm after culturing for 7 days at 25 °C.

Material examined – China, Hainan Province, Ledong Li Autonomous County, Jianfengling National Forest Park (18.700142 N, 108.812270 E, 126 m), on diseased leaves of *Pseudosasa japonica*, 4 December 2024, Y.L. Wang (HSAUP 14416-1, holotype), ex-type culture CGMCC 3.29238 = SAUCC 14416-1; *ibid.*, on diseased leaves of bamboo (*Poaceae* sp.), 04 October 2023, Q.Y. Liu (HSAUP 6449-4), living cultures SAUCC 6449-4.

Distribution – China, Hainan Province.

Ecology – Associated with diseased leaves of *Pseudosasa japonica* and bamboo.

Notes – The strains, representing *Nig. pseudosasa*, are closely related to *Nig. coryli* (W18, ex-type) (*tef1-α* 58/426 bp, *tub2* 28/325 bp). Morphologically, *Nig. pseudosasa* can be differentiated from *Nig. coryli* by its conidia (globose or elliptical, brown, shiny, aseptate,

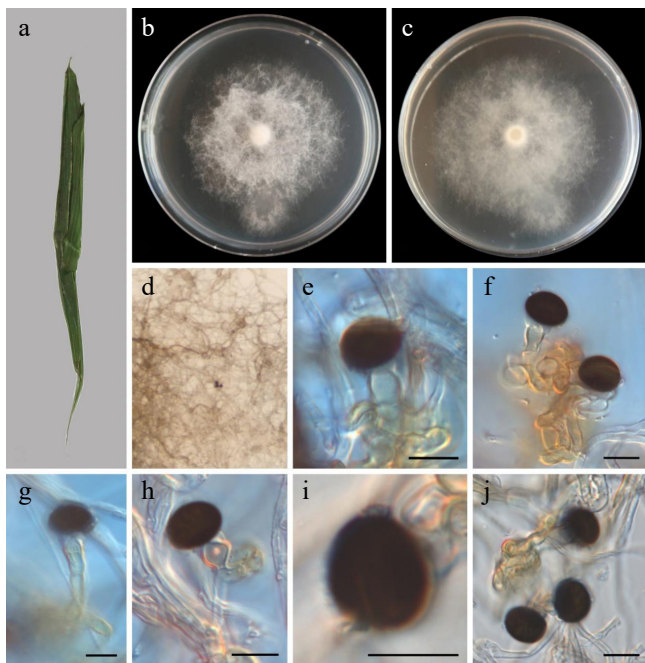


Fig. 32 *Nigrospora pseudosasae* (CGMCC 3.29238, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; top view (b) and bottom view (c). (d) Conidiomata formed in culture. (e–h) Conidia developed from conidiogenous cells. (i, j) Conidia. Scale bars: 10 µm (e–j).

10.81–13.67 × 7.91–11.71 µm vs. globose or subglobose, 13–20.5 µm diameter, acrogenous, smooth, solitary, shiny, aseptate, black; ellipsoidal, 13.5–17.5 × 11.5–14 µm^[126]. Based on comparison of morphology and phylogenetic trees, we described *Nig. pseudosasae* as a new species.

Beltraniaceae Nann

Notes – Beltraniaceae was first proposed by Nannizzi^[31] to accommodate the type genus *Beltrania* and several morphologically similar genera^[35]. Members of Beltraniaceae typically produce biconic, lageniform to navicular conidia that may possess a hyaline band and swollen separating cells; their conidiophores, which may arise independently or from radially lobed setal basal cells, are another diagnostic feature^[37,127,128]. To date, 11 genera validated by phylogenetic analysis have been accepted in Beltraniaceae^[16].

Beltraniella Subram.

Notes – *Beltraniella* is a genus distinguished by its setiform conidiophores, polyblastic, sympodial, denticulate conidiogenous cells, turbinate or biconic conidia with a truncate base, rostrate apex, and a hyaline transverse band. The genus *Beltraniella* was established by *Beltraniella odinae* as a type species from *Odina wodier* in India^[129,130].

In the phylogenetic tree consisting of 43 *Beltraniella* isolates, the strain of *Castanediella couratarii* (CBS 579.71) was used as the outgroup. The alignment sequences have 1,377 concatenated characters, viz. 1–583 (ITS) and 584–1,377 (LSU). Among these sequences, 1,242 characters were constant, 84 characters were variable and parsimony-uninformative, and 51 characters were parsimony-informative. The topologies were consistent in the ML and BI analyses; therefore, only the ML tree is displayed in this study. The 42 strains were identified to belong to 22 species by phylogenetic analysis of ITS and LSU gene sequences. BI analysis was performed over 1,780,000 generations in 3,562 trees; 3/4 of the trees were employed to compute the posterior probability using the majority-rule consensus tree (Fig. 33; first value: BIPP ≥ 0.90 displayed).

Beltraniella obovata D.H. Li, J.W. Xia & X.G. Zhang, sp. nov. Fig. 34

Fungal names: FN 573263

Etymology – The epithet "*obovata*" refers to the host of the holotype, specifically *Altingia obovata*.

Asexual morph: hyphomycetous. Mycelium mostly immersed in the substratum, composed of septate, branched subhyaline hyphae. *Setae* numerous, erect, straight or flexuous, unbranched, single or in small groups, thick-walled, verrucose, dark brown, 80.5–240.5 µm long, 5.5–9.0 µm wide at the base, tapering to a pointed apex, arising from radially lobed basal cells, 10.2–17.0 µm diameter. *Conidiophores* macronematous, sometimes setiform, single, straight, septate, partly verrucose, thick-walled to smooth-walled, 130.0–328.7 × 3.0–8.6 µm (mean ± SD = 228.0 ± 57.5 × 5.0 ± 1.2 µm, *n* = 30), sometimes branched at the apical region, dark brown swollen base, paler, and slightly tapering towards a pointed apex. *Conidiogenous cells* holoblastic, monoblastic to polyblastic, integrated, terminal. *Conidia* solitary to aggregated, acrogenous, simple, dry, straight, smooth, thin-walled, turbinate to pyriform, rostrate to pointed at the proximal end, rounded at the distal end, hyaline to subhyaline, 22.8–25.6 µm (mean ± SD = 24.2 ± 1.0 µm, *n* = 30) long, 6.0–8.0 µm wide (mean ± SD = 7.2 ± 0.6 µm, *n* = 30) in the broadest part. **Sexual morph:** *Ascomata* not seen. *Asci* 38.5–73.0 × 10.0–16.5 µm (mean ± SD = 56.5 ± 10.0 × 12.8 ± 1.6 µm, *n* = 30), unitunicate, 8-spored, subcylindrical to long obovoid, slightly curved. *Ascospores* 21.0–24.0 × 4.3–6.4 µm (mean ± SD = 22.5 ± 1.2 × 5.2 ± 0.5 µm, *n* = 30), overlapping uni- to bi-seriate, subhyaline to pale yellow, subcylindrical to long obovoid, slightly curved.

Culture characteristics – The colony surfaces are light yellowish-brown, verrucose, with moderate aerial mycelia, featuring a distinct circular growth zone; reverse fawn on the PDA medium. The diameter of the colony was 90 mm after culturing for 14 days at 25 °C.

Material examined – China, Hainan Province, Diaoluoshan National Forest Park (18.726546 N, 109.867095 E, 934 m), on diseased *Altingia obovata* leaves, 9 March 2023, D.H. Li (HSAUP 2895-5, holotype), ex-type culture CGMCC 3.29382 = SAUCC 2895-5; *ibid.*, HSAUP 2895-6, living culture SAUCC 2895-6.

Distribution – China, Hainan Province.

Ecology – Associated with diseased leaves of *Altingia obovata* leaves.

Notes – The strains, representing *Beltraniella obovata*, are closely related to *Beltraniella humicola* (CBS 203.64, ex-type) (ITS 9/556 bp; LSU 5/780 bp) and *Beltraniella hesseae* (BRIP 72433a, ex-type) (ITS 8/577 bp; LSU 3/781 bp)^[131,132]. Regarding *Beltraniella humicola* and *B. hesseae*, no morphological description was provided. Based on the comparison of phylogenetic trees, we described the collection of the two strains as a new species.

Sporocadaceae Corda

Notes – Sporocadaceae, a species-rich and cosmopolitan fungal family introduced by Corda^[38], includes plant pathogens, endophytes, saprobes, and parasites of humans and animals, and is typified by its appendage-bearing conidia^[44]. Now, 35 genera validated by phylogenetic analysis have been accepted in Sporocadaceae^[16].

Neopestalotiopsis Maharachch., K.D. Hyde & Crous

Notes – *Neopestalotiopsis* was proposed with the type species *Neopestalotiopsis protearum*^[42]. Members of *Neopestalotiopsis*, primarily found as plant pathogens, endophytes, or saprobes in tropical, subtropical ecosystems and other habitats such as caves^[44].

In the phylogenetic tree encompassing 259 *Neopestalotiopsis* isolates, the strains of *Pestalotiopsis colombiensis* (CBS 118553) and *Pestalotiopsis diversiseta* (MFLUCC 12-0287) were employed as the outgroups. The ultimate alignment was composed of 1928 concatenated characters, viz. 1–594 (ITS), 595–1,148 (*tef1-α*), and

