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# WITHDRAWN: The hidden diversity of diatrypaceous fungi in China; introducing Allodiatrypella gen. nov. and ten new species

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#### Research

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## EDITORIAL NOTE:

The full text of this preprint has been withdrawn by the authors while they make corrections to the work. Therefore, the authors do not wish this work to be cited as a reference. Questions should be directed to the corresponding author.

# Abstract

In this study, we investigated the diversity of diatrypaceous fungi from six regions in China based on morpho-molecular analyses (maximum parsimony, maximum likelihood and Bayesian inference analyses of combined ITS and *tub2* gene regions). We accept 24 genera in *Diatrypaceae* with 19 genera involved in the phylogram and the other five genera are lacking living materials with available sequences. Eleven species include in four genera (*viz. Allocryptovalsa, Diatrype, Eutypella* and *Allodiatrypella* gen. nov.) have been isolated from seven hosts species, of which ten novel species (*Allocryptovalsa castanea, Allodiatrypella betulae, A. betulicola, A. betulina, A. hubeiensis, A. xinjiangensis, Diatrype betulae, D. castaneicola, D. quercicola* and *Eutypella castaneicola*) are introduced in this study, while *Eutypella citricola* is a new record from *Morus* host. Current results show the high diversity of members of *Diatrypaceae* species which are wood-inhabiting fungi in China.

# Introduction

*Diatrypaceae* Nitschke is an important family in *Xylariales* Nannf. (*Sordariomycetes, Ascomycota*), containing many taxa with a worldwide distribution (Chlebicki 1986; Glawe and Jacobs 1987; Carmarán et al. 2006; Vasilyeva and Ma 2014; Dayarathne et al. 2016; de Almeida et al. 2016; Mayorquin et al. 2016; Senwanna et al. 2017; Shang et al. 2017, 2018; Moyo et al. 2018; Konta et al. 2020; Wijayawardene et al. 2020). The family *Diatrypaceae* was proposed by Nitschke (1867, as Diatrypaee) and accepted five genera (Table 1). Members of the *Diatrypaceae* are frequently saprobic on the decaying wood of angiosperms (Tendulkar 1970; Glawe and Rogers 1984; Acero et al. 2004; de Almeida et al. 2016), and Caroll et al. (1977) reported an asexual morph of *Diatrypaceae* (*Libertella* sp.) as an endophyte of *Picea abies*, a gymnosperm host. Few endophytes such as *Diatrypella frostii* and *Peroneutypa scoparia* were reported later (de Errasti et al. 2010; Vieira et al. 2011; Grassi et al. 2014). Strikingly, several plant pathogens of *Diatrypaceae* were reported causing cankers, dieback and grapevine trunk diseases, e.g., *Cryptosphaeria populina* was linked to canker in species of *Populus* (Glawe and Rogers 1984); *Cryptosphaeria pullmanensis* caused canker disease of *Populus alba* and *Salix alba* (Ma et al. 2016); *Cryptovalsa ampelina* caused grapevine trunk disease on species of *Vitis* (Luque et al. 2006); *Eutypa lata* was associated with canker and dieback of *Prunus armeniaca* and species of *Vitis* (Lardner et al. 2005); *Eutypa leptoplaca* contributed to the dieback of grapevines (Trouillas and Gubler 2004; Catal et al. 2007); and *Eutypella parasitica* caused canker in species of *Acer* (Rappaz 1987).

Kirk et. al (2001) accepted nine genera in this family. Later, Kirk et al. (2008) listed 13 genera and 229 species in *Diatrypaceae* (Table 1). *Diatrypasimilis* J.J. Zhou & Kohlm., *Monosporascus* Pollack & Uecker and *Pedumispora* K.D. Hyde & E.B.G. Jones have been added to the family in subsequent studies by Abdel-Wahab et al. (2014), Klaysuban et al. (2014), Maharachchikumbura et al. (2015). Wijayawardene et al. (2018) reported 17 genera in the family (Table 1). Later, Dayarathne et al. (2016), Senwanna et al. (2017), Phookamsak et al. (2019) introduced *Halodiatrype* Dayar. & K.D. Hyde, *Allocryptovalsa* Senwanna et al. and *Neoeutypella* M. Raza & Q.J. Shang respectively and accepted as members of *Diatrypaceae*. Wijayawardene et al. (2020) listed 20 genera in the family. Subsequently, Konta et al. (2020) and Dayarathne et. al (2020a, b) respectively added *Allodiatrype* Senwanna et al., *Halocryptosphaeria* Dayar. et al. and *Halocryptovalsa* Dayar. & K.D. Hyde to this family.

The sexual morph members of *Diatrypaceae* are characterized by perithecial ascomata, usually embedded in a black stroma, cylindricclavate to clavate, long pedicellate asci and allantoid ascospores (Glawe and Rogers 1984; Rappaz 1987; Mehrabi et al. 2015; Dayarathne et al. 2016; de Almeida et al. 2016). Asexual morphs of *Diatrypaceae* have been reported as *coelomycetes* or *hyphomycetes viz. Cytosporina* Sacc., *Libertella* Desm. and *Phaeoisaria* Höhn. (Glawe and Rogers 1984; Wijayawardene et al. 2012; Liu et al. 2015; Mehrabi et al. 2015; Dayarathne et al. 2016; de Almeida et al. 2016). However, the asexual morphs of many sexual species have to be determined (Acero et al. 2004). Kliejunas and Kuntz (1972) reported the asexual morph of *Eutypella parasitica* as coelomycetous, occurring on the host substrate and sporulating in cultures. The genus *Libertella* has been reported as the asexual morph of *Cryptovalsa ampelina* which was not seen on host substrate, but sporulated on culture (Mostert et al. 2004). Conidia of *Diatrypaceae* are usually unicellular, hyaline, cylindrical or filiform or allantoid, slightly curved and group in a slim mass (Glawe and Rogers 1982, 1984; Glawe 1983; Mostert et al. 2004; Luque et al. 2006). However, in most cases, it is difficult to differentiate diatrypaceous species based on asexual morphs (Glawe and Roger 1986; de Almeida et al. 2016). *Eutypella parasitica* was reported with both acervuli and pycnidial morphs on natural substrates and in cultures (Kliejunas and Kuntz 1972). Croxall (1950) reported that cultures of *Diatrypella favaceae* and *D. quercina* can produce microconidia and macroconidia at the same time.

*Diatrypaceae* species are difficult to identify based on morphology due to overlapping phenotypic characters (Glawe and Rogers 1984; Trouillas et al. 2011; Dayarathne et al. 2016; Senwanna et al. 2017; Shang et al. 2017; Konta et al. 2020). Polyphasic approaches to solve the taxonomy of fungi were very common in recent studies (Lawrence et al. 2016; Wijayawardene et al. 2016; Norphanphoun et al. 2017; Fan et al. 2018, 2020; Zhu et al. 2020). The first molecular phylogenetic analyse of *Diatrypaceae* based on ITS showed that *Cryptosphaeria*, *Diatrype*, *Diatrypella*, *Eutypa* and *Eutypella* were polyphyletic (Acero et al. 2004). The molecular (mostly based on ITS and *tub2* sequence data) and morphological data were widely applied for the primary identification and classification of diatrypaceous taxa recently (Phookamsak et al. 2019; Dayarathne et al. 2020b; Hyde et al. 2020b; Konta et al. 2020). Moreover, Konta et al. (2020) introduced one new genus *Allodiatrype* and five new species, *Allocryptovalsa elaeidis*, *Allodiatrype arengae*, *A. elaeidicola*, *A. elaeidis* and *Diatrypella elaeidis* from palms (Arecaceae) based on this criterion.

During the collecting program of forest pathogens that cause canker or dieback diseases in China, 86 diatrypaceous specimens associated with various disease symptoms were collected from Beijing City, Xinjiang Uygur Autonomous Region and four other provinces in China *viz.* Hubei, Hebei, Jiangsu and Yunnan. As the higher-level phylogeny of many genera within the *Diatrypaceae* remains unclear in China, the purpose of this study was to improve the phylogenetic systematics of *Diatrypaceae*.

# Methods

#### Sampling and isolation

Eighty-six fresh specimens of *Diatrypaceae* were collected from infected branches of seven tree hosts (*Betula albosinensis, B. davurica, B. platyphylla, Castanea mollissima, Juglans regia, Morus alba* and *Quercus mongolica*) from Beijing City, Xinjiang Uygur Autonomous Region and four other provinces in China *viz*. Hubei, Hebei, Jiangsu and Yunnan. Specimens were put into envelope with recording altitude, collector, collecting time, host, longitude and latitude. A total of 21 representative isolates were obtained by removing a mucoid spore mass from conidiomata or ascomata of fresh specimens and spreading suspension the on the surface of 1.8 % potato dextrose agar (PDA) and incubating at 25 °C for up to 24 h. Single germinating spores were transferred onto fresh PDA plates. Specimens and isolates were deposited in the Beijing Museum of Natural History (BJM) and the working Collection of X.L. Fan (CF) housed in the Beijing Forestry University (BJFU). Axenic cultures are maintained in the China Forestry Culture Collection Centre (CFCC).

#### Morphological analysis

Species identification was based on morphological features of the ascomata or conidiomata produced on infected plant tissues and micromorphology, supplemented by cultural characteristics. Microscopic photographs were captured using a Leica stereomicroscope (M205 FA) (Leica Microsystems, Wetzlar, Germany) (structure and size of stromata; structure and size of ectostromatic disc and ostioles). Microscopic lobservations (shape and size of conidiophores, asci and conidia/ascospores) were determined under a Nikon Eclipse 80i microscope (Nikon Corporation, Tokyo, Japan) equipped with a Nikon digital sight DS-Ri2 high definition colour camera, using differential interference contrast (DIC) illumination and the Nikon software NIS-Elements D Package v. 3.00. Adobe Bridge CS v. 6 and Adobe Photoshop CS v. 5 were used for the manual editing. More than 10 conidiomata/ascomata, 10 asci and 30 conidia/ascospores were measured to calculate the mean size/length and respective standard deviations (SD). Colony diameters were measured and the colony features were described using the colour charts of Rayner (1970). Nomenclatural novelties and descriptions were deposited in MycoBank (www.mycobank.org; Crous et al. 2004).

#### DNA extraction, PCR amplification and sequencing

Fungal mycelium grown on the cellophane of PDA was scraped for the extraction of genomic DNA following a modified CTAB method (Doyle and Doyle 1990). The ITS region was amplified with the primers ITS1 and ITS4 (White et al. 1990), the *tub2* region with the primers T1 (O'Donnell and Cigelnik 1997) and Bt2b (Glass and Donaldson 1995) firstly, and the additional combination of Bt2a and Bt2b (Glass and Donaldson 1995) was used in case of amplification failure of the primer T1 and Bt2b. The PCR mixture for all regions consisted of 1 µL genomic DNA, 3 mM MgCl<sub>2</sub>, 20 µM of each dNTP, 0.2 µM of each primer and 0.25 U BIOTAQ DNA polymerase (Bioline). Conditions for PCR of ITS gene constituted an initial denaturation step of 2 min at 95 °C, followed by 35 cycles of 30 s at 95 °C, 30 s at 51 °C and 140 s at 72 °C, and a final denaturation step of 10 min at 72 °C, while the *tub2* gene was performed using an initial denaturation step of 5 min at 72 °C. DNA sequencing was performed using an ABI PRISM® 3730XL DNA Analyser with a BigDye Terminater Kit v. 3.1 (Invitrogen, USA) at the Shanghai Invitrogen Biological Technology Company Limited (Beijing, China). The DNA sequences obtained from forward and reverse primers were combined using SeqMan v. 7.1.0 in the DNASTAR Lasergene Core Suite software (DNASTAR Inc., Madison, WI, USA).

#### Phylogenetic analyses

The current isolates were initially identified as *Diatrypaceae* species, based on both morphological observations and BLAST results. To clarify the phylogenetic position of our isolates, an analysis based on the combined ITS and *tub2* concatenated sequences was performed to compare *Diatrypaceae* species from the current study with other available species. Reference sequences were selected based on ex-type or ex-epitype sequences available from relevant recently published literature (de Almeida et al. 2016; Shang et al. 2017, 2018; Senwanna et al. 2017; Hyde et al. 2019; 2020b; Phookamsak et al. 2019; Dayarathne et al. 2020a, b; Konta et al. 2020) (Additional file 1: Table S1). *Xylaria hypoxylon* (CBS 122620) was selected as the outgroup. Subsequent alignments for each gene were generated using MAFFT v. 7 (Katoh and Standley 2013) and manually improved where it necessary using MEGA v. 6 (Tamura et al. 2013). Ambiguously aligned sequences were excluded from analysis. Phylogenetic analysis was performed by PAUP v. 4.0b10 for maximum parsimony (MP) method (Swofford 2003), MrBayes v. 3.1.2 for Bayesian Inference (BI) method (Ronquist and Huelsenbeck 2003) and PhyML v. 3.0 for maximum likelihood (ML) method (Guindon et al. 2010).

A partition homogeneity test (PHT) with heuristic search and 1000 replicates was performed using PAUP v. 4.0b10 to test the discrepancy among the ITS and tub2 sequence dataset in reconstructing phylogenetic trees. MP analysis was performed using a heuristic search option of 1000 random-addition sequences with a tree bisection and reconnection (TBR) branch swapping algorithm (Swofford et al. 2003). The branches of zero length were collapsed and all equally parsimonious trees were saved. Clade stability was assessed with a bootstrap analysis of 1,000 replicates (Hillis and Bull 1993). Other parsimony scores such as tree length (TL), consistency index (CI), retention index (RI) and rescaled consistency (RC) were calculated (Swofford et al. 2003). ML analysis was performed with GTR+G+I model of site substitution following recent studies (Konta et al. 2020), including estimation of gamma distributed rate heterogeneity and a proportion of invariant sites using PhyML v. 3.0 (Guindon et al. 2010). The branch support was evaluated with a bootstrapping method of 1000 replicates (Hillis and Bull 1993). BI analysis was performed using a Markov Chain Monte Carlo (MCMC) algorithm with Bayesian posterior probabilities (Rannala and Yang 1996). A nucleotide substitution model was estimated by MrModeltest v. 2.3 (Posada and Crandall 1998), and a weighted Bayesian analysis was considered. Two MCMC chains were run from random trees for 1000000 generations, and trees were sampled each 100th generations. The first 25 % of trees were discarded as the burn-in phase of each analysis, and the posterior probabilities (BPP) were calculated to assess the remaining trees (Rannala and Yang 1996). The branch support from MP and ML analyses were evaluated with a bootstrapping (BS) method of 1000 replicates (Hillis and Bull 1993). Phylograms were plotted in Figtree v. 1.4.4 (http://tree.bio.ed.ac.uk/software/figtree) and edited in Adobe Illustrator CS6 v. 16.0.0 (https://www.adobe.com/cn/products/illustrator.html). Novel sequences generated in the current study were deposited in GenBank (Table 2) and the aligned matrices used for phylogenetic analyses were submitted to TreeBASE (www.treebase.org; accession number: S27126).

