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Families and genera of diaporthalean fungi associated with canker and dieback of tree hosts

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Key words

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Abstract In this study we accept 25 families in *Diaporthales* based on phylogenetic analyses using partial ITS, LSU, *rpb2* and *tef1-α* gene sequences. Four different families associated with canker and dieback of tree hosts are morphologically treated and phylogenetically compared. These include three new families (*Diaporthostomataceae*, *Pseudomelanconidaceae*, *Synnemasporellaceae*), and one new genus, *Dendrostoma* (*Erythrogloeaceae*). *Dendrostoma* is newly described from *Malus spectabilis*, *Osmanthus fragrans* and *Quercus acutissima* having fusoid to cylindrical, bicellular ascospores, with three new species namely *D. mali*, *D. osmanthi* and *D. quercinum*. *Diaporthostomataceae* is characterised by conical and discrete perithecia with bicellular, fusoid ascospores on branches of *Machilus leptophylla*. *Pseudomelanconidaceae* is defined by conidiogenous cells with apical collarets and discreet annellations, and the inconspicuous hyaline conidial sheath when mature on *Carya cathayensis*, compared to morphologically similar families *Melanconidaceae* and *Juglanconidaceae*. *Synnemasporellaceae* is proposed to accommodate fungi with synnematous conidiomata, with descriptions of *S. toxicodendri* on *Toxicodendron sylvestre* and *S. aculeans* on *Rhus copallina*.

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INTRODUCTION

Diaporthales represents an important order in *Sordariomycetes* containing taxa that are mainly isolated as endophytes, saprobes or plant pathogens on various hosts. The order is characterised by perithecia with elongate beaks, often forming within stromatic tissues, deliquescent paraphyses and asci that generally deliquesce, become detached from the perithecial wall when mature, and have a characteristic refractive apical annulus (Rossman et al. 2007). Members of diaporthalean fungi are responsible for several diseases causing severe damage in plants with economic importance. The most notorious is chestnut blight caused by *Cryphonectria parasitica* (*Cryphonectriaceae*) that devastated American chestnut (*Castanea dentata*) populations in North America (Anagnostakis 1987, Gryzenhout et al. 2006). Other common diseases include ash anthracnose due to *Gnomoniella fraxinii* and birch canker caused by *Cryptosporella platyphylla* (*Gnomoniaceae*) (Redlin & Stack 1988, Fan et al. 2016a), stem-end rot of citrus fruits infected by *Diaporthe citri* and walnut canker by *Diaporthe rostrata* (*Diaporthaceae*) (Huang et al. 2013, 2015, Fan et al. 2015b, Guarnaccia & Crous 2017), willow and walnut canker disease caused by *Cytospora chrysosperma* (*Cytosporaceae*) (Fan et al. 2014, 2015a), birch dieback disease resulting from *Melanconis stilbostoma* (*Melanconidaceae*) (Fan et al. 2016b), walnut dieback disease by *Juglanconis juglandina* and *J. oblonga* (in *Juglanconidaceae*) (Voglmayr et al. 2017), foliar diseases of *Eucalyptus* by *Harknessia* spp. (*Harknessiaceae*) (Crous et al. 2012), and foliar, fruit and stem diseases by *Coniella* spp. (*Schizoparmaceae*) (Alvarez et al. 2016, Marin-Felix et al. 2017).

The classification of *Diaporthales* has changed drastically over the past decades because of the plasticity and variability in morphology. The order *Diaporthales* and *Valsales* were first introduced by Nannfeldt (1932), based on subfamilies *Eu-Diaportheen* and *Valseen* in *Diaportheaceae* proposed by Von Höhnel (1917). Later, *Diaporthaceae* and '*Valsaceae*' (now *Cytosporaceae*, and referred to as such below) were recognised in the *Diaporthales* by Von Arx & Müller (1954). Kobayashi (1970) proposed *Diaporthaceae* (including *Valsa* = *Cytospora*) in a wide concept including all taxa accepted in *Diaporthales* by Barr (1978). Wehmeyer & Hanlin (1975) accepted three families within this order, including non-allantoid spored *Gnomoniaceae* and *Diaporthaceae* separated on the presence or absence of a stroma, and *Cytosporaceae* with allantoid ascospores. Barr (1978) arranged four families (*Gnomoniaceae*, *Melanconidaceae*, *Pseudovalsaceae* and *Cytosporaceae*) in *Diaporthales* based on beak position of ascomata and thin or firm ascospore walls without special emphasis on allantoid or non-allantoid ascospores. Families within the *Diaporthales* have been segregated by several mycologists to utilise various criteria: stromatic tissues, arrangement of ascomata in the stroma or substrate, and ascospore shape, e.g., four families (*Cytosporaceae, Endoxylaceae*, *Gnomoniaceae* and *Melanconidaceae*) by Monod (1983), three families (*Cytosporaceae, Melanconidaceae* and *Phyllachoraceae*) by Cannon (1988), while Hawksworth et al. (1995) merged the *Cytosporaceae, Gnomoniaceae* and *Melanconidaceae* proposed by Barr (1990) to *Cytosporaceae* and *Melanconidaceae*. These changes and confusions suggested that phenotypic characters alone were unable to provide sufficient evidence to resolve phylogenetic and evolutionary patterns among these fungi.

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Molecular studies on fungi began in the early 1990s, and since then ribosomal DNA sequence data were accepted as the standard gene loci for fungi (Berbee & Taylor 1992, Schoch et al. 2012). Zhang & Blackwell (2001) recognised three lineages in *Diaporthales*, while Castlebury et al. (2002) postulated six major lineages, namely the *Cryphonectria-Endothia* complex, *Cytosporaceae* s.str., *Diaporthaceae* s.str., *Gnomoniaceae* s.str., *Melanconidaceae* s.str. and the *Schizoparme* complex. When Rossman et al. (2007) reviewed the *Diaporthales*, nine families were recognised, i.e., *Cryphonectriaceae*, *Cytosporaceae, Diaporthaceae*, *Gnomoniaceae*, *Melanconidaceae*, *Pseudovalsaceae*, *Schizoparmeaceae*, *Sydowiellaceae* and *Togniniaceae*. Kirk et al. (2008) added *Melogrammataceae* and listed 10 families in this order, whereas Jaklitsch & Voglmayr (2012) placed *Melogrammataceae* within *Xylariales* rather than *Diaporthales*. Subsequently, the *Pseudoplagiostomataceae*, *Harknessiaceae*, *Macrohilaceae* and *Tirisporellaceae* were also added to the *Diaporthales* (Cheewangkoon et al. 2010, Crous et al. 2012, 2015, Suetrong et al. 2015). Voglmayr & Jaklitsch (2014) resurrected *Stilbosporaceae*, while the *Togniniaceae* and *Tirisporellaceae* were reallocated to the *Togniniales* and *Tirisporellales* (Gramaje et al. 2015, Jones et al. 2015). Later, *Lamproconiaceae* and *Juglanconidaceae* were proposed as new families in this order (Norphanphoun et al. 2016, Voglmayr et al. 2017). The recent outline of *Diaporthales* published by Senanayake et al. (2017) used morphological and phylogenetic evidence to introduce seven new families and accepted a total of 21 families in the order. In spite of these changes, the phylogenetic placement of many genera in the *Diaporthales* remains unknown, and many families still wait to be elucidated.

During the trips to collect forest pathogens that cause canker or dieback diseases in China, several diaporthalean taxa associated with various disease symptoms were collected in Jiangxi and Zhejiang Provinces, China. Because the higher-level phylogeny of many genera within the *Diaporthales* remains largely unresolved, this project was initiated to address this issue. In this paper, we propose three new families and one new genus as well as several new species.

MATERIALS AND METHODS

Isolation

Fresh specimens of diaporthalean fungi were collected from infected branches of seven hosts during collection trips in China (Table 1). A total of 20 isolates were established by removing a mucoid spore mass from ascomata or conidiomata, spreading the suspension on the surface of 1.8 % potato dextrose agar (PDA), and incubating at 25 °C for up to 24 h. Single germinating conidia/ascospores were removed and plated onto fresh PDA plates. Specimens and isolates were deposited in the Key Laboratory for Silviculture and Conservation of the Ministry of Education in the Beijing Forestry University (BJFU) and the working Collection of X.L. Fan (CF) housed at the BJFU. Axenic cultures are maintained in the China Forestry Culture Collection Centre (CFCC).

Morphology

Species identification was based on morphological features of the ascomata or conidiomata produced on infected plant tissues and micromorphology, supplemented by cultural characteristics. Cross-sections were prepared by hand using a double-edge blade under a dissecting microscope. At least 10 conidiomata/ascomata, 10 asci and 30 conidia/ascospores were measured to calculate the mean size and standard deviation (SD). Microscopic photographs were captured with a Nikon Eclipse 80i microscope 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. Nomenclatural novelties and descriptions were deposited in MycoBank (Crous et al. 2004). Colony diameters were measured, and the colony colours described after 3 wk according to the colour charts of Rayner (1970).

DNA extraction, amplification and sequencing

Genomic DNA was extracted using a modified CTAB method, with fungal mycelium harvested from PDA plates with cellophane (Doyle & Doyle 1990). The ITS region was amplified with the primers ITS1 and ITS4 (White et al. 1990), the LSU region with the primers LR0R and LR5 (Vilgalys & Hester 1990), the *rpb2* region with primers fRPB2-5F and fRPB2-7cR (Liu et al. 1999), and the *tef1-α* gene with the primers EF1-728F and EF1-986R (Carbone & Kohn 1999). The PCR mixture for all regions consisted of 1 µL genomic DNA, 3 mM $MgCl_2$, 20 µM of each dNTP, 0.2 µM of each primer and 0.25 U BIOTAQ DNA polymerase (Bioline). Conditions for PCR of ITS and LSU genes constituted an initial denaturation step of 2 min at 95 °C, followed by 35 cycles of 30 s at 95 °C, 45 s at 51 °C and 1 min at 72 °C, and a final denaturation step of 8 min at 72 °C, while the *tef1-α* gene was performed using an initial denaturation step of 2 min at 95 °C, followed by 35 cycles of 30 s at 95 °C, 45 s at 56 °C and 1 min at 72 °C, and a final denaturation step of 8 min at 72 °C. For the *rpb2* amplification, conditions consisted of five cycles of 45 s at 95 °C, 45 s at 56 °C and 2 min at 72 °C, then five cycles with a 53 °C annealing temperature and 30 cycles with a 50 °C annealing temperature. The DNA sequencing was performed using an ABI PRISM® 3730XL DNA Analyzer with BigDye® Terminater Kit v. 3.1 (Invitrogen) at the Shanghai Invitrogen Biological Technology Company Limited (Beijing, China).

Molecular data analyses

DNA sequences generated by each primer combination were used to obtain consensus sequences using SeqMan v. 7.1.0 in the DNASTAR Lasergene Core Suite software (DNASTAR Inc., Madison, WI, USA). Reference sequences were selected based on ex-type or ex-epitype sequences available from relevant published literature (Rossman et al. 2007, Cheewangkoon et al. 2010, Crous et al. 2012, 2015, Suetrong et al. 2015, Norphanphoun et al. 2016, Hongsanan et al. 2017, Senanayake et al. 2017, Voglmayr et al. 2017) (Table 1). All sequences were aligned using MAFFT v. 6 (Katoh & Toh 2010) and edited manually using MEGA v. 6 (Tamura et al. 2013). Phylogenetic analyses were performed using PAUP v. 4.0b10 for maximum parsimony (MP) analysis (Swofford 2003), MrBayes v. 3.1.2 for Bayesian Inference (BI) analysis (Ronquist & Huelsenbeck 2003), and PhyML v. 7.2.8 for Maximum Likelihood (ML) analysis (Guindon et al. 2010). The first analyses were performed on the combined multi-gene dataset (ITS, LSU, *rpb2, tef1-α*) to compare isolates of *Diaporthales* species to ex-type sequence data from recent studies (Table 1).

A partition homogeneity test (PHT) with heuristic search and 1 000 replicates was performed using PAUP v. 4.0b10 to test the discrepancy among the ITS, LSU, *rpb2* and *tef1-α* sequence dataset in reconstructing phylogenetic trees. Maximum parsimony (MP) analysis was run using a heuristic search option of 1 000 search replicates with random-additions of sequences with a tree bisection and reconnection (TBR) algorithm. Maxtrees were set to 5 000, branches of zero length were collapsed and all equally parsimonious trees were saved. Other calculated parsimony scores were tree length (TL), consistency index (CI), retention index (RI) and rescaled consistency (RC). Maximum

Table 1 Details of the strains included for molecular study.

