

## Supplementary materials

**Table S1. The names, isolate numbers, and corresponding GenBank accession numbers of the taxa used in Figure 1. The taxa produced in this study are indicated in red, and the type strains are indicated in bold with “T”.**

Species	Isolate No.	GenBank accession No.	
		ITS	<i>tub2</i>
<i>Allocryptovalsa cryptovalsoidea</i>	HVFIG02 T	HQ692573	HQ692524
<i>Allocryptovalsa cryptovalsoidea</i>	HVFIG05	HQ692574	HQ692525
<i>Allocryptovalsa polyspora</i>	MFLUCC 17-0364 T	MF959500	MG334556
<i>Allocryptovalsa rabenhorstii</i>	WA07CO	HQ692620	HQ692522
<i>Allocryptovalsa rabenhorstii</i>	CreI	KC774567	/
<i>Allodiatrype arengae</i>	MFLUCC 15-0713 T	MN308411	MN340297
<i>Allodiatrype elaeidicola</i>	MFLUCC 15-0737a	MN308415	MN340299
<i>Allodiatrype elaeidis</i>	MFLUCC 15-0708b	MN308413	/
<i>Allodiatrype elaeidis</i>	MFLUCC 15-0708a	MN308412	MN340298
<i>Allodiatrype thailandica</i>	MFLUCC 15-0711	MN308414	/
<i>Anthostoma decipiens</i>	JL567	JN975370	JN975407
<i>Anthostoma decipiens</i>	IPV-FW349 T	AM399021	AM920693
<i>Cryptosphaeria avicenniae</i>	NFCCI-4248	MH304406	MH370273
<i>Cryptosphaeria bathurstensis</i>	AMH-9952 T	MN061366	MN431496
<i>Cryptosphaeria eunomia</i>	CBS 216.87	AJ302417	/
<i>Cryptosphaeria eunomia</i>	CBS223.87	AJ302421	/
<i>Cryptosphaeria ligniota</i>	CBS 273.87	AJ302418	KT425168
<i>Cryptosphaeria moravica</i>	CBS244.87	HM164735	HM164769
<i>Cryptosphaeria pullmanensis</i>	HBPF24	KT425202	GQ294014
<i>Cryptosphaeria pullmanensis</i>	ATCC 52655	KT425235	KT425170
<i>Cryptosphaeria subcutanea</i>	CBS 240.87	AJ302420	KT425167
<i>Cryptosphaeria subcutanea</i>	DSUB100A	KT425189	KT425124
<i>Cryptovalsa ampelina</i>	UCD779St	GQ293907	GQ293980
<i>Cryptovalsa ampelina</i>	A001	GQ293901	GQ293972
<i>Cryptovalsa ampelina</i>	DRO101	GQ293902	GQ293982
<i>Cryptovalsa ampelina</i>	IRAN 2281C	KJ767718	KY352426
<i>Diatrype bullata</i>	UCDDCh400	DQ006946	DQ007002
<i>Diatrype disciformis</i>	CBS 205.87 T	AJ302437	/
<i>Diatrype disciformis</i>	MFLUCC15-0538	KR605644	KY352434
<i>Diatrype exteroxantha</i>	HUEFS155114	KM396617	KT003700
<i>Diatrype exteroxantha</i>	HUEFS155116	KM396618	KT022236
<i>Diatrype macowaniana</i>	CBS 214.87	AJ302431	/
<i>Diatrype mangrovei</i>	MFLUCC 17-0412	MH304407	/