## Results

#### Phylogenetic analyses

The combined alignments matrix of ITS and *tub2* included 141 in-group accessions (21 from this study and 120 retrieved from GenBank) and counted 1081 characters including gaps (665 characters for ITS and 416 for *tub2*), of which 387 characters were constant, 132 variable characters were parsimony-uninformative and 562 characters were variable and parsimony-informative. The MP analysis generated 100 parsimonious trees of which the first tree is presented in Fig. 1 (TL = 3757, CI = 0.361, RI = 0.787, RC = 0.284). Tree topologies of ML and BI analyses were similar to the MP tree.

The phylogram based on the combined ITS and *tub2* sequence data belonging to the *Diatrypaceae* included 26 lineages, representing 18 known genera and one novel taxon as well as five *incertae sedis* clade. Eleven new lineages distinct from all known taxa, are herein described as one new genus and ten new species in *Diatrypaceae* (Fig. 1).

Clade 06 (*Allodiatrypella*): This clade comprises nine newly generated strains and *Allodiatrypella yunnanensis* (JZBH3380001) and supported with strong statistical values (MP/ML/BI = 83/91/1). *Allodiatrypella betulina* was the basal subclade with high support (MP/ML/BI = 100/100/1). *Allodiatrypella betulae* (CFCC 52404, CFCC 52405 and CFCC 52406) grouped together with high strong support (MP/ML/BI = 97/100/1) close to *Allodiatrypella betulina*. The two isolates (CFCC 52413 and CFCC 52409) formed two separate subclades representing two new species close to *Allodiatrypella yunnanensis*. *Allodiatrypella betulicola* (CFCC 52411 and CFCC 52412) also formed a distinct strongly supported clade (MP/ML/BI = 100/100/1).

Clade 13 (*Diatrype sensu stricto*): The type species of *Diatrype*, *D. disciformis* (CBS 205.87 and GB 5815) and other *Diatrype* and *Diatrypella* species grouped together with strong statistical supports (MP/ML/BI = 100/100/1) in Fig. 1. Six new strains group in this

clade as three different sub clades *viz. Diatrype quercicola* (CFCC 52418, CFCC 52419 and CFCC 52420), *Diatrype castaneicola* (CFCC 52425 and CFCC 52426) and *Diatrype betulae* (CFCC 52416).

Clade 14 (*Allocryptovalsa/Eutypella sensu stricto*): This clade comprises *Allocryptovalsa/Eutypella sensu stricto* grouped together with strong support values (MP/ML/BI = 99/100/1) in Fig. 1. Among six new isolates, two (CFCC 52433 and CFCC 52434) grouped together with *Eutypella citricola* (HVVIT07 and HVGRF01) with highly strong support (MP/ML/BI = 100/100/1). The isolates CFCC 52432 formed a separate branch which represented a new species *Eutypella castaneicola*. *Allocryptovalsa castanea* (CFCC 52427, CFCC 52428 and CFCC 52429) formed a distinct strongly supported clade (MP/ML/BI = 99/100/1).

#### Taxonomy

Allocryptovalsa Senwanna, Phook. & K.D. Hyde, Mycosphere 8(10): 1835 (2017)

Type:Allocryptovalsa polyspora Senwanna, Phook. & K.D. Hyde, Mycosphere 8(10): 1835 (2017).

*Known distribution*: Australia, China, Germany, Inidia, Thailand and USA (Saccardo 1882; Trouillas et al. 2011; Senwanna et al. 2017; Hyde et al. 2020a; Konta et al. 2020; This study).

*Notes: Allocryptovalsa* was introduced and typified by *A. polyspora* from *Hevea brasiliensis*. The genus is characterized by perithecia immersed in host tissue, polysporous asci and allantoid ascospores (Senwanna et al. 2017). This genus comprises another four species (*viz. A. cryptovalsoidea, A. elaeidis, A. rabenhorstii* and *A. truncata*) except the type species. In this study, we introduce the sixth species, *Allocryptovalsacastanea* based on morphological support along with molecular data (Fig. 1; clade 14; MP/ML/BI = 99/98/1).

Allocryptovalsa castanea H.Y. Zhu & X.L. Fan sp. nov. (Fig. 2)

MycoBank No: MB 837777

Etymology: Named after the host genus on which it was collected, Castanea.

Diagnosis: Phylogenetically sister to A. rabenhorstii, differs by the smaller size of ascospores.

*Type:* China: Hebei Province, Qinhuangdao City, Qinglong County (119°11'52.25" E 40°22'52.13" N, 246 m msl.), from branches of *Castanea mollissima*, 16 Oct. 2017, N. Jiang, deposited by X.L. Fan, *holotype* BJM 240506, ex-type living culture CFCC 52428,

*Description. Necrotrophic* on branches of *Castanea mollissima. Sexual morph: Stromata* solitary to gregarious, immersed in the bark, erumpent through the surface of bark,  $(350-)450-700(-750) \mu m$  in diam., with 3–5 perithecia arranged irregularly. *Ectostromatic disc* orange, unconspicuous, circular to oblong, with 3–5 ostioles arranged irregularly per disc. *Ostioles*  $(85-)120-130 \mu m$  in diam., numerous, brown to black, at the same level as the disc, scattered. *Perithecia*  $(320-)380-420 \mu m$  in diam., outer surface lacking powdery entostroma, black, flask-shaped to spherical, with discrete perithecial necks. *Asci*  $(52-)60-83(-92) \times (11-)12-17(-25) \mu m$  (av. =  $71.5 \pm 11.4 \times 15.4 \pm 2 \mu m$ , n = 30), clavate to elongate obovoid, polysporous, thin-walled, short pedicellate, apically rounded. *Ascospores*  $8-11(-13) \times 2.5-3.5 (-4) \mu m$  (av. =  $10.1 \pm 0.8 \times 3.1 \pm 0.4 \mu m$ , n = 30), elongate-allantoid, thin-walled, pale yellowish to pale brown at maturity, slightly curved, aseptate. *Asexual morph:* Coelomycetous. *Conidiomata* pycnidial, immersed in the bark, scattered, erumpent through the surface of bark. *Ectostromatic disc* flat or concave, orange, surrounded by bark flaps, circular to ovoid,  $(200-)250-320(-370) \mu m$  in diam., with 8-10 ostioles arranged circularly on per disc. *Ostioles* black, at the same level as the disc surface,  $(45-)60-70 \mu m$  in diam. *Conidiogenous cells*  $(15-)19-30(-31) \times (1-)1.5-2(-2.5) \mu m$  (av. =  $24.5 \pm 4.9 \times 1.7 \pm 0.2 \mu m$ , n = 30), holoblastic conidiogenesis, approximately cylindrical, hyaline, integrated, arising from pseudoparenchymatous cells unicellular, with wide base producing conidia at the apex. *Conidia*  $(4-)5-7(-8) \times (1-) 1.5-2(-2.5) \mu m$  (av. =  $5.9 \pm 0.9 \times 1.8 \pm 0.2 \mu m$ , n = 30), hyaline, elongate-allantoid, straight not curved, smooth, aseptate.

*Culture characteristics*: Cultures are initially white, growing up to 4 cm in diam. with irregular margin after 3 days, and stopping growing with 7 cm in diam. after 14 days, becoming dark green at the margin after 7–10 days. Colonies dense, irregular, flat.

Known host and distribution: Known on Castanea mollissima and Juglans regia in China.

*Notes*: Three new strains isolated from branches of *Castanea mollissima* and *Juglans regia* cluster in *Allocryptovalsa* (Fig. 1; Clade 14: *Allocryptovalsa/Eutypella sensu lato*). *Allocryptovalsa castanea* differs from *A. cryptovalsoidea* (from *Ficus carica*), *A. elaeidis* (from *Elaeis guineensis*), *A. polyspora* (from *Hevea brasiliensis*) and *A. rabenhorstii* (from *Vitis vinifera* and *Sambuscus nigra*) in host association (Saccardo 1882; Trouillas et al. 2011; Senwanna et al. 2017; Konta et al. 2020).

In morphology of asci and ascospores, *A. castanea* resembles *A. rabenhorstii*. Morphological comparison of members of *Allocryptovalsa* is provided in Table 3. Since, new strains showed a distinct lineage in phylogenetic analyses (Fig. 1; Clade 14; MP/ML/BI = 99/98/1) and it has different morphological characters (Table 3). *Allocryptovalsa castanea* is introduced as a noval species in *Allocryptovalsa* (Fig. 1).

Other species of this genus were not reported with asexual morph. *Allocryptovalsa castanea* showed coelomycetous asexual morph from host in China for the first time

*Material examined*: China: Hebei Province, Qinhuangdao City, Qinglong County (119°11'52.25" E 40°22'52.13" N, 246 m msl.), from branches of *Castanea mollissima*, 16 Oct. 2017, N. Jiang, deposited by X.L. Fan, *isotype* BJFU CF2020518, China: Yunnan Province, Chuxiong Yi Autonomous Prefecture, Dayao County (101°20'15.7" E 25°44'47.19" N, 2002 m msl.), from branches of *Juglans regia*, 7 Aug. 2015, N. Zhao, deposited by X.L. Fan, *paratype* BJFU CF2020516, ex-paratype living culture CFCC 52427.

#### Allodiatrypella H.Y. Zhu & X.L. Fan gen. nov.

MycoBank No: MB 837776

*Etymology*. In reference to the morphological resemblance to *Diatrypella*.

Diagnosis: Phylogenetically sister to Eutypa, differs by the polysporous asci.

*Description: Necrotrophic* on branches of *Betula* spp. *Sexual morph*: *Stromata* solitary, immersed in host bark, slightly erumpent from the bark surface. *Ectostromatic disc* yellowish to dark grey, ovoid to ellipsoid. *Perithecia* outer surface lacking powdery entostroma, flask-shape, surrounding the ectostromatic disc, irregularly scattered or arranged circularly, with discrete perithecial necks. *Ostioles* numerous, umbilicate, sulcate, scattered to gregarious, dark grey to black. *Asci* clavate to elongate obovoid, polysporous, thin-walled, long pedicellate, apically rounded to flat. *Ascospores* elongate-allantoid, thin-walled, pale yellowish to pale brown at maturity, straight to slightly curved, smooth or multiguttulate, containing 1–4 guttules per cell, aseptate. *Asexual morph*: not observed.

Type: Allodiatrypella betulae H.Y. Zhu & X.L. Fan.

Known distribution: China (Hyde et al. 2020b; This study).

*Notes*: Our phylogenetic analyses show that nine newly generated strains which have diatrypella-like morphology, cluster together but distinct to *Diatrypella sensu stricto* (Fig. 1). Moreover, this clade comprises *Diatrypella yunnanensis* Brahamanage, Thyagaraja & K.D. Hyde (Hyde et al. 2020b). Therefore, we introduce *Allodiatrypella* as a new genus in *Diatrypaceae* to accommodate five new species *Allodiatrypellabetulae, A. betulicola, A. betulina, A. hubeiensis* and *A. xinjiangensis. Diatrypella yunnanensis* which groups in *Allodiatrypella sensu stricto* (Fig. 1) is introduced as a new combination *viz. A.yunnanensis*. The morphology of *Allodiatrypella* species resemble *Diatrypella sensu stricto*. However, *Allodiatrypella* differs in having clavate to elongate obovoid asci and pale yellowish to pale brown ascospores at maturity, while asci of *Diatrypella* are cylindrical and ascospores are hyaline or yellowish (Vasilyeva and Stephenson 2005).

#### Allodiatrypella betulae H.Y. Zhu & X.L. Fan sp. nov. (Fig. 3)

MycoBank No: MB 837778

*Etymology*: Named after the host genus on which it was collected, *Betula*.

Diagnosis: Phylogenetically sister to Allodiatrypella betulina, differs by the by the number of perithecia.

*Type*: China: Hubei Province, Shennongjia Forest District, Shennong Stream (110°17'51.54" E 31°28'15.79" N, 2273 m msl.), from branches of *Betula albosinensis*, 17 Aug. 2017, Z. Du & Q. Yan, deposited by X.L. Fan, *holotype* BJM 240507, ex-type living culture CFCC 52406.

*Description: Necrotrophic* on branches of *Betula albosinensis. Sexual morph: Stromata* solitary, immersed in the bark, erumpent through the surface of bark, 1.7-2.1 mm in diam., with 7–10 perithecia arranged irregularly. *Ectostromatic disc* orange, circular to oblong, 830–1280(-1460) µm in diam., with 7–10 ostioles arranged regularly per disc. *Ostioles* (125–)175–240 µm in diam., numerous, scattered, umbilicate, sulcate, dark brown to black, at the same level as the disc. *Perithecia* (430–)530–870 µm in diam., outer surface lacking powdery entostroma, black, flask-shaped, with long discrete perithecial necks. *Asci* 132–140 × 7.5–10.5(-11.5) µm (av. = 136.2 ± 3 × 9.5 ± 1.4 µm, n = 10), clavate to elongate obovoid, polysporous, thin-walled, long pedicellate, apically rounded to flat. *Ascospores* (4.5–)5–7 × 1–2 µm (av. = 5.7 ± 0.5 × 1.5 ± 0.2 µm, n = 30), elongate-allantoid, thin-walled, pale yellowish to pale brown at maturity, slightly curved, smooth, aseptate. *Asexual morph*: not observed.

*Culture characteristics*: Cultures are white, flat, growing up to 4 cm in diam. after 3 days, and covering the 9 cm Petri dish after 7–10 days. Colonies white, rough on surface, not produced pigmentation on PDA media.

Known host and distribution: Known only on Betula albosinensis in Hubei Province, China.

*Notes: Allodiatrypella betulae* was isolated from branches of *Betula albosinensis* in Hubei Province, China. Three strains representing *Allodiatrypella betulae* cluster in a well-supported clade and appear most closely related to *A. betulina* which is also reported from *Betula* sp. In morphology of asci and ascospores, *Allodiatrypella betulae* resembles *A. betulina* but can be distinguished by the number of perithecia. Moreover, *Allodiatrypella betulae* can be distinguished from *A. betulina* based on ITS and *tub2* loci (67/665 in ITS and 13/416 in *tub2*).

*Material examined*: China: Hubei Province, Shennongjia Forest District, Shennong Stream (110°17'51.54" E 31°28'15.79" N, 2273 m msl.), from branches of *Betula albosinensis*, 17 Aug. 2017, Z. Du & Q. Yan, deposited by X.L. Fan, *isotype* BJFU CF2020501, ex-isotype living culture CFCC 52404; *ibid.*, BJFU CF2020502, living culture CFCC 52405.