Species	Culture	Location	Host	GenBank accession numbers			
				ITS	LSU	*rpb2*	*tef1-α*
Apiosporopsis carpinea	CBS 771.79	Switzerland	*Carpinus betulus*	NA	AF277130	NA	NA
Apiosporopsis sp.	Masuya 11Af2-1	Japan	*Alnus firma*	NA	AB669034	NA	NA
Apoharknessia insueta	**CBS 111377**	Brazil	*Eucalyptus pellita*	JQ706083	AY720814	NA	NA
	CBS 114575	Colombia	*Eucalyptus* sp.	NA	AY720813	NA	NA
Asterosporium asterospermum	MFLU 15-3555	Italy	*Fagus sylvatica*	NA	MF190062	MF377615	NA
	CBS 112404	Italy	*Fagus sylvatica*	NA	AB553745	NA	NA
	KT2138	Japan	*Fagus crenata*	NA	AB553744	NA	NA
Auratiopycnidiella tristaniopsidis	**CBS 132180 = CPC 16371**	Australia	*Tristaniopsis laurina*	JQ685516	JQ685522	NA	NA
Cainiella johansonii	**Kruys 731**	Sweden	*Dryas octopetala*	NA	JF701920	NA	NA
Chapeckia nigrospora	**AR 3809**	USA	*Betula* sp.	JF681957	EU683068	NA	NA
Chiangraiomyces bauhiniae	**MFLUCC 17-1669**	Thailand	*Bauhinia* sp.	MF190118	MF190064	MF377604	NA
	MFLUCC 17-1670	Thailand	*Bauhinia* sp.	MF190119	MF190065	MF377603	NA
Chrysocrypta corymbiae	**CBS 132528**	Australia	*Corymbia* sp.	JX069867	JX069851	NA	NA
Coniella diplodiella	CBS 111858 = CPC 3708	France	*Vitis vinifera*	AY339323	AY339284	KX833423	KX833603
Coniella koreana	CBS 143.97	Korea	NA	KX833584	AF408378	KX833490	KX833684
Coniella musaiensis var. *hibisci*	AR 3534 = CBS 109757	South Africa	*Hibiscus* sp.	KX833589	AF408337	NA	KX833689
Coniella straminea	CBS 149.22 = CPC 3932	USA	*Fragaria* sp.	AY339348	AF362569	KX833506	KX833704
Coniella wangiensis	CBS 132530 = CPC 19397	Australia	*Eucalyptus* sp.	JX069873	JX069857	KX833509	KX833705
Coryneum depressum	AR 3897	Austria	*Quercus cerris*	NA	EU683074	NA	NA
Coryneum modonium	AR 3558	Austria	*Castanea sativa*	NA	EU683073	NA	NA
Coryneum umbonatum	**AR 3541**	Austria	*Quercus cerris*	NA	EU683072	NA	NA
	MFLUCC 15-1110	Italy	*Quercus* sp.	MF190121	MF190067	MF377610	NA
	MFLUCC 13-0658	Italy	*Quercus* sp.	MF190120	MF190066	MF377609	NA
Cryphonectria macrospora	AR 3444 = CBS 109764	Russia	*Quercus mongolica*	EU199182	AF408340	EU220029	NA
Cryphonectria nitschkei	AR 3433 = CBS 109776	Russia	*Quercus mongolica*	DQ120761	AF408341	NA	NA
Cryphonectria parasitica	**ATCC 38755**	USA	*Castanea dentata*	AY141856	EU199123	DQ862017	EU222014
Cryptodiaporthe aesculi	**CBS 109765 = AFTOL-ID 1238**	Austria	*Aesculus hippocastanum*	DQ323530	AF408342	EU199138	GU354004
	AR3640 = CBS 121905	USA	*Aesculus hippocastanum*	EU254994	EU255164	EU219269	DQ313558
	LCM 447.01	Germany	*Aesculus hippocastanum*	GU367076	NA	GU367110	GU354002
Cryptosporella betulae	AR 3524 = CBS 109763	Austria	*Betula pendula*	EU199180	AF408375	EU199139	EU221884
Cryptosporella hypodermia	**AR 3552**	Austria	*Ulmus minor*	EU199181	AF408346	EU199140	NA
Cryptosporella suffusa	AR 3496 = CBS 109750	Austria	*Alnus incana*	EU199207	AF408376	EU199163	EU221945
Cytospora cenisia	AR 3522 = CBS 109752	Austria	*Juniperus communis*	NA	AF408385	NA	NA
Cytospora chrysosperma	**CFCC 89600**	China	*Sophora japonica*	KR045623	KR045623	KU710951	KU710915
Cytospora elaeagni	CFCC 89633	China	*Elaeagnus angustifolia*	KF765677	KF765693	KU710956	KU710919
Cytospora leucostoma	CFCC 50468	China	*Betula platyphylla*	KT732949	KT732968	NA	NA
Cytospora nivea	AR 3512	Austria	*Salix purpurea*	NA	AF408367	NA	NA
Cytospora sacculus	AR 3416= CBS 109756	Russia	*Quercus mongolica*	NA	AF408386	NA	NA
	AR 3426 = CBS 109777	Austria	*Quercus robur*	NA	AF408387	NA	NA
Dendrostoma mali	**CFCC 52102***	China	*Malus spectabilis*	MG682072	MG682012	MG682032	MG682052
Dendrostoma osmanthi	CFCC 52106*	China	*Osmanthus fragrans*	MG682073	MG682013	MG682033	MG682053
	CFCC 52107*	China	*Osmanthus fragrans*	MG682074	MG682014	MG682034	MG682054
	CFCC 52108*	China	*Osmanthus fragrans*	MG682075	MG682015	MG682035	MG682055
	CFCC 52109*	China	*Osmanthus fragrans*	MG682076	MG682016	MG682036	MG682056
Dendrostoma quercinum	CFCC 52103*	China	*Quercus acutissima*	MG682077	MG682017	MG682037	MG682057
	CFCC 52104*	China	*Quercus acutissima*	MG682078	MG682018	MG682038	MG682058
	CFCC 52105*	China	*Quercus acutissima*	MG682079	MG682019	MG682039	MG682059
Diaporthe decedens	AR 3459 = CBS 109772	Austria	*Corylus avellana*	KC343059	AF408348	NA	NA
Diaporthe detrusa	AR 3424 = CBS 109770	Austria	*Berberis vulgaris*	KC343061	AF408349	NA	KC343787
Diaporthe eres	**AR 3538 = CBS 109767**	Austria	*Acer campestre*	KC343075	AF408350	NA	KC343801
Diaporthella corylina	CBS 121124	China	*Corylus* sp.	KC343004	NA	NA	NA
Diaporthella sp.	CN 5	Italy	*Corylus avellana*	KP205483	NA	NA	NA
	CN13	Italy	*Corylus avellana*	KP205484	NA	NA	NA
Diaporthosporella cercidicola	**CFCC 51994**	China	*Cercis chinensis*	KY852492	KY852515	NA	NA
	CFCC 51995	China	*Cercis chinensis*	KY852493	KY852516	NA	NA
	CFCC 51996	China	*Cercis chinensis*	KY852494	KY852517	NA	NA
Diaporthostoma machili	**CFCC 52100***	China	*Machilus leptophylla*	MG682080	MG682020	MG682040	MG682060
	CFCC 52101*	China	*Machilus leptophylla*	MG682081	MG682021	MG682041	MG682061
Disculoides eucalypti	**CPC 17650**	Australia	*Eucalyptus* sp.	JQ685517	JQ685523	NA	NA
Disculoides eucalyptorum	CBS 132184 = CPC 17648	Australia	*Eucalyptus viminalis*	NR120090	JQ685524	NA	NA
Ditopella ditopa	**AR 3423 = CBS 109748**	Austria	*Alnus glutinosa*	EU199187	EU199126	EU199145	NA
Erythrogloeum hymenaeae	**CPC 18819**	Brazil	*Hymenaea courbaril*	JQ685519	JQ685525	NA	NA
Gnomonia gnomon	**CBS 199.53**	Italy	*Corylus avellana*	AY818956	AF408361	EU219295	EU221885
Harknessia eucalypti	**CBS 342.97**	Australia	*Eucalyptus regnans*	AY720745	AF408363	NA	NA
Harknessia molokaiensis	AR 3578 = CBS 109779	USA	*Eucalyptus robusta*	NA	AF408390	NA	NA
Hercospora tiliae	**AR 3526**	Austria	*Tilia tomentosa*	NA	AF408365	NA	NA
Hyaliappendispora galii	**MFLUCC 16-1208**	Italy	*Galium* sp.	MF190149	MF190095	NA	NA
Juglanconis appendiculata	D96	Austria	*Juglans nigra*	KY427139	KY427139	KY427189	KY427208
Juglanconis juglandina	**ME23**	Austria	*Juglans nigra*	KY427150	KY427150	KY427200	KY427219
Juglanconis oblonga	ME14	USA	*Juglans cinerea*	KY427151	KY427151	KY427201	KY427220
Juglanconis pterocaryae	ME20	Japan	*Pterocarya rhoifolia*	KY427155	KY427155	KY427205	KY427224
Lamproconium desmazieri	**MFLUCC 14-1047**	Russia	*Tilia cordata*	KX430132	KX430133	NA	MF377592
	MFLUCC 15-0870	Russia	*Tilia tomentosa*	KX430134	KX430135	MF377605	MF377591
Lasmenia sp.	CBS 124123	Puerto Rico	*Nephelium lappaceum*	GU797406	JF838338	NA	NA
	CBS 124124	Puerto Rico	*Nephelium lappaceum*	JF838336	JF838341	NA	NA
Luteocirrhus shearii	**CBS 130776**	Australia	*Banksia baxteri*	NR120254	NG042770	NA	NA
Macrohilum eucalypti	**CPC 10945**	New Zealand	*Eucalyptus* sp.	DQ195781	DQ195793	NA	NA
	CPC 19421	Australia	*Eucalyptus piperita*	KR873244	KR873275	NA	NA

Table 1 (cont.)

Species	Culture	Location	Host	GenBank accession numbers			
				ITS	LSU	*rpb2*	*tef1-α*
Melanconiella ellisii	BPI 878343	USA	*Carpinus caroliniana*	JQ926271	JQ926271	JQ926339	JQ926406
Melanconiella hyperopta	AR 3832 = CBS 131492	Austria	*Carpinus betulus*	JQ926278	JQ926278	NA	NA
Melanconiella spodiaea	**MSH**	Austria	*Carpinus betulus*	JQ926298	JQ926298	JQ926364	JQ926431
Melanconis alni	AR 3748	Austria	*Alnus viridis*	EU199195	EU199130	EU199153	NA
Melanconis betulae	CFCC 50471	China	*Betula albosinensis*	KT732952	KT732971	KT732984	KT733001
Melanconis itoana	CFCC 50474	China	*Betula albosinensis*	KT732955	KT732974	KT732987	KT733004
Melanconis marginalis	AR 3442 = CBS 109744	Canada	*Alnus rubra*	EU199197	AF408373	EU219301	EU221991
Melanconis stilbostoma	**CFCC 50475**	China	*Betula platyphylla*	KT732956	KT732975	KT732988	KT733005
Nakataea oryzae	**CBS 243.76**	NA	NA	KM484861	DQ341498	NA	NA
Ophiodiaporthe cyatheae	**YMJ1364**	China	*Cyathea lepifera*	JX570889	JX570891	JX570893	NA
Pachytrype princeps	**Rogers S**	USA	NA	NA	FJ532382	NA	NA
Pachytrype rimosa	FF1066	Costa Rica	NA	NA	FJ532381	NA	NA
Paradiaporthe artemisiae	**MFLUCC 14-0850**	Italy	*Artemisia* sp.	MF190155	MF190100	NA	NA
	MFLUCC 17-1663	Italy	*Artemisia* sp.	MF190156	MF190101	NA	NA
Phaeoappendispora thailandensis	**MFLUCC 13-0161**	Thailand	*Quercus* sp.	MF190157	MF190102	MF377613	NA
Phaeodiaporthe appendiculata	**CBS 123821 = D77**	Austria	*Acer campestre*	KF570156	KF570156	NA	NA
	CBS 123809 = D76	Austria	*Acer campestre*	KF570155	KF570155	NA	NA
Phragmoporthe conformis	**AR 3632 = CBS 109783**	Canada	*Alnus rubra*	DQ323527	AF408377	NA	NA
Plagiostoma euphorbiae	**CBS 340.78**	Netherlands	*Euphorbia palustris*	EU199198	AF408382	DQ368643	NA
Plagiostoma salicellum	AR 3455 = CBS 109775	Austria	*Salix* sp.	DQ323529	AF408345	EU199141	EU221916
Prosopidicola mexicana	**CBS 113530**	USA	*Prosopis glandulosa*	AY720710	NA	NA	NA
	CBS 113529	USA	*Prosopis glandulosa*	AY720709	KX228354	NA	NA
Pseudomelanconis caryae	**CFCC 52110***	China	*Carya cathayensis*	MG682082	MG682022	MG682042	MG682062
	CFCC 52111*	China	*Carya cathayensis*	MG682083	MG682023	MG682043	MG682063
	CFCC 52112*	China	*Carya cathayensis*	MG682084	MG682024	MG682044	MG682064
	CFCC 52113*	China	*Carya cathayensis*	MG682085	MG682025	MG682045	MG682065
Pseudoplagiostoma eucalypti	**CBS 124807**	Venezuela	*Eucalyptus urophylla*	GU973512	GU973606	NA	NA
	CBS 116382	Thailand	*Eucalyptus camaldulensis*	GU973514	GU973608	NA	NA
Pseudoplagiostoma oldii	CBS 115722	Australia	*Eucalyptus camaldulensis*	GU973535	GU973610	NA	NA
Pseudoplagiostoma variabile	CBS 113067	Uruguay	*Eucalyptus globulus*	GU973536	GU973611	NA	NA
Pyricularia grisea	**Ina168**	NA	NA	AB026819	AB026819	NA	NA
Rossmania ukurunduensis	**AR 3484**	Russia	*Acer ukurunduense*	NA	EU683075	NA	NA
Sillia ferruginea	**AR 3440 = CBS 126567**	Austria	*Corylus avellana*	JF681959	EU683076	NA	NA
Stegonsporium protopyriforme	CBS 117041	Austria	*Acer pseudoplatanus*	NR126119	EU039992	NA	NA
Stegonsporium pyriforme	**CBS 124487**	UK	*Acer heldreichii*	KF570160	KF570160	KF570190	NA
Stilbospora macrosperma	**CBS 121883**	Austria	*Carpinus betulus*	JX517290	JX517299	KF570196	NA
	CBS 121695	Netherlands	*Carpinus betulus*	JX517288	JX517297	NA	NA
Sydowiella depressula	CBS 813.79	Switzerland	*Rubus* sp.	NA	EU683077	NA	NA
Sydowiella fenestrans	**AR 3777 = CBS 125530**	Russia	*Chamerion angustifolium*	JF681956	EU683078	NA	NA
Synnemasporella aculeans	CFCC 52094*	China	*Rhus chinensis*	MG682086	MG682026	MG682046	MG682066
	CFCC 52095*	China	*Rhus chinensis*	MG682087	MG682027	MG682047	MG682067
	CFCC 52096*	China	*Rhus chinensis*	MG682088	MG682028	MG682048	MG682068
	AR 3878 = CBS 126566	USA	*Rhus glabra*	NA	EU255134	NA	NA
Synnemasporella toxicodendri	**CFCC 52097***	China	*Toxicodendron sylvestre*	MG682089	MG682029	MG682049	MG682069
	CFCC 52098*	China	*Toxicodendron sylvestre*	MG682090	MG682030	MG682050	MG682070
	CFCC 52099*	China	*Toxicodendron sylvestre*	MG682091	MG682031	MG682051	MG682071

