Phylogeny of Graphostromataceae with Three Species Isolated in China

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Abstract

Three species possessing characteristics of Graphostromataceae were observed in China. Morphology of the described species with illustrations and their phylogeny based on regions of internal transcribed spacers (ITS), the second largest subunit of the RNA polymerase II (RPB2), β-tubulin (TUB2) and α-actin (ACT) are provided. Two new species and one new record from China were identified. Morphologically, Biscogniauxia glaucae sp. nov. differs from B. atropunctata var. maritima, B. citriformis var. macrospora, B. fuscella and B. mediterranea by its stromata with raised margins, with clear outlines, with punctate ostioles openings and ascospores which are equilateral with broadly rounded ends, with a straight germ slit on the more concave side, nearly full spore length, lacking appendages and sheathes. ITS sequence difference between Graphostroma guizhouensis sp. nov and type strain of G. platystomum is 7%, which support identifying it as a new species. Camillea broomeana with scanning electron microscope description of ascospores was illustrated as a new record from China. Cryptostroma was proposed in Graphostromataceae based on molecular data. Vivantia was accepted in Graphostromataceae based on its morphological characteristics and Nodulisporium anamorphs which is similar with that of Biscogniauxia.

Introduction

Graphostromataceae M.E. Barr, J.D. Rogers & Y.M. Ju was erected to accommodate Graphostroma platystomum (Schwein.) Piroz. which was first belonged to Xylariaceae (Barr et al. 1993, Pirozynski 1974). Graphostroma platystomum was separeated from Diatrypaceae, and placed in Xylariaceae (Pirozynski 1974). Up to now, five genera, Biscogniauxia Kuntze, Camillea Fr., Graphostroma Piroz., Obolarina Pouzar, and Vivantia J.D. Rogers, Y.M. Ju & Cand. were listed in the family of Graphostromataceae (Wijayawardene et al. 2020).

Graphostroma was introduced to accommodate some fungi resembling Diatrype stigma (Hoffm. ex Fr.) Fr. as a monotypic genus of Xylariaceae (Pirozynski 1974). Graphostroma platystomum (Schw.) Piroz. was designated as type species. Since the features of two-layered stroma, diatrysoid configuration of short-breaked ascomata, holoblastic conidiogenesis of the Nodulosporium anamorph, faintly amyloid apical ring of asci, G. platystomum was proposed to under a new family of Graphostromataceae (Barr et al. 1993). Currently, only one species was accepted in the genus of Graphostroma.

Nummularia Tul. & C. Tul. was introduced in 1863 (Tulasne and Tulasne 1863). The name, Biscogniauxia Kuntze was used for the sexual morph of genus (Pouzar, 1979). Biscogniauxia was reviewed by Ju et al. (1998), and forty-nine taxa were accepted. In their study, morphological differences between similar genera were discussed, and a key to the species of Biscogniauxia was provided. The morphological characteristics of Biscogniauxia are as follows: stromata widely effuse with separate ostioles at the surface; perithecia mostly in a layer, but sometimes polystichous; asci 8-spored, cylindrical, with or without an amyloid apical ring; ascospores uniseriate, rarely biseriate, ellipsoid, and brown, with or without germ slits (Ju et al. 1998; Vasilyeva et al. 2007).
*Camillea* was erected to include taxa with applanate, carbonaceous, cylindrical, or broadly conic-truncate, bipartite stromata with light coloured ascospores (Fries 1849). *Camillea leprieurii* (Mont.) Mont. was designated as the lectotype by Montagne (1855). Læaessøe et al. (1989) reviewed the *Camillea* and made morphological descriptions of most species. Based on phylogenetic analysis, Wendt et al. (2018) accepted it as a genus of Graphostromataceae, which was followed by Daranagama (2018).

During investigation of Xylariales from Chian, three taxa possessing features of Graphostromataceae were collected. Based on morphological and molecular data, we identified them as *Biscogniauxia glaucae*, *Graphostroma guizhouensis*, *Camillea broomeana*. Detail descriptions were given in this paper. Meanwhile, we discuss the systematic classification of Grapholomataceae and suggest that *Vivantia* and *Cryptostroma corticale* (Ellis & Everh.) P.H. Greg. & S. Waller should be included in this family.

**Materials And Methods**

**Collection, isolation and morphology**

Specimens with black spots on their surfer were collected from Guizhou province, China. Materials were placed into paper bags with desiccant silica gel and taken to laboratory for examinations. Specimen collection information including location and collection time was recorded. Pure cultures were isolated using single-spore isolation (Chomnunti et al. 2014). Cultures were stored in screw cap centrifuge tubes containing potato-dextrose agar (PDA) medium at 4°C and were preserved in 2 mL screw cap centrifuge tubes with 10% glycerol at −20°C. Macroscopic characteristics were observed using Olympus SZ61 stereomicroscope and photographed with a fitted Canon 700D digital camera (Liu et al. 2018). The contents of the stomata were picked out and mounted in water and Melzer’s reagent for anatomical examination. Characteristics of asci, ascospores, and ascus apical apparatus were photographed using a Nikon digital camera (700D) fitted to a microscope (Nikon Ni). The dimensions of 30 ascospores, 20 asci, and 20 ascus apical apparatus were measured with Tarosoft ® image framework (v. 0.9.0.7). Microphotographs were modified appropriately without changing features, and were arranged as a plate using Adobe Photoshop CS6. The specimens were deposited in herbarium of Guizhou medical university (GMB), herbarium of Guizhou agricultural college (GACP) and herbarium of Kunming Institute of Botany (KUN), and living cultures were deposited in Guizhou medical university culture collection (GMBC).