#### Allodiatrypella betulicola H.Y. Zhu & X.L. Fan sp. nov. (Fig. 4)

MycoBank No: MB 837779

Etymology. Named after the host genus on which it was collected, Betula.

*Diagnosis*: Allodiatrypella betulicola is different from other species of Allodiatrypella on host association and the size of asci and ascospores.

*Type*: China: Beijing City, Mentougou District, Mount Dongling, Xiaolongmen Forestry Centre (115°26'51.27" E 39°58'19.62" N, 1209 m msl.), from branches of *Betula davurica*, 21 Aug. 2017, H.Y. Zhu & X.L. Fan, deposited by X.L. Fan, *holotype* BJM 240508, ex-type living culture CFCC 52411.

*Description: Necrotrophic* on branches of *Betula davurica* and *B. platyphylla.* **Sexual morph**: Stromata solitary, immersed in the bark, erumpent through the surface of bark, (1.3-)1.5-1.9(-2.1) mm in diam., with 7–10 perithecia arranged regularly. *Ectostromatic disc* brown to black, circular to oblong, (0.5-)0.9-1.2(-1.4) mm in diam., with more than 10 ostioles arranged regularly per disc. *Ostioles* (145-)185-240(-270) µm in diam., numerous, scattered, umbilicate, sulcate, dark brown to black, at the same level as the disc. *Perithecia* (520-)600-750(-790) µm in diam., outer surface lacking powdery entostroma, black, flask-shaped, with short discrete perithecial necks. *Asci*  $117-133 \times 10-12$  µm (av. =  $124.9 \pm 7.7 \times 10.6 \pm 0.5$  µm, n = 10), clavate to elongate obvoid, polysporous, thinwalled, long pedicellate, apically flat. *Ascospores*  $5-8 \times 1-2$  µm (av. =  $6.6 \pm 0.6 \times 1.6 \pm 0.2$  µm, n = 30), elongate-allantoid, thin-walled, pale yellowish to pale brown at maturity, slightly curved, aseptate, smooth or multiguttulate, occasionally containing one guttule per cell. *Asexual morph*: not observed.

*Culture characteristics*: Cultures are initially white, fluffy, growing up to 4 cm in diam. after 3 days, and covering the 9 cm Petri dish after 7–10 days, becoming pale yellow at the margin after 14 days. Colonies dense with aerial mycelium at the centre, sparse at the margin.

Known host and distribution: Known on Betula davurica and B. platyphylla in Beijing City, China.

*Notes: Allodiatrypella betulicola* was isolated from branches of *Betula davurica* and *Betula platyphylla* in Beijing Province, China. Phylogenetically, two strains representing *Allodiatrypella betulicola* cluster in a well-supported clade in *Allodiatrypella sensu stricto.* Morphologically, it is different from other species of *Allodiatrypella* on host association and the size of asci and ascospores (Table 4).

*Material examined*: China: Beijing City, Mentougou District, Mount Dongling, Xiaolongmen Forestry Centre (115°26'51.27" E 39°58'19.62" N, 1209 m msl.), from branches of *Betula davurica*, 21 Aug. 2017, H.Y. Zhu & X.L. Fan, deposited by X.L. Fan, *isotype* BJFU CF2020505. China: Beijing City, Mentougou District, Mount Dongling, Xiaolongmen Forestry (115°26'51.27" E 39°58'19.62" N, 1209 m msl.), from branches of *Betula platyphylla*, 21 Aug. 2017, H.Y. Zhu & X.L. Fan, deposited by X.L. Fan, *isotype* BJFU CF2020506, ex-paratype living culture CFCC 52412.

Allodiatrypella betulina H.Y. Zhu & X.L. Fan sp. nov. (Fig. 5)

#### MycoBank No: MB 837780

Etymology. Named after the host genus on which it was collected, Betula.

Diagnosis: Phylogenetically sister to Allodiatrypella betulae, differs by ITS and tub2 loci (67/665 in ITS and 13/416 in tub2).

*Type*: China: Hubei Province, Shennongjia Forest District, Shennong Ding, Shennong Camp (110°17'28.39" E 31°26'34.59" N, 2647 m msl.), from branches of *Betula albosinensis*, 17 Aug. 2017, Z. Du & Q. Yan, deposited by X.L. Fan, *holotype* BJM 240509, ex-type living culture CFCC 52415.

*Description: Necrotrophic* on branches of *Betula albosinensis.* **Sexual morph**:*Stromata* solitary, immersed in the bark, erumpent through the surface of bark, causing a pustulate bark surface, (1.9-)2.0-2.8(-3.7) mm in diam., with more than 10 perithecia arranged irregularly. *Ectostromatic disc* orange, circular to oblong, (1.0-)1.1-1.8(-2.6) mm in diam., with more than 10 ostioles arranged regularly to irregularly per disc. *Ostioles* 160-215 µm in diam., numerous, scattered, umbilicate, sulcate, dark brown to black, at the same level as the disc. *Perithecia* (530-)630-810(-970) µm in diam., outer surface lacking powdery entostroma, black, flask-shaped to spherical, with long discrete perithecial necks. *Asci* 129-140 × (5-)8-12 µm (av. =  $135 \pm 4.5 \times 9.8 \pm 1.7$  µm, n = 10), clavate to elongate obovoid, polysporous, thin-walled, long pedicellate, apically rounded to flat. *Ascospores*  $5-7 \times 1-2$  µm (av. =  $5.9 \pm 0.6 \times 1.4 \pm 0.2$  µm, n = 30), elongate-allantoid, thin-walled, pale yellowish to pale brown at maturity, slightly curved, smooth, aseptate. *Asexual morph*: not observed.

*Culture characteristics*: Cultures are white, fluffy, growing up to 4 cm in diam. after 3 days, and covering the 9 cm Petri dish after 7–10 days. Colonies dense, uniform, not produced pigmentation on PDA media.

Known host and distribution: Known only on Betula albosinensis in Hubei Province, China.

*Notes: Allodiatrypella betulina* was isolated from branches of *Betula albosinensis* in Hubei Province, China. It can be distinguished from its closest relative, *Allodiatrypella betulae* by its number of perithecia (less than 10 vs. more than 10) in one stroma and base number difference (67/665 in ITS and 13/416 in *tub2*).

*Material examined*: China: Hubei Province, Shennongjia Forest District, Shennong Ding, Shennong Camp (110°17'28.39" E 31°26'34.59" N, 2647 m msl.), from branches of *Betula albosinensis*, 17 Aug. 2017, Z. Du & Q. Yan, deposited by X.L. Fan, *isotype* BJFU CF2020508, ex-isotype living culture CFCC 52414.

Allodiatrypella hubeiensis H.Y. Zhu & X.L. Fan sp. nov. (Fig. 6)

MycoBank No: MB 837781

Etymology: Named after the location where it was collected, Hubei Province.

Diagnosis: Phylogenetically sister to Allodiatrypella yunnanensis, differs by larger size of asci and smaller size of ascospores.

*Type*: China: Hubei Province, Shennongjia Forest District, Tianyan Scenic Area (110°27'36.71" E 31°42'59.10" N, 2140 m msl.), from branches of *Betula davurica*, 16 Aug. 2017, Z. Du & Q. Yan, deposited by X.L. Fan, *holotype* BJM 240510, ex-type living culture CFCC 52413.

*Description. Necrotrophic* on branches of *Betula davurica.* **Sexual morph**: Stromata solitary, immersed in the bark, erumpent through the surface of bark, (1.4-)1.7-2.6(-3.0) mm in diam., with 5–7 perithecia arranged regularly. *Ectostromatic disc* brown to black, circular to oblong, 0.9-1.2(-2.6) mm in diam., with 5–7 ostioles arranged irregularly per disc. *Ostioles* 120-150(-195) µm in diam., numerous, gregarious, umbilicate, sulcate, dark brown to black, at the same level as the disc. *Perithecia* (510-)600-720 µm in diam., outer surface lacking powdery entostroma, black, flask-shaped to spherical, with long discrete perithecial necks. *Asci*  $189-240 \times 18-21$  µm (av. =  $213.4 \pm 13.3 \times 19.8 \pm 0.5$  µm, n = 10), clavate to elongate obvoid, occasionally similar to an inverted volumetric flask, polysporous, thinwalled, long pedicellate, apically rounded to flat. *Ascospores*  $6-8.5(-9) \times 1-2$  µm (av. =  $7.4 \pm 0.7 \times 1.6 \pm 0.2$  µm, n = 30), elongate-allantoid, thin-walled, slightly curved, aseptate, multiguttulate, often containing two symmetrical guttules per cell. *Asexual morph*: not observed.

*Culture characteristics*: Cultures are white, fluffy, growing up to 4 cm in diam. after 3 days, and covering the 9 cm Petri dish after 7–10 days. Colonies dense, slightly raised with aerial mycelium, not produced pigmentation on PDA media.

Known host and distribution: Known only on Betula davurica in Hubei Province, China.

*Notes: Allodiatrypella hubeiensis* was isolated from branches of *Betula davurica* in Hubei Province, China. The only strain CFCC 52413 is representing *Allodiatrypella hubeiensis* which clusters in a separate lineage and differs from its closest relative *Allodiatrypella yunnanensis* by larger size of asci (189–240 × 18–21 vs. 105–210 × 15–30  $\mu$ m) and smaller size of ascospores (6–8.5 × 1–2 vs. 18–22 ×3–4  $\mu$ m).

*Material examined*: China: Hubei Province, Shennongjia Forest District, Tianyan Scenic Area (110°27'36.71" E 31°42'59.10" N, 2140 m msl.), from branches of *Betula davurica*, 16 Aug. 2017, Z. Du & Q. Yan, deposited by X.L. Fan, *isotype* BJFU CF2020507.

Allodiatrypella xinjiangensis H.Y. Zhu & X.L. Fan sp. nov. (Fig. 7)

#### MycoBank No: MB 837782

*Etymology*: Named after the location where it was collected, Xinjiang Uygur Autonomous Region.

Diagnosis: Phylogenetically sister to Allodiatrypella hubeiensis, differs by smaller size of asci and smaller size of ascospores.

*Type*: China: Xinjiang Uygur Autonomous Region, Bortala Mongol Autonomous Prefecture, Wenquan County (81°46'22.96" E 45°13'08.47" N, 1439 m msl.), from branches of *Betula platyphylla*, 15 Jul. 2017, C.M. Tian & R. Ma, deposited by X.L. Fan, *holotype* BJM 240511, ex-type living culture CFCC 52409.

*Description: Necrotrophic* on branches of *Betula platyphylla.* **Sexual morph**: *Stromata* solitary, consisting of an inconspicuous pale yellow ectostromatic disc, immersed in the bark, erumpent through the surface of bark, (1.9-)2.9-3.2(-3.3) mm in diam., with 7–10 perithecia arranged irregularly. *Ectostromatic disc* brown to black, circular to oblong, (0.5-)1.8-2.3(-2.4) mm in diam., with 5–7 ostioles arranged irregularly per disc. *Ostioles* 230–260(-280) µm in diam., numerous, gregarious, umbilicate, sulcate, dark brown to black, at the same level as the disc. *Paraphyses* 118–125 × 2–3.5 µm (av. = 121.6 ± 2.7 × 2.7 ± 0.7 µm, n = 10), elongate cylindrical. *Perithecia* (690–)780–940 µm in diam., outer surface lacking powdery entostroma, black, flask-shaped to spherical, with long discrete perithecial necks. *Asci* 88–133 × (7–)8–10(–11) µm (av. = 113.6 ± 18.5 × 8.8 ± 1.2 µm, n = 10), clavate to elongate obvoid, polysporous, thin-walled, long pedicellate, apically rounded. *Ascospores* 4–6 × 1–2 µm (av. = 4.9 ± 0.5 × 1.6 ± 0.2 µm, n = 30) µm, short-allantoid, thin-walled, pale yellowish to pale brown at maturity, slightly curved, aseptate, multiguttulate, often containing one guttulae per cell. *Asexual morph*: not observed.

*Culture characteristics*: Cultures are white, uniform, growing up to 4 cm in diam. after 3 days, and covering the 9 cm Petri dish after 7–10 days. Colonies sparse at the center, medium dense at the margin, rough on the surface, not produced pigmentation on PDA media.

Known host and distribution: Known only on Betula platyphylla in Xinjiang Uygur Autonomous Region, China.

*Notes: Allodiatrypella xinjiangensis* was isolated from branches of *Betula platyphylla* in Xinjiang Uygur Autonomous Region, China. The only strain CFCC 52409 representing *Allodiatrypella xinjiangensis* and it clusters in a separate lineage. It differs from its closest species, *Allodiatrypella hubenensis* by smaller size of asci (88–133 × 8–10 vs. 189–240 × 18–21  $\mu$ m) and smaller size of ascospores (4–6 × 1– 2 vs. 6–8.5 × 1–2  $\mu$ m).

*Material examined*: China: Xinjiang Uygur Autonomous Region, Bortala Mongol Autonomous Prefecture, Wenquan County (81°46'22.96" E 45°13'08.47" N, 1439 m msl.), from branches of *Betula platyphylla*, 15 Jul. 2017, C.M. Tian & R. Ma, deposited by X.L. Fan, *isotype* CF 2020504.

*Allodiatrypella yunnanensis* (Brahamanage, Thyagaraja & K.D. Hyde) Brahamanage, Thyagaraja & K.D. Hyde comb. nov.

Basionym.Diatrypella yunnanensis Brahamanage, Thyagaraja & K.D. Hyde, Fungal Diversity 100: 226 (2020)

MycoBank No: MB 837783

Description: See Hyde et al. (2020b).

Known host and distribution: Only known on dead twigs of an unidentified plant in China (Hyde et al. 2020b).

*Notes*: Hyde et al. (2020b) introduced *Diatrypella yunnanensis* from twigs of an unidentified plant in China. *Diatrypella yunnanensis* is similar to *Allodiatrypella betulae, A. betulicola, A. betulina, A. hubeiensis* and *A. xinjiangensis* in having polysporous asci (Hyde et al. 2020b). Based on phylogenetic analyses this species clustered with the species of *Allodiatrypella* (Fig. 1; Clade 06: *Allodiatrypella*). Therefore, we transfer the species to the genus *Allodiatrypella* as *A. yunnanensis*.

Diatrype Fr., Summa veg. Scand., Sectio Post. (Stockholm): 384 (1849)

Type: Diatrype disciformis (Hoffm.) Fr., Summa veg. Scand., Sectio Post. (Stockholm): 385 (1849).

*Known distribution*: Asia, Europe, North America, Oceania and South Africa (Doidge 1950; **Munk** 1957; Conners 1967; Rappaz 1987; Mulenko et al. 2008; Trouillas et al. 2010a; b).