Note: CBS: Westerdijk Fungal Biodiversity Institute (CBS-KNAW Fungal Biodiversity Centre), Utrecht, The Netherlands; CFCC: China Forestry Culture Collection Center, Beijing, China; CPC: Culture collection of Pedro Crous, The Netherlands; MFLU: Mae Fah Luang University herbarium, Thailand; MFLUCC: Mae Fah Luang University Culture Collection, Thailand; NA: not applicable. All the new isolates used in this study are marked by an asterisk (*) and the strains from generic type species are in **bold**.

likelihood (ML) analysis was performed with a GTR site substitution model, including a gamma-distributed rate heterogeneity and a proportion of invariant sites (Guindon et al. 2010). The branch support was evaluated with a bootstrapping (BS) method of 1 000 replicates (Hillis & Bull 1993).

MrModeltest v. 2.3 was used to estimate the best nucleotide substitution model settings for each gene (Posada & Crandall 1998). Bayesian inference (BI) was performed based on the DNA dataset from the results of the MrModeltest, using a Markov Chain Monte Carlo (MCMC) algorithm in MrBayes v. 3.1.2 (Ronquist & Huelsenbeck 2003). Two MCMC chains were run from random trees for 1 000 M generations and stopped when average standard deviation of split frequencies fell below 0.01. Trees were saved each 1 000 generations. The first 25 % of trees were discarded as the burn-in phase of each analysis, and the posterior probabilities (BPP) were calculated from the remaining trees (Rannala & Yang 1996). *Nakataea oryzae* (CBS 243.76) and *Pyricularia grisea* (Ina168) were selected as outgroups in all analyses (Fan et al. 2016b). Phylograms were shown using FigTree v. 1.3.1 (Rambaut & Drummond 2010). Novel sequences generated in the current study were deposited in GenBank (Table 1) and the aligned matrices used for phylogenetic analyses in TreeBASE (www.treebase.org; accession number: S22175).

RESULTS

Molecular phylogenetic analyses

The alignment based on the sequence dataset (ITS, LSU, *rpb2* and *tef1-α*) included 122 ingroup taxa, comprising 3 261 characters in the aligned matrix. Of these, 1 562 characters were constant, 184 variable characters were parsimony-uninformative and 1 515 characters were parsimony informative. The MP analysis resulted in 119 equally most parsimonious trees (TL = 8 082, CI = 0.385, RI = 0.761, RC = 0.293) and the first tree is shown in Fig. 1. For BI analyses, the general time reversible model, additionally assuming a proportion of invariant sites with gamma-distributed substitution rates of the remaining sites (GTR + I + G) was determined to be the best for the ITS, LSU and *tef1-α* loci by MrModeltest, while the most appropriate

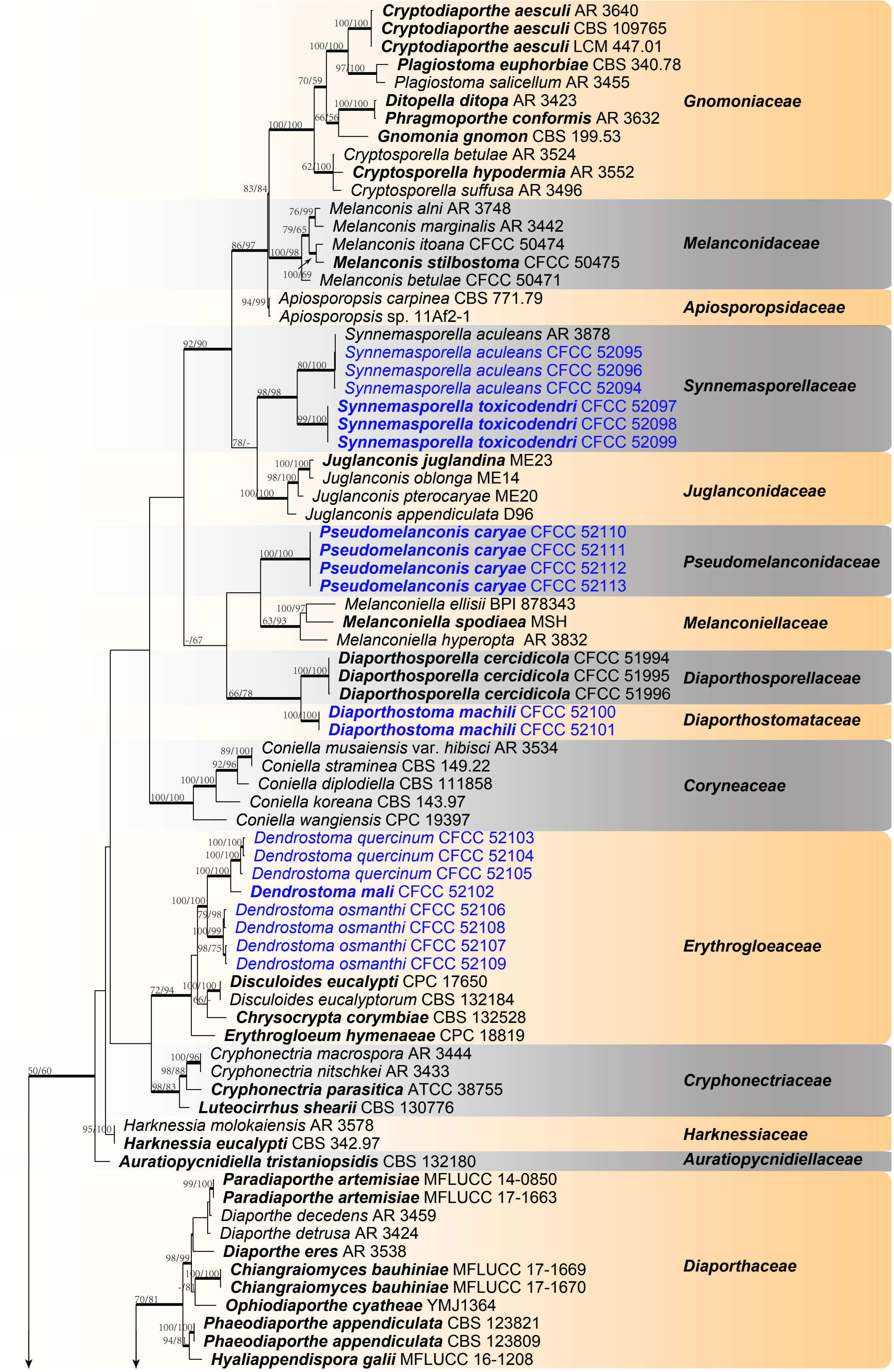

Fig. 1 Phylogram of *Diaporthales* resulting from MP analysis based on combined ITS, LSU, *rpb2* and *tef1-α*. MP and ML bootstrap support values above 70 % are shown at the first and second position. Thickened branches represent posterior probabilities above 0.95 from BI. Type species are in **bold**. Strains obtained in the current study are in blue. — Scale bar = 200 changes.

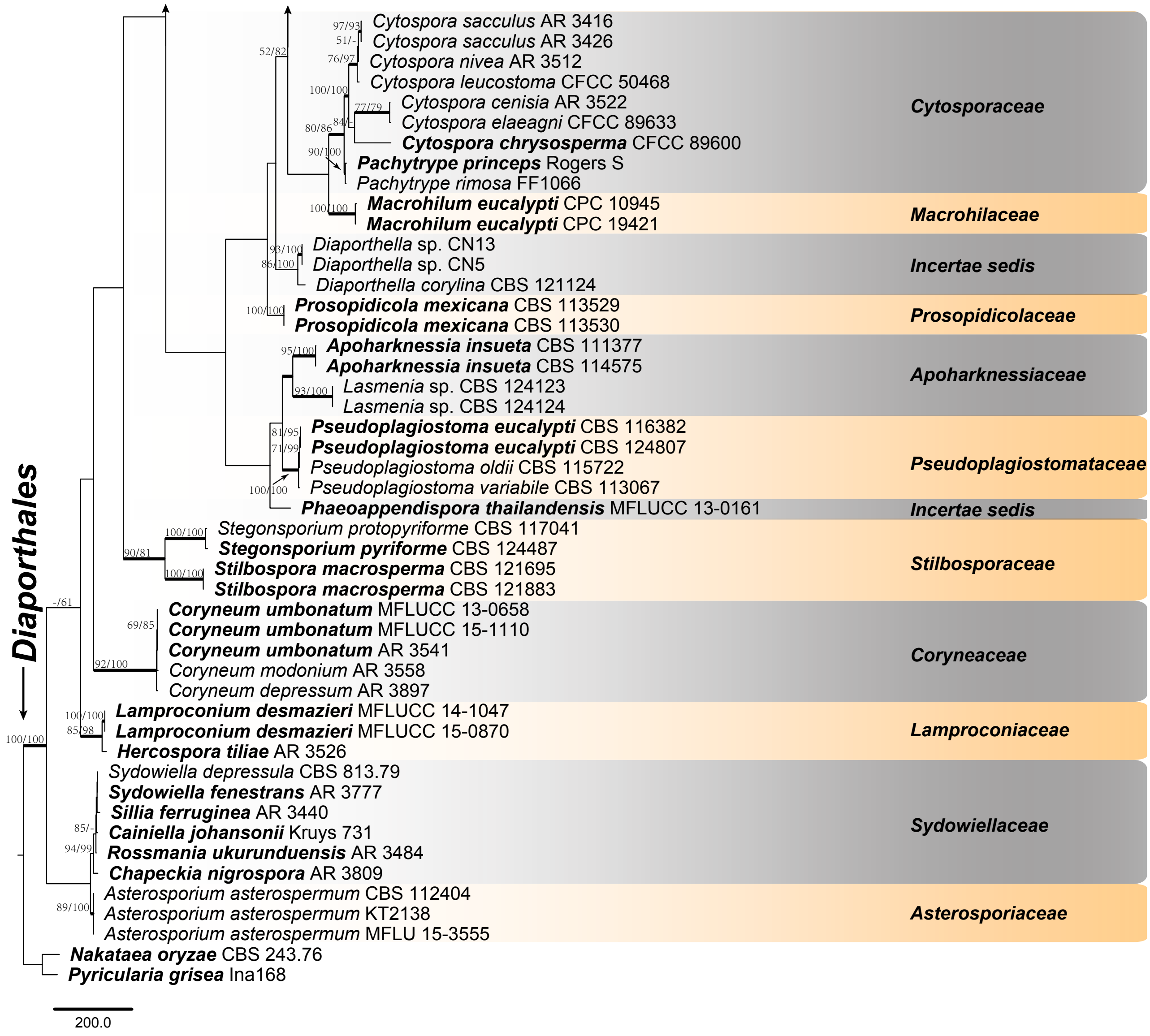

Fig. 1 (cont.)

model for the *rpb2* locus was the Tamura-Nei model, additionally assuming a proportion of invariant sites with gamma-distributed substitution rates of the remaining sites (TrN + I + G). The MP and ML bootstrap support values above 70 % are shown at the first and second position, respectively. Branches with significant Bayesian posterior probability (≥ 0.95) in Bayesian analyses were thickened in the phylogenetic tree. The phylogram based on four genes indicated 24 known lineages, representing 22 known families and two unknown taxa lacking typification studies, namely *Diaporthella* and *Phaeoappendispora*. Four new lineages belonging to the *Diaporthales*, distinct from all known taxa, are herein described as three new families and a new genus in *Erythrogloeaceae* (Fig. 1).

Taxonomy

Diaporthostomataceae X.L. Fan & C.M. Tian, *fam. nov.* — MycoBank MB823983

Etymology. Name derived from the type genus, *Diaporthostoma*.

Type genus. *Diaporthostoma*.

Sexual morph: *Pseudostromata* immersed in host bark and slightly erumpent from host tissues. *Ectostromatic disc* ovoid to ellipsoid, yellowish to dark grey. *Central column* beneath the disc more or less conical. *Stromatic zones* lacking. *Perithecia* conical, surrounding the ectostromatic disc. *Ostioles* single, dark grey to black. *Paraphyses* deliquescent. *Asci* 8-spored, with an apical ring. *Ascospores* hyaline, fusoid, bicellular. *Asexual morph*: not observed.