**DNA extraction, PCR amplification and sequencing**

Pure cultures were grown on PDA at 25°C for 2 weeks. The fungal mycelia were scratched off with sterilized scalpel. Genomic DNA was extracted from fresh fungal mycelia using the BIOMIGA fungus genomic DNA extraction kit (GD2416, Biomiga, USA), following the manufacturer's instructions. DNA extractions were stored at −20°C. Region of internal transcribed spacers (ITS) was amplified with primers ITS4 and ITS1 (White et al. 1990; Gardes and Bruns 1993). Partial β-tubulin (*TUB2*) was amplified with primers Bt2a and Bt2b (Glass and Donaldson 1995). The second largest subunit of the RNA polymerase II
was amplified using primers (RPB2-5F, -7cF, and -7cR) introduced by Liu et al. (1999). The PCR primer pair ACT-512F/ACT-783R (Carbone and Kohn 1999) was used to amplify portions of the α-actin gene (ACT). The components of a 25 µL volume PCR mixture were as follows: double distilled water 9.5 µL, PCR Master Mix 12.5 µL, 1 µL of each primer, 1 µL template DNA. Qualified PCR products were checked with 1.5% agarose gel electrophoresis stained with GoldenView and sent to Sangon Co., China, for sequencing. The PCR conditions were: initial denaturation step at 95°C for 2 min, 35 cycles of 95°C for 30 seconds, 52°C (ITS), 61°C (TUB2), 54°C (RPB2), 58°C (ACT) for 45 s, 72°C for 1 min, and a final extension at 72°C for 5 min.

Sequence alignment and phylogenetic analyses

All strains for phylogenetic analyses were chosen based on Wendt et al. (2018) and top hits of ITS blasted in the GenBank database. Sequences downloaded from GenBank database for construction of phylogenetic tree are listed in supplement table. ITS, TUB2, RPB2 and ACT sequence data were assembled respectively using the MAFFT v.7.110 online programme (http://mafft.cbrc.jp/alignment/server/) with the default settings. Multiple sequence alignments of ITS, TUB2, RPB2 and ACT were combined and manually adjusted to reduced redundant gaps using BioEdit v.7.0.5.3 (Hall 1999). The maximum likelihood analyses were carried out in RAxML 7.4.2 Black Box (https://www.phylo.org/, Stamatakis et al. 2008). The final ML search was conducted using the GTR GAMMA + I model. All free model parameters were estimated by RAxML with ML estimates of 25 per site rate categories. The phylogenetic analyses were performed for Bayesian inference in MrBayes 3.2.7 online with default parameters (https://www.phylo.org/, Stamatakis et al. 2008). Markov chain Monte Carlo (MCMC) sampling in MrBayes v.3.2.2 (Ronquist et al. 2012) was used to determine the posterior probabilities (PP) (Rannala and Yang 1996). Six simultaneous Markov chains were run for 1000000 generations and trees were sampled every 1000th generation. Phylogenetic trees were viewed and arranged using FigTree v1.4.0. and edited with Microsoft PowerPoint and Adobe Photoshop CS6. The alignment was uploaded in TreeBASE (www.treebase.org/treebase-web/home.html) under ID 27791 for ITS-RPB2-TUB2-ACT alignment and tree.

Results

Phylogenetic analyses

Graphostromataceae taxa and closely related families were included in the phylogenetic analyses with two strains of Hypoxylon rickii (MUCL 53309) and H. pulicicidum (MUCL49879) as outgroup (Fig. 1). Datasets of ITS, RPB2, ACT and TUB2 were aligned respectively, and were combined to form a dataset of ITS-RPB2-TUB2-ACT. The dataset of ITS-RPB2-TUB2-ACT consisted 67 taxa, including the two sequences from two outgroup taxa, and contained 2785 alignable characters, 1347 constant characters, 1248 phylogenetically informative characters, and 190 parsimony-uninformative variable characters. Final ML optimization likelihood is -43391.566516. Topology of the complete RAxML and MrBayes trees were
consistent. The tree showed that *Camillea, Obolarina, Graphostroma* and *Cryptostroma* were nested within *Biscogniauxia* with a well-supported (100/1). Sequences of *Biscogniauxia glaucae* showed a close relationship with *B. formosana* with bootstrap (100/1), and showed as a distinct branch. GMBC0218 was nested in group of *Camillea*, which showed a very close kinship with *Camillea obularia* (Fr.) Læssøe, J.D. Rogers & Lodge. *Graphostroma guizhouensis* formed a distinctly branch within the group of *Graphostroma*.