*Notes*: The genus *Diatrype* was established by Fries (1849) with *Diatrype disciformis* as the type species. There are 380 epithets of *Diatrype* listed in Index Fungorum (2020). It commonly inhabits decaying wood. A few species are reported as pathogens that from cankers on forest trees (Senanayake et al. 2015). The asexual morph of *Diatrype* is reported as libertella-like and dumortieria-like (Kirk et al. 2008; Wijayawardene et al. 2012, 2017; Maharachchikumbura et al. 2015, 2016; Senanayake et al. 2015; Dayarathne et al. 2020a, b). *Diatrype* may require reconsideration in the future together with a revision for the entire family.

Diatrype betulae H.Y. Zhu & X.L. Fan sp. nov. (Fig. 8)

MycoBank No: MB 837784

Etymology: Named after the host genus on which it was collected, Betula.

Diagnosis: Phylogenetically, Diatrype castaneicola formed a separate clade.

*Type*: China: Beijing City, Mentougou District, Mount Dongling, Xiaolongmen ForestryCentre (115°26'51.27" E 39°58'19.62" N, 1302 m msl.), from branches of *Betula davurica*, 21 Aug. 2017, H.Y. Zhu & X.L. Fan, deposited by X.L. Fan, *holotype* BJM 240512, ex-type living culture CFCC 52416.

*Descriptic: Necrotrophic* on branches of *Betula davurica.* **Sexual morph**: not observed. **Asexual morph**: Coelomycetous. *Conidiomata* pycnidial, immersed in the bark, scattered, erumpent slightly through the surface of bark, with multiple locules and orange colloid conidial drops exuding from the ostioles. *Locules* numerous, buff, circular to ovoid,  $1200-1320 \mu m$  in diam. *Conidiogenous cells*  $(12-)14-20 \times 1-2 \mu m$  (av. =  $16.6 \pm 2.5 \times 1.2 \pm 0.2 \mu m$ , n = 10), approximately cylindrical, mostly straight, discrete or integrated, arising from pseudoparenchymatous cells, hyaline, unicellular, with wide base producing conidia at the apex, holoblastic conidiogenesis. *Conidia*  $10-13 \times 1-2 \mu m$  (av. =  $11.7 \pm 1.2 \times 1.5 \pm 0.1 \mu m$ , n = 30), hyaline, filiform, smooth or rough, aseptate.

*Culture characteristics*: Cultures are white, uniform, dense, growing up to 4 cm in diam. after 14 days, not produced pigmentation on PDA media.

Known host and distribution: Known only on Betula davurica in Beijing City, China.

*Notes*: *Diatrype betulae* was isolated from branches of *Betula davurica* in Beijing City, China. The only strain of *Diatrype betulae* (CFCC 52416) clusters as a single lineage (Fig. 1).

*Diatrype albopruinosa* (a sexual fungus) was reported by Vasilyeva and Ma (2014) from *Betula* sp. (Tiffany and Gilman 1965; Goos 2010). However, it lacks the asexual morph and sequences are unavailable. Therefore, more study of *D. albopruinosa* and *D. betulae* is needed.

*Material examined*: China: Beijing City, Mentougou District, Mount Dongling, Xiaolongmen ForestryCentre (115°26'51.27" E 39°58'19.62" N, 1302 m msl.), from branches of *Betula davurica*, 21 Aug. 2017, H.Y. Zhu & X.L. Fan, deposited by X.L. Fan, *isotype* BJFU CF2020510.

Diatrype castaneicola H.Y. Zhu & X.L. Fan sp. nov. (Fig. 9)

MycoBank No: MB 837785

Etymology: Named after the host genus on which it was collected, Castanea.

Diagnosis: Phylogenetically, Diatrype castaneicola formed a separate clade.

*Type*: China: Hebei Province, Qinhuangdao City, Qinglong County (119°11'52.25" E 40°22'52.13" N, 246 m msl.), from branches of *Castanea mollissima*, 16 Oct. 2017, N. Jiang, deposited by X.L. Fan, *holotype* BJM 240513, ex-type living culture CFCC 52425.

*Description: Necrotrophic* on branches of *Castanea mollissima.* **Sexual morph**: not observed. **Asexual morph**: Coelomycetous. *Conidiomata* pycnidial, immersed in the bark, scattered, erumpent slightly through the surface of bark, with multiple locules. *Ectostromaticdisc* brown, unconspicuous, circular to ovoid. *Ostiole* unconspicuous, grey to black, at the same the level as the disc surface, covered by ectostroma tissue. *Locules* numerous, circular to ovoid, 1.3-1.5 mm in diam. *Conidiogenous cells* (15-)18-26(-33)  $\times 1-1.5 \mu$ m (av. =  $22.5 \pm 3.5 \times 1.2 \pm 0.2 \mu$ m, n = 30), approximately cylindrical, mostly straight, discrete or integrated, arising from pseudoparenchymatous cells, hyaline, unicellular, with wide base producing conidia at the apex, holoblastic conidiogenesis. *Conidia* 4-6  $\times 1-1.5 \mu$ m (av. =  $5.3 \pm 0.6 \times 1.3 \pm 0.2 \mu$ m, n = 30), hyaline, elongate-allantoid, slightly curved, smooth, aseptate, multiguttulate, often containing 1-2 guttules per cell.

*Culture characteristics*: Colonies are white, dense, not produced pigmentation on PDA media. Pycnidia distributed irregularly on colony surface with yellow cream conidial drops exuding from the ostioles.

Known host and distribution: Known only on Castanea mollissima in Hebei Province, China.

*Notes: Diatrype castaneicola* was isolated from branches of *Castanea mollissima* in Hebei Province, China. Our new isolates (CFCC 52425 and CFCC 5246) grouped in *Diatrype sensu stricto* as a separate clade with high statistical support (MP/ML/BI =100/100/1) (Fig. 1). Hence, we introduce new strain as a new species, *D. castaneicola*. Currently, this species is reported with only the asexual morph thus more studies are essential to report the sexual morph.

*Material examined*: China: Hebei Province, Qinhuangdao City, Qinglong County (119°11'52.25" E 40°22'52.13" N, 246 m msl.), from branches of *Castanea mollissima*, 16 Oct. 2017, N. Jiang, deposited by X.L. Fan, *isotype* BJFU CF2020515, ex-isotype living culture CFCC 52426.

Diatrype quercicola H.Y. Zhu & X.L. Fan sp. nov. (Fig. 10)

MycoBank No: MB 837786

Etymology: Named after the host genus on which it was collected, Quercus.

*Diagnosis*: Phylogenetically, *Diatrype quercicola* formed a separate clade, and its asci are polysporous and is different from the common 8-ascospores asci of *Diatrype*.

*Type*: China: Beijing City, Mentougou District, Mount Dongling, Xiaolongmen Forestry (115°26'51.27" E 39°58'19.62" N, 1267 m msl.), from branches of *Quercus mongolica*, 21 Aug. 2017, H.Y. Zhu & X.L. Fan, deposited by X.L. Fan, *holotype* BJM 240514, ex-type living culture CFCC 52418.

*Description: Necrotrophic* on branches of *Quercus mongolica.* **Sexual morph:** Stromata solitary, immersed in the bark, erumpent through the surface of bark, (2.3-)2.5-2.9 mm in diam., with more than 10 perithecia arranged irregularly. *Ectostromatic disc* brown, circular to oblong, (1.5-)1.7-2.4 µm in diam., with more than 10 ostioles arranged regularly per disc. *Ostioles* dark brown to black, at the same level as the disc, scattered, 210-275(-335) µm in diam. *Perithecia* outer surface coated with yellow, powdery entostromablack, flask-

shaped, with discrete perithecial necks,  $475-665 \mu m$  in diam. *Asci*  $172-183 \times (16-)20-43 \mu m$  (av. =  $178 \pm 3.3 \times 31.7 \pm 10.9 \mu m$ , n = 10), clavate to elongate obovoid, polysporous, thin-walled, long pedicellate, apically rounded. *Ascospores*  $17-27 \times 4-6 \mu m$  (av. =  $22.6 \pm 2.6 \times 5.4 \pm 0.6 \mu m$ , n = 30), elongate-allantoid, thin-walled, pale yellowish to pale brown at maturity, slightly curved, aseptate, multiguttulate, often containing 1-3 symmetrical guttules per cell. *Asexual morph*: not observed.

*Culture characteristics*: Colonies are white, irregular, growing up to 9 cm in diam. after 7 days, not produced pigmentation on PDA media.

Known host and distribution: Known only on Quercus mongolica in Beijing City, China.

*Notes: Diatrype quercicola* was isolated from the branches of *Quercus mongolica* in Beijing City, China. Our three isolates (CFCC 52418, CFCC 52419 and CFCC 52420) grouped in *Diatrype sensu stricto* but as a separate clade with high statistical support (MP/ML/BI = 100/100/1) (Fig. 1). Asci of this species are polysporous and differs from the common 8-ascospores asci of *Diatrype*. Nevertheless, based on phylogeny analyses, this taxon appears best placed in *Diatrype*. However, because of the taxonomic confusion around *Diatrypaceae* and the difficulty in segregating the various genera, the assignment of this isolate to the genus *Diatrype* may require reconsideration in the future.

*Diatrype albopruinosa, D. standleyi* and *D. stigmaoides* were both isolated from *Quercus* sp. (Tiffany and Gilman 1965; Rappaz 1987; Mendez-Mayboca et al. 2008; Vasilyeva and Stephenson 2009). *Diatrype albopruinosa* and *D. standleyi* differs from *D. quercicola* by its 8-ascospores asci (Vasilyeva and Ma 2014). *Diatrype stigmaoides* differs from *D. quercicola* by its hyaline ascospores (Vasilyeva and Stephenson 2009).

*Material examined*: China: Beijing City, Mentougou District, Mount Dongling, Xiaolongmen Forestry (115°26'51.27" E 39°58'19.62" N, 1267 m msl.), from branches of *Quercus mongolica*, 21 Aug. 2017, H.Y. Zhu & X.L. Fan, deposited by X.L. Fan, *isotype* BJFU CF2020512, ex-isotype living culture CFCC 52419; *ibid.*, BJFU CF2020513, living culture CFCC 52420.

Eutypella (Nitschke) Sacc., Atti Soc. Veneto-Trent. Sci. Nat., Padova, Sér. 4 4: 80 (1875)

Type: Eutypella cerviculata (Fr.) Sacc., Syll. Fung. (Abellini) 1: 146 (1882).

*Known distribution*: Asia, Europe, North America, Oceania, South Africa and South America (**Doidge** 1950; **Rappaz** 1987; **Trouillas 2011;** Jayawardena et al. 2018).

*Notes*: The genus *Eutypella* was established by Saccardo (1875) with *E. cerviculata* as the type species (Saccardo 1882). *Eutypella* is characterized by ascostromata erumpent through the host bark by clustered, sulcate perithecial beaks, 8-spored, clavate asci, with long stalks, and allantoid, hyaline or yellowish ascospores (Vasilyeva and Stephenson 2006; Senwanna et al. 2017). *Eutypella* species have been found on a wide range of hosts, especially associated with canker diseases in *Vitis vinifera* (Vasilyeva and Stephenson 2006; Trouillas et al. 2011; Luque et al. 2012). Currently, 251 species epithets of *Eutypella* are listed in Index Fungorum (2020), but only a few species have sequence data. Phylogenetic analyses of *Diatrypaceae* from previous studies show that *Eutypella* is polyphyletic (Acero et al. 2004; Chacón et al. 2013; de Almeida et al. 2016; Shang et al. 2017). Therefore, further study of the taxa in this genus is needed.

#### Eutypella castaneicola H.Y. Zhu & X.L. Fan sp. nov. (Fig. 11)

MycoBank No: MB 837787

Etymology: Named after the host genus on which it was collected, Castanea.

Diagnosis: Eutypella castaneicola differs from other Eutypella species by its polysporous asci.

*Type*: China: Hebei Province, Chende City, Kuancheng Manchu Nationality Autonomous County (118°27'54" E 40°38'37" N, 450 m msl.), from branches of *Castanea mollissima*, 14 Oct. 2017, N. Jiang, deposited by X.L. Fan, *holotype* BJM 240515, ex-type living culture CFCC 52432,

*Description: Necrotrophic* on branches of *Castanea mollissima*. *Sexual morph: Stromata* scattered to gregarious, immersed in the bark, erumpent through the surface of bark, (1.5-)1.7-1.9(-2.0) mm in diam., with 8–10 perithecia arranged irregularly. *Ectostromatic disc* brown, circular to oblong, (680-)750-920(-990) µm in diam., with more than 10 ostioles arranged circularly per disc. *Ostioles* 103–112

 $\mu$ m in diam., numerous, gregarious, umbilicate, 4-sulcate dark brown to black, at the same level as the disc. *Perithecia* (200–)250–320(– 380)  $\mu$ m in diam., outer surface coated with yellow, powdery entostromablack, flask-shaped, perithecial necks erumpent in groups. *Asci* 194–202 × 15–21  $\mu$ m (av. = 198.4 ± 3.3 × 18.9 ± 0.5  $\mu$ m, n = 10), clavate to elongate obovoid, polysporous, thin-walled, long pedicellate, apically flat. *Ascospores* 22–25 × 5–6  $\mu$ m (av. = 23.8 ± 1.1 × 5.4 ± 0.3  $\mu$ m, n = 30), elongate-allantoid, thin-walled, pale yellowish to pale brown at maturity, slightly curved, aseptate, smooth. *Asexual morph*: not observed.

*Culture characteristics*: Colonies are initially white, uniform, becoming dark after 14 days. Pycnidia distributed irregularly on colony surface with yellow cream conidial drops exuding from the ostioles.

Known host and distribution: Known only on Castanea mollissima in Hebei Province, China.

*Notes*: The present species displays some features of morphology typical of *Cryptovalsa* (polysporous ascus) as well as *Eutypella* (perithecial necks erumpent in groups) (Spooner 1981; Vasilyeva and Stephenson 2005; Trouillas et al. 2011). However, based on phylogentic analyses, this fungus appears best placed in *Eutypella*. Because of the taxonomic confusion around *Diatrypaceae* and the difficulty in segregating the various genera, the assignment of this isolate to the genus *Eutypella* may require reconsideration in the future.

*Eutypella castaneicola* differs from other *Eutypella* species by its polysporous asci (Trouillas et al. 2010a). The ascomatal outer surface of *Cryptovalsa* species is often a white powdery entostroma (Dayarathne et. al 2020a), while *Eutypella castaneicola* have a yellow powdery entostroma. Also, phylogenetic analyses show affinities of this fungus with *Allocryptovalsa* spp. and *Eutypella* spp. Therefore, the assignment of this isolate to the genus *Eutypella* may require future reconsideration.