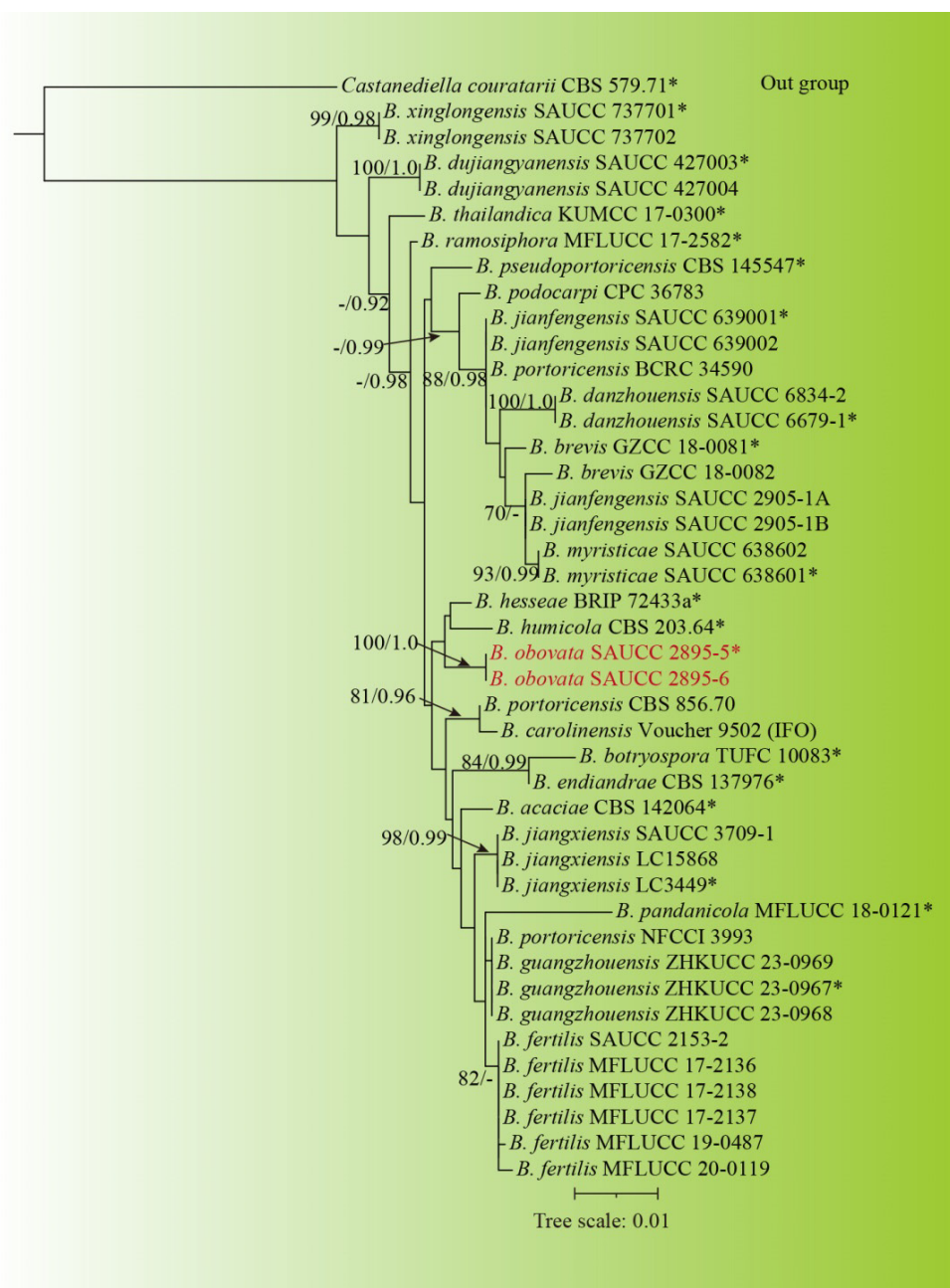


Fig. 33 Phylogenetic tree of the genus *Beltraniella* based on a concatenated alignment of ITS and LSU sequences, with *Castanediella couratarii* serving as the outgroup. The Bayesian inference posterior probability (right, BIPP ≥ 0.90) and the maximum likelihood bootstrap value (left, MLBV $\geq 70\%$) are shown as MLBV/BIPP above the nodes. Strains marked "*" in the tree are represented as ex-type or ex-epitype. Strains in this study are highlighted in red. The scale bar at the bottom indicates 0.01 substitutions per site.

1,149–1,928 (*tub2*). Among these sequences, 1,190 characters were constant, 271 characters were variable and parsimony-uninformative, and 467 characters were parsimony-informative. The topologies were consistent in the ML and BI analyses; therefore, only the ML tree is shown in this study. The 257 strains were identified as 140 species based on phylogenetic analysis of ITS, *tef1- α* , and *tub2* gene sequences. BI analysis was carried out for 5,000,000 generations in 10,002 trees; 3/4 of the trees were utilized to compute the posterior probability using the majority-rule consensus tree (Fig. 35; first value: BIPP ≥ 0.90 displayed).

Neopestalotiopsis bamboensis Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov.
Fig. 36

Fungal names: FN 573262

Etymology – The epithet "*bamboensis*" refers to the host of the holotype, specifically bamboo.

Asexual morph on PDA: *conidiomata* acervular, globose, black, solitary, releasing conidia in a black, slimy, globose mass. *Conidiophores* indistinct and reduced to conidiogenous cells. *Conidiogenous cells* discrete, smooth-walled, hyaline, and cylindrical, $5.21\text{--}13.54 \times 1.58\text{--}3.80 \mu\text{m}$ (av. = $8.70 \pm 2.63 \times 2.93 \pm 0.73 \mu\text{m}$). *Conidia* fusiform, slightly curved or straight, $17.53\text{--}25.37 \times 5.47\text{--}7.80 \mu\text{m}$ (av. = $21.32 \pm 2.22 \times 6.46 \pm 0.68 \mu\text{m}$, $n = 19$); mostly 4-septate, occasionally 3-septate, slightly constricted at the septa; basal cells obconic with a truncate base, $2.37\text{--}3.49 \mu\text{m}$ (av. = $3.06 \mu\text{m}$) long, hyaline, smooth, thin-walled; the two or three intermediate cells columnar or cylindrical, concolorous or versicolor, brown to pale

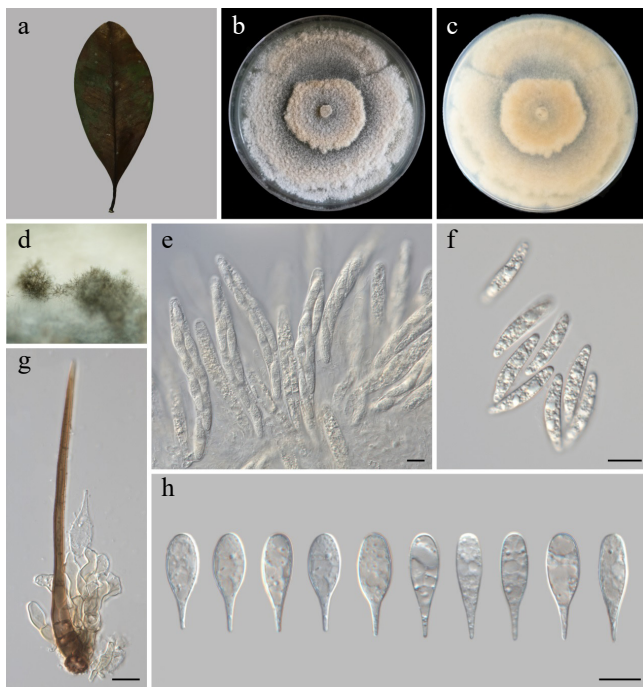


Fig. 34 *Beltraniella obovata* (CGMCC 3.29382, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 14 days; (b) top view and (c) bottom view. (d) Conidiophores and setae on pine needle. (e) Asci. (f) Ascospores. (g) Seta. (h) Conidia. Scale bars: 10 μ m (e–h).

brown, 12.23–15.97 μ m (av. = 13.95 $\pm$ 0.98 μ m) long, septa and periclinal walls darker than the rest of the cell; second cell from the base pale brown, 3.43–5.96 μ m (av. = 4.38 $\pm$ 0.68 μ m) long; third cell brown or pale brown, 2.90–7.34 μ m (av. = 4.75 $\pm$ 1.08 μ m) long; fourth cell pale brown, 3.51–6.10 μ m (av. = 4.77 $\pm$ 0.83 μ m) long; apical cell hyaline, subcylindrical, 1.25–4.87 μ m (av. = 3.40 $\pm$ 1.12 μ m) long; with 0–3 tubular apical appendages (mostly 2), unbranched, 17.67–38.39 μ m (av. = 29.11 $\pm$ 6.06 μ m) long; basal appendage single, tubular, unbranched, 2.65–8.57 μ m (av. = 5.53 $\pm$ 2.08 μ m) long. Sexual morph not observed.

Culture characteristics – The colony surfaces are cream-colored, prominent, floccose, forming concentric rings and reverse white on the PDA medium. The diameter of the colony was 78 mm after culturing for 7 days at 25 °C.

Material examined – China, Hainan Province, Diaoluoshan National Forest Park (18.660546 N, 109.936445 E, 94 m), on diseased leaves of bamboo (*Poaceae* sp.), 17 March 2023, Q.Y. Liu (HSAUP 7656-2A, holotype), ex-type culture CGMCC 3.29364 = SAUCC 7656-2A; *ibid.*, HSAUP 7656-2B, living culture SAUCC 7656-2B.

Distribution – China, Hainan Province.

Ecology – Associated with diseased leaves of bamboo (*Poaceae* sp.).

Notes – *Neopestalotiopsis bamboensis* (SAUCC 7656-2A and SAUCC 7656-2B) formed a distinct branching relationship with *Neo. brasiliensis* (COAD 2166, ex-type). The isolates are closely related to *Neo. brasiliensis* (COAD 2166, ex-type) and show nucleotide differences in the *tef1- α* (10/457 bp) and *tub2* (1/430 bp) gene regions. *Neopestalotiopsis bamboensis* was morphologically distinct from *Neo. brasiliensis* in its number of septa (4-septate, occasionally 3-septate vs. 4-septate) and apical appendages (0–3 vs. 1–3)^[133]. Thus, we described this fungus as a new species.

Pestalotiopsis Steyaert

Notes – Steyaert^[41] established the genus *Pestalotiopsis* with *Pestalotiopsis guepinii* as the type species to accommodate species

possessing 4-septate conidia, a key feature that differentiates it from *Pestalotia*. *Pestalotiopsis* is a common fungal genus that inhabits plant tissues as an endophyte, pathogen, or saprophyte, and it is well-known as a causal agent of leaf spot diseases^[134].

In the phylogenetic tree containing 306 *Pestalotiopsis* isolates, the strain of *Nonappendiculata quercina* (CBS 270.82) was selected as the outgroup. The ultimate alignment comprised 1,646 concatenated characters, viz. 1–533 (ITS), 534–1,044 (*tef1- α*), and 1,045–1,646 (*tub2*). Among the sequences, 932 characters were constant, 180 characters were variable and parsimony-uninformative, and 534 characters were parsimony-informative. The topologies were consistent in the ML and BI analyses; therefore, only the ML tree is shown in this study. The 305 strains were identified as 173 species by phylogenetic analysis of ITS, *tef1- α* , and *tub2* gene sequences. BI analysis was performed for 19,000,000 generations in 38,002 trees; 3/4 of the trees were used to compute the posterior probability using the majority-rule consensus tree (Fig. 37; first value: BIPP $\geq$ 0.90 displayed).

Pestalotiopsis castanopsis Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. Fig. 38
Fungal names: FN 573303

Etymology – The epithet "*castanopsis*" refers to the host of the holotype, specifically *Castanopsis carlesii*.

Asexual morph on PDA: *conidiomata* acervular, globose, black, solitary, releasing conidia in a black, slimy, globose mass. *Conidiophores* indistinct and reduced to conidiogenous cells. *Conidiogenous cells* discrete, smooth-walled, hyaline, cylindrical, 4.75–9.90 $\times$ 1.67–3.11 μ m (av. = 7.54 $\pm$ 1.46 $\times$ 2.15 $\pm$ 0.50 μ m). *Conidia* fusiform, straight or slightly curved, 21.77–27.39 $\times$ 4.08–6.14 μ m (av. = 24.70 $\pm$ 1.49 $\times$ 5.06 $\pm$ 0.58 μ m, n = 17); 1-septate, 2-septate, 3-septate, 4-septate, slightly constricted at the septa; basal cells obconic with a truncate base, 3.31–8.32 μ m (av. = 5.28 μ m) long, hyaline, smooth, thin-walled; the intermediate cells columnar or cylindrical, versicolor, hyaline to pale brown, 11.92–23.98 μ m (av. = 16.01 $\pm$ 2.04 μ m) long, septa, and periclinal walls darker than the rest of the cell; second cell from the base pale brown, 3.79–6.44 μ m (av. = 5.08 $\pm$ 0.79 μ m) long; third cell pale brown, 5.10–8.17 μ m (av. = 6.77 $\pm$ 0.72 μ m) long; fourth cell pale brown, 4.48–9.53 μ m (av. = 9.54 $\pm$ 1.17 μ m) long; apical cell hyaline, subcylindrical, 4.45–7.72 μ m (av. = 7.72 $\pm$ 0.86 μ m) long; with 1–5 tubular apical appendages (mostly 2), unbranched, 15.59–43.35 μ m (av. = 27.83 $\pm$ 6.55 μ m) long; basal appendages 1–2, tubular, unbranched, 2.10–8.17 μ m (av. = 4.99 $\pm$ 1.48 μ m) long. Sexual morph not observed.