**SEM**

About 5 mm sample of stromata for SEM investigations was processed by gold coating under critical point dryer (K850). Scanning electron microscopy (SEM Inspect) was carried out to examine the preparations. The images were saved and processed using Adobe Photoshop CS6.

**Taxonomy**

*Biscogniauxia glaucae* Q.R. Li, J.C. Kang & K.D. Hyde, sp. nov. Figure 2

MycoBank number: MB 835896;

Etymology: In reference to the host, *Quercus glauca* Thunb..

Holotype: GMB0007

*Saprobic* on dead bark of *Q. glauca*. **Sexual morph:** *Stromata* 3–5 cm long, 1–2 cm wide and 0.3–0.4 cm high, widely effused, flat, black, bipartite, confluent, with raised margins, perithecium immersed, with black ostioles. Stromatal tissue between perithecia composed entirely of carbonaceous tissue. **Ostioles** openings punctate, discretely encased by carbonaceous stromatal tissue, equal or slightly lower than stromatal surface, black. **Perithecia** 250–350 μm high, 130–260 μm wide (av. = 285 × 183 μm, n = 10), solitary, black, carbonaceous, immersed, in vertical section, obovoid, globose to subglobose, ostiolate. **Peridium** 45–70 μm thick, black. **Paraphyses** not observed. **Asci** 131–180 × 10.5–12.5 μm (av. = 152.5 × 11.5 μm, n = 20), 8-spored, unitunicate, cylindrical, short-pedicellate, apically round, with a J+, wedge apical apparatus in Melzer’s reagent, 3–4 μm high, 7.5–9.5 μm wide. **Ascospores** 13.5–16 × 7.5–9.5 μm (av. = 15 × 8.5 μm, n = 30), uniseriate, unicellular, dark brown to black, more or less equilateral with broadly rounded ends, smooth-walled, with a straight germ slit on the more concave side, nearly full spore length, lacking appendages and sheathes. **Asexual morph:** undetermined.

Culture characteristics: Colonies growing on PDA, reached 5 cm diam. after one week at 25 ºC, white, cottony, flat, low, dense, fructifications were not observed in culture.

Material examined: CHINA, Guizhou province, Guiyang city, Forest Park of Guiyang, on dead bark of *Q. glauca*, March, 2014, Q.R. Li, GZ72, (GMB0007, holotype, extype living culture GMBC0007; GACP2014QR58, isotype).
Other material examined: CHINA, Guizhou province, Guiyang city, Huaxi Park, on dead bark of unknown plant, June, 2014, Q.R. Li, GZH96 (GMB0029, living culture GMBC0029; GACP2014QR79).

Note

There were four species collected from China in the examined specimens by Ju et al. (1998). Most of them were obtained and published in Taiwan (Ju and Rogers 2001; Kuo et al. 2018). Currently, nine species were collected and introduced from China (Ju and Rogers 2001; Vasilyeva et al. 2009; Ariyawansa et al. 2015; Ma et al. 2020). Here we introduce a new species of Biscogniauxia found from China mainland. Molecular phylogenetic studies based on ITS, β-tubulin, RPB2 and ACT sequences indicated that B. glaucae form a distinct branch from other species and supported B. glaucae as a new species of Biscogniauxia. In morphology, this species has a similar ascospores size range to B. atropunctata var. maritima (Lar. N. Vassiljeva) Y.M. Ju & J.D. Rogers, B. citriformis var. macrospora Van der Gucht & Whalley, B. fuscella (Rehm) F. San Martín & J.D. Rogers and B. mediterranea (De Not.) Kuntze. However, stromata of B. glaucae have clear raised margins, with clear outlines which differ from those of them (Ju et al. 1998; Ju and Rogers 2001). Moreover, B. fuscella has white outer dehiscing layer and nearly equilateral ascospores with a cellular appendage on immature ascospores and some mature ascospores (Ju et al. 1998). Biscogniauxia atropunctata var. maritime shows different characteristics in having ostioles of slightly higher than the stromatal surface, with openings papillate and ascospores with narrowly rounded ends (Ju et al. 1998; Ju and Rogers 2001). Ascospores of B. citriformis var. macrospora are almost C-shaped with pinched ends, with spore-length on more convex side (Ju et al. 1998). Biscogniauxia mediterranea can be readily separated from the B. glaucae in having ostioles higher than stromatal surface, with openings coarsely papillate (Ju et al. 1998). The phylogenetic tree (Fig. 2) shows that B. glaucae, B. formosana and B. cylindrispora have a close relationship. However, B. formosana (15–22.5 × 8–11 µm) and B. cylindrispora (20–26 × 10–14 µm) has larger ascospores than those of B. glaucae.