*Eutypella elegans* was reported from *Castanea sativa* (Unamuno 1941), which differs from *E. castaneicola* from *Castanea mollissima* by its smaller ascospores  $(7-9 \times 2.5 \text{ vs. } 22-25 \times 5-6 \text{ } \mu\text{m})$  (Saccardo 1882).

*Material examined*: China: Hebei Province, Chende City, Kuancheng Manchu Nationality Autonomous County (118°27'54" E 40°38'37" N, 450 m msl.), from branches of *Castanea mollissima*, 14 Oct. 2017, N. Jiang, deposited by X.L. Fan, *isotype* BJFU CF2020519.

Eutypella citricola Speg., Anales del Museo Nacional de Buenos Aires 6: 245 (1898)

Description: See Trouillas et al. (2011).

Known host and distribution: Known from Citrus limon, C. sinensis, C. paradisi, Schinus molle var. areira, Ulmus procera in Australia; Vitis vinifera in USA, Morus alba in China.

*Notes:Eutypella citricola* (CFCC 52433 and CFCC 52434) clustered in a well-supported clade with high support values (MP/ML/BI =100/100/1) based on combined multilocus gene phylogenetic analyses (Fig. 1). Collections from China were morphologically identical to the type specimen of *E. citricola*. Therefore, we identified CFCC 52433 and CFCC 52434 as known species *E. citricola*. It is the first record of this species from *Morus alba*.

*Material examined*: China: Jiangsu Province, Yangzhou City, (119°28'11.81" E, 32°47'25.10" N, 1 m msl.), from branches of *Morus alba*, 12 Nov. 2017, N. Jiang, deposited by X.L. Fan, BJFU CF2020520, living culture CFCC 52433; *ibid.*, BJFU CF2020521, living culture CFCC 52433.

#### Other genera included in Diatrpaceae

In here, we follow Hyde et al. (2020a) and Wijayawardene et al. (2020) to list the genera in Diatrapaceae. A taxonomic key to distinguish 24 genera of *Diatrypaceae* is provided.

Allodiatrype Konta & K.D. Hyde, Mycosphere 11(1): 247 (2020)

Type: Allodiatrype arengae Mycosphere 11(1): 249 (2020).

Known distribution: Thailand (Li et al. 2016; Konta et al. 2020).

*Notes: Allodiatrype* was established by Konta et al. (2020) to accommodate *A. arengae* Konta & K.D. Hyde , *A. elaeidicola* Konta & K.D. Hyde, *A. elaeidis* Konta & K.D. Hyde and *A. thailandica* (R.H. Perera, Jian K. Liu & K.D. Hyde) Konta & K.D. Hyde. The genus is

characterised by 8-spored, cylindrical, apex flat, with J-, cylindrical, conspicuous apical ring, long pedicellate asci. Ascospores are hyaline becoming yellowish at maturity, allantoid, with small fat globules at each end.

Anthostoma Nitschke, Pyrenomyc. Germ. 1: 110 (1867)

Type: Anthostoma decipiens (DC.) Nitschke, Pyrenomyc. Germ. 1: 111 (1867).

Known distribution: Asia, Europe, North America and South America (Cash 1952; Ahmad 1969; Farr 1973; Rappaz 1995).

*Notes*: Both sexual and asexual morphs of *Anthostoma decipiens* were studied by Rappaz (1992, 1993) and concluded that the genus belongs in *Diatrypaceae*. Phylogenetic analyses of sequence data suppoted these results (Rocchi et al. 2010; Jaklitsch et al. 2014). The genus is characterised by dark brown to dark, globose to subglobose ascomata, immersed in a stroma, with cylindrical, prominent ostioles, cylindrical to clavate asci, with apically rounded to truncate apices, with a short pedicel and brown to black brown ascospores (Nitschke 1867).

Cryptosphaeria Ces. & De Not., Comm. Soc. crittog. Ital. 1(4): 231 (1863)

Type: Cryptosphaeria millepunctata Grev., Fl. Edin.: 360 (1824).

*Known distribution*: Asia, Europe, North America, Oceania and South Africa (**Teodoro 1937; Trouillas et al. 2015; Jayawardena et al. 2018; Moyo et al. 2019**).

*Notes: Cryptosphaeria* has been widely accepted in *Diatrypaceae* (Nitschke 1867; 1870; Rappaz 1989; Trouillas et al. 2010a; 2015). The genus comprises corticolous species and is characterised by widely effuse and poorly developed stromata, often covered by a periderm, which is penetrated only by the separately emerging ostioles, generally 8-spored, spindle-shaped, long pedicellate asci and sub-olivaceous to brown ascospores (Glawe 1984; Rappaz 1987).

Cryptovalsa Ces. & De Not. ex Fuckel, Jb. Nassau. Ver. Naturk. 23-24: 212 (1870)

Type: Cryptovalsa protracta (Pers.) De Not., Hedwigia 2: 178 (1863).

*Known distribution*: Asia, Europe, North America, Oceania, South Africa and South America (**Teodoro 1937;Trouillas et al. 2010a, 2011;Jayawardena et al. 2018; Moyo et al. 2019**).

*Notes: Cryptovalsa* was established by Cesati and De Notaris to accommodate *C. protracta* (Pers.) De Not., *C. ampelina* (Nitschke) Fucke, *C. nitschkei* Fuckel and *C. effusa* Fuckel. The genus is characterised by eutypoid stromata that are rather variable, when erumpent separately diatrypelloid, often immersed in wood, but sometimes invading bark tissues. Asci are cylindrical or clavate, polysporous, with short or long pedicels. Ascospores are crowded, allantoid and yellowish (Spooner 1981; Vasilyeva and Stephenson 2005). At present, 55 species epithets of *Cryptovalsa* are listed in Index Fungorum (2020), but only *Cryptovalsa ampelina* has sequence data. And the type species of *Cryptovalsa*, *C. protracta* lacks sequence data in GenBank. Therefore, until more species are collected and sequenced, understanding of the *Cryptovalsa* will remain incomplete.

#### Diatrypasimilis J.J. Zhou & Kohlm., Mycologia 102(2): 432 (2010)

Type: Diatrypasimilis australiensis J.J. Zhou & Kohlm., Mycologia 102(2): 432 (2010).

Known distribution: Australia (Chalkley et al. 2010).

*Notes: Diatrypasimilis* was established by Chalkley et al. (2010) based on conventional taxonomic criteria and molecular phylogeny to accommodate a species from mangroves. The genus is characterised by carbonaceous, black stromata, 8-spored, cylindrical asci and ellipsoidal, dark brown ascospores with a germ slit.

Diatrypella (Ces. & De Not.) De Not., Sfer. Ital.: 29 (1863)

Type: Diatrypella verruciformis (Ehrh.) Nitschke, Pyrenomyc. Germ. 1: 76 (1867).

*Known distribution*: Asia, Europe, North America, Oceania, South Africa and South America (**Unamuno 1941; Doidge 1950; Rao 1966; Conners 1967; Hanlin 1992; Crous et al. 2016**).

*Notes: Diatrypella* was introduced by Cesati and De Notaris (1863) with *D. verruciformis* (Ehrh.) Nitschke as the type species. There are 146 epithets of *Diatrypella* listed in Index Fungorum (2020). *Diatrypella* is characterised by conical-truncate, cushion-like or discoid ascostromata, usually delimited by a black zone on host tissues, perithecial ascomata, umbilicate or sulcate ostioles and numerous small ovoid to allantoid ascospores (Simmons 1948; Rao 1964; Vasilyeva and Stephenson 2005; Mehrabi et al. 2015; Mehrabi et al. 2016; Shang et al. 2017). *Diatrypella* species have a libertella-like asexual morph (Kirk et al. 2008). In morphology, *Diatrypella* has polysporous asci resembling *Cryptovalsa*. *Diatrypella* was mentioned as the polysporous complement of *Diatrype,* while *Cryptovalsa* was a polysporous complement of *Eutypa* (Vasilyeva and Stephenson 2005). Nevertheless, it is still difficult to determine the differences between *Diatrypella* and *Cryptovalsa* based on morphological characters (Acero et al. 2004; Vasilyeva and Stephenson 2005). Therefore, phylogenetic analyses including more representative taxa with multigene regions are needed to clarify the phylogenetic affinity of *Diatrypella* for the better understanding of its taxonomic relationships (Mehrabi et al. 2015).

Dothideovalsa Speg., Anal. Mus. Nac. B. Aires, Ser. 3(12): 414 (1909)

Type: Dothideovalsa tucumanensis Speg., Anal. Mus. Nac. B. Aires, Ser. 3(12): 414 (1909).

Known distribution: Argentina, Brazil and USA (Rappaz 1987; Hanlin 1992).

*Notes: Dothideovalsa* was introduced to accommodate *D. diantherae*, *D. eutypoides*, *D. tucumanensis* and *D. turnerae*. At present, only four species epithets of *Dothideovalsa* is listed in Index Fungorum (2020). However, there was no available sequence data in GenBank. Therefore, this genus is still doubtful and needs further studies.

Endoxylina Romell, Bot. Notiser 1892: 173 (1892)

*Type*: *Endoxylina stellulata* Romell, Bot. Notiser 1892: 173 (1892).

Known distribution: Asia, Europe and North America (Tai 1979; Ju et al. 1996).

*Notes: Endoxylina* was introduced and assigned to *Diatrypales* (Current name: *Xylarialesfide* Kirk et al. 2008) without assigning the familial position by Romell (1892). Based on previous morphological literature and herbarium studies, Hyde et al. (2017) transferred *Endoxylina* to *Diatrypaceae*. The concept of genus *Endoxylina* is rather broad, and it is characterized as having stromata of valsoid or eutypoid configurations and 8-spored, long pedicellate, asci, with J-, apical ring, as well as uni- to triseptate, ascospores (Romell 1892; Ju et al. 1996; Vasilyeva 2010; Hyde et al. 2017). At present, 21 species epithets of *Endoxylina* are listed in Index Fungorum (2020), however, some of these *Endoxylina* species have now been transferred and synonymised with other genera (Ellis and Everhart 1892; Wehmeyer 1975; Rappaz 1987; Barr 1993). Therefore, currently, there is a great deal of taxonomic uncertainty and nomenclatural instability for *Endoxylina* species (Hawksworth et al. 1995) and the number of species recognized for this genus is not well-established.

*Eutypa* Tul. & C. Tul., Select. Fung. Carpol. (Paris) 2: 52 (1863)

Type: Eutypa lata (Pers.) Tul. & C. Tul., Select. Fung. Carpol. (Paris) 2: 56 (1863).

*Known distribution*: Asia, Europe, North America, Oceania, South Africa and South America (Ahmad 1978; **Rappaz** 1987; Schmid-Heckel 1988; Eriksson and Yue 1998; **Mulenko et al. 2008;Moyo et al. 2019**).

*Notes*: Species of *Eutypa* are the causal agents of *Eutypa* dieback of grapevine, apricots and cherries (Trouillas and Gubler 2004; Baumgartner et al. 2010; Camps et al. 2010; Trouillas and Gubler 2010; Blanco-Ulate et al. 2013; Camps et al. 2014). The genus is characterised by stromata which are irregular in shape, as confluent bumps, with conspicuous, scattered, roundish to prominent ostioles on the host surface. Asci are 8-spored, clavate, apically rounded to truncate, with indistinct apical rings, and long pedicels. Ascospores are allantoid to ellipsoidal, aseptate and pale yellowish.

Halocryptosphaeria Dayar., Devadatha, V.V. Sarma & K.D. Hyde, Mycosphere 11(1): 136 (2020)

Type: Halocryptosphaeria bathurstensis (K.D. Hyde & Rappaz) Dayar. & K.D. Hyde, Mycosphere 11(1): 136 (2020).

Known distribution: India (Dayarathne et al. 2020b).

*Notes: Halocryptosphaeria* was established by Dayarathne et al. (2020b) to accommodate species resembling *Cryptosphaeria* <u>but</u> <u>phylogenetically distinct</u>. *Halocryptosphaeria* is characterized in having poorly developed entostroma, dorsally limited by a black zone binding the stromatic area, submerged or occasionally deeply buried long necked ascomata and olive-brown, aseptate ascospores.

#### Halocryptovalsa Dayar. & K.D. Hyde, Cryptog. Mycol. 41(3): 49 (2020)

Type: Halocryptovalsa avicenniae (Abdel-Wahab, Bahkali & E.B.G. Jones) Dayar. & K.D. Hyde, Cryptog. Mycol. 41(3): 50 (2020).

Known distribution: India, Saudi Arabia and Thailand (Abdel-Wahab et al. 2017; Dayarathne et al. 2020a, b).

*Notes: Halocryptovalsa* was established by Dayarathne et al. (2020a) to accommodate species resembling *Cryptovalsa* from marine environments namely *Cryptovalsa avicenniae* and a new species *Halocryptovalsa salicorniae*. The genus is characterised by poorly developed stromata and poly-spored asci, with a J-, cylindrical, conspicuous apical or subapical ring. Ascospores are hyaline or yellow-brown to brown, allantoid, with small, fat globules at the end (Dayarathne et al. 2020a).

Halodiatrype Dayar. & K.D. Hyde, Phytotaxa 7(5): 617 (2016)

*Type: Halodiatrype salinicola* Dayar. & K.D. Hyde, Mycosphere 7(5): 617 (2016).

Known distribution: Thailand (Dayarathne et al. 2016, 2020a).

*Notes: Halodiatrype* was established by Dayarathne et al. (2016) to accommodate *H. avicenniae* and *H. salinicola* isolated from mangroves. The genus is characterised by 8-spored, cylindrical to clavate, pedicellate asci, with apically rounded or flattened, lacking an apical ring and deliquescing early. Ascospores are oblong to allantoid or sub-inequilateral, aseptate or septate, not constricted at the septa, light brown, with one to few small guttules and slightly curved. The asexual morphs are libertella-like (Dayarathne et al. 2016; 2020a).

Leptoperidia Rappaz, Mycol. Helv. 2(3): 544 (1987)

Type: Leptoperidia macropunctata (Rehm) Rappaz, Mycol. Helv. 2(3): 545 (1987).

Known distribution: Congo, Mexico, Philippines (Ellis and Everhart 1896; Rehm 1913).

*Notes: Leptoperidia* was introduced to accommodate *L. applanata, L. asperrima, L. macropunctata* and *L. trifida* (Rappaz 1987). The genus is characterised by relatively small stroma, asci and ascospores, perithecia with very thin and slightly melanized walls (Rappaz 1987). At present, only four species epithets of *Leptoperidia* are listed in Index Fungorum (2020). Sequence data are unavailable in GenBank.

Libertella Desm., Annls Sci. Nat., Bot. 19: 275 (1830)

Type: Libertella betulina Desm., Annls Sci. Nat., Bot. 19: 276 (1830).

*Known distribution*: Asia, Europe, North America, Oceania, South Africa and South America (**Doidge** 1950; Conners 1967; **Ahmad 1969;Farr** 1973; Sosnowski et al. 2007; Mulenko et al. 2008).