Notes — The current phylogenetic analyses placed the new family *Diaporthostomataceae* in a highly supported clade (MP/ML/BI = 100/100/1) closely related to *Diaporthosporellaceae*. *Diaporthostomataceae* is morphologically distinct from *Diaporthosporellaceae* (Yang et al. 2018) by discrete perithecia and fusoid, straight to curved ascospores with a median septum.

Diaporthostoma X.L. Fan & C.M. Tian, *gen. nov.* — MycoBank MB823984

Etymology. Name derived from the morphological similarity with the genus *Diaporthe*.

Type species. *Diaporthostoma machili* X.L. Fan & C.M. Tian.

Sexual morph: *Pseudostromata* immersed in host bark, slightly erumpent from the bark surface. *Ectostromatic disc* yellowish to dark grey, nearly flat, ovoid to ellipsoid. *Central column* beneath the disc more or less conical. *Stromatic zones* lacking. *Perithecia* conical, surrounding the ectostromatic disc, regularly scattered. *Ostioles* single, dark grey to black. *Paraphyses* deliquescent. *Asci* oblong to cylindrical-clavate, 8-spored,

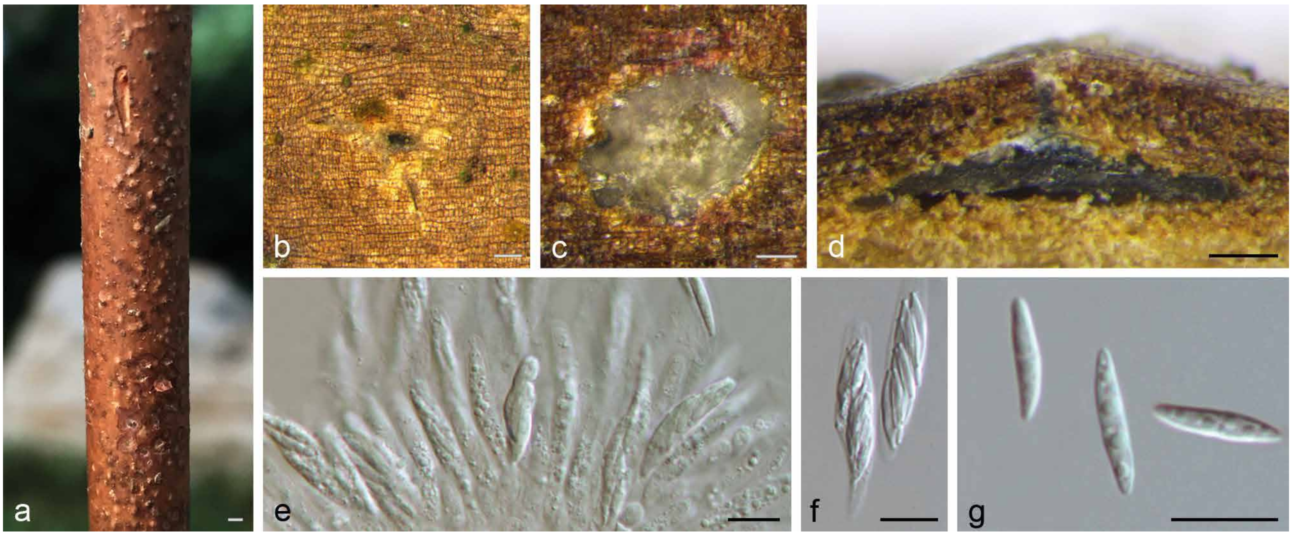

Fig. 2 Morphology of *Diaporthostoma machili* from *Machilus leptophylla*. a, b. Habit of pseudostromata on branches; c. transverse section through pseudostroma; d. longitudinal section through pseudostroma; e, f. asci and ascospores; g. ascospores. — Scale bars: a = 1 mm; b–d = 100 µm; e–g = 10 µm.

2–3-seriate, with a more or less distinct apical ring. *Ascospores* hyaline, smooth, fusoid, multiguttulate, straight to curved, bicellular, with an inconspicuous median septum. *Asexual morph*: not observed.

Diaporthostoma machili X.L. Fan & C.M. Tian, *sp. nov.* — MycoBank MB823985; Fig. 2

Etymology. Name derived from the host genus, *Machilus*.

Sexual morph: *Pseudostromata* immersed in host bark, slightly erumpent, 400–700 µm diam. *Ectostromatic disc* yellowish to dark grey, nearly flat, ovoid to ellipsoid, 120–140 µm diam. *Central column* beneath the disc more or less conical. *Stromatic zones* lacking. *Perithecia* conical, surrounding the ectostromatic disc, regularly scattered, 380–420 µm diam. *Ostioles* single, dark grey to black, 65–85 µm diam. *Paraphyses* deliquescent. *Asci* oblong to cylindrical-clavate, 8-spored, 2–3-seriate, with a more or less distinct apical ring, (26–)30–38(–40) × 6–8 µm ($\bar{x}$ = 33.5 ± 1.5 × 7 ± 0.5 µm, n = 20). *Ascospores* hyaline, smooth, fusoid, multiguttulate, straight to slight curved, bicellular, with a median septum, not constricted at the septum, 11–14 × 2–2.5 ($\bar{x}$ = 12 ± 1.1 × 2.3 ± 0.2 µm, n = 30) µm. *Asexual morph*: not observed.

On PDA, cultures are initially white, becoming dark vinaceous after 3 wk. The colonies are flat with an irregular edge, producing white, sparse aerial mycelium; texture initially uniform, producing a dark brick-coloured circular ring on the margin after 3 d; sterile.

Host & Distribution — On *Machilus leptophylla* in China.

Materials examined (all on twigs and branches of *Machilus leptophylla*). China, Zhejiang Province, Hangzhou City, Linan, Tianmu Mountain, N30°19'18.21" E119°26'18.21", 354 m asl, 20 Apr. 2017, *Q. Yang & Z. Du* (holotype CF 2017475; living ex-type culture CFCC 52100); Zhejiang Province, Hangzhou City, Linan, Tianmu Mountain, N30°19'17.33" E119°26'15.60", 350 m asl, 20 Apr. 2017, *Q. Yang & Z. Du* (CF 2017479; living culture CFCC 52101).

Notes — *Diaporthostoma machili* is the type species of *Diaporthostoma*, and is thus far only known to occur on *Machilus leptophylla*. Morphologically, it is characterised by the scattered, conical perithecia and fusoid, straight to curved ascospores with a median septum, which differs with other species in *Diaporthales*.

Erythrogloeaceae Senan. et al., Stud. Mycol. 86: 258. 2017. emend.

Type genus. *Erythrogloeum* Petr.

Sexual morph: *Pseudostromata* small to large, erumpent, consisting of an inconspicuous ectostromatic disc generally with orange colour, semi-immersed to superficial, causing a more or less pustulate bark surface. *Central column* beneath the disc more or less conical. *Stromatic zones* lacking. *Perithecia* umber to fuscous black, covered with orange to umber pseudostromatic tissue, surrounding the ectostromatic disc, with small to long ostioles that emerge within the ectostromatic disc. *Paraphyses* deliquescent. *Asci* 8-spored, with an apical ring, grouped at the base with other asci, becoming detached from the perithecial wall. *Ascospores* hyaline, fusoid to cylindrical, bicellular. *Asexual morph*: foliicolous, associated with leaf spots. *Conidiomata* epiphyllous, subepidermal, sometimes eustromatic, acervular or subglobose, brown to black or yellow-orange, amphigenous, opening by irregular rupture, wall of 2–6 layers of orange-brown *textura angularis*, exuding slimy orange masses of conidia. *Conidiophores* hyaline to amber. *Conidiogenous cells* lining the inner cavity of conidioma, hyaline to olivaceous, smooth, subcylindrical to ampulliform, tapering to a long, thin neck, at times apical part elongated into a long neck, proliferating several times percurrently near apex, with flaring collarettes, or apex truncate, with minute periclinal thickening. *Conidia* hyaline to olivaceous, smooth, guttulate or not, thin-walled, ellipsoid, fusoid, ovoid to somewhat obclavate, straight to curved, apex subobtuse, obtusely rounded, base truncate, with prominent marginal frill, or dimorphic, intermixed in same conidiomata. *Macroconidia* broadly ellipsoid to obovoid, hyaline, smooth, granular to guttulate, thick-walled, apex obtuse, base flattened. *Microconidia* hyaline, smooth, guttulate, fusoid-ellipsoid, acutely rounded at apex, truncate at base (emended from Senanayake et al. 2017).

Notes — The family *Erythrogloeaceae* was recently introduced by Senanayake et al. (2017) to accommodate *Chrysocrypta*, *Disculoides* and *Erythrogloeum* species having epiphyllous acervuli, and subcylindrical to ampulliform conidiogenous cells. These authors did not report any sexual morph associated with these genera. During our investigation, phylogenetic inferences using DNA sequences from some materials with a sexual morph placed these samples in a highly supported clade (MP/ML/BI = 100/100/1) in the *Erythrogloeaceae*. The family *Erythrogloeaceae* is emended here to include the morphological features of the new sexual morphs observed during our study. These fungi have typical diaporthalean perithecia with clavate asci, and fusoid to cylindrical, bicellular ascospores.

Dendrostoma X.L. Fan & C.M. Tian, *gen. nov.* — MycoBank MB823986

Etymology. Name derived from pseudostromata emerging from woody host tissue.

Type species. Dendrostoma mali X.L. Fan & C.M. Tian.

Sexual morph: *Pseudostromata* small to large, distinct, circular, erumpent, consisting of an inconspicuous, usually orange ectostromatic disc, semi-immersed to superficial, causing a pustulate bark surface. *Ectostromatic disc* flat or concave, orange, surrounded by bark flaps. *Central column* beneath the disc more or less conical. *Stromatic zones* lacking. *Perithecia* conspicuous, umber to fuscous black, embedded in orange to umber pseudostromatic tissue, regularly scattered, surrounding the ectostromatic disc, with small to long ostioles that emerge within the ectostromatic disc. *Ostioles* flat in the disc or sometimes slightly projecting, cylindrical, sometimes obscuring the disc, covered by an orange, umber to fuscous black crust. *Paraphyses* deliquescent. *Asci* fusoid, 8-spored, 2–3-seriate, with an apical ring, becoming detached from the perithecial wall. *Ascospores* hyaline, fusoid to cylindrical, symmetrical to asymmetrical, straight to curved, bicellular, with a median septum, constricted at the septum, smooth, multiguttulate. *Asexual morph*: observed on PDA. *Conidiomata* pycnidial, hemispherical, somewhat erumpent, coated with aerial mycelium. *Conidiophores* hyaline to amber. *Conidiogenous cells* enteroblastic, polyphialidic, hyaline, verruculose, ampulliform to doliiform. *Conidia* hyaline, aseptate, ovoid to ellipsoid, or fusoid.

Notes — The current phylogenetic analyses placed the new genus *Dendrostoma* in a highly supported clade (MP/ML/BI = 100/100/1) closely related to other genera in *Erythrogloeaceae* (Senanayake et al. 2017). *Dendrostoma* is described based on the typical diaporthalean perithecia with clavate asci and fusoid to cylindrical, bicellular ascospores. This study describes one genus and four species from China, and the host association appears to provide an important character for reliable identification. However, further collections are needed to confirm the host ranges and geographical distributions.

Dendrostoma mali X.L. Fan & C.M. Tian, *sp. nov.* — MycoBank MB823987; Fig. 3

Etymology. Name derived from the host genus, *Malus*.

Pseudostromata erumpent, consisting of an inconspicuous orange ectostromatic disc, semi-immersed to superficial, causing a pustulate bark surface, 1300–2100 µm diam. *Ectostromatic disc* flat or concave, orange, or brown to black, sometimes concealed by ostioles, surrounded by bark flaps, 350–800 µm diam. *Central column* yellowish to brownish. *Stromatic zones* lacking. *Perithecia* conspicuous, umber to fuscous black, regularly scattered, surrounding the ectostromatic disc, 300–500 µm diam. *Ostioles* 2–6 per disc, flat in the disc or sometimes slightly projecting, cylindrical, covered by an orange, umber to fuscous black crust, 70–100 µm diam. *Paraphyses* deliquescent. *Asci* fusoid, 8-spored, biseriate, with an apical ring, 40–60(–65) × 7–10(–11) µm ($\bar{x}$ = 47 ± 5.3 × 8.5 ± 1.1 µm, n = 10). *Ascospores* hyaline, fusoid to cylindrical, smooth, multiguttulate, often containing two guttules per cell, symmetrical to asymmetrical, straight to slightly curved, bicellular, with a median septum distinctly constricted, 12–14 × 3–4 µm ($\bar{x}$ = 13 ± 1 × 3.4 ± 0.3 µm, n = 30). *Conidiomata* pycnidial, hemispherical, somewhat erumpent, coated with white aerial mycelium, 1200–2500 µm, conidial masses extruding from the ostioles. *Conidiophores* hyaline, occasionally amber at the base, aseptate. *Conidiogenous cells* enteroblastic, polyphialidic, with 1–2 integrated loci, hyaline, verruculose, ampulliform to doliiform. *Conidia* hyaline, aseptate, ovoid to ellipsoid, apex obtuse, 3–4.5 × 2–2.5 µm ($\bar{x}$ = 3.6 ± 0.5 × 2.2 ± 0.2 µm, n = 30).