Camillea broomeana (Berk. & M.A. Curtis) Læssøe, J.D. Rogers & Whalley, Mycol. Res. 93(2): 149 (1989) Fig. 3

MycoBank number: MB 135957;

Saprobic on the surface of stem of deciduous plant, Cerasus sp.. Sexual morph: Stromata widely effused, irregular in outline, black, erumpent through bark, edges raised, up to 4 cm length, up to 3 mm thick, first covered with an ectostromatal and host tissue layer which is readily lost. Ectostroma brown to black, crust, easily separated without clear ostioles. Entostroma carbonaceous, black, with a layer of ostioles on the surface, perithecia embedded. Ostioles indistinct papillate, central. Perithecia 295–380 × 195–264 µm (av. = 320 × 245 µm), ovoid to cylindrical. Paraphyses abundant, persistent, smooth, 3 µm wide, slightly longer than asci. Asci 144.5–190.5 × 7.5–15.5 µm (av. = 167 × 10 µm, n = 30), 8 -spored, unitunicate, cylindrical, rounded at apex, with a J+, jar-shape apical apparatus in Melzer's reagent, 2–4 µm high, 3–5 µm wide. Ascospores 10–15 × 4.5–6.5 µm (av. = 13 × 5.5 µm, n = 30), one-celled, uniseriate,
dilute brown, ellipsoid, mostly 1-guttulate, rounded ends, with rough warty ornamentation, without a germ slit. Asexual morph: Not observed on the surface of stromata and PDA medium.

Material examined: CHINA, Hainan province, Wuzhishan city, Emerald Park, (18°48′46.17″N, 109°30′45.54″E), on stem of Cerasus sp., November, 2020, Q.R. Li, 2020FCGY11, altitude: 475 m (GMB0218, extype living culture GMBC0218; HKAS 112698).

Note

There are two species of Camillea with echinulate ascospores, Camillea broomeiana and C. signata (Jong & Benjamin) Læaessøe, J. D. Rogers & Whalley. Camillea signata differs from C. broomeiana by its annulate ostioles (Læaessøe et al. 1989). Most species of Camillea have been discovered from in the Neotropics and the largest concentration of species occurs in the Amazon region (Læaessøe et al. 1989). No Camillea species by far was reported from China mainland. This is the first discovery of Camillea species in China mainland.

Graphostroma guizhouensis sp. nov. Q.R. Li Fig. 4

MycoBank number: MB XXX;

Etymology: In reference to the collection location.

Holotype: GMB0219

Saprobic on the surface of small branches of unknown deciduous plant. Sexual morph: Stromata black, widely effused, irregular in outline, black, up to 3 cm length, containing two layers. Ectostroma brown to black, crust, carbonaceous, easily separated, with cracks, without clear ostioles. Entostroma cracked, with a layer of ostioles on the surface, perithecia embedded. Ostioles crater-like, central. Perithecia 285–322 × 175–234 µm (av. = 302 × 198 µm), bottle-shaped, pyriform with a neck, with hyaline wall. Paraphyses not observed. Asci 25–39 × 3.5–6 µm (av. = 31.5 × 5 µm), 8-spored, unitunicate, clavate, short-stalked, rounded at apex, with a non-amyloid ring in the apical apparatus. Ascospores 6–7.5 × 1–1.5 µm (av. = 6.8 × 1.4 µm), one-celled, colorless, reniform, equilateral, rounded ends, without germ slit. Asexual morph: Not observed on the surface of stromata and PDA medium.

Examined specimen: CHINA, Guizhou Province; Guiyang city, Aha lake (26°36′50.21″N, 106°40′15.78″E), on dead wood, August, 2020, collector: Sihan Long, 2020AH23, altitude: 1108 m (GMB0219, holotype, extype living culture GMBC0219; HKAS 112684, isotype).

Additional examined specimen: CHINA, Guizhou Province; Guiyang, Aha lake (26°32′50.37″N, 106°40′16.65″E), on dead wood, August, 2020, collector: Yinhui Pi, 2020AH28, Altitude: 1090 m (GMB0008, living culture GMBC0008).

Note
Here we would like to propose a new species of *Graphostroma*, although *Graphostroma guizhouensis* shows similar features with *G. platystomum*. A comparison of the ITS region DNA sequence data between *G. guizhouensis* and *G. platystomum* (CBS 270.87, type material of *G. platystomum*) revealed base pair differences of 7% which supports establishment of *G. guizhouensis* as a new taxon. We speculate that *Graphostroma platystomum* should be a group containing some cryptic species. Their morphological characteristics are very similar, but their DNA sequences are quite different. And DNA sequences should be a main diagnostic feature for the genus of *Graphostroma*.

**Discussion**

*Nummularia* was introduced in 1863 to accommodate the fungi which have flattened dis-shaped stromata reminiscent of coins. *Obolarina, Camillea* and *Biscogniauxia* all possess *Nummularia*-like anamorphs. *Biscogniauxia* was adopted for the genus (Pouzar 1979). *Obolarina* was separated from *Biscogniauxia* with *Obolarina dryophila* (Tul. & C. Tul.) Pouzar (= *Nummularia dryophila* Tul. & C. Tul.) as the type species (Pouzar 1986). *Obolarina dryophila* possesses spiral germination slits of rather large spores which differ from those of *Biscogniauxia*. *Obolarina* and *Biscogniauxia* have almost the same morphological characteristics, such as the morphology of the stromata, asci, ascospores. Ju et al. (1998) reviewed the *Biscogniauxia* and presented a key that contained genera with close affinities. They figured out that the main difference between *Obolarina* and *Biscogniauxia* is that *Obolarina* lacks an ascal apical ring. *Camillea* is characterized by dark brown or black and carbonaceous bipartite stromata, asci with blue apical rings in Melzer’s iodine reagent and hyaline or light brown ornamented ascospores lacking a germ slit (Læaessøe et al. 1989). These characteristics of *Camillea* can clearly distinguish it from *Obolarina* and *Biscogniauxia*.