Culture characteristics – The colony is nearly circular, with undulate edge, flat, white, floccose, forming concentric rings and reverse pale yellow on the PDA medium. The diameter of the colony was 72 mm after culturing for 7 days at 25 °C.

Material examined – China, Hainan Province, Diaoluoshan National Forest Park (18.660546 N, 109.936445 E, 94 m), on diseased leaves of *Castanopsis carlesii*, 26 June 2024, X.Y. Liu (HSAUP 7607-2A, holotype), ex-type culture CGMCC 3.29376 = SAUCC 7607-2A; *ibid.*, HSAUP 7607-2B, living culture SAUCC 7607-2B.

Distribution – China, Hainan Province.

Ecology – Associated with diseased leaves of *Castanopsis carlesii*.

Notes – *Pestalotiopsis castanopsis* (SAUCC 7607-2A and SAUCC 7607-2B) formed a distinct branching relationship with *P. shorea* (MFLUCC 12–0314, ex-type). The isolates are closely related to *P. shorea* (MFLUCC 12–0314, ex-type) and showed nucleotide differences in the ITS (12/513 bp), *tef1- α* (17/408 bp), and *tub2* (6/411 bp) gene regions. *Pestalotiopsis castanopsis* was morphologically distinct from *P. shorea* in its apical appendages (1–5 vs. 1–3) and the number of septa in conidia (1-septate, 2-septate, 3-septate, 4-septate vs. 4-septate)^[135]. Thus, we described *P. castanopsis* as a new species.

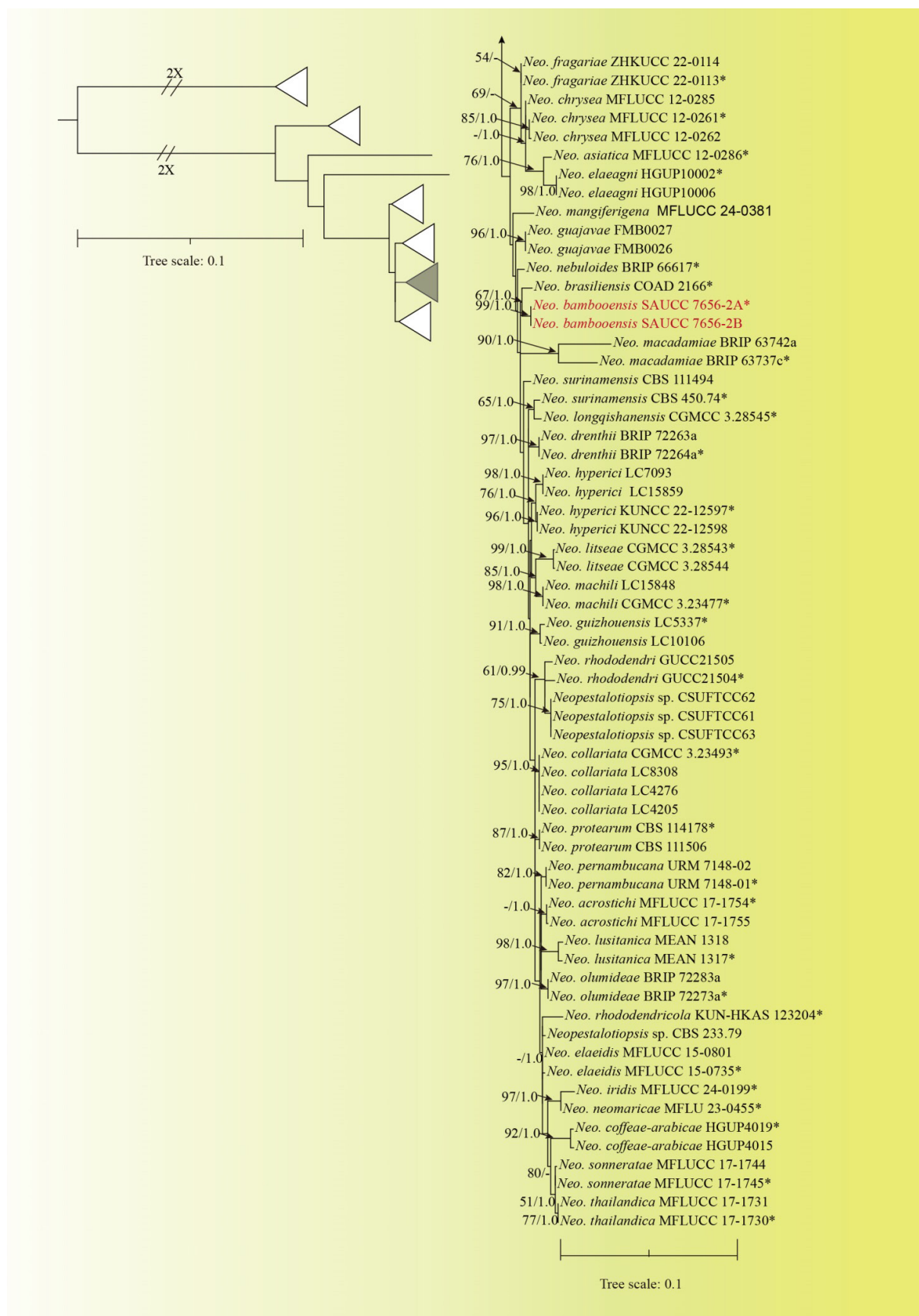


Fig. 35 to be continued



Fig. 35 Phylogenetic tree of the genus *Neopestalotiopsis* based on a concatenated alignment of ITS, *tef1-α*, and *tub2* sequences, with *Pestalotiopsis colombiensis* and *P. diversiseta* serving as outgroups. The Bayesian inference posterior probability (right, BIPP ≥ 0.90) and the maximum Likelihood bootstrap value (left, MLBV ≥ 50%) are shown as MLBV/BIPP above the nodes. Strains marked "*" in the tree are represented as ex-type or ex-epitype. Strains in this study are highlighted in red. The scale bar at the bottom indicates 0.1 substitutions per site. To enhance the visual appeal of the evolutionary tree layout, certain branches are shortened by two diagonal lines ("//") with the number of times. The figure shows partial branches of the evolutionary tree and the full evolutionary tree can be found in [Supplementary Information 12](#).

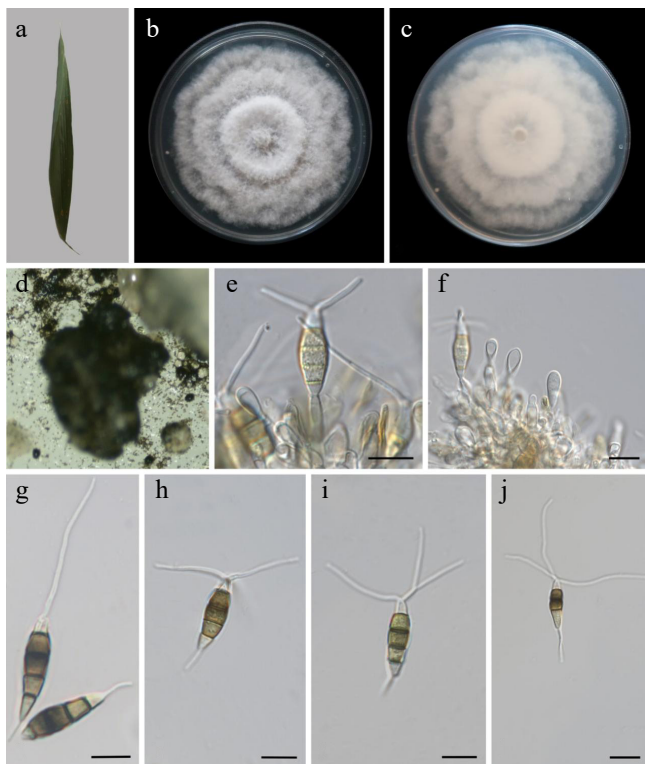


Fig. 36 *Neopestalotiopsis bamboensis* (CGMCC 3.29364, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; top view (b) and bottom view (c). (d) Conidiomata formed in culture. (e–f) Conidia developed from conidiogenous cells. (g–j) Conidia. Scale bars: 10 μ m (e–j).

Pestalotiopsis nanpingensis Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. [Fig. 39](#)

Fungal names: FN 573304

Etymology – The epithet "*nanpingensis*" refers to the host of the holotype collected from Nanping City, Fujian Province.

Asexual morph on PDA: *conidiomata* acervular, globose, black, solitary, releasing conidia in a black, slimy, globose mass. *Conidiophores* indistinct and reduced to conidiogenous cells. *Conidiogenous cells* discrete, smooth-walled, hyaline, cylindrical. *Conidia* fusiform, straight or slightly curved, hyaline to pale brown $15.85\text{--}22.69 \times 4.55\text{--}5.82 \mu\text{m}$ (av. = $19.47 \pm 2.10 \times 5.14 \pm 0.38 \mu\text{m}$, $n = 17$); 4-septate, slightly constricted at the septa; basal cells obconic with a truncate base, $3.19\text{--}6.27 \mu\text{m}$ (av. = $4.18 \mu\text{m}$) long, hyaline, smooth, thin-walled; the three intermediate cells columnar or cylindrical, concolourous, pale brown, $10.41\text{--}13.72 \mu\text{m}$ (av. = $12.10 \pm 0.97 \mu\text{m}$) long, septa and periclinal walls darker than the rest of the cell; second cell from the base pale brown, $4.07\text{--}5.11 \mu\text{m}$ (av. = $4.53 \pm 0.30 \mu\text{m}$) long; third cell pale brown, $3.49\text{--}5.64 \mu\text{m}$ (av. = $4.71 \pm 0.53 \mu\text{m}$) long; fourth cell pale brown, $3.17\text{--}5.57 \mu\text{m}$ (av. = $4.38 \pm 0.58 \mu\text{m}$) long; apical cell hyaline, subcylindrical, $2.18\text{--}4.32 \mu\text{m}$ (av. = $3.22 \pm 0.54 \mu\text{m}$) long; with 0–4 tubular apical appendages (mostly 2), unbranched, $2.05\text{--}15.46 \mu\text{m}$ (av. = $11.31 \pm 4.04 \mu\text{m}$) long; basal appendage 0–1, tubular, unbranched, $2.61\text{--}6.67 \mu\text{m}$ (av. = $4.17 \pm 1.11 \mu\text{m}$) long.

Culture characteristics – The colony is nearly circular, granular, flat, white, floccose, reverse pale yellow on the PDA medium. The diameter of the colony was 65 mm after culturing for 7 days at 25 $^{\circ}\text{C}$.

Material examined – China, Fujian Province, Nanping City, Wuyishan Rare and Precious Botanical Garden (27.747133 N, 117.677600 E, 723 m), on decaying leaves, 19 October 2024, Y.L. Wang (HSAUP

10887-3A, holotype), ex-type culture CGMCC 3.29375 = SAUCC 10887-3A; *ibid.*, HSAUP 10887-3B, living culture SAUCC 10887-3B.