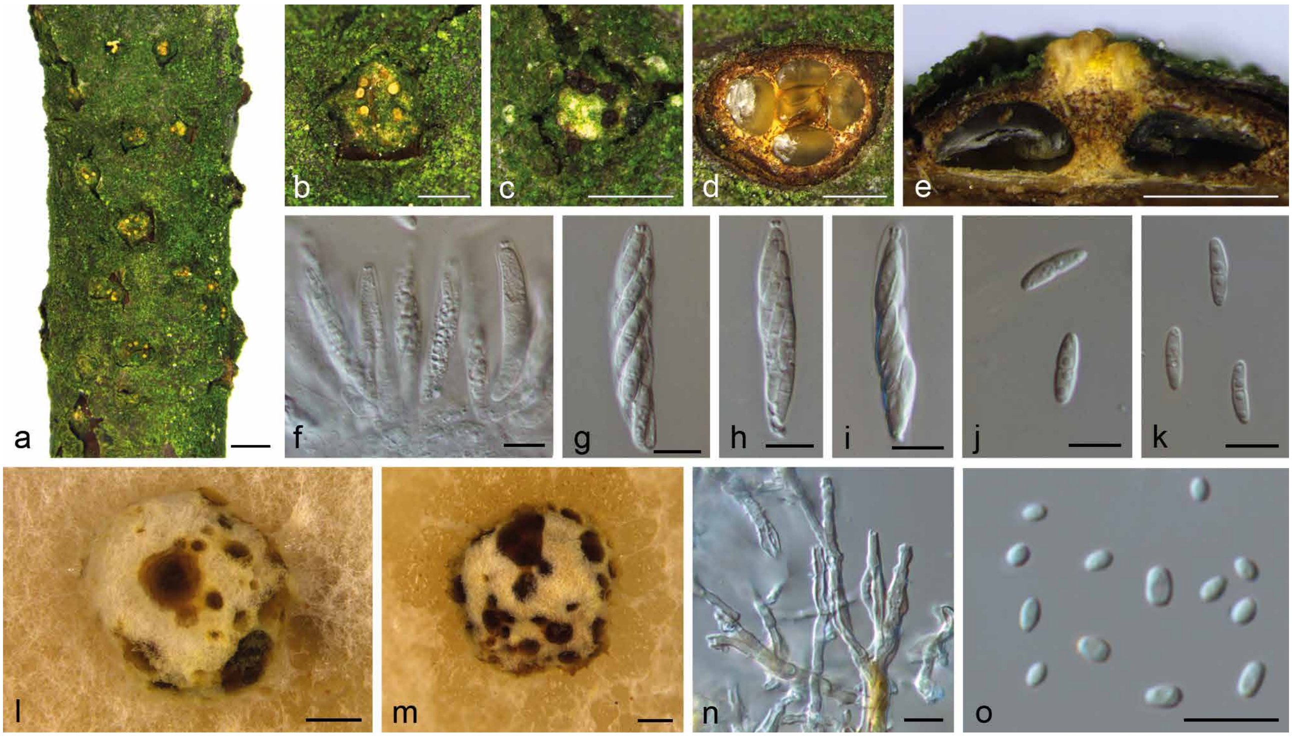

Fig. 3 Morphology of *Dendrostoma mali* from *Malus spectabilis*. a–c. Habit of pseudostromata on branches; d. transverse section of perithecia; e. longitudinal section through perithecia; f–i. asci and ascospores; j, k. ascospores; l, m. conidiomata on PDA; n. conidiophores and conidiogenous cells; o. conidia. — Scale bars: a = 1 mm; b–e, l, m = 500 µm; f–k, n, o = 10 µm.

On PDA, cultures are white. Colonies are flat with regular edge; texture initially uniform, producing concentric circles after 3 wk with sparse conidiomata irregularly distributed on the agar surface.

Host & Distribution — On *Malus spectabilis* in China.

Material examined. China, Zhejiang Province, Hangzhou City, Linan, Tianmu Mountain, N30°19'02.62" E119°26'34.33", 320 m asl, on twigs and branches of *Malus spectabilis*, 21 Apr. 2017, *Q. Yang & Z. Du* (holotype CF 2017445; living ex-type culture CFCC 52102).

Notes — *Dendrostoma mali* is the type species of *Dendrostoma*, and presently is only known on *Malus spectabilis*. It can be distinguished from other known *Dendrostoma* spp. by the fusoid to cylindrical ascospores, and the ovoid to ellipsoid conidia with obtuse apices. *Dendrostoma mali* is assumed to be host specific which needs to be confirmed by additional studies.

Dendrostoma quercinum X.L. Fan & C.M. Tian, *sp. nov.* — MycoBank MB823989; Fig. 4

Etymology. Name derived from the host genus, *Quercus*.

Pseudostromata erumpent, consisting of an inconspicuous orange ectostromatic disc, semi-immersed to erumpent, causing a pustulate bark surface, 800–1500 µm diam. *Ectostromatic disc* flat or concave, orange, or brown to black, sometimes concealed by ostioles, surrounded by bark flaps, 500–1100 µm diam. *Central column* yellowish to brownish. *Stromatic zones* lacking. *Perithecia* conspicuous, umber to fuscous black, regularly scattered, surrounding the ectostromatic disc, 250–500 µm. *Ostioles* 3–8 per disc, flat in disc or sometimes slightly projecting, cylindrical, covered by an orange, umber to fuscous black crust, 100–150 µm diam. *Paraphyses* deliquescent. *Asci* fusoid, 8-spored, 2–3-seriate, with an apical ring, 53–70 × 9.5–10 µm ($\overline{x}$ = 60.5 ± 4 × 9.8 ± 0.3 µm, n = 10). *Ascospores* hyaline, fusoid to cylindrical, smooth, multi-guttulate, often containing two guttules per cell, symmetrical to asymmetrical, straight to slightly curved, bicellular, with a median septum distinctly constricted, 16–22(–24) × 3–4 µm ($\overline{x}$ = 20 ± 1.7 × 3.5 ± 0.4 µm, n = 30). *Conidiomata* pycnidial, hemispherical, somewhat erumpent, covered with cinnamon aerial mycelium, 900–2200 µm diam; conidial masses extruding from ostioles. *Conidiophores* hyaline, occasionally amber at the base, aseptate. *Conidiogenous cells* enteroblastic, polyphialidic, with 1–2 integrated loci, hyaline, verruculose, ampulliform to doliiform. *Conidia* hyaline, aseptate, fusoid, acute at each end, 10.5–14 × 2.5(–3) µm ($\overline{x}$ = 12 ± 1 × 2.5 ± 0.2 µm, n = 30).
On PDA, cultures are white, becoming hazel in the centre after 2 wk. The colonies are flat with regular edge; texture initially uniform, becoming dense in the centre after 2 wk, producing circular conidiomata at the margin of the compact centre.

Host & Distribution — On *Quercus acutissima* in China.

Materials examined (all on twigs and branches of *Quercus acutissima*). China, Zhejiang Province, Hangzhou City, Hangzhou Botanical Garden, N30°15'13.25" E120°06'56.33", 49 m asl, 17 Apr. 2017, *Q. Yang & Z. Du* (holotype CF 2017461; living ex-type culture CFCC 52103); Zhejiang Province, Hangzhou City, Hangzhou Botanical Garden, N30°15'12.52", E120°06'57.02", 50 m asl, 17 Apr. 2017, *Q. Yang & Z. Du* (CF 2017462; living culture CFCC 52104); Hangzhou City, Hangzhou Botanical Garden, N30°15'13.77" E120°06'59.93", 46 m asl, 17 Apr. 2017, *Q. Yang & Z. Du* (CF 2017470; living culture CFCC 52105).

Notes — *Dendrostoma quercinum* can be distinguished from *D. mali* and *D. osmanthi* by its larger ascospores (16–24 × 3–4 µm), and DNA sequence data.

Dendrostoma osmanthi X.L. Fan & C.M. Tian, *sp. nov.* — MycoBank MB823990; Fig. 5

Etymology. Name derived from the host genus, *Osmanthus*.

Pseudostromata erumpent, consisting of an inconspicuous orange ectostromatic disc, semi-immersed to superficial, causing a pustulate bark surface, 1200–1400 µm diam. *Ectostromatic disc* flat or concave, orange, brown to black, sometimes concealed by ostioles, surrounded by bark flaps, 500–1100 µm

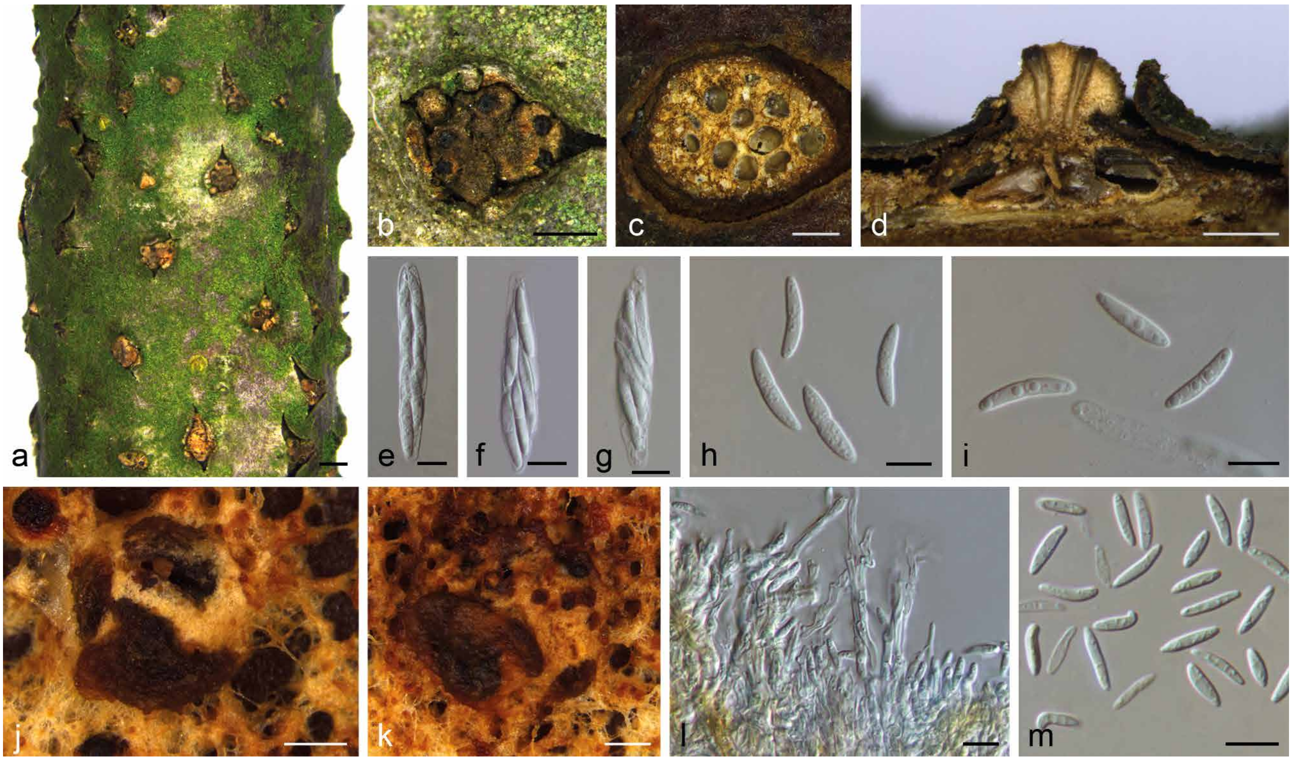

Fig. 4 Morphology of *Dendrostoma quercina* from *Quercus acutissima*. a, b. Habit of pseudostromata on branches; c. transverse section of pseudostroma; d. longitudinal section through pseudostroma; e–g. asci and ascospores; h, i. ascospores; j, k. conidiomata on PDA; l. conidiophores and conidiogenous cells; m. conidia. — Scale bars: a = 1 mm; b–d, j, k = 500 µm; e–i, l, m = 10 µm.