The anamorphic fungi *Cryptostroma corticale* introduced as type species of *Cryptostroma* can cause sooty bark disease of *Acer pseudoplatanus* L. (Gregory et al. 1951). Stroma was described as two layers of “floor stroma” and “roof stroma” by Gregory et al. (1951). Pirozynski (1974) established a new genus, *Graphostroma* to accommodate *G. platystomum*, and placed it among Xylariaceae. Molecular systematic studies indicated the close affinity of *Graphostroma* and *Biscogniauxia* (Smith et al. 2003). Based on ITS rDNA sequences, Koukol et al. (2015) treated *C. corticale* as a Hypoxyloideae clade of Xylariaceae which closed to *G. platystomum* and *Biscogniauxia*. In this study, we get the similar result. *Cryptostroma* was listed in Xylariales genera incertae sedis (Wijayawardene et al. 2020). Here, we propose to place *Cryptostroma* in Graphostromataceae.

*Vivantia* was accepted in the Amphisphaeriaceae to include species with features of bipartite, carbonaceous, applano-pulvinate stromata, cylindrical asci with apical ring bluing in Melzer's reagent and two-celled, subhyaline ascospores without germ slit (Rogers et al. 1996). Two-layers, carbonaceous stromata and *Nodulisporium* anamorphs indicate its affinity with *Biscogniauxia*. *Vivantia* was listed in the family of Graphostromataceae without any evidences (Wijayawardene et al. 2020). In this paper we provides evidences and would like accept *Cryptostroma* and *Vivantia* in Graphostromataceae, based on
their common features, bipartite stromata, asci with apical ring bluing in Melzer's reagent, light-colored ascospores, *Nodulisporium* or *Xylocladium* like anamorphs.

Molecular phylogenetic analysis indicated that species of Graphostromataceae form monotypic family with high value (100/1), and *Biscogniauxia* is not a monotypic genus. *Biscogniauxia* was divided into 8 clades. *Obolarina, Camillea* and *Graphostroma* clusted in the branch of *Biscogniauxia*, have close relationship with *Biscogniauxia*. *Obolarina, Camillea* and *Graphostroma* form a monophyletic group respectively. *Biscogniauxia mediterranea* and *B. rosacearum* (clade 1) indicate a close relationship with *Obolarina*. Nevertheless, *Biscogniauxia mediterranea* have an apical ring of ascus bluing in Melzer's iodine reagent and dark brown ascospores (Ju et al. 1998). *Biscogniauxia_rosacearum* was published as an endophytic fungus without description of sexual morph. *Biscogniauxia granmoi* and *B. marginata* (clade 6) have close genetic relationship with *Cryptostroma* and *Graphostroma*. However, the ascospores of *B. granmoi* and *B. marginata* are brown which distinct from those of *Cryptostroma* and *Graphostroma* (Ju et al. 1998, Læssøe et al. 1999). In terms of the morphological characteristics of ascospores, the differences between *Camillea, Graphostroma, Cryptostroma* and *Biscogniauxia* are very obvious. However, phylogeny showed that *Camillea, Graphostroma,* and *Cryptostroma* were in the branch of *Biscogniauxia*. We speculate that the morphological diagnostic features currently used are insucient for the systematic classification of *Biscogniauxia* and its related genera. *Biscogniauxia* may be divided into some genera to maintain the uniformity of genus characteristics. Compared with the published morphological species, there are relatively few species with available DNA sequences of *Biscogniauxia* and *Camillea*, which leads to the confusion of kinship of *Camillea, Obolarina* and *Cryptostroma*. We will not make arbitrary divisions of this genus for the time being. We look forward to more available DNA sequences or new diagnostic features to solve the systematic classification problem of *Biscogniauxia*.

**Declarations**

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**References**

1. Ariyawansa H, Hyde DK, Jayasiri S, Buyck B, Thilini Chethana KW, Dai DQ, Dai, YC, Daranagama DA, Jayawardena RS, Lücking R, Ghobad-Nejhad M et al (2015) Fungal Diversity Notes 111–252—
taxonomic and phylogenetic contributions to fungal taxa. Fungal Divers 75(1): 27–274. https://doi.org/10.1007/s13225-015-0346-5

2. Barr ME, Rogers JD, Ju YM (1993) Revisionary studies in the calosphaeriales. Mycotaxon, 48:529–535.

3. Bills GF, Victor GM, Jesús M, Gonzalo P, Jacques F, P Derek Stadler M, Maria-Jose F (2012) Hypoxylon pulicicidum sp. nov. (Ascomycota, Xylariales), a pantropical insecticide-producing endophyte. Plos One 7(10):e46687. https://doi.org/10.1371/journal.pone.0046687