Distribution – China, Fujian Province.

Ecology – Associated with decaying leaves.

Notes – *Pestalotiopsis nanpingensis* (SAUCC 10887-3A and SAUCC 10887-3B) formed a distinct branching relationship with *P. shaanxiensis* (CFCC 54958, ex-type), *P. biciliata* (CBS 124463, ex-type), *P. ficicrescens* (HGUP 861, ex-type), *P. camelliae-oleiferae* (CSUFTCC 08, ex-type), and *P. cyclosora* (HJAUP C1724.221, ex-type). Sequence comparisons with *P. shaanxiensis* (CFCC 54958, ex-type) revealed nucleotide differences in ITS (1/503 bp), *tef1- α* (3/406 bp), and *tub2* (3/431 bp) gene regions, morphologically distinct from *P. shaanxiensis* in its conidia size ($15.85\text{--}22.69 \times 4.55\text{--}5.82 \mu\text{m}$ vs. $(21)\text{--}22\text{--}24.5(25)$ by $(7)7.5\text{--}8.5(9) \mu\text{m}$) and apical appendages (0–4 vs. 3)^[134]. Sequence comparisons with *P. biciliata* (CBS 124463, ex-type strain) revealed differences in ITS (1/503 bp), *tef1- α* (7/406 bp), and *tub2* (3/431 bp) gene regions, morphologically distinct from *P. biciliata* in its conidia size ($15.85\text{--}22.69 \times 4.55\text{--}5.82$ vs. $(21)\text{--}22\text{--}28.5(30) \times (5.5)\text{--}6\text{--}7.5(8) \mu\text{m}$), apical appendages (0–4 vs. 2–3) and basal appendages (0–1 vs. 2)^[42]. Sequence comparisons with *P. ficicrescens* (HGUP 861, ex-type) revealed differences in ITS (4/502 bp), *tef1- α* (8/406 bp), and *tub2* (6/431 bp) gene regions, morphologically distinct from *P. ficicrescens* in its number of apical appendages (0–4 vs. 2–3) and basal appendage (0–1 vs. single)^[136]. Sequence comparisons with *P. camelliae-oleiferae* (CSUFTCC 08, ex-type) revealed differences in ITS (5/498 bp), *tef1- α* (8/406 bp), and *tub2* (5/431 bp) gene regions, morphologically distinct from *P. camelliae-oleiferae* in its number of apical appendages (0–4 vs. 2–3)^[137]. Sequence comparisons with *P. cyclosora* (HJAUP C1724.221, ex-type) revealed differences in ITS (1/503 bp), *tef1- α* (6/219 bp), and *tub2* (5/431 bp) gene regions, morphologically distinct from *P. cyclosora* in its conidia size ($15.85\text{--}22.69 \times 4.55\text{--}5.82$ vs. $16.3\text{--}26.1 \times 5.4\text{--}7.1 \mu\text{m}$) and number of apical appendages (0–4 vs. 1–4 (mostly 2 or 3))^[138]. Thus, we described *P. nanpingensis* as a new species.

Pestalotiopsis rhizomaticola Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. [Fig. 40](#)

Fungal names: FN 573305

Etymology – The epithet "*rhizomaticola*" refers to the host of the holotype, specifically *Dioscoreae rhizoma*.

Asexual morph on PDA: *conidiomata* acervular, globose, black, solitary, releasing conidia in a black, slimy, globose mass. *Conidiophores* indistinct and reduced to conidiogenous cells. *Conidiogenous cells* discrete, smooth-walled, hyaline, cylindrical, $6.04\text{--}12.90 \times 1.72\text{--}4.16 \mu\text{m}$ (av. = $9.05 \pm 2.31 \times 2.38 \pm 0.82 \mu\text{m}$). *Conidia* fusiform, straight or slightly curved, $17.83\text{--}26.76 \times 4.58\text{--}6.62 \mu\text{m}$ (av. = $21.39 \pm 2.93 \times 5.80 \pm 0.81 \mu\text{m}$, $n = 15$); 4-septate, slightly constricted at the septa; basal cells obconic with a truncate base, $3.61\text{--}6.41 \mu\text{m}$ (av. = $4.80 \mu\text{m}$) long, hyaline, smooth, thin-walled; the three intermediate cells columnar or cylindrical, concolourous, pale brown, $11.42\text{--}14.85 \mu\text{m}$ (av. = $13.20 \pm 0.89 \mu\text{m}$) long, septa and periclinal walls darker than rest of the cell; second cell from the base pale brown, $3.40\text{--}6.10 \mu\text{m}$ (av. = $4.74 \pm 0.66 \mu\text{m}$) long; third cell brown or light brown, $3.71\text{--}6.07 \mu\text{m}$ (av. = $4.87 \pm 0.73 \mu\text{m}$) long; fourth cell pale brown, $3.91\text{--}6.00 \mu\text{m}$ (av. = $4.64 \pm 0.60 \mu\text{m}$) long; apical cell hyaline, subcylindrical, $2.68\text{--}6.19 \mu\text{m}$ (av. = $4.00 \pm 1.05 \mu\text{m}$) long; with 0–4 tubular apical appendages (mostly 2), unbranched, $1.96\text{--}16.16 \mu\text{m}$ (av. = $11.88 \pm 4.23 \mu\text{m}$) long; basal appendages 0–2, tubular, unbranched, $2.56\text{--}5.54 \mu\text{m}$ (av. = $4.24 \pm 0.92 \mu\text{m}$) long.

Culture characteristics – The colony is nearly circular, flat, and floccose, with yellow centers and white margins; the reverse exhibited the same color on the PDA medium. The diameter of the colony was 78 mm after culturing for 7 days at 25 $^{\circ}\text{C}$.