*Notes: Libertella* was introduced by Desmazières (1830) to accommodate *L. betulina*, *L. faginea* and *L. rosae*. This genus was mostly reported as the asexual morph of *Diatrypella*, however, some species were reported as asexual *Eutypa*, *Eutypella*, *Diaporthe* and *Polystigma* (Kirk et al. 2001). The genus is characterised by subcortical, erumpent and yellow to red acervula conidiomata and branched conidiophores that produce hyaline, 1-celled, filiform conidia (Barnett and Hunter 1972; Sutton 1980; von Arx 1981).

#### Monosporascus Pollack & Uecker, Mycologia 66(2): 348 (1974)

Type: Monosporascus cannonballus Pollack & Uecker, Mycologia 66(2): 348 (1974).

*Known distribution*: Africa, Asia, Europe, North America and South America (**Pande**, 2008; Sales et al. 2010; Chew-Madinaveitia et al. 2012; Salem et al. 2013; Aleandri et al. 2017).

*Notes: Monosporascus* was introduced by Pollack and Uecker (1974) with *M. cannonballus* as the type species. The genus is characterised by pyriform asci and the formation of one (rarely two) single large, sphaerical ascospores (Pollack and Uecker 1974).

#### Neoeutypella M. Raza, Q.J. Shang, Phook. & L. Cai, Fungal Diversity 95: 167 (2019)

Type: Neoeutypella baoshanensis M. Raza, Q.J. Shang, Phook. & L. Cai, Fungal Diversity 95: 168 (2019).

Known distribution: China and France (Phookamsak et al. 2019).

*Notes: Neoeutypella* was introduced by Phookamsak et al. (2019) to accommodate two fungal strains under the name *Eutypella caricae* and a new strain isolated from *Pinus armandii* (Pinaceae). *Neoeutypella* is characterised by carbonaceous stromata, erumpent through host epidermis, producing yellow pigments surrounding the stroma. Asci are 8-spored, spindle-shaped, with long pedicellate, apically rounded, with refractive cytoplasmic strands, with a J+, subapical ring. Ascospores overlapping 1–3-seriate, allantoid, slightly or moderately curved, initially hyaline, becoming pale brown at maturity, aseptate, mostly with small 1–2 guttules.

*Pedumispora* K.D. Hyde & E.B.G. Jones, Mycol. Res. 96(1): 78 (1992)

*Type: Pedumispora rhizophorae* K.D. Hyde & E.B.G. Jones, Mycol. Res. 96: 78 (1992).

Known distribution: Australia, India and Thailand (Hyde and Jones 1992; Pande 2008; Dayarathne et al. 2020a).

*Notes: Pedumispora* was introduced by Hyde and Jones (1992) to accommodate a taxon from mangrove habitats. A phylogenetic study based on nuclear ITS and LSU regions showed the taxonomic position of *Pedumispora* was in *Diatrypaceae* (Klaysuban et al. 2014). The genus is characterised by 8-spored, fusiform, pedicellate, unitunicate, apically truncate asci. Ascospores are filiform, mutli-septate, curved, longitudinally striate, with tapering poles, with one or both ends crook-like (Hyde and Jones 1992).

#### Peroneutypa Berl., Icon. Fung. 3: 80 (1902)

Type: Peroneutypa bellula (Desm.) Berl., Icon. Fung. 3: 81 (1902).

Known distribution: Asia, Europe, South Africa and South America (**Teodoro** 1937; Moyo et al. 2018; Castilla-Cayuman et al. 201; Moyo et al. 2019).

*Notes: Peroneutypa* was introduced by Berlese (1902) to accommodate *P. bellula*, *P. corniculata and P. heteracantha* without designating the type species. Rappaz (1987) proposed *P. bellula* as the type species and synonymized *Peroneutypa* under *Eutypella*. However, based on morphological characters and phylogenetic (Acero et al. 2004), *Peroneutypa* was reinstated by Carmarán et al. (2006). The genus is characterised by valsoid stromata, with packed, long prominent necks, sessile to long pedicels, small asci with truncate apices and allantoid ascospores (Carmarán et al. 2006, 2014; Senwanna et al. 2017; Shang et al. 2017).

#### Quaternaria Tul. & C. Tul., Select. Fung. Carpol. 2: 104 (1863)

Type: Quaternaria persoonii Tul. & C. Tul., Select. Fung. Carpol. 2: 105 (1863).

Known distribution: Asia, Europe and South America (Mujica and Vergara 1945; Munk 1957; Srinivasulu and Sathe 1970).

*Notes: Quaternaria* was introduced by Tulasne and Tulasne (1863) and was typified by *Q. persoonii*. Clements and Shear (1931) lectotypified the illegitimate name *Q. quaternata* to *Q. persoonii* considered *Quaternaria* as a synonym of *Eutypella* (Tulasne and Tulasne 1863). Based on analyses of ITS and LSU sequence data and the discussion of Gams (1994), *Quaternaria* was considered to be an independent genus by Acero et al. (2004). The genus is characterised by stromata that are cryptosphaeroid in appearance and develop within the bark parenchyma.

#### Rostronitschkia Fitzp., Mycologia 11(4): 165 (1919)

Type: Rostronitschkia nervincola Fitzp., Mycologia 11(4): 166 (1919).

Known distribution: Puerto Rico and Virgin Islands (Stevenson 1975).

*Notes: Rostronitschkia* was introduced to accommodate the type species *R. nervincola*. At present, only the type species epithets of *Rostronitschkia* was listed in Index Fungorum (2020). However, there were no available sequence data and strains. Therefore, this genus is still doubtful and needs to further study.

## Key to genera of Diatrypaceae

1 Asexual morph2
1 Sexual morph3
<b>2</b> Conidiomata acervuli, yellow to red
<b>2</b> Conidiomata pycnidial, brownish yellow, watery, bubble-like <b>Diatrype</b>
<b>3</b> Ascospores globose, fusiform, or oblong to ellipsoidal <b>4</b>
3 Ascospores allantoid7
<b>4</b> Ascospores fusiform, septate <b>Pedumispora</b>
4 Ascospores aseptate
<b>5</b> Ascospores globose, with 1–2 spores in each ascus
5Ascospores oblong to ellipsoidal, with 8 spores in each ascus
6Ascospores with a germ slit
6Ascospores lacking a germ slit
7 Asci with more than 8 spores
7Asci with 8 spores
• <b>8</b> Stromata erumpent through host surface, discoid <b>9</b>
<b>8</b> Stromata immersed in wood but sometimes invading bark tissues, eutypoid <b>10</b>
9 Asci clavate to spindle shaped
<b>9</b> Asci cylindrical <b>Diatrypella</b>
10Habitats marine
10 Habitats terrestrial11
12 Perithecia outer surface lacking powdery entostroma
12 Perithecia outer surface coated with white, powdery entostroma Cryptovalsa
11 Ascospores 0-1 septate13
11 Ascospores uni- to triseptate
<b>13</b> Stromata semi-immersed to erumpent through the host periderm (ectostromatic) <b>14</b>
13Stromata deeply immersed in the host periderm (entostromatic)16

<b>14</b> Asci lacking an apical ring	Halodiatrype
<b>14</b> Asci with J-, cylindrical, conspicuous apica	al ring <b>15</b>
15Ascospores hyaline becoming yellowish a	t maturity Allodiatrype
15Ascospores hyaline	Diatrype
<b>16</b> Ascomata clustered, forming valsoid confinecks	iguration, breaking through entostroma by short to long <b>17</b>
16Ascomata scattered, arranged in linear ent	tostroma, with short to long necks <b>19</b>
<b>17</b> Entostromata immersed in the host, with in center	
17Entostromata slightly raised on the host, v	vith long cylindrical, packed necks <b>18</b>
18Hosts range wide	Eutypella
18Host Pinus armandii	Neoeutypella
<ul><li>19 Ascomata forming very long necks, throug</li><li>19 Ascomata forming short papilla protruding</li></ul>	
<b>20</b> Peridium thin-walled, composed of a singl entostroma	e layer of melanized cells, difficult to separate from the <i>Leptoperidia</i>
<b>20</b> Peridium thick-walled, composed of not o entostroma	
<b>21</b> Asci cylindric-clavate, with pale yellow asc	cospores <i>Eutypa</i>
21Asci generally spindle-shaped, with sub-oli	ivaceous to brown ascospores22
22Peridium compose of two distinct layers	Cryptosphaeria
22Peridium compose of three distinct layers.	Halocryptosphaeria
Key to <i>Diatrypaceae</i> species on <i>Bet</i>	tula spp.
1Asexual morph present	Diatrype betulae
Sexual morph present	2
2 Asci containing 8 biseriate ascospores	
<b>2</b> Asci polysporous	5
<b>3</b> Apical ring amyloid	Diatrype undulata
<b>3</b> Apical ring indistinguishable	4
<b>4</b> Size of asci more than 25 μm	Cryptosphaeria venusta
<b>4</b> Size of asci less than 25 μm	Diatrype platystoma
5Stromata immersed in wood but sometimes	s invading bark tissues, eutypoid
	Eutypella halseyana
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Stromata erumpent through host surface, discoid
Asci cylindrical <b>Diatrypella favacea</b>
Asci clavate to spindle shaped7
More than 10 perithecia arranged irregularly8
Less than 10 perithecia arranged regularly9
Size of asci more than 130 μm
Size of asci less than 130 μm
More than one host
Only one host10
<b>0</b> Size of asci less than 140 μm
<b>0</b> Size of asci more than 140 μm

# Discussion

In this study, 21 isolates were identified as diatrypaceous fungi from *Betula albosinensis*, *B. davurica* and *B. platyphylla* (Betulaceae), *Castanea mollissima* and *Quercus mongolica* (Fagaceae), *Juglans regia* (Juglandaceae) and *Morus alba* (Moraceae). Morpho-molecular analyses confirmed that these strains belong in one new genus (*Allodiatrypella*) and ten novel species (*Allocryptovalsa castanea*, *Allodiatrypella betulae*, *A. betulicola*, *A. betulina*, *A. hubeiensis*, *A. xinjiangensis*, *Diatrype betulae*, *D. castaneicola*, *D. quercicola* and *Eutypella castaneicola*). *Eutypella citricola* which was reported from *Morus* host for the first time, thus it's a new host record. Of these, *Allodiatrypella* was provided to accommodate the new combination species *Allodiatrypella yunnanensis* (Basionym: *Diatrypella yunnanensis*) and another five novel *Allodiatrypella* species.

The generic concepts of *Diatrypaceae* have been unstable, thus many species being transferred from one genus to another (Phookamsak et al. 2019; Konta et al. 2020). The current study revised the *Diatrypaceae* and accepted 24 genera in this family (Table 1). However, there only exist 19 genera in current phylogenetic analyses due to limited available molecular data (Fig. 1). In China, 11 genera and 63 species belongs in *Diatrypaceae* have been recorded (Additional file 2: Table S2). However, 46 species (73.01%) do not have molecular data until now since they have been reported.

Birch is of high economic, medicinal and ornamental value. Six species of *Diatrypaceae* were recorded from *Betula* spp. with available materials and DNA sequences in current study, including *Allodiatrypella betulae*, *A. betulicola*, *A. betulina*, *A. hubeiensis*, *A. xinjiangensis* and *Diatrype betulae*. All *Allodiatrypella* species except *A. yunnanensis* which was iasolated from unidentified plant was isolated from *Betula* spp. It may indicate that many *Allodiatrypella* species have obvious host specificity. The other five species of *Diatrypaceae* were recorded from *Betula* spp. in China with available materials but no DNA sequences, including *Cryptosphaeria venusta*, *Diatrype platystoma*, *D. undulata*, *Diatrypella favacea*, *Eutypella halseyana* (Teng 1996; Vasilyeva and Ma 2014). A morphological key was provided to separate them in the current study.

Some confused taxa were excluded in the current phylogram. *Diatrype decorticata* (ANM 1498), *Diatrype enteroxantha* (HUEFS 155116), *Diatrype macowaniana* (CBS 214.8), *Diatrype oregonensis* (DCA600), *Diatrype polycocca* (CBS 213.87), *Diatrype prominens* (ATCC MYA-4410), *Diatrype whitmanensis* (CDB011), *Eutypella parasitica* (CBS 210.39) and *Eutypella prunastri* (CBS 277.87) are not the type strains, which have single clade in phylogenetic tree or mixed with in clade of other genera. And the sequence data of *Halocryptovalsa avicenniae* (MAW 2017a) is inconsistent with the position of genus. Therefore, fresh collections and sequence data of type materials are required for revising *Diatrypaceae*.

The *Allocryptovalsa* species clustered with the *Eutypella* species which cannot divided into two separate clades representing two different genera in phylogenetic analyses (Fig. 1; Clade 14: *Allocryptovalsa/Eutypella sensu lato*). And the *Allocryptovalsa cryptovalsoide* (syn. *Eutypella cryptovalsoide*) and *Eutypella castaneicola* both display some features of morphology typical of *Cryptovalsa* (polysporous ascus) as well as *Eutypella* (perithecial necks erumpent in groups) (Spooner 1981; Vasilyeva and Stephenson 2005;

Trouillas et al. 2011). *Allocryptovalsa* was introduced by Senwanna et al. (2017) which resembles *Cryptovalsa* in morphology which both have polysporous asci different from the 8-spored asci of *Eutypella*. The number of spores per ascus (eight spores vs. more than eight spores) has been used traditionally to differentiate the genera of *Diatrypaceae* (*Diatrype* vs. *Diatrypella* and *Cryptovalsa* vs. *Eutypella*). However, the polysporous ascus feature has been shown to be not significant in *Diatrypaceae* based on recent studies (Acero et al. 2004; Vasilyeva and Stephenson 2005; Trouillas et al. 2011; Chacon et al. 2013; Liu et al. 2015) and the phylogenies showed that the genera *Cryptovalsa* and *Eutypella*, as well as *Diatrype* and *Diatrypella* have molecular affinities. Therefore, we suggest to combine this species from clade 14 into one genus in further study.