4. Carbone I, Kohn LM (1999) A method for designing primer sets for speciation studies in filamentous ascomycetes. Mycologia 91: 553–556. https://doi.org/10.2307/3761358

5. Chomnunti P, Hongsanan S, Aguirre-Hudson B, Tian Q, Peršoh D, Dhami MK, Alisa AS, Xu JC, Liu XZ, Stadler M, Hyde KD (2014) The sooty moulds. Fungal Divers 66: 1–36. https://doi.org/10.1007/s13225-014-0278-5

6. Crous PW, Wingfield MJ, Schumacher RK, Akulov A, Bulgakov TS, Carnegie AJ, Jurjevič Ž, Decock C, Denman S et al. (2020) New and Interesting Fungi. 3. Fungal Syst Evol 6(1): 157–231. https://doi.org/10.3114/fuse.2020.06.09

7. Daranagama DA, Camporesi E, Tian Q, Liu XZ, Chamuyang S, Stadler M, Hyde KD (2015) Anthostomella is polyphyletic comprising several genera in Xylariaceae. Fungal Divers 73(1):203-238. https://doi.org/10.1007/s13225-015-0329-6

8. Daranagama DA, Hyde KD, Sir EB, Thambugala K, Tian Q, Samarakoon MC, Mckenzie E, Jayasiri SC, Tibpromma S, Bhat DJ, Liu XZ, Stadler M (2018) Towards a natural classification and backbone tree for Graphostromataceae, Hypoxylaceae, Lopadostomataceae and Xylariaceae. Fungal Divers 88:1–165. https://doi.org/10.1007/s13225-017-0388-y

9. Fries EM (1849). Summa Vegetabilium Scandinaviae. Part 2. Stockholm & Leipzig: Bonnier.

10. Gardes M, Bruns TD (1993) ITS primers with enhanced specificity for basidiomycetes – application to the identification of mycorrhizae and rusts. Mol Ecol 2: 113–118. https://doi.org/10.1111/j.1365-294X1993tb00005x

11. Glass NL, Donaldson GC (1995) Development of primer sets designed for use with the PCR to amplify conserved genes from filamentous ascomycetes. Appl Environ Microbiol 61: 1323–1330.

12. Gregory PH, Waller S (1951) Cryptostroma corticale and sooty bark disease of sycamore (Acer pseudoplatanus). Trans Br Mycol Soc 34: 579, IN8–597, IN10.

13. Hall TA (1999) BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symp Ser 41: 95–98.

14. Hsieh HM, Lin CR, Fang MJ, Rogers JD, Fournier J, Lechat C, Ju, YM (2010) Phylogenetic status of Xylaria subgenus Pseudoxyllaria among taxa of the subfamily Xylarioideae (Xylariaceae) and phylogeny of the taxa involved in the subfamily. Mol Phylogenet Evol 54: 957e969. https://doi.org/10.1016/j.mpev.2009.12.015

15. Jaklitsch WM, Gardiennnet, Voglmayr H (2016) Resolution of morphology-based taxonomic delusions: Acrocordiella, Basiseptospora, Blogiascospora, Clypeosphaeria, Hymenopleella, Lepteutypa,
Pseudapispora, Requienella, Seiridium and Strickeria. Persoonia 37:82–105. https://doi.org/10.3767/003158516X690475

16. Jaklitsch WM, Voglmayr H. (2012) Phylogenetic relationships of five genera of Xylariales and Rosasphaeria gen. nov. (Hypocreales). Fungal Divers 52(1):75–98. https://doi.org/10.1007/s13225-011-0104-2

17. Ju YM, Rogers JD, San Martín F, Granmoi A (1998) The genus Biscogniauxia. Mycotaxon 66: 1–98.

18. Ju YM, Rogers JD (2001) New and interesting Biscogniauxia taxa, with a key to the world species. Mycol Res 105: 1123–1133. https://doi.org/10.1016/s0953-7562(08)61976-0

19. Koukol O, Kelnarová I, Černý K. (2015) Recent observations of sooty bark disease of sycamore maple in Prague (Czech Republic) and the phylogenetic placement of Cryptostroma corticale. Forest Pathol 45: 21–27. https://doi.org/10.1111/efp.12129

20. Kuhnert E, Fournier PF, Peršoh D, Luangsa-ard JJ, Stadler M (2013) New Hypoxylon species from Martinique and new evidence on the molecular phylogeny of Hypoxylon based on ITS rDNA and β-tubulin data. Fungal Divers 64:181–203. https://doi.org/10.1007/s13225-013-0264-3

21. Kuo WH, Chen CY, Kuo CH, Goh TK (2018) Some ascomycetes from the alishan national scenic area, Chiayi County, Taiwan. Nova Hedwigia 107: 531–542. https://doi.org/10.1127/nova_hedwigia/2018/0490