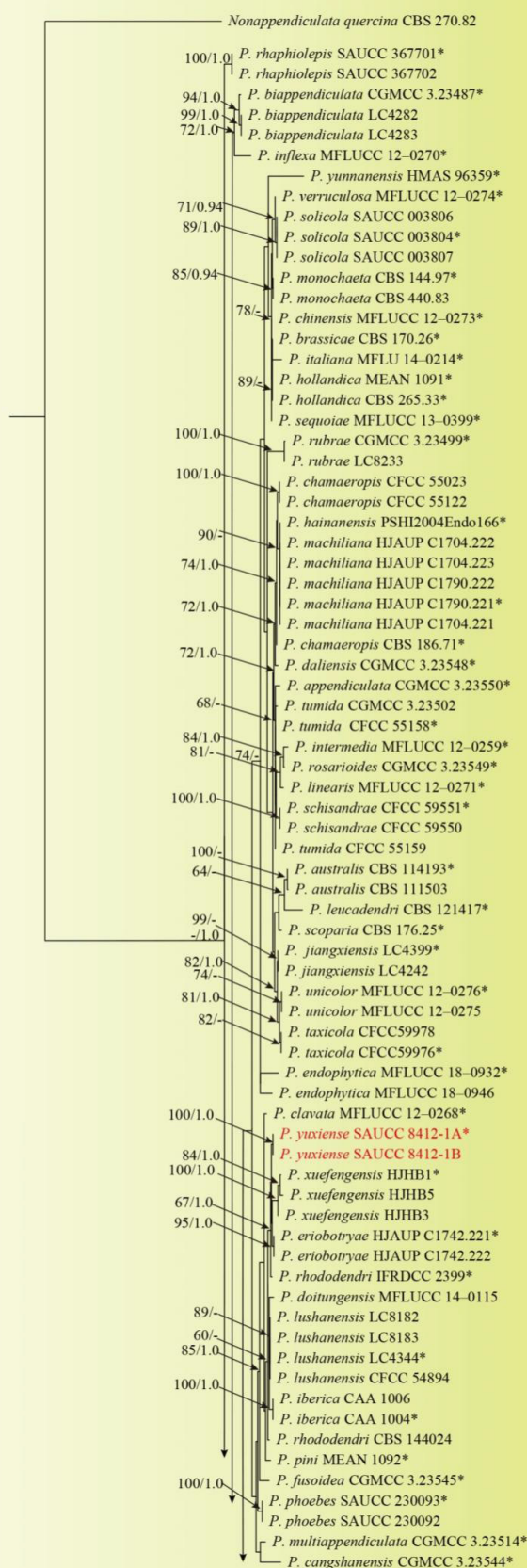


Fig. 37 to be continued

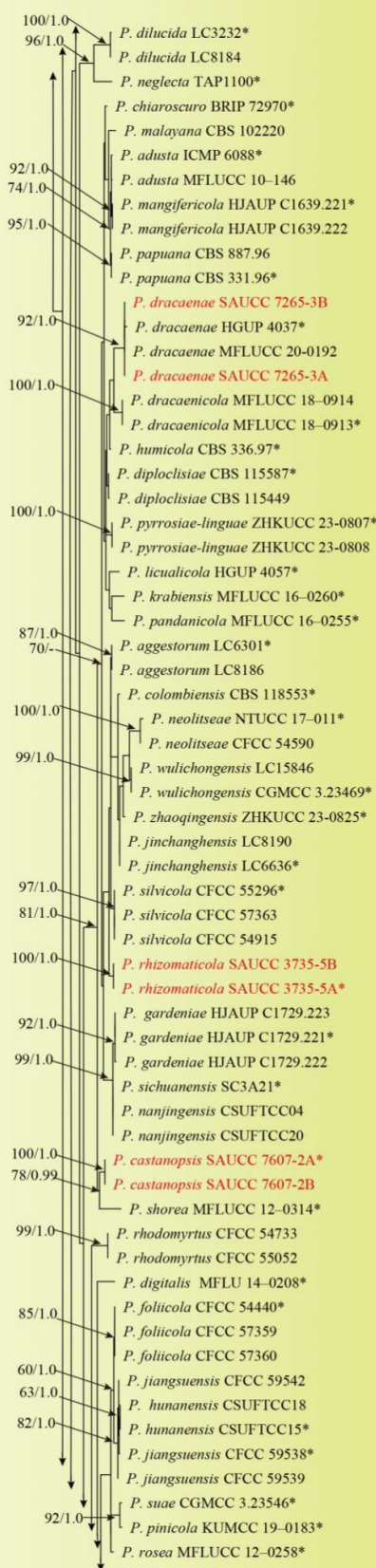


Fig. 37 to be continued

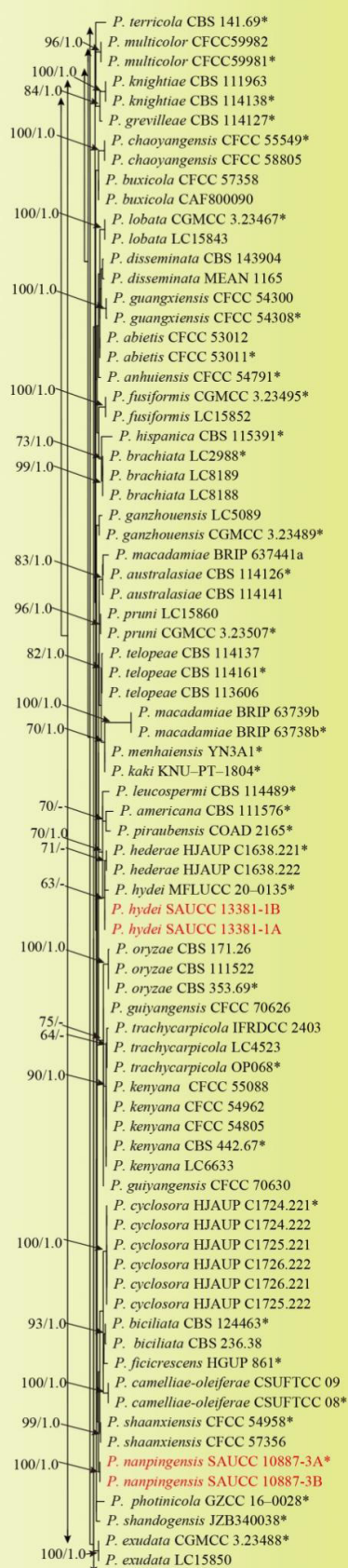


Fig. 37 to be continued

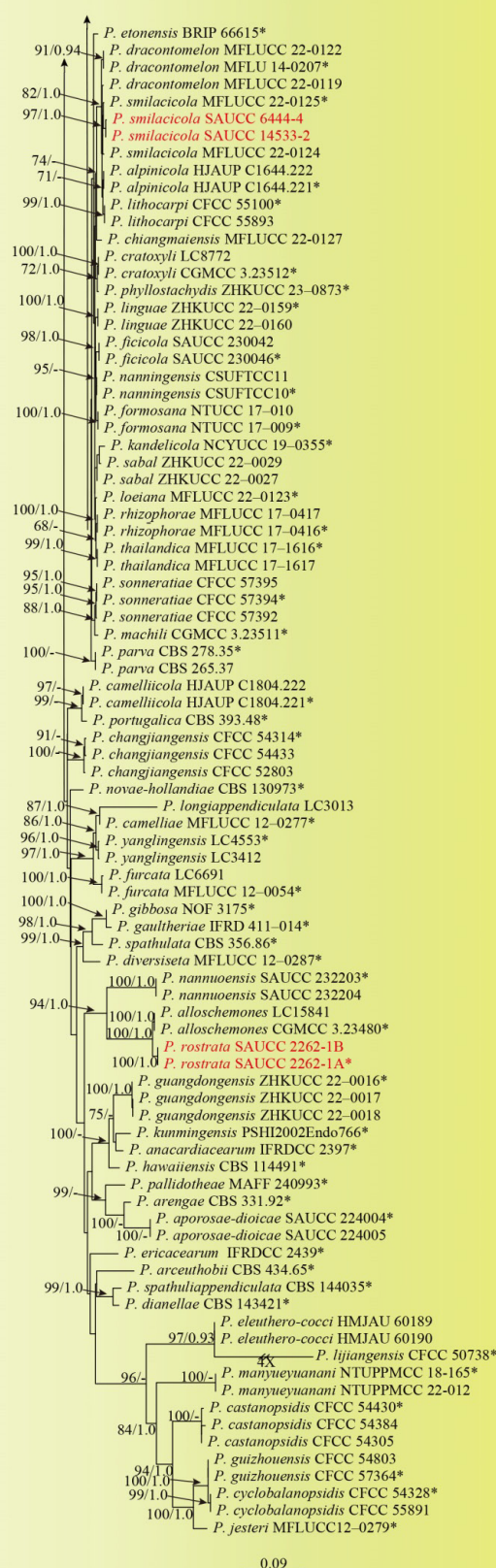


Fig. 37 Phylogenetic tree of the genus *Pestalotiopsis* based on a concatenated alignment of ITS, *tef1-α*, and *tub2* sequences, with *Nonappendiculata quercina* serving as the outgroup. The Bayesian inference posterior probability (right, BIPP ≥ 0.90) and the maximum likelihood bootstrap value (left, MLBV $\geq 60\%$) are shown as MLBV/BIPP above the nodes. Ex-type cultures are indicated in boldface and strains from the present study are highlighted in red. The scale bar at the bottom indicates 0.09 substitutions per site. To enhance the visual appeal of the evolutionary tree layout, certain branches are shortened by four diagonal lines ("/") with the number of times. Furthermore, three single-gene trees were evaluated for *Pestalotiopsis* (Supplementary Information 13).

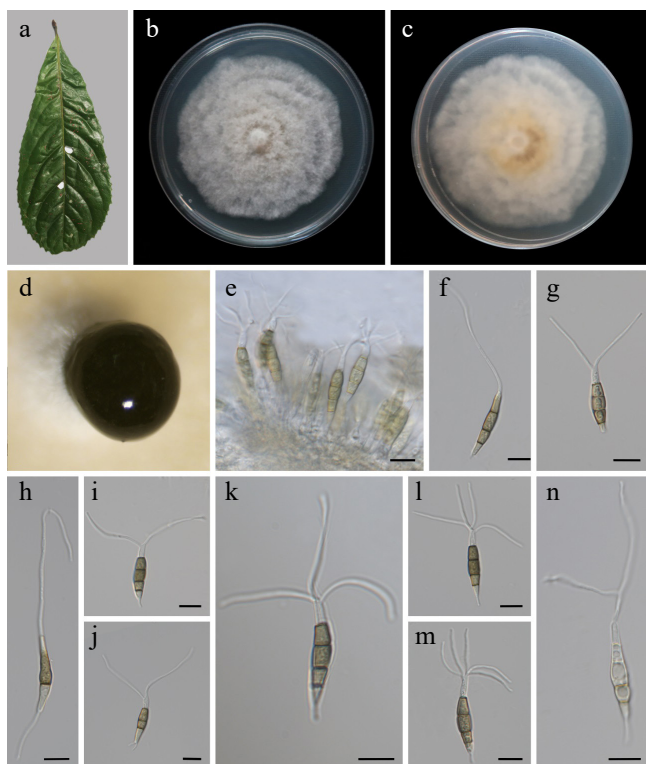


Fig. 38 *Pestalotiopsis castanopsis* (CGMCC 3.29376, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; top view (b) and bottom view (c). (d) Conidiomata formed in culture. (e) Conidia developed from conidiogenous cells. (f–n) Conidia. Scale bars: 10 μ m (e–n).

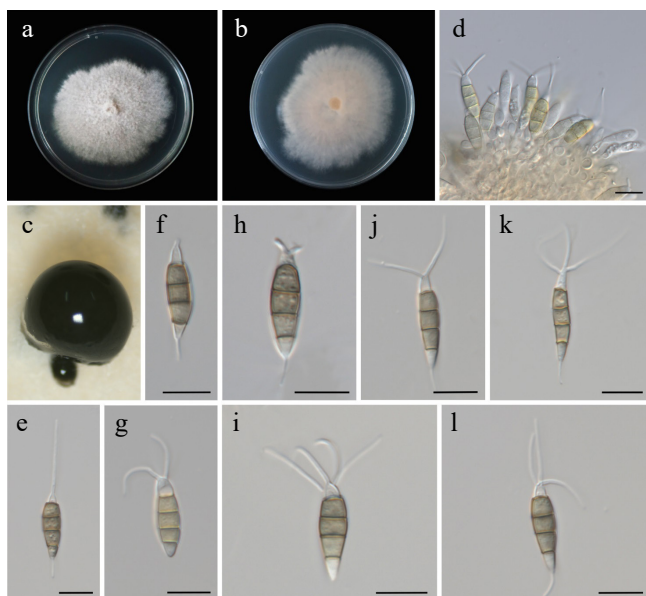


Fig. 39 *Pestalotiopsis nanpingensis* (CGMCC 3.29375, ex-type culture). (a–b) Colonies after incubation on PDA for 7 days; (a) top view and (b) bottom view. (c) Conidiomata formed in culture. (d) Conidia developed from conidiogenous cells. (e–l) Conidia. Scale bars: 10 μ m (d–l).

Material examined – China, Hainan Province, Ledong Li Autonomous County, Jianfeng Town (18.688815 N, 108.858742 E, 697 m), on leaves of *Dioscoreae rhizoma*, 12 April 2023, D.H. Li (HSAUP 3735-5A, holotype), ex-type culture CGMCC 3.29378 = SAUCC 3735-5A; *ibid.*, HSAUP 3735-5B, living culture SAUCC 3735-5B.

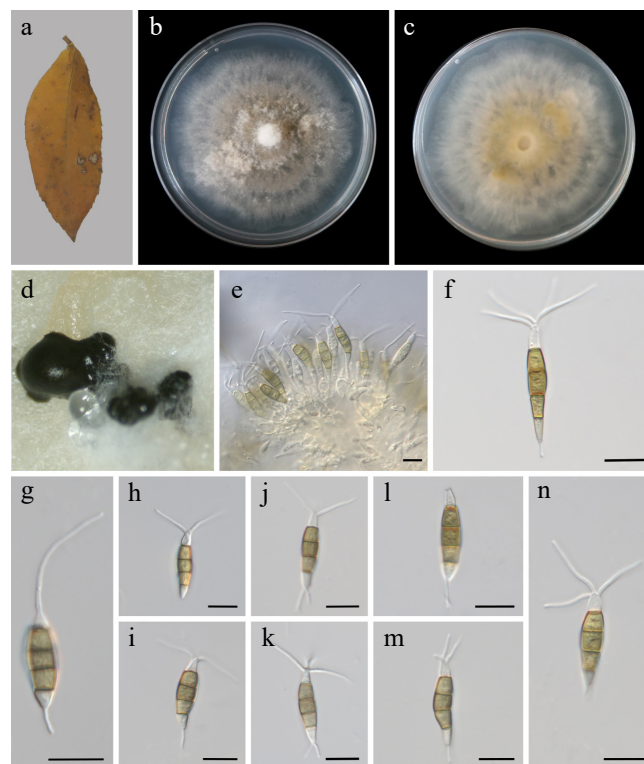


Fig. 40 *Pestalotiopsis rhizomaticola* (CGMCC 3.29378, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; top view (b) and bottom view (c). (d) Conidiomata formed in culture. (e) Conidia developed from conidiogenous cells. (f–n) Conidia. Scale bars: 10 μ m (e–n).

Distribution – China, Hainan Province.

Ecology – Associated with leaves of *Dioscoreae rhizoma*.

Notes – *Pestalotiopsis rhizomaticola* (SAUCC 3735-5A and SAUCC 3735-5B) formed a distinct branching relationship with *P. aggestorum* (LC6301, ex-type) and *P. silvicola* (CFCC 55296, ex-type). *Pestalotiopsis rhizomaticola* and *P. aggestorum* differed by 10 bp across three loci: 1/503 bp in ITS, 6/413 bp in *tef1- α* , and 3/436 bp in *tub2* gene regions. *Pestalotiopsis rhizomaticola* was morphologically distinct from *P. aggestorum* in the length of its apical appendages (2.68–6.19 vs. 18–28 μ m) and basal appendages (2.56–5.54 vs. 5–14 μ m)^[139]. The isolates are closely related to *P. silvicola* (CFCC 55296, ex-type) and comparisons of their sequences revealed 10 bp differences across three loci (1/502 bp in ITS, 5/413 bp for *tef1- α* , 4/435 bp for *tub2*). *Pestalotiopsis rhizomaticola* differed morphologically from *P. silvicola* in the shape of its apical cell (subcylindrical vs. conic with an acute apex) and the color of its median cells (pale brown vs. brown)^[134]. Thus, we described this fungus as a new species.

Pestalotiopsis rostrata Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. Fig. 41

Fungal names: FN 573306

Etymology – The epithet “*rostrata*” refers to the host of the holotype, specifically *Magnolia rostrata*.