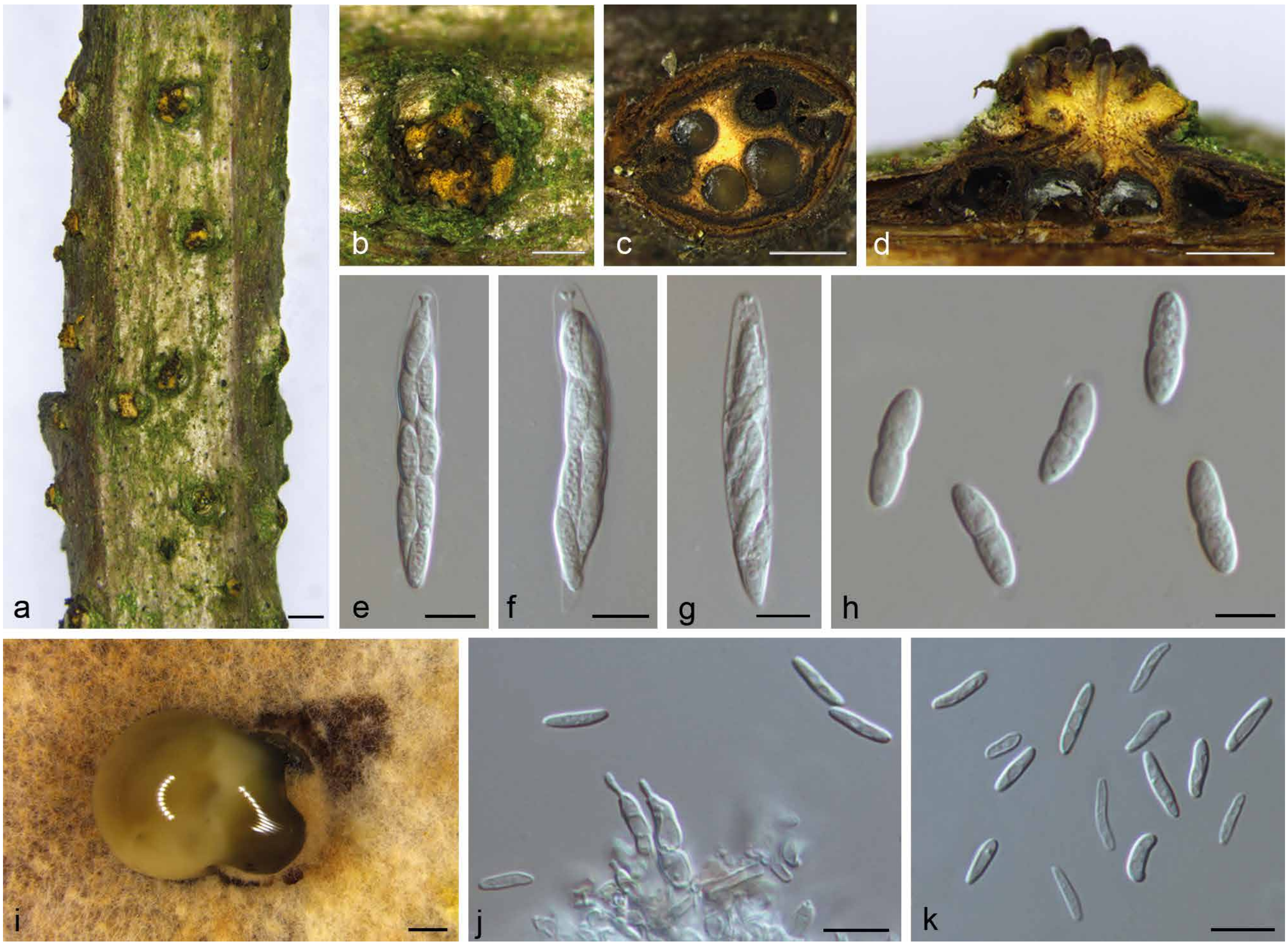

Fig. 5 Morphology of *Dendrostoma osmanthi* from *Osmanthus fragrans*. a, b. Habit of pseudostromata on branches; c. transverse section of pseudostroma; d. longitudinal section through pseudostroma; e–g. asci and ascospores; h. ascospores; i. conidiomata on PDA; j. conidiophores and conidiogenous cells; k. conidia. — Scale bars: a = 1 mm; b–d, i = 500 µm; e–h, j, k = 10 µm.

diam. *Central column* yellowish to brownish. *Stromatic zones* lacking. *Perithecia* conspicuous, umber to fuscous black, regularly scattered, surrounding the ectostromatic disc, 300–400 µm diam. *Ostioles* 4–16 per disc, flat in the disc or sometimes slightly projecting, cylindrical, covered by an orange, umber to fuscous black crust, 80–130 µm diam. *Paraphyses* deliquescent. *Asci* fusoid, 8-spored, biseriate, with an apical ring, 55–65 × 7.5–9.5(–10) µm ($\bar{x}$ = 59 ± 2.1 × 8.7 ± 0.7 µm, n = 10). *Ascospores* hyaline, fusoid to cylindrical, smooth, often containing two guttules per cell to multiguttulate, symmetrical to asymmetrical, straight to slightly curved, bicellular, with a median septum distinctly constricted, 11.5–14.5 × 3.5–4 µm ($\bar{x}$ = 13 ± 1.2 × 3.7 ± 0.2 µm, n = 30). *Conidiomata* pycnidial, hemispherical, somewhat erumpent, coated with cinnamon aerial mycelium, 900–2200 µm diam, with translucent conidial droplets emerging from ostioles. *Conidiophores* hyaline, aseptate. *Conidiogenous cells* enteroblastic, polyphialidic, with 1–2 integrated loci, hyaline, ampulliform to doliiform. *Conidia* hyaline, aseptate, fusoid, acute at each end, 7.5–10.5(–12) × 2–2.5 µm ($\bar{x}$ = 9.5 ± 1.2 × 2.3 ± 0.2 µm, n = 30).
On PDA, cultures are white, becoming slight isabelline after 2 wk. The colonies are flat with irregular edge; texture initially uniform, producing concentric circles after 2 wk with sparse conidiomata irregularly distributed on the agar surface.

Host & Distribution — On *Osmanthus fragrans* in China.

Materials examined (all on twigs and branches of *Osmanthus fragrans*). China, Zhejiang Province, Hangzhou City, Linan, Xijing Mountain, N30°17'00.77" E119°43'28.70", 139 m asl, 23 Apr. 2017, *Q. Yang & Z. Du* (holotype CF 2017473; living ex-type culture CFCC 52106); Zhejiang Province, Hangzhou City, Linan, Xijing Mountain, N33°17'00.35" E119°43'26.70", 154 m asl, 23 Apr. 2017, *Q. Yang & Z. Du* (CF 2017476; living culture CFCC 52108); Zhejiang Province, Hangzhou City, Linan, Xijing Mountain, N30°17'30.67" E119°43'20.30", 139 m asl, 23 Apr. 2017, *Q. Yang & Z. Du* (CF 2017474; living culture CFCC 52107); Zhejiang Province, Hangzhou City, Linan, Xijing Mountain, N33°17'32.33" E119°43'22.15", 154 m asl, 23 Apr. 2017, *Q. Yang & Z. Du* (CF 2017477; living culture CFCC 52109).

Notes — The bark surface of *Osmanthus fragrans* is pustulate, with the fungus appearing to be pathogenic to this host. *Dendrostoma osmanthi* is similar to *D. mali* but differs by having fusoid to cylindrical ascospores that are distinctly constricted at the median septum. The phylogenetic inferences indicated this species as an individual well-supported clade (MP/ML/BI = 100/99/1) in the genus *Dendrostoma*.

Pseudomelanconidaceae C.M. Tian & X.L. Fan, *fam. nov.* — MycoBank MB823991

Etymology. Name derived from the type genus, *Pseudomelanconis*.

Type genus. *Pseudomelanconis* C.M. Tian & X.L. Fan.

Asexual morph: melanconium-like. *Conidiomata* in bark, acervular, with an inconspicuous ectostromatic disc causing a more or less pustulate bark surface. *Central column* beneath the disc more or less conical and becoming pale brown or olive at maturity. The marginal part of ectostroma comprises conidiophores and their basal cell layers. *Conidiophores* aseptate, unbranched, cylindrical, hyaline to pale brown, smooth-walled. *Conidiogenous cells* annellidic. *Conidia* ellipsoid to elongate pyriform, brown at maturity with hyaline sheath. *Sexual morph*: not observed.

Notes — The asexual morph of the new family *Pseudomelanconidaceae* is similar to members of *Melanconiellaceae*, *Melan-*

conidaceae and *Juglanconidaceae* (Fan et al. 2016b, Voglmayr et al. 2017), but differs mainly by having conidiogenous cells with discreet annellations and an inconspicuous hyaline conidial sheath when mature. The phylogenetic inferences resolved this family as an individual group with well-supported value (MP/ML/BI = 100/100/1) from other families of *Diaporthales*.

Pseudomelanconis C.M. Tian & X.L. Fan, *gen. nov.* — MycoBank MB823992

Etymology. Name derived from pseudo- (false-, in Greek) and the genus name *Melanconis*.

Type species. Pseudomelanconis caryae C.M. Tian & X.L. Fan.

Asexual morph: melanconium-like. *Conidiomata* in bark, acervular, immersed in host bark to erumpent. *Ectostromatic disc* inconspicuous, causing a more or less pustulate bark surface. *Central column* beneath the disc more or less conical. The marginal part of the central column comprises conidiophores and their basal cell layers. *Conidiophores* unbranched, aseptate, cylindrical, hyaline to pale brown, smooth-walled, sometimes reduced to conidiogenous cells. *Conidiogenous cells* annellidic, sometimes with apical collarette. *Conidia* hyaline when immature, becoming brown at maturity, ellipsoid to oblong, aseptate, multiguttulate, with distinct hyaline sheath, becoming inconspicuous when mature. *Conidial wall* smooth on the outer surface, with inconspicuous to distinct, sometimes confluent irregular verrucae on the inner surface. *Sexual morph*: not observed.

Pseudomelanconis caryae C.M. Tian & X.L. Fan, *sp. nov.* — MycoBank MB823993; Fig. 6

Etymology. Named after the host genus from which it was isolated, *Carya*.

Asexual morph: melanconium-like. *Conidiomata* acervular, 500–800 µm diam, immersed in host bark to erumpent, covered by brown to blackish exuding conidial masses at maturity. *Central column* beneath the disc more or less conical. *Conidiophores* unbranched, aseptate, cylindrical, hyaline to pale brown, smooth-walled, 14–30 µm. *Conidiogenous cells* annellidic, occasionally with distinct annellations and collarettes. *Conidia* hyaline when immature, becoming greyish sepia to olivaceous, ellipsoid to oblong, multiguttulate, aseptate, (12.5–)13–15(–16) × 4–5 µm ($\overline{x}$ = 14 ± 1.1 × 4.5 ± 0.3 µm, n = 30), with distinct hyaline sheath, 0.5–1 µm diam, becoming inconspicuous when mature. *Conidial wall* smooth on the outer surface. *Sexual morph*: not observed.

On PDA, cultures are initially white, becoming grey olivaceous. The colonies are flat, with irregular margins; texture initially uniform, becoming compact in centre after 3 wk. Conidiomata sparse, producing black conidial droplets, irregularly distributed over the agar surface.

Host & Distribution — On *Carya cathayensis* in China.

Materials examined (all on twigs and branches of *Carya cathayensis*). China, Zhejiang Province, Hangzhou City, Linan, Tianmu Mountain, N30°18'48.85" E119°26'36.99", 288 m asl, 21 Apr. 2017, *Q. Yang & Z. Du* (holotype CF 2017466; living ex-type culture CFCC 52110); Zhejiang Province, Hangzhou City, Linan, Tianmu Mountain, N30°18'49.19" E119°26'37.24", 281 m asl, 21 Apr. 2017, *Q. Yang & Z. Du* (CF 2017467; living culture CFCC 52111); Hangzhou City, Linan, Tianmu Mountain, N30°18'48.77" E119°26'36.56", 287 m asl, 21 Apr. 2017, *Q. Yang & Z. Du* (CF 2017468; living culture CFCC 52112); Hangzhou City, Linan, Tianmu Mountain, N30°18'49.14" E119°26'30.44", 285 m asl, 21 Apr. 2017, *Q. Yang & Z. Du* (CF 2017469; living culture CFCC 52113).

Notes — *Pseudomelanconis caryae* is the type species of *Pseudomelanconis*, and only occurs on *Carya cathayensis* in China. Isolates were identified as *P. caryae* based on their characteristic morphology, host, and DNA phylogeny (MP/ML/BI = 100/100/1). *Juglanconis oblonga* is similar to *P. caryae*, but it can be distinguished by larger brown to blackish conidia (18–22.7 × 9.2–12), and distinctly integrated annellations, as well as DNA sequence data (Voglmayr et al. 2017). *Melanconis juglandis* var. *caryae* was recorded from *Carya cathayensis*, which was considered as a distinct species by Wehmeyer (1941). However, it differs from *P. caryae* primarily by hyaline alpha (10.5–14 × 5–7 µm) and beta conidia (2–2.5 × 0.8–1 µm; Wehmeyer 1941). Wehmeyer (1937) also transferred *Melanconiella pallida* from *Carya* spp. to *Melanconis*, which differs from *P. caryae* in dark brown, subspherical to ovoid or oblong-cylindrical conidia (18–26.5 × 13.3–16.5 µm). Although *Pseudomelanconis* has acervular conidiomata covered by a pustulate conidial mass on the bark surface similar to *Melanconis* and *Juglanconis*, DNA sequence data confirmed them to represent a distinct phylogenetic lineage. Results of recent molecular phylogenetic investigations revealed a remarkably high diversity of corticolous melanconium-like fungi in *Diaporthales* (Fan et al. 2016b, Voglmayr et al. 2012, 2017).