22. Læssøe T, Rogers JD, Whalley AJS. (1989) Camillea, Jongiella and light spored species of Hypoxylon. Mycol Res 93(2): 121 155. https://doi.org/10.1016/S0953-7562(89)80111-X

23. Læssøe T, Scheuer S, Granmoi A (1999) Biscogniauxia granmoi (Xylariaceae) in Europe. Östen. Z. Pilzk 8:139–147.

24. Li QR, Wen TC, Kang JC, Hyde KD (2015) A new species of Collocliscula (Xylariaceae) from China. Phytotaxa 205:187–196. https://doi.org/10.11646/phytotaxa.205.3.6

25. Liu LL, Long QD, Kang JC, Zhang X, Hyde KD, Shen XC, Li QR (2018) Morphology, and phylogeny of Mycopepon. Mycosphere 9: 779–789. https://doi.org/10.1093/mycosphere/9/4/6

26. Liu YL, Whelen S, Hall BD (1999) Phylogenetic relationships among ascomycetes: evidence from an RNA polymerase II subunit. Mol Biol Evol 16: 1799–1808. https://doi.org/10.1093/oxfordjournals.molbev.a026092

27. Malysheva EF, Malysheva VF, Kovalenko AE, Gromyko MN, Pimenova EA (2012) The participation of Biscogniauxia maritima (Xylariaceae, Ascomycota) in oak dieback revealed in the Sikhote-Alinsky Nature Reserve. Mikol. Fitopatol. 46: 217–225.

28. Ma XY, Nontachaiyapoom S, Hyde KD, Jeewon R, Doilom M, Chomnunti P; Kang JC (2020) Biscogniauxia dendrobii sp. nov. and B. petrensis from Dendrobium orchids and the first report of cytotoxicity (towards A549 and K562) of B. petrensis (MFLUCC 14-0151) in vitro. S Afr J Bot 134: 382–393. https://doi.org/10.1016/j.sajb.2020.06.022

29. Mirabolfathy M, Ju YM, Hsieh HM, Roger JD (2013) Obolarina persica sp nov, associated with dying Quercus in Iran. Mycoscience 54: 315–320. https://doi.org/10.1093/sysbio/sys029
30. Montagne JFC (1855) *Cryptogamia guyanensis.* Annales des Sciences Naturelles 4. Serie, Botanique 3: 91–144.

31. Pažoutová S, Šrůtka P, Holuša J, Chudíčková M, Kolařík, M (2010) The phylogenetic position of *Obolarina dryophila* (Xylariales). Mycol Prog 9: 501–507. https://doi.org/10.1007/s11557-010-0658-5

32. Pirozynski KA (1974) *Xenotypa* Petrak and *Graphostroma* gen. nov. segregates from Diatrypaceae. Can J Bot, 52:2129–2135.

33. Pouzar Z (1979) Notes on taxonomy and nomenclature of *Nummularia* (Pyrenomycetes). Czech Mycol 33: 207–219.

34. Pouzar Z (1986) A key and conspectus of central European species of *Biscogniauxia* and *Obalarina* (Pyrenomycetes). Czech Mycol 40: 11–10.

35. Raimondo ML, Lops F, Carlucci A (2016) Charcoal canker of pear, plum, and quince trees caused by *Biscogniauxia rosacearum* sp nov in Southern Italy. Plant Dis 100: 1813–1822. https://doi.org/10.1094/PDIS-09-15-1037-RE

36. Rannala B, Yang, Z (1996) Probability distribution of molecular evolutionary trees: a new method of phylogenetic inference. J Mol Evol 43: 304–311. https://doi.org/10.1007/BF02338839

37. Rogers JD, Ju YM, Candoussau F (1996) *Biscogniauxia anceps* comb. nov. and *Vivantia guadalupensis* gen. et sp. nov. Mycol Res 100:669–674. https://doi.org/10.1016/S0953-7562(96)80196-1

38. Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck J (2012) MrBayes 32: efficient Bayesian phylogenetic inference and model choice across a large model space. Syst Biol 61: 539–42. https://doi.org/10.1093/sysbio/sys029

39. Senanayake IC, Maharachchikumbura SSN, Hyde KD, Bhat JD, Jones EBG, McKenzie EHC, Dai DQ, Daranagama DA, et al. (2015) Towards unraveling relationships in Xylariomycetidae (Sordariomycetes). Fungal Divers 73:73–144. https://doi.org/10.1007/s13225-015-0340-y

40. Smith GJ, Liew ECY, Hyde KD (2003) The Xylariales: a monophyletic order containing 7 families. Fungal Divers 13: 175–208.