Asexual morph on PDA: *conidiomata* acervular, globose, black, solitary, releasing conidia in a black, slimy, globose mass. *Conidiophores* indistinct and reduced to conidiogenous cells. *Conidiogenous cells* discrete, smooth-walled, hyaline, cylindrical, 6.09–13.63 $\times$ 2.08–3.80 μ m (av. = 9.52 $\pm$ 2.56 $\times$ 2.75 $\pm$ 0.69 μ m). *Conidia* fusiform, straight or slightly curved, 22.46–31.30 $\times$ 4.71–6.02 μ m (av. = 26.07 $\pm$ 2.28 $\times$ 5.63 $\pm$ 0.58 μ m, n = 16); 4-septate, slightly constricted at the septa; basal cells obconic with a truncate base, 3.41–6.77 μ m (av. = 5.19 μ m) long, hyaline, smooth, thin-walled; the three intermediate cells columnar or cylindrical, concolourous, pale brown, 14.27–19.32

μm (av. = $17.10 \pm 1.50 \mu\text{m}$) long, septa and periclinal walls are darker than the rest of the cell; the second cell from the base is pale brown, $5.30\text{--}7.82 \mu\text{m}$ (av. = $6.39 \pm 0.67 \mu\text{m}$) long; the third cell is pale brown, $4.41\text{--}7.06 \mu\text{m}$ (av. = $5.89 \pm 0.67 \mu\text{m}$) long; the fourth cell is pale brown, $4.76\text{--}7.72 \mu\text{m}$ (av. = $7.72 \pm 0.82 \mu\text{m}$) long; the apical cell is hyaline, subcylindrical, $3.75\text{--}6.68 \mu\text{m}$ (av. = $4.93 \pm 0.87 \mu\text{m}$) long; with 1–4 and six tubular apical appendages (mostly 2), unbranched, $9.19\text{--}20.18 \mu\text{m}$ (av. = $15.27 \pm 3.20 \mu\text{m}$) long; basal appendage single, tubular, unbranched, $2.48\text{--}6.07 \mu\text{m}$ (av. = $3.86 \pm 1.20 \mu\text{m}$) long.

Culture characteristics – The colony is nearly circular, with undulate edge, flat, white, floccose, reverse white on the PDA medium. The diameter of the colony was 71 mm after culturing for 7 days at 25°C .

Material examined – China, Yunnan Province, Jinghong City (22.1695431 N, 100.863829 E, 736 m), on diseased leaves of *Magnolia rostrata*, 19 March 2023, X.Y. Liu (HSAUP 2262-1A, holotype), ex-type culture CGMCC 3.29374 = SAUCC 2262-1A; *ibid.*, HSAUP 2262-1B, living culture SAUCC 2262-1B.

Distribution – China, Yunnan Province.

Ecology – Associated with diseased leaves of *Magnolia rostrata*.

Notes – *Pestalotiopsis rostrata* (SAUCC 2262-1A and SAUCC 2262-1B) formed a distinct branching relationship to *P. alloschemones* (CGMCC 3.23480, ex-type). The isolates are closely related to *P. alloschemones* (CGMCC 3.23480, ex-type) and comparisons of their sequences revealed 13 bp differences across two loci (8/376 bp for *tef1- α* , 5/380 bp for *tub2*). *Pestalotiopsis rostrata* is distinct from *P. alloschemones* in its conidia ($22.46\text{--}31.30 \times 4.71\text{--}6.02$ vs. $17\text{--}22.5 \times 4.5\text{--}6 \mu\text{m}$) and *P. alloschemones* possesses branched apical appendages and a basal appendage^[44]. Thus, we described this fungus as a new species.

Pestalotiopsis yuxiensis Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. Fig. 42
Fungal names: FN 573307

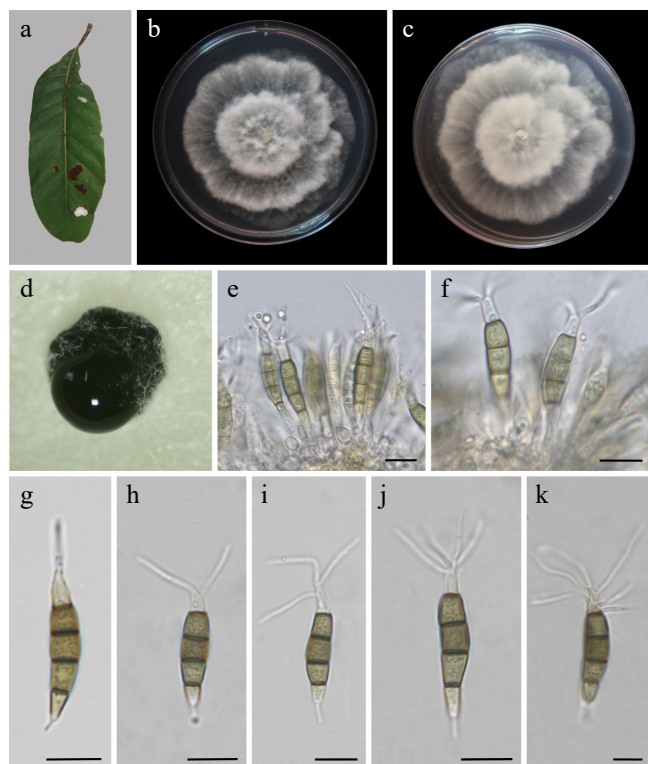


Fig. 41 *Pestalotiopsis rostrata* (CGMCC 3.29374, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; top view (b) and bottom view (c). (d) Conidiomata formed in culture. (e, f) Conidia developed from conidiogenous cells. (g–k) Conidia. Scale bars: $10 \mu\text{m}$ (e–k).

Etymology – The epithet "*yuxiensis*" refers to the host of the holotype collected from the Yuxi City, Yunnan Province.

Asexual morph on PDA: *conidiomata* acervular, globose, black, solitary, releasing conidia in a black, slimy, globose mass. *Conidiophores* indistinct and reduced to conidiogenous cells. *Conidiogenous cells* discrete, smooth-walled, hyaline, cylindrical, $6.97\text{--}20.24 \times 1.41\text{--}2.96 \mu\text{m}$ (av. = $13.34 \pm 5.86 \times 1.95 \pm 0.59 \mu\text{m}$). *Conidia* fusiform, straight or slightly curved, $18.91\text{--}25.61 \times 6.72\text{--}9.29 \mu\text{m}$ (av. = $22.91 \pm 2.34 \times 7.80 \pm 0.81 \mu\text{m}$, $n = 15$); 4-septate, slightly constricted at the septa; basal cells obconic with a truncate base, $3.17\text{--}8.39 \mu\text{m}$ (av. = $5.77 \mu\text{m}$) long, hyaline, smooth, thin-walled; the three intermediate cells columnar or cylindrical, versicolor, brown to pale brown, $14.32\text{--}17.16 \mu\text{m}$ (av. = $15.73 \pm 0.91 \mu\text{m}$) long, septa and periclinal walls darker than the rest of the cell; second cell from the base pale brown, $4.25\text{--}6.94 \mu\text{m}$ (av. = $5.65 \pm 0.79 \mu\text{m}$) long; third cell brown or light brown, $4.89\text{--}7.82 \mu\text{m}$ (av. = $6.23 \pm 0.68 \mu\text{m}$) long; fourth cell pale brown, $3.47\text{--}7.13 \mu\text{m}$ (av. = $5.71 \pm 0.85 \mu\text{m}$) long; apical cell hyaline, subcylindrical, $2.80\text{--}4.58 \mu\text{m}$ (av. = $3.50 \pm 0.50 \mu\text{m}$) long; with 2–4 tubular apical appendages (mostly 2), unbranched, $2.78\text{--}29.02 \mu\text{m}$ (av. = $19.99 \pm 6.82 \mu\text{m}$) long; basal appendages 0–2, tubular, spatulate, or sometimes knobbed, curved, centric, mostly branched, $2.38\text{--}14.11 \mu\text{m}$ (av. = $5.75 \pm 2.89 \mu\text{m}$) long.

Culture characteristics – The colony is nearly circular, with undulate edge, flat, white, floccose, reverse white on the PDA medium. The diameter of the colony was 80 mm after culturing for 7 days at 25°C .

Material examined – China, Yunnan Province, Yuxi City, Xinping Yi and Dai Autonomous County (23.960428 N, 101.937698 E, 2123 m), on unidentified diseased leaves, 13 May 2023, Q.Y. Liu (HSAUP 8412-1A, holotype), ex-type culture CGMCC 3.29373 = SAUCC 8412-1A; *ibid.*, HSAUP 8412-1B, living culture SAUCC 8412-1B.

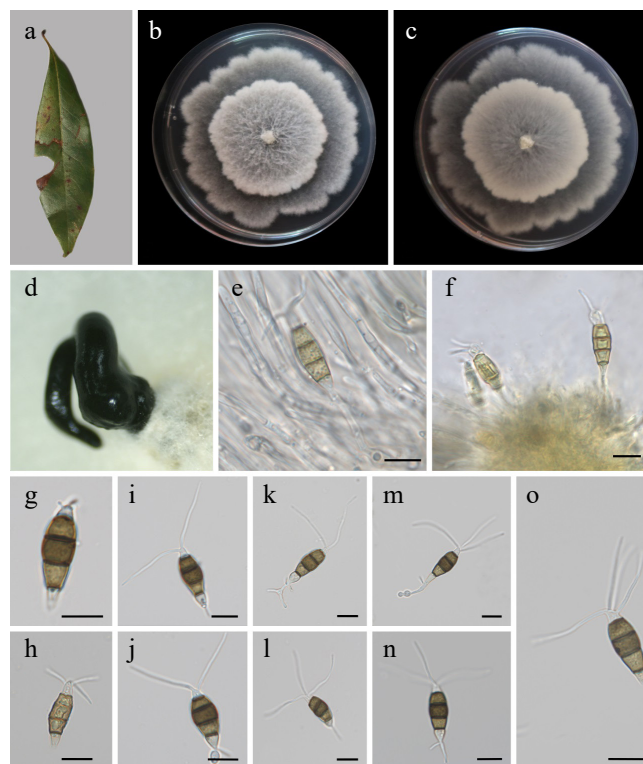


Fig. 42 *Pestalotiopsis yuxiensis* (CGMCC 3.29373, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; top view (b) and bottom view (c). (d) Conidiomata formed in culture. (e, f) Conidia developed from conidiogenous cells. (g–o) Conidia. Scale bars: $10 \mu\text{m}$ (e–o).

Distribution – China, Yunnan Province.

Ecology – Associated with unidentified diseased leaves.

Notes – *Pestalotiopsis yuxiensis* (SAUCC 8412-1A and SAUCC 8412-1B) formed a distinct branching relationship with *P. eriobotryae* (HJAUP C1742.221, ex-type) and *P. xuefengensis* (HJHB1, ex-type), and comparisons of their nucleotide sequences revealed 5 and 18 bp differences, respectively. Moreover, *P. yuxiensis* is morphologically distinguished from *P. eriobotryae* and *P. xuefengensis* in its basal appendages (0–2, tubular, spatulate, or sometimes knobbed, curved, centric, mostly branched basal appendages vs. single filiform, unbranched)^[138,140]. The PHI test in [Supplementary Information 14](#) did not find statistically significant evidence for recombination ($p = 0.5$). Thus, we described this fungus as a new species.