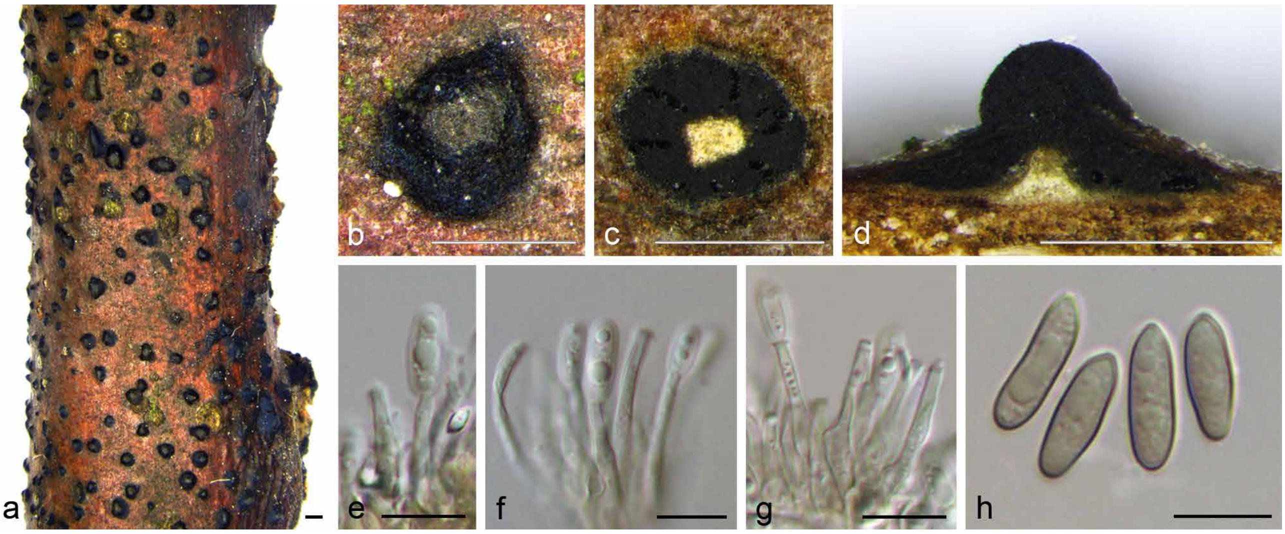

Fig. 6 Morphology of *Pseudomelanconis caryae* from *Carya cathayensis*. a, b. Habit of conidiomata on branches; c. transverse section of conidioma; d. longitudinal section through conidioma; e–g. conidiophores and conidiogenous cells; h. conidia. — Scale bars: a = 1 mm; b–d = 500 µm; e–h = 10 µm.

Synnemasporellaceae X.L. Fan & J.D.P. Bezerra, *fam. nov.* — MycoBank MB823994

Etymology. Name derived from the type genus, *Synnemasporella*.

Type genus. *Synnemasporella* X.L. Fan & J.D.P. Bezerra.

Pseudostromata appearing upon the bark surface as pustules containing small groups of a few ostioles emergent through the adherent periderm, covered by a whitish pulverulence. *Stromatic zones* lacking. *Perithecia* spherical or flattened, with long necks, thickly clustered beneath the ectostromatic disks. *Asci* clavate. *Ascospores* biseriate, fusoid-ellipsoid, two-celled, hyaline, usually with a short, hyaline, bristle-like appendage at each end. *Conidiomata* synnematal or pycnidial. *Synnemata* determinate, parallel, consisting of slender, cylindrical black stalks and a spherical, capitate, shiny black mass of conidia which was cut off from the ends of the numerous entwined hyphae of the stalk; conidiogenous cells zone concave. *Pycnidia* with a central circular ostiole, hemispherical, immersed, somewhat erumpent. *Conidiophores* aggregated, straight to curved. *Conidiogenous cells* aggregated, hyaline, straight to curved, cylindrical. *Conidia* cylindrical to clavate, with a discrete hilum, smooth, pale brown.

Notes — The new family *Synnemasporellaceae* is proposed to accommodate fungi without the typical characters of any of the two-celled, hyaline-spored, stromatic genera. Also, the synnematal and pycnidial conidiomata differ widely from melanconium-like fungi, having pale brown conidia with a distinct hilum (Wehmeyer 1933). The phylogenetic inferences resolved this family as a well-supported clade (MP/ML/BI = 98/98/1) between the families *Juglanconidaceae* and *Apiosporopsidaceae*. Members of the new family differ from *Juglanconidaceae* and *Apiosporopsidaceae* (Senanayake et al. 2017, Voglmayr et al. 2017) mainly in the type of the host plant association, disease symptoms, ascomatal and/or conidiomatal characters, shape of ascospores, conidiogenous cells and conidia, and distinct synnemata.

Synnemasporella X.L. Fan & J.D.P. Bezerra, *gen. nov.* — MycoBank MB823995

Etymology. Name derived from the synnematous conidiomata.

Type species. *Synnemasporella toxicodendri* X.L. Fan & J.D.P. Bezerra.

Sexual morph (based on Wehmeyer 1933): *Pseudostromata* appearing upon the surface as pustules containing small groups of a few ostioles emergent through the adherent periderm, or as larger dense fascicles of elongate-cylindrical ostioles, erumpent through a whitish pulverulent disk. *Ectostromatic disc* often obliterated by the erumpent ostioles, many of which are covered by a whitish pulverulence. *Perithecia* spherical or somewhat flattened, with long slender necks, thickly clustered beneath the ectostromatic disks. *Asci* clavate. *Ascospores* biseriate, long fusoid-ellipsoid, two-celled, hyaline, constricted at the septum, usually with a short, hyaline, bristle-like appendage at each end. *Asexual morph*: *Conidiomata* synnematal or pycnidial. *Synnemata* long and determinate, erumpent, growing from the host tissue, pale brown, straight to curved, parallel, conidiogenous cells zone concave and dark, with some host tissue at the base of synnema. *Pycnidia* with a central circular ostiole, hemispherical, immersed, somewhat erumpent. *Conidiophores* aggregated, aseptate, straight to curved. *Conidiogenous cells* aggregated, hyaline, straight to curved, cylindrical, arranged alongside one another, each producing one conidium. *Conidia* cylindrical to oblong-cylindrical, with a discrete hilum, smooth, multiguttulate, pale brown.

Synnemasporella aculeans (Schwein.) X.L. Fan & J.D.P. Bezerra, *comb. nov.* — MycoBank MB823996; Fig. 7

Basionym. *Sphaeria aculeans* Schwein., Trans. Amer. Philos. Soc. 4: 204. 1832.

Synonym. *Cryptodiaporthe aculeans* (Schwein.) Wehm., Monogr. Gen. *Diaporthe* Nitschke & Segreg., Univ. Michigan Stud., Sci. Ser. 9: 212. 1933.

Sexual morph (based on Wehmeyer 1933): *Pseudostromata* appearing upon the surface as pustules containing small groups of a few ostioles emergent through the adherent periderm, or as larger dense fascicles of elongate-cylindrical ostioles, erumpent through a whitish pulverulent disk, 0.3–1 mm diam, covered by a whitish pulverulence. *Stromatic zones* lacking. *Perithecia* spherical or flattened, with long slender necks, thickly clustered beneath the ectostromatic disks, 260–480 × 250–400 µm. *Asci* clavate, 47–65 × 5–8 µm. *Ascospores* biseriate, long fusoid-ellipsoid, two-celled, hyaline, constricted at the septum, 12–18 × 2.5–3 µm, and usually with a short, hyaline, bristle-like appendage at each end, 2–2.5 µm length. *Asexual morph*: *Conidiomata* synnematal or pycnidial. *Synnemata* long and determinated, growing from the host tissue, pale to brown, straight to curved, parallel, with convex and dark conidiogenous cells zone, and some host tissue at the base of synnema, 1100–1500 µm high, 200–400 µm diam. *Conidiophores* aggregated, aseptate, straight to curved, 20–30 µm. *Conidiogenous cells* aggregated, hyaline, straight to curved, cylindrical, arranged alongside one another at the end of the synnemata, each producing one conidium. *Conidia* oblong-cylindrical, with a distinct hilum, smooth, multiguttulate, hyaline when young and becoming pale brown at maturity, 8–10(–11) × 3–3.5 µm ($\bar{x}$ = 9.3 ± 0.9 × 3.2 ± 0.3 µm, n = 30). *Pycnidia* with a central circular ostiole, hemispherical, immersed, somewhat erumpent, containing an irregular one-chambered locule with black conidial mass, 700–1000 µm. *Conidiophores* aggregated, aseptate, straight to curved, 20–35 µm. *Conidiogenous cells* aggregated, hyaline, straight to curved, cylindrical, arranged alongside one another at the base of the pycnidia, each producing one conidium. *Conidia* ovoid to oblong-fusoid, one-celled, hyaline, multiguttulate, (6.5–)7–8.5(–9) × 2.5–3(–3.5) µm ($\bar{x}$ = 7.6 ± 0.6 × 3 ± 0.3 µm, n = 30).
On PDA, cultures are initially white, becoming straw on the margin after 3 wk. The colonies are felty with regular edge; texture initially uniform, producing concentric circle on the margin after 3 d; sterile.

Host & Distribution — On *Rhus copallina*, *R. diversiloba*, *R. glabra, R. javanica, R. typhina* and *R. vernix* in Japan and USA (Wehmeyer 1933, Kobayashi 1970, Mejía et al. 2011), and on *R. chinensis* in China.

Materials examined (all on twigs and branches of *Rhus chinensis*). China, Zhejiang Province, Hangzhou City, Linan, Xijing Mountain, N30°15'32.83" E119°43'30.73", 47 m asl, 22 Apr. 2017, *Q. Yang & Z. Du* (CF 2017464; living culture CFCC 52094); Jiangxi Province, Dexing City, Phoenix Lake, N28°56'15.20" E117°35'32.12", 40 m asl, 8 Apr. 2017, *B. Cao* (CF 2017401; living culture CFCC 52096); Jiangxi Province, Dexing City, Phoenix Lake, N28°56'14.11" E117°35'32.84", 41 m asl, 8 Apr. 2017, *B. Cao* (CF 2017400; living culture CFCC 52095).

Notes — *Synnemasporella aculeans* is proposed as a new combination in the new genus *Synnemasporella* based on the description of *Cryptodiaporthe aculeans*, which was introduced producing perithecial ascomata, and an asexual morph producing sporodochial and/or pycnidial conidiomata (Wehmeyer 1933). Wehmeyer (1933) placed *C. aculeans* provisionally in *Cryptodiaporthe* and suggested this genus as a 'heterogeneous group of species which will probably be segregated into several genera when the relationships of its species are better known', highlighting that *C. aculeans* could be proposed as a new genus based on its atypical morphological features (see notes of *Synnemasporellaceae*). Sogonov et al. (2008) treated

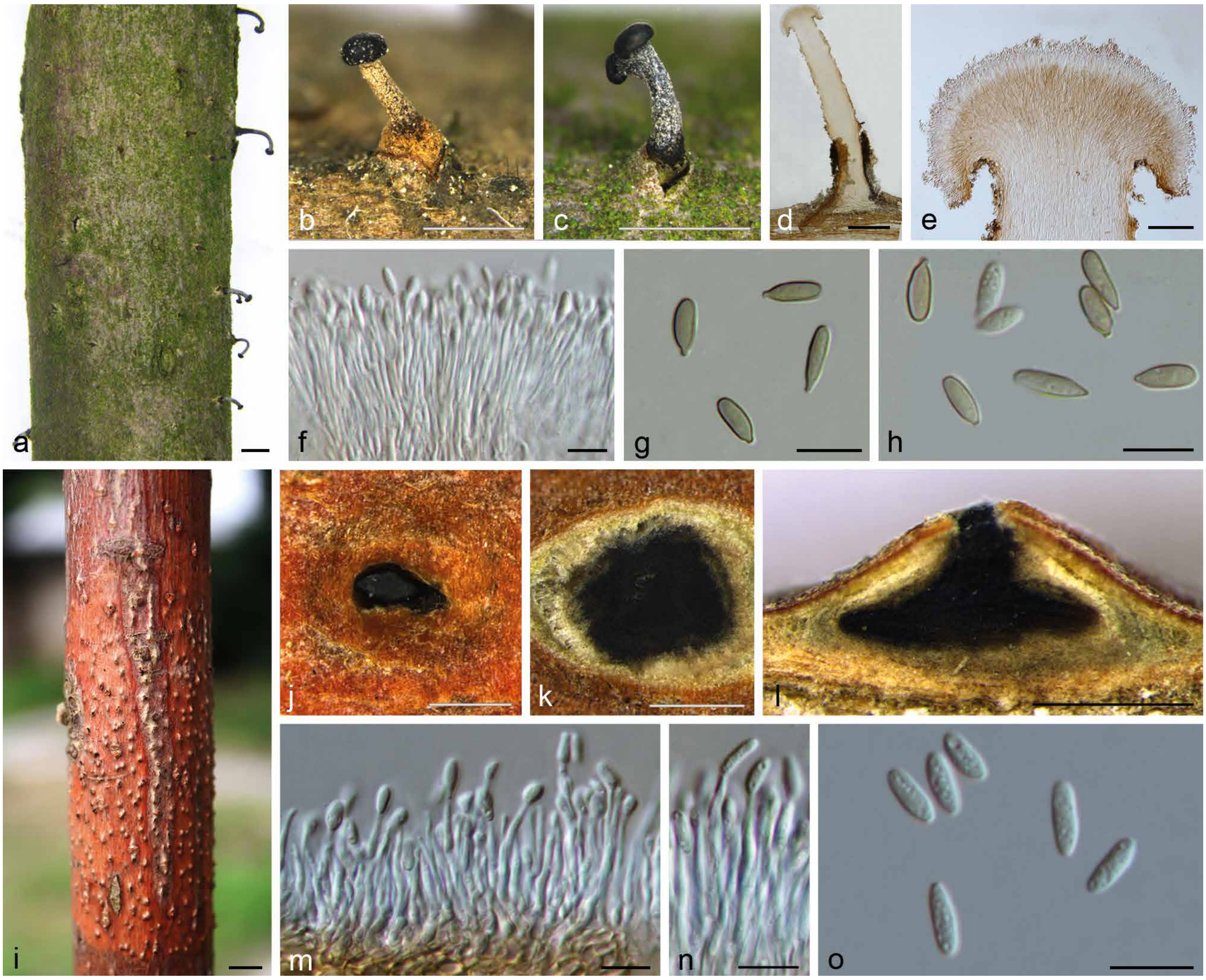

Fig. 7 Morphology of *Synnemasporella aculeans* from *Rhus chinensis*. a–c. Habit of synnemata on branches; d, e. longitudinal section through synnema; f, m, n. conidiophores and conidiogenous cells; g, h, o. conidia; i, j. habit of pycnidia on branches; k. transverse section of pycnidium; l. longitudinal section through pycnidium. — Scale bars: a–c = 1 mm; d, j–l = 500 µm; e = 100 µm; f–h, m–o = 10 µm; i = 5 mm.