<i>Diatrype mangrovei</i>	MFLUCC 17-0391	MH304408	/
<i>Diatrype mangrovei</i>	MFLUCC 17-0394	MH304409	/
<b><i>Diatrype palmicola</i></b>	<b>MFLU 15-0040 T</b>	<b>KP744439</b>	/
<i>Diatrype stigma</i>	DCASH200	GQ293947	GQ294003
<i>Diatrype undulate</i>	CBS 271.87	AJ302436	/
<i>Diatrypella favaceae</i>	Isolate 380	KU320616	/
<i>Diatrypella pulvinata</i>	H048	FR715523	FR715495
<i>Eutypa astroidea</i>	CBS 292.87	AJ302458	DQ006966
<i>Eutypa cremea</i>	STEU 8087	KY111646	KY111603
<i>Eutypa cremea</i>	STEU 8082	KY111656	KY111598
<i>Eutypa laevata</i>	CBS 291.87	HM164737	HM164771
<i>Eutypa lata</i>	SAPN01	HQ692616	HQ692500
<i>Eutypa lata</i> va. <i>aceri</i>	CBS 290.87	HM164736	HM164770
<i>Eutypa lejoplaca</i>	020202-5	AY684221	AY684196
<i>Eutypa leptoplaca</i>	CBS 287.87	AY684226	AY684204
<i>Eutypa leptoplaca</i>	CBS 288.88	AY684227	AY684205
<i>Eutypa sparsa</i>	3802-3b	AY684220	AY684201
<i>Eutypella caricae</i>	EL51C	AJ302460	/
<i>Eutypella cerviculata</i>	CBS 221.87	AJ302468	/
<b><i>Eutypella cerviculata</i></b>	<b>M68 T</b>	<b>JF340269</b>	/
<i>Eutypella leprosa</i>	EL54C	AJ302463	/
<i>Eutypella leprosa</i>	Isolate 60	KU320622	/
<i>Eutypella microtheca</i>	BCMX01	KC405563	KC405560
<i>Eutypella microtheca</i>	ADEL200	HQ692559	HQ692527
<i>Halodiatrype avicenniae</i>	MFLUCC 16-0532	MH304411	MH370275
<i>Halodiatrype avicenniae</i>	MFLUCC 17-0396	MH304413	MH370277
<i>Halodiatrype avicenniae</i>	MFLUCC 15-0948	MH304414	MH370278
<i>Halodiatrype avicenniae</i>	MFLUCC 16-0533	MH304412	MH370276
<b><i>Halodiatrype salinicola</i></b>	<b>MFLUCC15-1277 T</b>	<b>KX573915</b>	<b>KX573932</b>
<i>Kretzschmaria deusta</i>	CBS 826.72	KU683767	KU684190
<i>Libertella blepharis</i>	LBAg	AY620998	/
<i>Libertella</i> sp.	F6	OL336844	/
<b><i>Mangifericola hongheensis</i></b>	<b>HKAS 122665 T</b>	<b>OM030351</b>	<b>ON468664</b>
<i>Mangifericola hongheensis</i>	HKAS 122666	OM030348	ON468665
<b><i>Melanostictus longiostiolatus</i></b>	<b>MFLU 19-2146 T</b>	<b>NR_175675</b>	<b>MW775595</b>
<b><i>Melanostictus thailandicus</i></b>	<b>MFLU 19-2123 T</b>	<b>NR_175671</b>	<b>MW775590</b>
<i>Monosporascus cannonballus</i>	CMM3646	JX971617	/
<b><i>Monosporascus cannonballus</i></b>	<b>ATCC 26931 T</b>	<b>FJ430598</b>	/
<i>Neoeutypella baoshanensis</i>	GMB:0052	MW797106	MW814878
<b><i>Neoeutypella baoshanensis</i></b>	<b>HMAS 255436 T</b>	<b>NR_164038</b>	<b>MH822888</b>