Pseudopestalotiopsis Maharachch., K.D. Hyde & Crous

Notes – *Pseudopestalotiopsis* was proposed with the type species *Pseudopestalotiopsis theae*^[42]. Morphologically, *Pseudopestalotiopsis* is morphologically distinguished from *Neopestalotiopsis* by its concolorous median cells, while *Neopestalotiopsis* possesses versicolored ones^[42].

In the phylogenetic tree encompassing 58 *Pseudopestalotiopsis* isolates, the strain of *Neopestalotiopsis clavispora* (MFLUCC 12-0281) acted as the outgroup. The ultimate alignment contained 1,486 concatenated characters, viz. 1–535 (ITS), 536–1,043 (*tef1-α*), and 1,044–1,486 (*tub2*). Among these sequences, 1,113 characters were constant, 232 characters were variable and parsimony-uninformative, and 141 characters were parsimony-informative. The topologies were consistent in the ML and BI analyses; thus, only the ML tree is displayed in this study. The 57 strains were defined as 34 species by phylogenetic analysis of ITS, *tef1-α*, and *tub2* gene sequences. BI analysis was conducted on 4,095,000 generations in 8,192 trees; 3/4 of the trees were utilized to compute the posterior probability using the majority-rule consensus tree ([Fig. 43](#); first value: BIPP ≥ 0.90 displayed).

Pseudopestalotiopsis xishuangbannaensis Q.Y. Liu, Z. Li & X.G. Zhang, sp. nov. [Fig. 44](#)

Fungal names: FN 573261

Etymology – The epithet "*xishuangbannaensis*" refers to the location where the type was collected, Xishuangbanna Primeval Forest Park, Yunnan Province.

Asexual morph on PDA: *conidiomata* acervular, globose, black, solitary, releasing conidia in a black, slimy, globose mass. *Conidiophores* indistinct and reduced to conidiogenous cells. *Conidiogenous cells* discrete, smooth-walled, pale yellow, cylindrical or ampulliform, $3.63\text{--}11.19 \times 2.18\text{--}3.82 \mu\text{m}$ (av. = $8.20 \pm 2.35 \times 2.85 \pm 0.64 \mu\text{m}$). *Conidia* fusiform, straight or slightly curved, $24.97\text{--}29.30 \times 4.86\text{--}6.98 \mu\text{m}$ (av. = $27.51 \pm 1.29 \times 6.11 \pm 0.67 \mu\text{m}$, $n = 25$); mostly 4-septate, occasionally 5-septate, slightly constricted at the septa; basal cells obconic with a truncate base, $3.16\text{--}5.31 \mu\text{m}$ (av. = $4.67 \mu\text{m}$) long, hyaline to pale yellow, smooth, thin-walled; the three or four intermediate cells columnar or cylindrical, homochromatic, pale brown, $16.43\text{--}21.13 \mu\text{m}$ (av. = $18.62 \pm 1.51 \mu\text{m}$) long, septa and periclinal walls darker than the rest of the cell; second cell from the base pale brown, $4.83\text{--}7.23 \mu\text{m}$ (av. = $6.12 \pm 0.72 \mu\text{m}$) long; third cell brown, $4.28\text{--}7.36 \mu\text{m}$ (av. = $5.95 \pm 0.98 \mu\text{m}$) long; fourth cell pale brown to brown, $2.81\text{--}8.52 \mu\text{m}$ (av. = $6.38 \pm 1.77 \mu\text{m}$) long; fifth cell pale brown to brown, $3.12\text{--}4.63 \mu\text{m}$ (av. = $3.98 \pm 0.80 \mu\text{m}$) long; apical cell hyaline, subcylindrical, collapsed, $2.70\text{--}6.00 \mu\text{m}$ (av. = $4.05 \pm 0.89 \mu\text{m}$) long; with 1–4 tubular apical appendages (mostly 2), unbranched or branched, $16.03\text{--}28.45 \mu\text{m}$ (av. = $22.59 \pm 4.09 \mu\text{m}$) long; basal appendages 0–1, tubular, unbranched, $1.44\text{--}6.74 \mu\text{m}$ (av. = $4.76 \pm 1.55 \mu\text{m}$) long.

Culture characteristics – The colony surfaces are white, flat, floccose, with concentric rings, and reverse pale yellow on the PDA

medium. The diameter of the colony was 75 mm after culturing for 7 days at 25 °C.

Material examined – China, Yunnan Province, Jinghong City, Near Xishuangbanna Primitive Forest Park (22.0312884 N, 100.8769031 E, 678 m), on unidentified leaves, 17 March 2023, D.H. Li (HSAUP 2069-2A, holotype), ex-type culture CGMCC 3.29371 = SAUCC 2069-2A; *ibid.*, HSAUP 2069-2B, living culture SAUCC 2069-2B.

Distribution – China, Yunnan Province.

Ecology – Associated with unidentified diseased leaves.

Notes – *Pseudopestalotiopsis xishuangbannaensis* (SAUCC 2069-2A and SAUCC 2069-2B) formed a distinct branching relationship with *Ps. kawthaungina* (MM14-F0083, ex-type). The isolates are closely related to *Ps. kawthaungina* (MM14-F0083, ex-type), and sequence comparisons revealed 17 bp differences across three loci (1/488 bp in ITS, 1/475 bp in *tef1-α*, 15/420 bp in *tub2*). *Pseudopestalotiopsis xishuangbannaensis* was morphologically distinct from *Ps. kawthaungina* in its number of conidia septa (4-septate, occasionally 5-septate vs. four-septate) and conidia size ($24.97\text{--}29.30 \times 4.86\text{--}6.98$ vs. $29.5\text{--}34.5 \times 7\text{--}9 \mu\text{m}$)^[141]. Based on the comparison of morphology and phylogenetic trees, we described this fungus as a new species.

List of accepted genera in Amphisphaeriales

Amphisphaeriaceae G. Winter

Amphisphaeria Ces. & De Not. (= *Lepteutypa* Petr.)

Labridella Brenckle (= *Griphosphaerioma* Höhn., *fide*)

Appendicosporaceae Samarak. & K.D. Hyde

Appendicospora K.D. Hyde

Neoamphisphaeria Samarak. & K.D. Hyde

Apiosporaceae K.D. Hyde, J. Fröhl., Joanne E. Taylor & M.E. Barr

Apiospora Sacc.

Arthrimum Kunze

Nigrospora Zimm.

Beltraniaceae Nann.

Anabeltraniomyces R.F. Castañeda, Mardones, P.M. Kirk & Gusmão

Beltrania Penz.

Beltraniella Subram.

Beltraniopsis Bat. & J.L. Bezerra

Hemibeltrania Piroz.

Parabeltrania Rambelli ex R.F. Castañeda, Gusmão & P.M. Kirk

Parapleurotheciopsis P.M. Kirk

Porobeltraniella Gusmão

Pseudobeltrania Henn.

Pseudosubramaniomyces Crous

Subsessila C.G. Lin & K.D. Hyde

Castanediellaceae Hern.-Restr., Guarro & Crous

Castanediella Hern.-Restr., Crous & M.J. Wingf.

Clypeophysalosporaceae Giraldo & Crous

Bagadiella Cheew. & Crous

Clypeophysalospora H.J. Swart

Neophysalospora Crous & M.J. Wingf.

Paraphysalospora Crous (1)

Plectosphaera Theiss.

Hyponectriaceae Petr.

Apiothyrium Petr.

Arecomyces K.D. Hyde

Arwidsonia B. Erikss.

Cesatiella Sacc.

Chamaeascus L. Holm, K. Holm & M.E. Barr

Discosphaerina Höhn.

Exarmidium P. Karst.

Fronidicola K.D. Hyde

Hyponectria Sacc.

Lichenoverruculina Etayo (1)

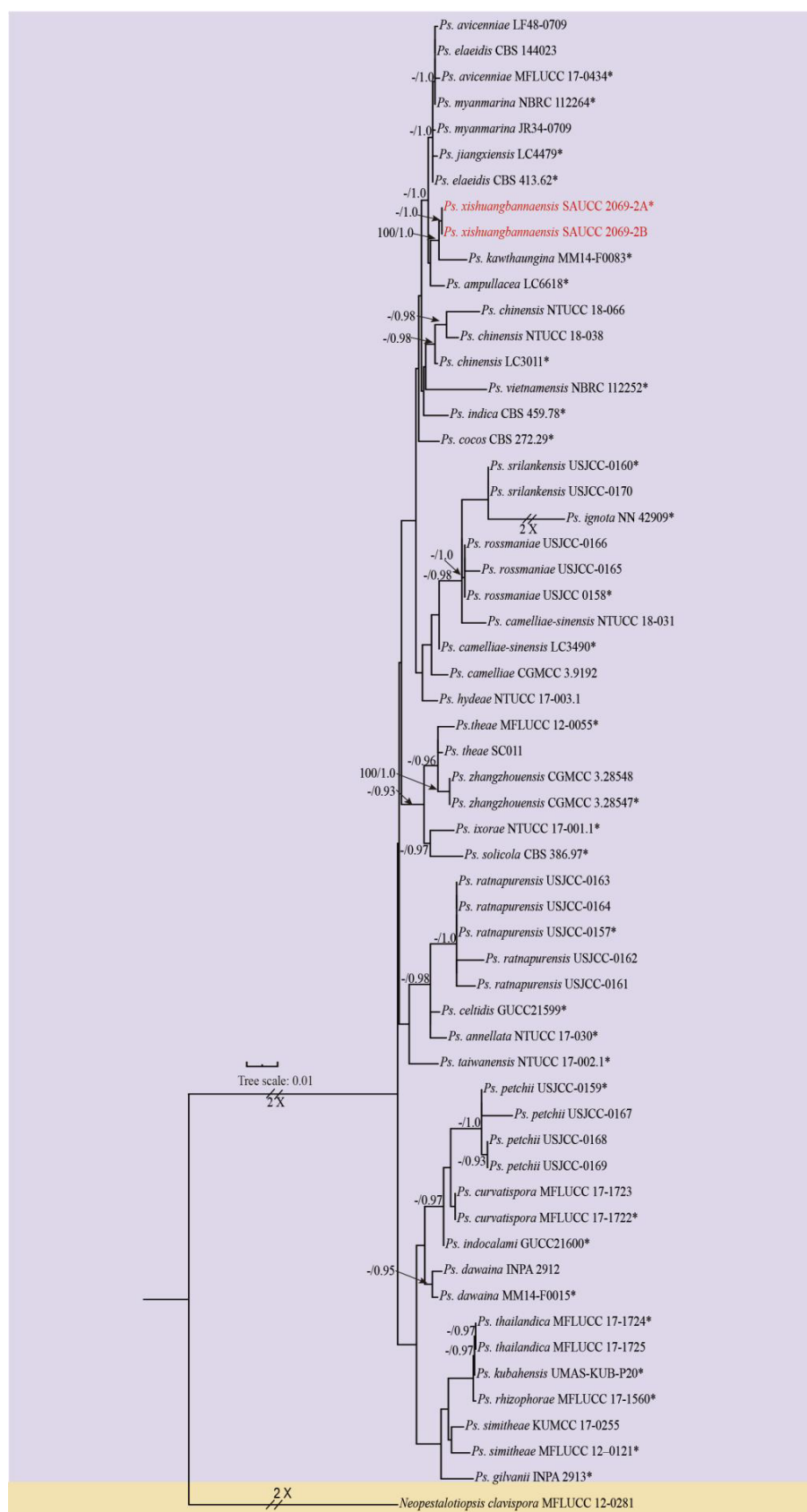


Fig. 43 Phylogenetic tree of the genus *Pseudoestalotiopsis* based on a concatenated ITS, *tef1-α*, and *tub2* sequences alignment, with *Neopestalotiopsis clavisporea* serving as outgroup. The Bayesian Inference Posterior Probability (right, BIPP ≥ 0.90) and the Maximum Likelihood Bootstrap Value (left, MLBV ≥ 95%) are shown as BIPP/MLBV above the nodes. Those marked "*" in the tree are represented as ex-type or ex-epitype strains. Strains isolated in this study were highlighted in red. The scale bar at the bottom indicates 0.01 substitutions per site. To enhance the visual appeal of the evolutionary tree layout, certain branches are shortened by two diagonal lines (//) with the number of times.