The strains of *Diatrype* formed a well-resolved clade (Fig. 1; Clade 13: *Diatrype sensu stricto*). However, in this clade, some strains of *Diatrypella* (*D. quercina*, *D. iranensis* and *D. macrospora*) were placed between *Diatrype* species. Acero et al. (2004) reported that *Cryptosphaeria*, *Diatrype*, *Diatrypella*, *Eutypa* and *Eutypella* based on ITS sequence data were polyphyletic and confused probably lacking of *tub2* gene sequences or misidentified species. However, these five genera are still polyphyletic within the family from previous studies (Trouillas et al. 2011; Chacón et al. 2013; de Almeida et al. 2016; Shang et al. 2017; Mehrabi et al. 2019; Konta et al. 2020; Dayarathne et al. 2020a, b) based on the ITS and *tub2* sequences data. In our study, the *Diatrype* and *Diatrypella* are not polyphyletic with the five novel taxa and one novel combination constituting separate lineages (Fig. 1; Clade 06: *Allodiatrypella*). *Allodiatrype* and *Halodiatrype* were reported the morphological resemblance to *Diatrype* (Dayarathne et al. 2016, Konta et al. 2020). However, different from the asci of *Halodiatrype* lacking an apical ring, the asci of *Allodiatrype* have J-, cylindrical, conspicuous apical ring (Dayarathne et al. 2016; Maharachchikumbura et al. 2016; Konta et al. 2020). Additionally, *Diatrype* can be differentiated from *Allodiatrype* in color of ascospores. The ascospores of *Diatrype* are hyaline becoming yellowish ascospores at maturity, whereas the ascospores of *Allodiatrype* are hyaline (Maharachchikumbura et al. 2016; Konta et al. 2020). Though the genes *Diatrype* and *Diatrypella* are not polyphyletia

In same case, some strains of *Diatrype* species (*D. brunneospora* and *D. palmicola*), *Diatrypella* species (*D. banksiae*), *Eutypa* species (*E. guttalata*) and *Eutypalla* species (*E. cearensis*) formed distinct lineages within *Diatrypaceae* (Fig. 1; *Incertae sedis*). *Diatrypella banksiae* is closely related to the genus *Neoeutypella* with high support values from the phylogenetic analyses (MP/ML/BI = 98/98/1) (Fig. 1) which produced an asexual morph (Crous et al. 2016; Phookamsak et al. 2019). Nevertheless, *Neoeutypella* can be differentiated from *Diatrypella banksiae* in shape and size of conidia. *Neoeutypella baoshanensis* has filiform conidia, whereas *Diatrypella banksiae* has spindle-shaped conidia (Crous et al. 2016; Phookamsak et al. 2019). However, the asexual morphs of *Diatrypaceae* are not generally useful in separating species (Glawe and Rogers 1982, 1984; Rappaz 1987; Konta et al. 2020). Therefore, sexual morph of *Diatrypella banksiae* is to be studied.

*Diatrypella banksiae* probably belongs the genus *Neoeutypella*. Further study of the relationship between *Neoeutypella* and *Diatrypella banksiae* is needed. *Eutypa guttulata* is closely related to the genus *Halodiatrype* and *Pedumispora* from the phylogenetic analyses (Fig. 1) as basal branch. *Eutypa guttulata* can be distinguished by fusiform ascospores, whereas *Pedumispora* has allantoid ascospores (Hyde and Jones 1992). It is also different from *Halodiatrype* because of lacking an apical ring (Dayarathne et al. 2016). *Diatrype brunneospora* is closed to *Eutypa guttulata* (Fig. 1) which has morphological similarity with members of the genus *Eutypa* (Trouillas et al. 2010a). Therefore, the assignment of this isolate to the genus *Diatrype* may require reconsideration in the future. *Diatrype palmicola* is closely related to the genus *Allodiatrypella* with no support (Fig. 1). *Allodiatrypella* can be distinguished by hyaline to subhyaline, rarely pale olivaceous ascospores, whereas *Diatrype palmicola* has pale yellowish to pale brown ascospores at maturity (Liu et al. 2015). For those species, the assignment of these isolates still remain unclear, which may require reconsideration in the future.

*Eutypa microasca* appeared in a strongly supported clade along with two *Peroneutypa* species with fusiform asci in Fig. 1 (Clade 21: *Peroneutypa*), suggesting that the divergent characters of the stromata, perithecia necks, and shape of the asci are probably primitive and retained in *Eutypa microasca*. Carmarán et al. (2006) suggested that the morphology of the ascus could explain the phylogenetic relationships within *Diatrypaceae* better than stromata, although our study indicates that it is not entirely supported in *Peroneutypa*. The phylogenetic signal of the ascus shape and the phylogenetic placement of *Eutypa microasca* should be further tested in future study.

# Conclusions

The current study focuses on *Diatrypaceae* species in China, which is considered as a biodiversity hotspot with a high diversity for fungal species (Yang et al. 2018; Fan et al. 2020; Pan et al 2020). We hope that the descriptions and molecular data of *Diatrypaceae* in this study could provide a resource for future studies in this family.

# Abbreviations

ITS: Ribosomal DNA internal transcribed spacer region; *tub2*:beta-tubulin; PDA:Potato dextrose agar.

# Declarations

#### Ethics approval and consent to participate

Not applicable.

#### Adherence to national and international regulations

Not applicable.

#### Consent for publication

Not applicable.

#### Availability of data and materials

Alignments and tree files generated during the current study are available in the TreeBASE (accession https://www.treebase.org/treebase-web/home.html; study S27126). All sequence data are available in NCBI Genbank following the accession numbers in the manuscript.

#### **Competing interests**

The authors declare no competing interests.

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#### Authors' contributions

All authors contributed extensively to the work presented in the manuscript. XF, CT and CY conceived and designed the experiments. HZ, MP, GZ, RM and MH performed the experiments. HZ MP and GZ analyzed the data. NW and DD polished the language. HZ wrote the manuscript. XF revised and approved the final version of the manuscript.

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## Tables

**Table 1.** Placement of genera in Diatrypaceae by different authors.

Nitschke (1867) (5 gen.)	Kirk et al. (2001) (9 gen.)	Kirk et al. (2008) (13 gen.)	Senanayake et al. (2015) (17 gen.)	Wijayawardene et al. (2018) (17 gen.)	Wijayawardene et al. (2020) Hyde et al. (2020a) (20 gen.)	This study (24 gen.)
Calosphaeria	Cryptosphaeria	Cryptosphaeria	Anthostoma	Allocryptovalsa	Allocryptovalsa	Allocryptovalsa
Diatrype	Cryptovalsa	Diatrype	Cryptosphaeria	Anthostoma	Anthostoma	Allodiatrype
Diatrypella	Diatrype	Dothideovalsa	Cryptovalsa	Cryptosphaeria	Cryptosphaeria	Allodiatrypella
Quaternaria	Diatrypella	Diatrypella	Diatrype	Cryptovalsa	Cryptovalsa	Anthostoma
Scoptria	Eutypella	Eutypa	Diatrypella	Diatrypasimilis	Diatrypasimilis	Cryptosphaeria
	Echinomyces	Echinomyces	Diamantinia	Diatrype	Diatrype	Cryptovalsa
	Eutypa	Endoxylina	Diatrypasimilis	Diatrypella	Diatrypella	Diatrypasimilis
	Fassia	Eutypella	Echinomyces	Echinomyces	Echinomyces	Diatrype
	Leptoperidia	Leptoperidia	Eutypa	Endoxylina	Endoxylina	Diatrypella
		Libertella	Eutypella	Eutypa	Eutypa	Dothideovalsa*
		Quaternaria	Leptoperidia	Eutypella	Eutypella	Endoxylina*
		Peroneutypa	Libertella	Leptoperidia	Halocryptovalsa	Eutypa
		Rostronitschkia	Monosporascus	Halodiatrype	Halodiatrype	Eutypella
			Pedumispora	Libertella	Leptoperidia	Halocryptosphaeria
			Peroneutypa	Monosporascus	Libertella	Halocryptovalsa
			Phaeoisaria	Peroneutypa	Monosporascus	Halodiatrype
			Quaternaria	Quaternaria	Neoeutypella	Leptoperidia*
					Pedumispora	Libertella*
					Peroneutypa	Monosporascus
					Quaternaria	Neoeutypella
						Pedumispora
						Peroneutypa
						Quaternaria
						Rostronitschkia*

Notes: Genera without available sequence data in this study are marked by an asterisk (\*).

 $\label{eq:table2} \textbf{Table 2.} \ \textbf{Isolates and GenBank accession numbers in the current study}.$ 

Species	Strain	Host/Substrate	Origin	GenBank accession numbers		
				ITS	TUB2	
Allocryptovalsa castanea	CFCC 52428	Castanea mollissima	China	XXXXXX	XXXXXX	
Allocryptovalsa castanea	CFCC 52427	Juglans regia	China	XXXXXX	XXXXXX	
Allocryptovalsa castanea	CFCC 52429	Castanea mollissima	China	XXXXXX	XXXXXX	
Allodiatrypella betulae <sup>TS</sup>	CFCC 52406	Betula albosinensis	China	XXXXXX	XXXXXX	
Allodiatrypella betulae <sup>TS</sup>	CFCC 52404	Betula albosinensis	China	XXXXXX	XXXXXX	
Allodiatrypella betulae <sup>TS</sup>	CFCC 52405	Betula albosinensis	China	XXXXXX	XXXXXX	
Allodiatrypella betulicola	CFCC 52411	Betula davurica	China	XXXXXX	XXXXXX	
Allodiatrypella betulicola	CFCC 52412	Betula platyphylla	China	XXXXXX	XXXXXX	
Allodiatrypella betulina	CFCC 52414	Betula albosinensis	China	XXXXXX	XXXXXX	
Allodiatrypella betulina	CFCC 52415	Betula albosinensis	China	XXXXXX	XXXXXX	
Allodiatrypella hubeiensis	CFCC 52413	Betula davurica	China	XXXXXX	XXXXXX	
Allodiatrypella wenquanensis	CFCC 52409	Betula platyphylla	China	XXXXXX	XXXXXX	
Diatrype betulae	CFCC 52416	Betula davurica	China	XXXXXX	XXXXXX	
Diatrype castaneicola	CFCC 52425	Castanea mollissima	China	XXXXXX	XXXXXX	
Diatrype castaneicola	CFCC 52426	Castanea mollissima	China	XXXXXX	XXXXXX	
Diatrype querquecina	CFCC 52418	Quercus mongolica	China	XXXXXX	XXXXXX	
Diatrype querquecina	CFCC 52419	Quercus mongolica	China	XXXXXX	XXXXXX	
Diatrype querquecina	CFCC 52420	Quercus mongolica	China	XXXXXX	XXXXXX	
Eutypella castaneicola	CFCC 52432	Castanea mollissima	China	XXXXXX	XXXXXX	
Eutypella citricola	CFCC 52433	Morus alba	China	XXXXXX	XXXXXX	
Eutypella citricola	CFCC 52434	Morus alba	China	XXXXXX	XXXXXX	

Notes: Ex-type strains are in bold and type species are denoted with the superscript "TS".

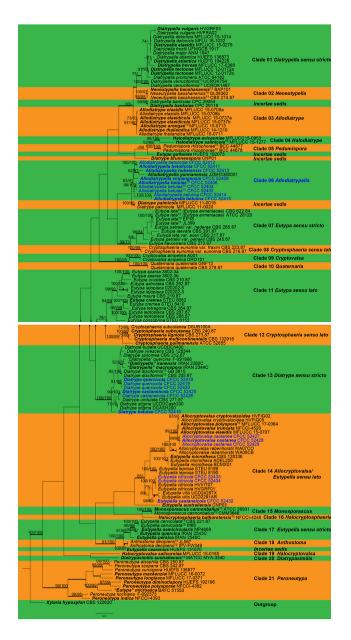
 Table 3. Synopsis of Allocryptovalsa castanea and other species of Allocryptovalsa.

Species	Host	Asci length (µm)	Asci width (μm)	Ascospores length (µm)	Ascospore width (µm)	Reference
A. castanea	Castanea mollissima Juglans regia	(52-)60- 83(-92)	(11–)12– 17(–25)	8-11(-13)	2.5-3.5 (-4)	This study
A. cryptovalsoidea	Ficus carica	65-120	15-20	8-12(-13.5)	2-3	Trouillas et al. (2011)
A. elaeidis	Elaeis guineensis	(55–)68– 147(–157)	14-26	(6-)7.5-9(-10.5)	2-4	Konta et al. (2020)
A. polyspora	Hevea brasiliensis	(33–)70– 120(–177)	(4-)13-19(-21)	5-14	2-4	Senwanna et al. (2017)
A. rabenhorstii	Vitis vinifera Sambuscus nigra	(55-)70-90(-95)	(15-)18-22(-27)	(10-)13.5-15(-17.5)	(3-)4-5(-6)	Trouillas et al. (2011)
A. truncata	NA	(84–)89–117(– 122)	(10-)12-15(- 16.5)	(7-)7.2-10.7	2.1-2.7	Hyde et al. (2020)

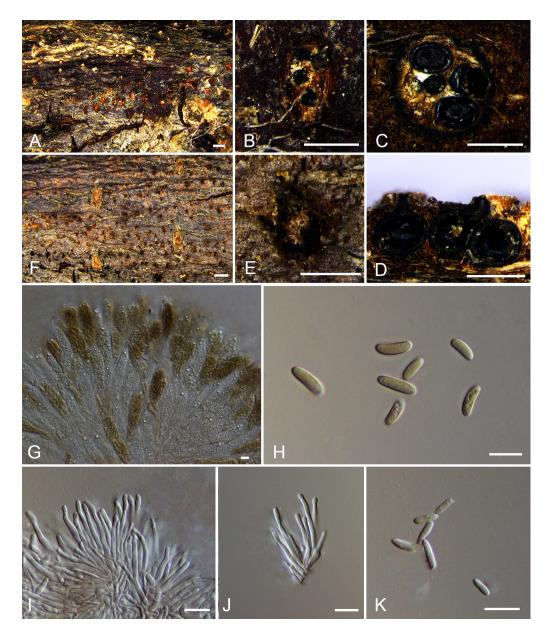
## Table 4. Synopsis of species of Allodiatrypella.