Cryptodiaporthe (type *C. aesculi*) as a synonym of *Plagiostoma*, which was followed by Mejía et al. (2011) and Voglmayr et al. (2017). Recently, Senanayake et al. (2017) separated the genera *Plagiostoma* and *Cryptodiaporthe* in their phylogenetically inferences, and pointed out that *Gnomoniaceae* comprised 24 genera, including *Plagiostoma* and *Cryptodiaporthe*. In the current study, the phylogram indicated that our isolates clustered into the same clade (MP/ML/BI = 80/100/1) with the only available culture of *C. aculeans* (AR3878). Based on the phylogenetic inferences and morphological features, we transferred *C. aculeans* to the new genus *Synnemasporella*, as a new combination *S. aculeans*. *Synnemasporella aculeans* is similar to *S. toxicodendri*, but differs from it in having shorter synnemata (1100–1500 µm vs 1200–1800 µm), a convex conidiogenous cells zone on top of synnemata, and larger, oblong-cylindrical conidia (8–11 × 3–3.5 µm).

This species also represents two types of conidiomata in *Diaporthales*, namely pycnidia and synnemata. This uncommon phenomenon was also recorded by Wehmeyer (1933), who observed the production of sporodochia on twigs of *Rhus*. Wehmeyer (1933) also reported the production of conidiomata when cultures were grown on agar, 'showing all intergradations between true pycnidia and true sporodochia'.

Synnemasporella toxicodendri X.L. Fan & J.D.P. Bezerra, *sp. nov.* — MycoBank MB823997; Fig. 8

Etymology. Name derived from the host genus, *Toxicodendron*.

Conidiomata synnematal. *Synnemata* long and determinate, growing from host tissue, pale to brown, straight to curved, parallel, with flat to slightly concave and dark conidiogenous cells zone and some host tissue at the base of synnema, 1200–1800 µm high, 150–300 µm diam. *Conidiophores* aggregated, aseptate, straight to curved, reduced to conidiogenous cells, 20–30 µm. *Conidiogenous cells* aggregated, hyaline, straight to curved, cylindrical, arranged adjacent to one another at the end of the synnema, producing one conidium each. *Conidia* cylindrical to oblong-cylindrical, with a discrete hilum, smooth, multiguttulate, pale brown, 6–8 × 2.5–4 µm ($\overline{x}$ = 7.3 ± 0.6 × 3.1 ± 0.3 µm, n = 30). *Sexual morph*: not observed.
On PDA, cultures are initially white, becoming sepia on the bottom after 3 d. The colonies are felty with an irregular edge; texture initially uniform, producing concentric circles after 3 wk; sterile.

Host & Distribution — From *Toxicodendron sylvestre* in China.

Materials examined (all on twigs and branches of *Toxicodendron sylvestre*). China, Zhejiang Province, Hangzhou City, Linan, Xijing Mountain, N30°15'32.84" E119°43'31.21", 54 m asl, 22 Apr. 2017, *Q. Yang & Z. Du* (holotype CF 2017481; living ex-type culture CFCC 52097); Zhejiang Province, Hangzhou City, Linan, Xijing Mountain, N30°15'32.21" E119°43'31.55", 51 m asl, 22 Apr. 2017, *Q. Yang & Z. Du* (CF 2017483; living culture CFCC 52099);

Fig. 8 Morphology of *Synnemasporella toxicodendri* from *Toxicodendron sylvestre*. a, b. Habit of synnemata on branches; c, d. longitudinal section through synnema; e. conidiophores and conidiogenous cells; f, g. conidia. — Scale bars: a, b = 1 mm; c, d = 100 µm; e–g = 10 µm.

Zhejiang Province, Hangzhou City, Linan, Xijing Mountain, N30°15'31.12" E119°43'30.77", 52 m asl, 22 Apr. 2017, *Q. Yang & Z. Du* (CF 2017482; living culture CFCC 52098).

Notes — Structures of *S. toxicodendri* were observed growing on diseased wood of *Toxicodendron sylvestre* in China, and so far, only occurs on *T. sylvestre*. Morphologically, it can be distinguished from *S. aculeans* and other genera in *Diaporthales* because it is characterised by the higher synnemata (1200–1800 µm) growing from the host tissue, with flat to slightly concave and dark conidiogenous cells zone on the top. The sexual morph of this species is not known and further collections are required to resolve its life cycle.

DISCUSSION

In this study we propose three new families, namely *Diaporthostomataceae*, *Pseudomelanconidaceae*, *Synnemasporellaceae*, and a new genus, *Dendrostoma* (*Erythrogloeaceae*), including three new species. The new materials studied here were collected in Zhejiang Province, China. This province was chiefly selected due to Tianmu Mountain, which is considered as a biodiversity hotspot with a high diversity for forest species (Zhou 1995). In the current study, all specimens were collected from symptomatic branches and twigs associated with canker or dieback disease of *Anacardiaceae* (*Rhus chinensis*, *Toxicodendron sylvestre*), *Fagaceae* (*Quercus acutissima*), *Juglandaceae* (*Carya cathayensis*), *Lauraceae* (*Machilus leptophylla*), *Oleaceae* (*Osmanthus fragrans*) and *Rosaceae* (*Malus spectabilis*), suggesting that many additional undiscovered species of diaporthalean fungi exist in China.

The classification of *Diaporthales* presented here integrates results from prior analyses (Castlebury et al. 2002, Rossman et al. 2007) and discoveries of new taxa from many other research groups (Cheewangkoon et al. 2010, Crous et al. 2012, 2015, Suetrong et al. 2015, Norphanphoun et al. 2016, Senanayake et al. 2017, Voglmayr et al. 2017). *Diaporthales* are mostly characterised by diaporthalean perithecia with an elongate beak and unitunicate asci with a characteristic refractive apical annulus when mature (Rossman et al. 2007). However, these characters are difficult to fully study *in vivo* due to the absence of various morphological morphs. As a result, the family concepts have thus been unstable, with many species being transferred from one genus or family to another (Rossman et al. 2007, Hongsanan et al. 2017, Senanayake et al. 2017). Based on newly generated molecular data, the current systematic framework provides good support for this order and related families (Castlebury et al. 2002, Rossman et al. 2007, Crous et al. 2015, Senanayake et al. 2017, Voglmayr et al. 2017). The current study revised the *Diaporthales* and accepted 25 families in the order (Table 2). However, some nodes remain weakly supported, and genera such as *Diaporthella* and *Phaeoappendispora* require further collection and study (Senanayake et al. 2017).

As the morphological features in *Diaporthales* are highly diverse, phylogenetic studies have been useful to elucidate the diversity in this group, and the inclusion or exclusion of taxa in this order. In this study we proposed a new genus in *Erythrogloeaceae*, namely *Dendrostoma*, which is characterised by typical diaporthalean perithecia with clavate asci, and fusoid to cylindrical, bicellular ascospores. The family *Erythrogloeaceae* was recently proposed by Senanayake et al. (2017) to accommodate *Chrysocrypta*, *Disculoides* and *Erythrogloeum* based on morphological features and phylogenetic analyses. Members of this family are mainly characterised by acervular conidiomata, hyaline to olivaceous conidia, and the presence of macro- and microconidia. Although Senanayake et al. (2017) did not observe any sexual morph in this family, we did collect a sexual morph in the present study, and thus emended the family description accordingly.

The new family *Diaporthostomataceae* is introduced here based on phylogenetic inferences and morphology of its members, which are mainly characterised by conical and discrete perithecia, and bicellular, fusoid ascospores. The new family is morphologically distinct from its sister family *Diaporthosporellaceae,* which is also distinguished from other diaporthalean families by irregularly uniseriate, allantoid or subreniform ascospores, phialidic conidiophores, and cylindrical to ellipsoidal, aseptate conidia (Yang et al. 2018). Members of *Diaporthosporellaceae* are known from twigs and branches of *Cercis chinensis* (Yang et al. 2018), and representatives of *Diaporthostomataceae* occur on *Machilus leptophylla*, both occurring in China.

Pseudomelanconidaceae is described here (on *Carya cathayensis* in China) based on phylogenetic inferences, and on few morphological features which distinguish it from members of *Melanconium*-related *Melanconiellaceae*, *Melanconidaceae* and *Juglanconidaceae*. Senanayake et al. (2017) introduced

Table 2 Placement of families in *Diaporthales* by different authors.

Nannfeldt (1932)	Von Arx & Müller (1954)	Wehmeyer & Hanlin (1975)	Barr (1978)	Rossman et al. (2007)	Senanayake et al. (2017)	This paper (2018)
Diaportheaceae	*Diaportheaceae*	*Diaportheaceae*	*Diaportheaceae*	*Cryphonectriaceae*	*Apiosporopsidaceae*	*Apiosporopsidaceae*
	Valsaceae	*Gnomoniaceae*	*Gnomoniaceae*	*Diaportheaceae*	*Apoharknessiaceae*	*Apoharknessiaceae*
		Valsaceae	*Melanconidaceae*	*Gnomoniaceae*	*Asterosporiaceae*	*Asterosporiaceae*
			Valsaceae	*Melanconidaceae*	*Auratiopycnidiellaceae*	*Auratiopycnidiellaceae*
				Pseudovalsaceae	*Coryneaceae*	*Coryneaceae*
				Schizoparmeaceae	*Cryphonectriaceae*	*Cryphonectriaceae*
				Sydowiellaceae	*Cytosporaceae*	*Cytosporaceae*
				Togniniaceae	*Diaporthaceae*	*Diaporthaceae*
				Valsaceae	*Erythrogloeaceae*	*Diaporthosporellaceae*
					Gnomoniaceae	*Diaporthostomataceae*
					Harknessiaceae	*Erythrogloeaceae*
					Juglanconidaceae	*Gnomoniaceae*
					Lamproconiaceae	*Harknessiaceae*
					Macrohilaceae	*Juglanconidaceae*
					Melanconidaceae	*Lamproconiaceae*
					Melanconiellaceae	*Macrohilaceae*
					Prosopidicolaceae	*Melanconidaceae*
					Pseudoplagiostomataceae	*Melanconiellaceae*
					Schizoparmeaceae	*Prosopidicolaceae*
					Stilbosporaceae	*Pseudomelanconidaceae*
					Sydowiellaceae	*Pseudoplagiostomataceae*
						Schizoparmeaceae
						Stilbosporaceae
						Sydowiellaceae
						Synnemasporellaceae

Melanconiellaceae to accommodate the previous unresolved *Melanconiella* clade in *Diaporthales*. *Melanconiella* species were previously observed to be highly host-specific to the host family *Betulaceae*, and confined to the north temperate zone, namely Europe and North America (Voglmayr et al. 2012). Du et al. (2017) extended the host and geographic range to include *Cornus controversa* and *Juglans regia* in China. The *Melanconidaceae* was recently revised by Senanayake et al. (2017), and included a single genus, *Melanconis*, which is characterised by perithecial ascomata having 8-spored asci, hyaline, ellipsoid, 1-septate ascospores, and acervular conidiomata with hyaline to brown, ellipsoid or subglobose conidia. Members of this family include saprobic and plant pathogenic species in North America and Europe (Senanayake et al. 2017). *Juglanconidaceae* was introduced by Voglmayr et al. (2017) and it comprises a single genus, *Juglanconis,* which occurs on dead, corticated twigs and branches of *Juglandaceae* species. Morphologically, members of this family have perithecial ascomata, octosporous asci with an apical ring, hyaline, bicellular ascospores with or without gelatinous appendages, and acervular conidiomata with brown conidia with gelatinous sheaths (Senanayake et al. 2017, Voglmayr et al. 2017).

The molecular phylogenetic analyses also revealed another well-supported family, *Synnemasporellaceae*, which is closely related to *Juglanconidaceae* (Fig. 1). We identified one species of this clade as *Cryptodiaporthe aculeans* based on the ambiguous asexual features of this species, which can produce synnemata and pycnidia. Interestingly, *C. aculeans* was ‘arbitrarily placed in the genus *Cryptodiaporthe*’ by Wehmeyer (1933), who also suggested that this species could be described as a new genus ‘since it does not show the typical characters of any of the two-celled, hyaline-spored, stromata genera’. Recent studies, however, did not include *Cryptodiaporthe aculeans* in their phylogenetic analyses (Sogonov et al. 2008, Mejía et al. 2011, Senanayake et al. 2017). In the present study, this fungus was transferred to *Synnemasporella* as a new combination, based on the original description of Wehmeyer (1933), and the only sequenced culture (AR3878) available in GenBank. *Synnemasporellaceae* comprises fungi distinguished by the presence of spherical or flattened perithecia with long necks, clavate asci, fusoid-ellipsoid, two-celled, hyaline ascospores, usually with a short, hyaline, bristle-like appendage at each end, and synnematal and/or pycnidial conidiomata producing cylindrical to clavate, smooth, pale brown conidia.

As shown in this study, future studies addressing the family-level organization of the *Diaporthales* should routinely include data for protein-coding genes, especially *rpb2* and *tef1-α*. It is hoped that the classification proposed here will also provide an updated phylogenetic framework that will facilitate further revision of the *Diaporthales*.

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