Micronectria Speg.
Papilionovela Aptroot
Pellucida Dulym., Sivan., P.F. Cannon & Peerally
Phragmitensis M.K.M. Wong, Poon & K.D. Hyde
Physalospora Niessl
Rachidicola K.D. Hyde & J. Fröhl.
Xenothecium Höhn.
 Iodosphaeriaceae O. Hilber
Iodosphaeria Samuels, E. Müll. & Petrini
 Melogrammataceae G. Winter
Melogramma Fr.
 Oxydothidaceae Konta & K.D. Hyde
Oxydothis Penz. & Sacc.
 Phlogicylindriaceae Senan. & K.D. Hyde
Ciferriascosea Senan., Bhat, Camporesi & K.D. Hyde
Idriellomyces Crous
Phlogicylindrium Crous, Summerb. & Summerell
Polyscytulum Riess
 Pseudomassariaceae Senan. & K.D. Hyde
Leiosphaerella Höhn.
Pseudapiospora Petr.
Pseudomassaria Jacz.
Pseudomassariella Petr.
 Pseudosporidesmiaceae Crous
Pseudosporidesmium K.D. Hyde & McKenzie
 Pseudotruncatellaceae Crous
Pseudotruncatella R.H. Perera, Camporesi, Maharachch. & K.D. Hyde
 Hyde
 Sporocadaceae Corda
Allelochaeta Petr.
Annellolacinia B. Sutton
Bartalinia Tassi
Broomella Sacc.
Cavernicola P. Razaghi, F. Liu & L. Cai
Ciliochorella Syd.
Diploceras (Sacc.) Died.
Disaeta Bonar
Discosia Lib.
Distononappendiculata F. Liu, L. Cai & Crous
Diversimediispora F. Liu, L. Cai & Crous
Doliomyces Steyaert
Heterotruncatella F. Liu, L. Cai & Crous
Hyalotiella Papendorf
Hymenopleella Munk
Immersidiscosia Kaz. Tanaka, Okane & Hosoya
Millesimomyces Crous & M.J. Wingf.
Monochaetia (Sacc.) Allesch.
Morinia Berl. & Bres.
Neopestalotiopsis Maharachch., K.D. Hyde & Crous
Nonappendiculata F. Liu, L. Cai & Crous
Nothoseiridium Crous
Parabartalinia F. Liu, L. Cai & Crous
Pestalotiopsis Steyaert (= *Pestalopezia* Seaver
Pseudopestalotiopsis Maharachch., K.D. Hyde & Crous
Pseudosarcostroma F. Liu, L. Cai & Crous
Robillarda Sacc.
Sarcostroma Cooke
Seimatosporium Corda
Seiridium Nees
Sporocadus Corda
Strickeria Körb.
Synnemapestaloides T. Handa & Y. Harada
Truncatella Steyaert

Xenoseimatosporium F. Liu, L. Cai & Crous
 Vialaeaceae P.F. Cannon
Vialaea Sacc.
 Amphisphaeriales genera incertae sedis
Chitonospora E. Bommer, M. Rousseau & Sacc.
Neoarthrinium Ning Jiang

Discussion

Molecular phylogenetic and evolutionary analyses have established a clear understanding of Amphisphaeriales, recognizing it as a distinct order within the subclass of Xylariomycetidae^[7,8,10,142,143]. As is well known, *Apiospora* is a genus of the Apiosporaceae family, which belongs to the order Amphisphaeriales. In this study, the geographical distributions of all tested *Apiospora* strains were mainly collected from the tropical region of Hainan Province. All of them showed a high association with Poaceae hosts. 76% and 72% of these genus strains were derived from Poaceae and bamboo, respectively (Supplementary Information 15). These findings support the previous studies that *Apiospora* is primarily associated with Poaceae plants in tropical and subtropical climates^[28,29,65,66]. The genus *Apiospora* exhibits diverse ecological roles, functioning not only as plant pathogens but also as endophytes. For instance, *A. marii* is associated with olive tree dieback in Italy^[144], and *A. phaeospermum* causes leaf necrosis in Sicily^[145]. Conversely, the endophytic *A. saccharicola* is known for producing industrial enzymes^[146]. Furthermore, *Apiospora* species produces a wide array of metabolic products; the ones that are obtained from *A. arundinis* perform antifungal activity against *Mucor hiemalis*^[14].

In this study, we isolated several strains of multiple species from a single infected leaf (Supplementary Information 16). For example, three species (e.g., *Apiospora baihualingensis*, *A. hydei*, and *A.*

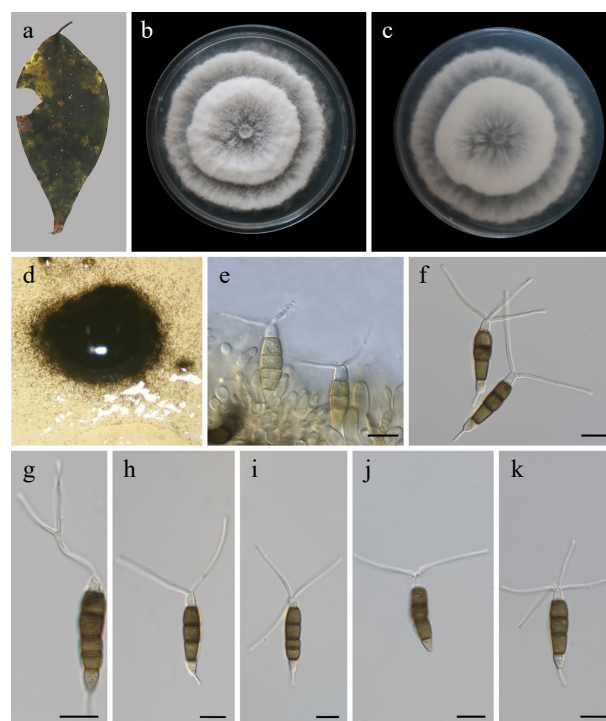


Fig. 44 *Pseudopestalotiopsis xishuangbannaensis* (CGMCC 3.29371, ex-type culture). (a) Leaf of the host plant. (b, c) Colonies after incubation on PDA for 7 days; top view (b) and bottom view (c). (d) Conidiomata formed in culture. (e) Conidia developed from conidiogenous cells. (f–k) Conidia. Scale bars: 10 µm (e–k).

qiongzhongensis) were identified from one diseased bamboo leaf. The co-infection (or mixed infection) phenomenon has been noted and discussed in previous studies^[147–151]. Therefore, these cases of multi-species infection in the same leaf reflect the pathobiome concept rather than the obsolete "one pathogen–one disease"^[152,153]. Recently, Han et al.^[151] demonstrated that the co-infection exemplified prominent advantages of the pathobiome concept: Firstly, microbes such as pathogens, endophytes, and saprophytes are often ambiguous and can mutually transition in nature^[154–156]. For example, for many so-called "pathogens", plant symptoms require high concentrations of conidia as a prerequisite^[157,158]. Secondly, these microbes can generate new pathogenic variants through hybridization or gene transfer, serving as a potential driver of pathogen evolution^[159–163]. Thirdly, since co-infection can enhance reproduction and transmission of pathogens^[164], the pathobiome concept provides a mechanistic explanation for the positive correlation between the richness of fungal pathogens and the severity of threats to plant health^[165]. Therefore, the widespread co-infection in the nature suggests that pathogens may closely interact with each other during disease development (Supplementary Information 16).

Species of pestalotioid taxa are known to cause various plant diseases, primarily manifesting as leaf spots, blights, and diebacks^[40,44,166]. However, these pestalotioid taxa pose a challenge for accurate identification due to their high degree of morphological similarity, particularly in the absence of molecular data^[12]. The advancement of knowledge regarding pestalotioid taxa relies on the collection, isolation, sequencing, and global sharing of new fungal data, thus enabling the precise delineation and distinction of these taxonomic groups through systematic species-level comparisons^[10]. Modern classification provides more accurate and reliable phylogenetic placements^[44,138,140]. Therefore, phylogenetic analysis is superior to morphological characteristics in the classification of pestalotioid taxa. Integrating phylogenetic analysis with chemical data provides a robust foundation for elucidating the relationships among species in pestalotioid taxa, which is crucial for constructing a more accurate and coherent taxonomic framework for this fungal taxa.

In this study, we revealed through phylogenetic analysis that several species of *Apiospora*, *Neopestalotiopsis*, and *Pestalotiopsis* exhibited abnormal long-branch attraction, as reported in previous publications^[63,140,167]. This phenomenon may be attributed to several factors, including sequencing errors, unequal evolutionary rates among different lineages, the absence of closely related taxa, alignment sequences containing many introns, or horizontal gene transfer^[168,169]. Therefore, phylogenetic resolution can be improved by expanding taxon sampling of extant species and applying suitable evolutionary models alongside informative outgroups^[170].

Amphisphaeriales comprises sixteen families and two incertae sedis genera^[16]. To determine the familial placements of these two incertae sedis genera in Amphisphaeriales, we advance the understanding of three families (Apiosporaceae, Beltraniaceae, and Sporocadaceae) and six genera (*Apiospora*, *Nigrospora*, *Beltraniella*, *Neopestalotiopsis*, *Pestalotiopsis*, and *Pseudopestalotiopsis*) using morphology and multilocus sequence analysis. All these studies contribute to refining taxonomic boundaries and clarifying phylogenetic relationships, thereby establishing a robust framework of classification for this fungal taxa. To further conduct the taxonomic study of this fungal taxa, genomic analysis, enzyme activity assays, and biogeographical analysis should be used to understand their distribution patterns in different ecological environments.

Ethical statements

No ethical statement was reported.

Author contributions

The authors confirm their contributions to the paper as follows: study conception and design: Liu QY and Zhang XG; data collection: Wang YL, Zhang MY, Dong ZX, Shang YX, Li DH, Yuan JY, Li XH, Jiang Y, Liu WW, and Wang XS; analysis and interpretation of results: Zhang ZX, Xia JW, Ai CC, Wang S, and Liu XY; draft manuscript preparation: Liu QY, Li Z, and Zhang XG. All authors reviewed the findings and approved the final manuscript.

Data availability

All of the data that support the findings of this study are available in the main text or Supplementary Information.

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Conflict of interest

The authors declare that they have no conflict of interest.

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