<i>Paraeutypella citricola</i>	IRAN 2349C	KR605647	KY352439
<i>Paraeutypella citricola</i>	KUMCC 21-0461	OL989101	ON468663
<i>Paraeutypella citricola</i>	HVVIT07	HQ692579	HQ692512
<i>Paraeutypella citricola</i>	HVGRF01	HQ692589	HQ692521
<i>Paraeutypella citricola</i>	KUMCC 20-0023	MW040050	MW239663
<i>Paraeutypella guizhouensis</i>	KUMCC 20-0017	MW039348	MW239661
<b><i>Paraeutypella guizhouensis</i></b>	<b>KUMCC 20-0016 T</b>	<b>MW036142</b>	<b>MW239660</b>
<i>Paraeutypella quatemata</i>	CBS 196.30	MH855110	/
<i>Paraeutypella vitis</i>	UCD2291AR	HQ288224	HQ288303
<i>Paraeutypella vitis</i>	UCD2428TX	FJ790851	GU294726
<i>Pedumispora rhizophorae</i>	BCC44877	KJ888854	/
<i>Pedumispora rhizophorae</i>	BCC44878	KJ888853	/
<i>Peroneutypa alsophila</i>	CBS 250.87	AJ302467	/
<i>Peroneutypa comosa</i>	BAFC 393	KF964568	/
<i>Peroneutypa curvispora</i>	HUEFS 136877	KM396641	/
<b><i>Peroneutypa diminutispora</i></b>	<b>HUEFS 192196 T</b>	<b>KM396647</b>	/
<i>Peroneutypa kochiana</i>	EL53M	AJ302462	/
<b><i>Peroneutypa microasca</i></b>	<b>BAFC 51550 T</b>	<b>KF964566</b>	<b>KF964572</b>
<b><i>Peroneutypa rubiformis</i></b>	<b>MFLUCC 17-2142 T</b>	<b>MG873477</b>	/
<i>Peroneutypa scoparia</i>	DFMAL100	GQ293962	GQ294029
<i>Peroneutypa scoparia</i>	IRAN 2345C	KR605646	KY352452
<i>Quaternaria quaternata</i>	CBS 278.87	AJ302469	/
<i>Quaternaria quaternata</i>	IRAN 2348C	KR605645	KY352464
<b><i>Xylaria berteroi</i></b>	<b>YMJ 95101511 T</b>	<b>KC473562</b>	<b>KC473561</b>

**Table S2. The names, isolate numbers, and corresponding GenBank accession numbers of the taxa used in figure 3. The taxa produced in this study are indicated in red, and the type strains are indicated in bold with “T”.**

Species name	Isolate No.	GenBank accession No.			
		ITS	LSU	<i>rpb2</i>	<i>tub2</i>
<i>Annulohypoxyton annulatum</i>	CBS 140775	KY610418	KY610418	KY624263	KX376353
<i>Annulohypoxyton truncatum</i>	CBS 140778	KY610419	KY610419	KY624277	KX376352
<i>Biscogniauxia nummularia</i>	MUCL 51395	KY610382	KY610427	KY624236	KX271241
<i>Daldinia concentrica</i>	CBS 113277	AY616683	KY610434	KY624243	KC977274
<b><i>Daldinia dennisii</i></b>	<b>CBS 114741 T</b>	<b>JX658477</b>	<b>KY610435</b>	<b>KY624244</b>	<b>KC977262</b>
<i>Daldinia loculatoides</i>	CBS 113279	AF176982	KY610438	KY624247	KX271246
<i>Daldinia steglichii</i>	MUCL 43512	KY610399	KY610479	KY624250	KX271269
<i>Entonaema liquescens</i>	ATCC 46302	KY610389	KY610443	KY624253	KX271248
<i>Htfoxptflon eurasiaticum</i>	MUCL 57722	MW367853	/	MW373854	MW373863
<b><i>Hypomontagnella barbarensis</i></b>	<b>STMA 14081 T</b>	<b>MK131720</b>	<b>MK131718</b>	<b>MK135891</b>	<b>MK135893</b>
<i>Hypomontagnella monticulosa</i>	MUCL 54604	KY610404	KY610487	KY624305	KX271273
<i>Hypomontagnella monticulosa</i>	CLL 205	MK131719	MK131717	MK135890	MK135892
<i>Hypomontagnella monticulosa</i>	HKAS 122664	OL989326	OM001328	ON392010	ON468657
<i>Hypomontagnella submonticulosa</i>	CBS 115280	KC968923	KY610457	KY624226	KC977267
<b><i>Hypoxyton addis</i></b>	<b>MUCL 52797 T</b>	<b>KC968931</b>	/	/	<b>KC968931</b>
<i>Hypoxyton anthochroum</i>	YMJ 9	JN660819	/	/	AY951703
<b><i>Hypoxyton aurantium</i></b>	<b>MFLU 16-1202 T</b>	<b>MN047114</b>	<b>NG_068298</b>	/	/
<i>Hypoxyton aurantium</i>	MFLU 18-0531	MN047115	MN017879	MN077081	/
<b><i>Hypoxyton aveirensis</i></b>	<b>CMG 29 T</b>	<b>MN053021</b>	/	/	<b>MN066636</b>
<b><i>Hypoxyton baihualingense</i></b>	<b>FCATAS 477 T</b>	<b>MG490190</b>	/	/	<b>MH790276</b>
<i>Hypoxyton baruense</i>	UCH9545	MN056428	/	/	MK908142