Species	Host	Asci length	igth (μm)	Ascospores length	Ascospores width	Reference
		(µm)		(µm)	(µm)	
A. betulae	Betula albosinensis	132- 140	7.5– 10.5(–11.5)	(4.5-)5-7	1-2	This study
A. betulicola	Betula davurica, Betula platyphylla	117- 133	10-12	5-8	1-2	This study
A. betulina	Betula albosinensis	129- 140	(5-)8-12	5-7	1-2	This study
A. hubeiensis	Betula davurica	189- 240	18-21	6-8.5(-9)	1-2	This study
A. xinjiangensis	Betula platyphylla	88-133	(7-)8- 10(-11)	4-6	1-2	This study
A. yunnanensis	NA	105- 210	15-30	18-22	3-4	Hyde et al. (2020b)

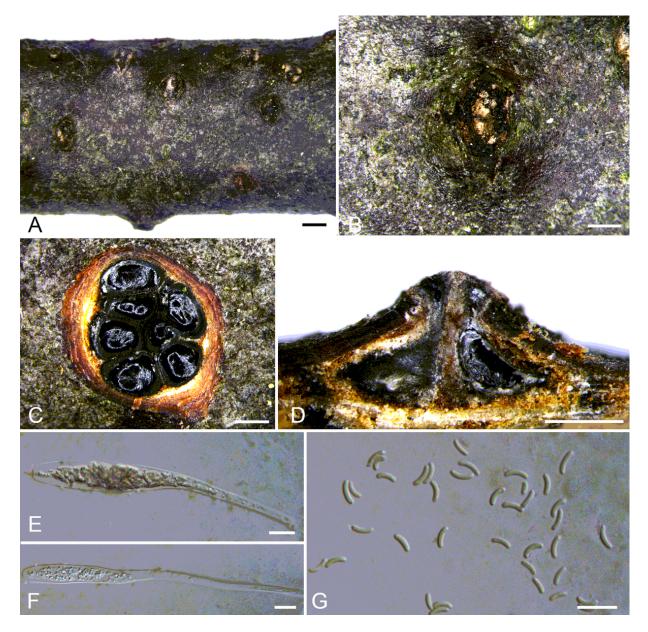
# Figures



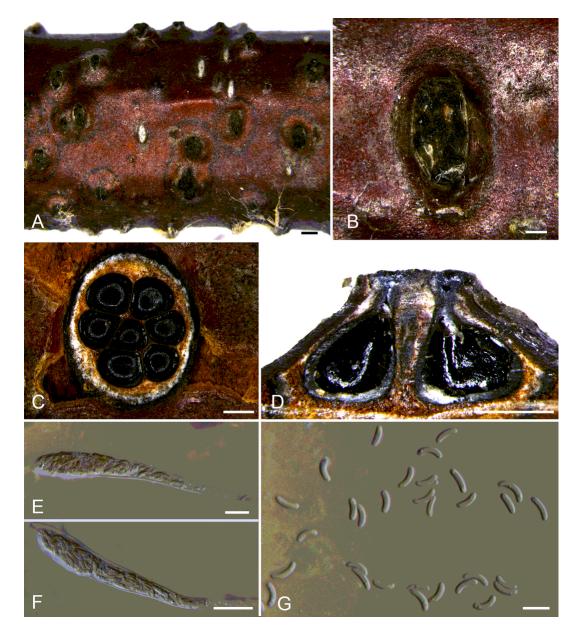
Phylogram of Diatrypaceae based on combined ITS and tub2 sequence data. The MP and ML bootstrap support values above 70 % are shown at the first and second positions, respectively. Thickened branches represent posterior probabilities above 0.95 from the BI. Extype strains are in bold and type species are denoted with the superscript "TS". Strains from the current study are in blue.



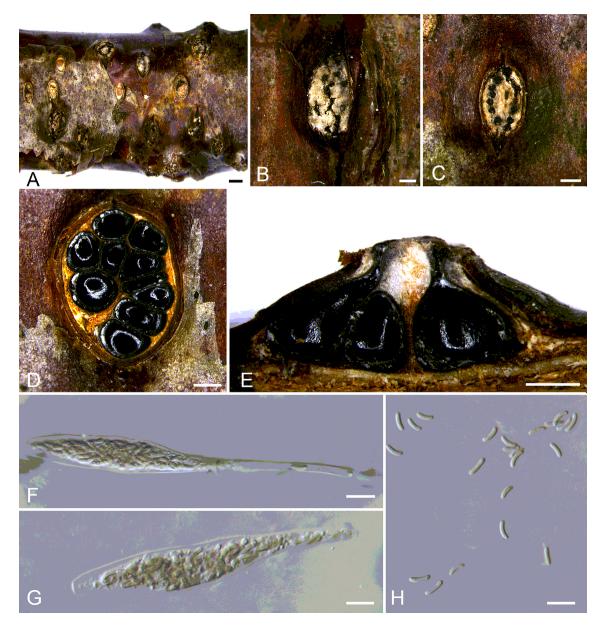
Holomorph of Allocryptovalsa castanea (BJM 240506, holotype). a, b Habit of stromata on twig. c Transverse section of stroma. d Longitudinal section through stroma. e, f Conidiomata on twig. g Asci and ascospores. h Ascospores. i–j Conidia attatch to conidiogenous cells. k Conidia. Scale bars: 1 mm (a, f); 500  $\mu$ m (b–e); 10  $\mu$ m (g–k).



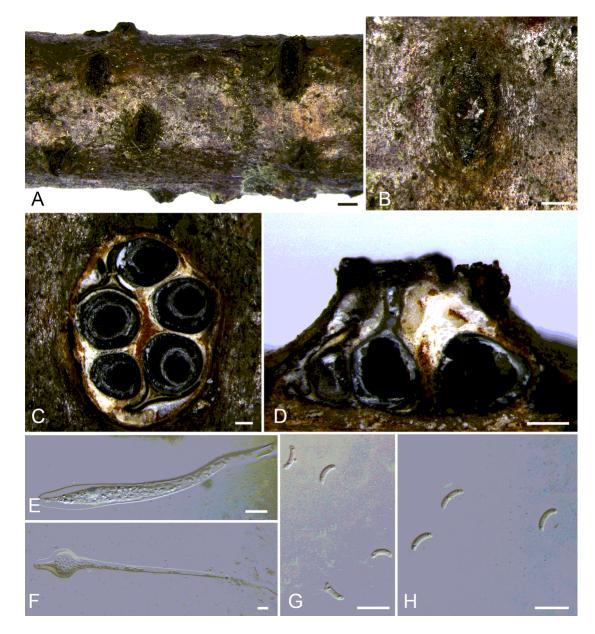
Sexual morph of Allodiatrypella betulae (BJM 240507, holotype). a-b Habit of stromata on twig. c Transverse section of stroma. d Longitudinal section through stroma. e-f Asci and ascospores. g Ascospores. Scale bars: 1 mm (a); 500 µm (b-d); 10 µm (e-g).



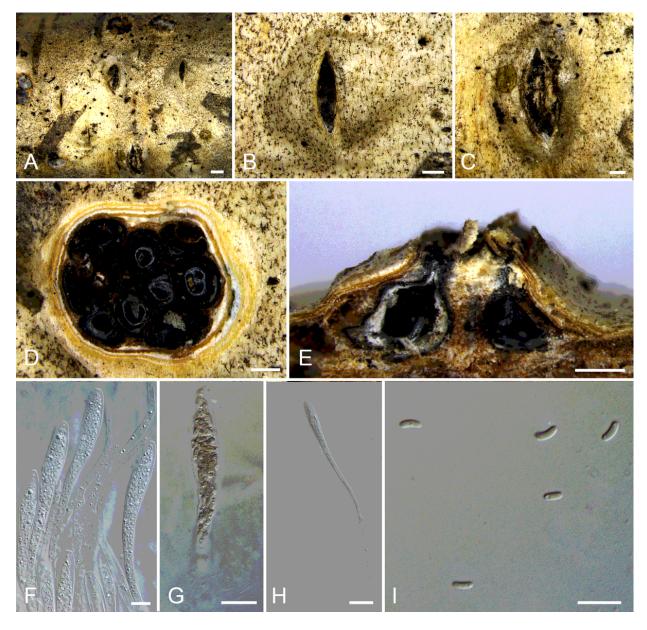
Sexual morph of Allodiatrypella betulicola (BJM 240508). a-b Habit of stromata on twig. c Transverse section of stroma. d Longitudinal section through stroma. e-f Asci and ascospores. g Ascospores. Scale bars: 1 mm (a); 500  $\mu$ m (b-d); 10  $\mu$ m (e-g).



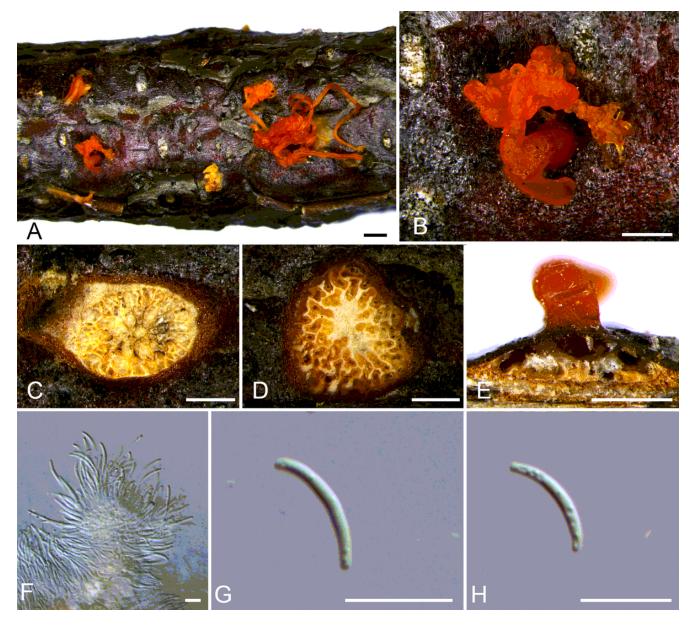
Sexual morph of Allodiatrypella betulina (BJM 240509). a-c Habit of stromata on twig. d Transverse section of stroma. e Longitudinal section through stroma. f-g Asci and ascospores. h Ascospores. Scale bars: 1 mm (a); 500  $\mu$ m (b-e); 10  $\mu$ m (f-h).



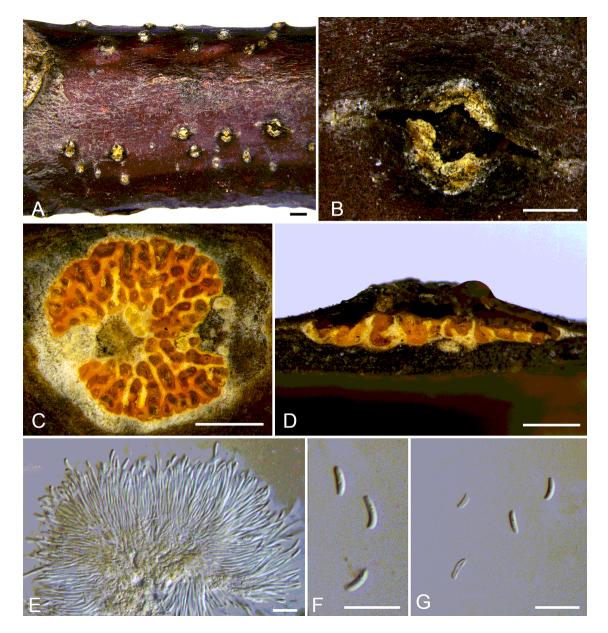
Sexual morph of Allodiatrypella hubeiensis (BJM 240510). a–b Habit of stromata on twig. c Transverse section of stroma. d Longitudinal section through stroma. e–f Asci and ascospores. g Ascospores. Scale bars: 1 mm (a); 500 µm (b–d); 10 µm (e–g).



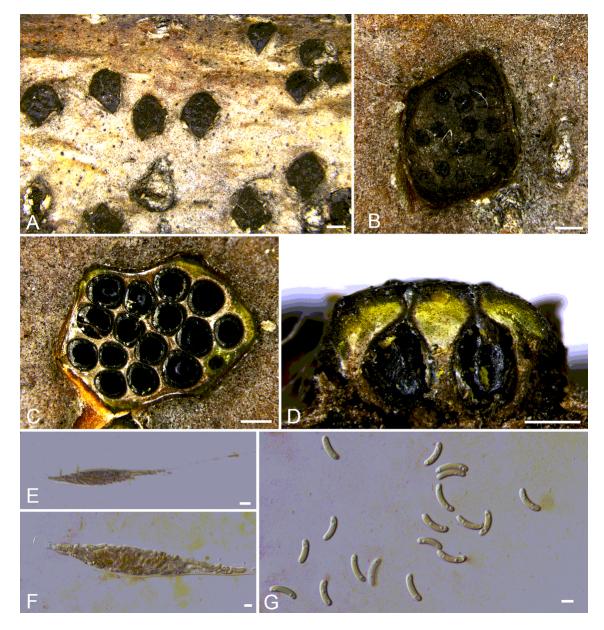
Sexual morph of Allodiatrypella xinjiangensis (BJM 240511). a-c Habit of stromata on twig. d Transverse section of stroma. e Longitudinal section through stroma. f-h Asci and ascospores. i Ascospores. Scale bars: 1 mm (a); 500  $\mu$ m (b-e); 10  $\mu$ m (f-i).



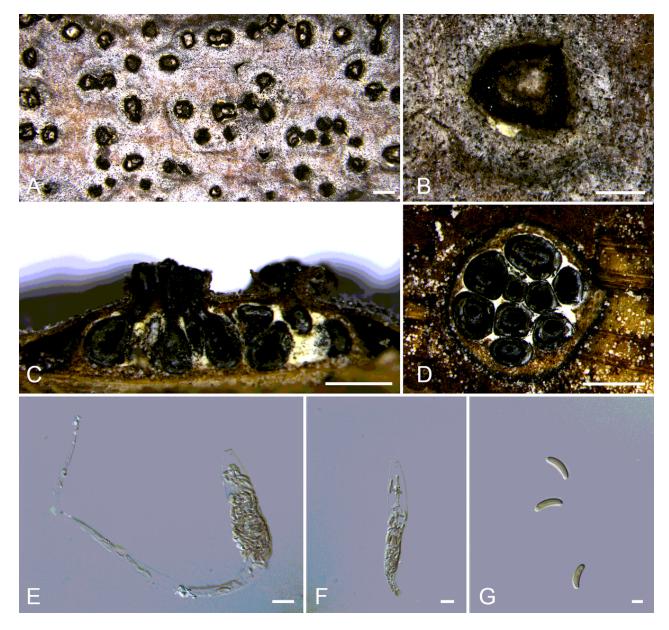
Asexual morph of Diatrype betulae (BJM 240512). a-b Habit of conidiomata on twig. c-d Transverse section of conidioma. e Longitudinal section through conidioma. f Conidiogenous cells. g-h Conidia. Scale bars: 1 mm (a); 500  $\mu$ m (b-e); 10  $\mu$ m (f-h).



Asexual morph of Diatrype castaneicola (BJM 240513). a-b Habit of conidiomata on twig. c Transverse section of conidioma. d Longitudinal section through conidioma. e Conidiogenous cells. f Conidia. Scale bars: 1 mm (a); 500  $\mu$ m (b-d); 10  $\mu$ m (e-f).



Sexual morph of Diatrype quercicola (BJM 240514). a-b Habit of stromata on twig. c Transverse section of ascoma. d Longitudinal section through ascoma. e-f Asci and ascospores. g Ascospores. Scale bars: 1 mm (a); 500  $\mu$ m (b-d); 10  $\mu$ m (e-g).



Sexual morph of Cryptovalsa castaneicola (BJM 240515). a-b Habit of stromata on twig. c Transverse section of stroma. d Longitudinal section through stroma. e-f Asci and ascospores. g Ascospores. Scale bars: 1 mm (a); 500 µm (b-d); 10 µm (e-g).

# **Supplementary Files**

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- TableS1.docx
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