41. Stadler M, Kuhnert E, Peroh D, Fournier J (2013) The Xylariaceae as model example for a unified nomenclature following the "One Fungus-One Name" (1F1N) concept. Mycology 4(1): 5–21. http://dx.doi.org/10.1080/21501203.2013.782478

42. Stamatakis A, Hoover P, Rougemont J (2008) A rapid bootstrap algorithm for the RAxML web servers. Syst Biol 75: 758–771. https://doi.org/10.1080/10635150802429642

43. Tulasne LR, Tulasne C (1863) Selecta fungorum Carpologia 2: 363p

44. U'Ren, Jana M, Miadlikowska J, Zimmerman NB, Lutzoni F (2016) Contributions of North American endophytes to the phylogeny, ecology, and taxonomy of Xylariaceae (Sordariomycetes, Ascomycota). Mol Phylogenet Evol 98: 210–232. https://doi.org/10.1016/j.mpev.2016.02.010

45. Vasilyeva L, Li Y, Stephenson S (2009) Some pyrenomycetous fungi new to China. Mycotaxon 109: 415–428. https://doi.org/10.5248/109415
46. Vasilyeva LN, Stephenson SL, Miller AN (2007) Pyrenomycetes of the Great Smoky Mountains National Park IV Biscogniauxia, Camaropella, Camarops, Camillea, Peridoxylon and Whalleya. Fungal Divers 25: 219–231

47. Voglmayr H, Beenken L (2020) Linosporopsis, a new leaf-inhabiting scolecosporous genus in Xylariaceae. Mycol Prog 19(3):205–222. https://doi.org/10.1007/s11557-020-01559-7

48. Voglmayr H, Friebes G, Gardiennet A, Jaklitsch WM (2018) Barrmaelia and Entosordaria in Barrmaeliaceae (fam. nov. Xylariales) and critical notes on Anthostomella-like genera based on multigene phylogenies. Mycol Prog 17:155–177. https://doi.org/10.1007/s11557-017-1329-6

49. Vu D, Groenewald M, De Vries M, Gehrmann T, Stielow B, Eberhardt U, Al-Hatmi A, Groenewald JZ, Cardinali G, Houbraken J, Boekhout T, Crous PW, Robert V, Verkley GJM (2019) Large-scale generation and analysis of filamentous fungal DNA barcodes boosts coverage for kingdom fungi and reveals thresholds for fungal species and higher taxon delimitation. Stud Mycol 92: 135–154. https://doi.org/10.1016/jstudmycol.2018.05.001

50. Wendt L, Sir EB, Kuhnert E, Heitkämper S, Lambert C, Hladki Al, Romero Al, Luangsa-ard JJ, Srikitikulchai P, Peršoh D, Stadler M (2018) Resurrection and emendation of the Hypoxylaceae, recognised from a multigene phylogeny of the Xylariales. Mycol Prog 17: 115–154. https://doi.org/10.1007/s11557-017-1311-3

51. Wijayawardene NN, Hyde KD, Al-Ani LKT, Tedersoo L, Haelewaters D, Rajeshkumar KC, Zhao RL, Aptroot A, et al. (2020) Outline of Fungi and fungi-like taxa. Mycosphere 11: 1060–1456. https://doi.org/10.5943/mycosphere/11/1/8

52. White TJ, Bruns T, Lee S, Taylor JW (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics PCR protocols: a guide to methods and applications Academic Press, San Diego, California, pp 315–322. https://doi.org/10.1016/B978-0-12-372180-850042-1

53. Zhang ZF, Liu F, Zhou X, Liu XZ, Liu SJ, Cai, L (2017) Culturable mycobiota from Karst caves in China, with descriptions of 20 new species. Persoonia 39: 1–31. https://doi.org/10.3767/persoonia20173901

Figures
Figure 1

Phylogeny of Graphostromataceae and its allies obtained from a Maximum Likelihood analysis of the combines of ITS, RPB2, TUB2 and ACT using RAxML-HPC BlackBox software online. Hypoxylon rickii (MUCL 53309) and H. pulicicidum (MUCL49879) were taken as outgroup. Strains numbers were followed by their names. Bayesian posterior probabilities >0.95 and bootstrap support values for maximum
likelihood (ML) higher than >75% are marked above the nodes; an en-dash ("-") indicates a value <0.95 (PP) or <75% (BS). The bold branches indicate the support values are 100/1.

Figure 2

Biscogniauxia glaucae (GMB0007, holotype) a Material. b Ascomata on the surface of host. c Section of ascomata. d–j Asci with ascospores (stained in Melzer’s reagent). h–j Ascospores. l Ascus apex with a J+ apical apparatus. Scale bars: b, c=200 μm, d–g=10 μm, h–l=5 μm
Figure 3

Camillea broomeiana (GMB0218). a Material. b the stromata on stem surface of Cerasus yedoensis. c longitudinal section of ascomata. d Cross-section of ascomata. e,f Ascus apex with a J+ apical apparatus (stained in Melzer’s reagent). g Fragments of stromata in KOH without pigments. h–k Asci with ascospores l–o Ascospores with one guttulat and rough warty ornamentation e. Scale bars: e,f =10 μm, h–n=10 μm.
Figure 4

Graphostroma guizhouensis. (GMBC0219, holotype) a Material. b the inner layer of stromata c the outer layer of stromata. d the stromata on the surface of unknown plant. e Cross-section of ascomata (inner layer of stromata). f Longitudinal section of ascomata (inner layer of stromata) g Ascus apex with a non-amyloid ring in Melzer's reagent. h–k Asci with ascospores. l–q Ascospores. Scale bars: g–k =10 μm
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