<i>Hypoxylon begae</i>	YMJ 215	JN660820	/	/	AY951704
<i>Hypoxylon bellicolor</i>	UCH9543	MN056425	/	/	MK908139
<i>Hypoxylon brevisporum</i>	YMJ 36	JN660821	/	/	AY951705
<i>Hypoxylon carneum</i>	MUCL 54177	KY610400	KY610480	KY624297	KX271270
<i>Hypoxylon cercidicola</i>	CBS 119009	KC968908	KY610444	KY624254	KC977263
<b><i>Hypoxylon chrysalidosporum</i></b>	<b>FCATAS 2710 T</b>	<b>OL467294</b>	<b>OL615106</b>	<b>OL584222</b>	<b>OL584229</b>
<i>Hypoxylon crocop eplum</i>	CBS 119004	KC968907	KY610445	KY624255	KC977268
<i>Hypoxylon crocopeplum</i>	ANM 1118	JN673047	/	/	/
<b><i>Hypoxylon cyclobalanopsidis</i></b>	<b>FCATAS 2714 T</b>	<b>OL467298</b>	<b>OL615108</b>	<b>OL584225</b>	<b>OL584232</b>
<b><i>Hypoxylon damuense</i></b>	<b>FCATAS4207 T</b>	<b>ON075427</b>	<b>ON075433</b>	<b>ON093251</b>	<b>ON093245</b>
<b><i>Hypoxylon delonicis</i></b>	<b>MFLU 16-1031 T</b>	<b>NR_171100</b>	<b>NG_074451</b>	/	<b>MT212215</b>
<i>Hypoxylon dieckmannii</i>	YMJ 89041203	JN979413	/	/	AY951713
<i>Hypoxylon duranii</i>	YMJ 85	JN979414	/	/	AY951714
<i>Hypoxylon erythrostroma</i>	YMJ 90080602	JN979416	/	/	AY951716
<i>Hypoxylon eurasiaticum</i>	MUCL 57720	MW367851	/	MW373852	MW373861
<i>Hypoxylon eurasiaticum</i>	MUCL 57721	MW367852	/	MW373853	MW373862
<i>Hypoxylon eurasiaticum</i>	MUCL 57723	MW367854	/	MW373855	MW373864
<i>Hypoxylon eurasiaticum</i>	DSM 112037	MW367855	/	MW373856	MW373865
<i>Hypoxylon fendleri</i>	MUCL 54792	KF234421	KY610481	KY624298	KF300547
<i>Hypoxylon ferrugineum</i>	CBS 141259	KX090079	/	/	KX090080
<i>Hypoxylon fragiforme</i>	MUCL 51264	KC477229	KM186295	KM186296	KX271282
<i>Hypoxylon fraxinophilum</i>	MUCL 54176	KC968938	/	/	KC977301
<b><i>Hypoxylon fulvosulphureum</i></b>	<b>MFLUCC13-0589 T</b>	<b>KP401576</b>	/	/	<b>KP401584</b>
<i>Hypoxylon fuscum</i>	DSM 112039	MW367856	MW367847	MW373857	MW373866
<i>Hypoxylon fuscum</i>	CBS 113049	KY610401	KY610482	KY624299	KX271271
<b><i>Hypoxylon griseobrunneum</i></b>	<b>CBS 331.73 T</b>	<b>KY610402</b>	<b>KY610483</b>	<b>KY624300</b>	<b>KC977303</b>

<i>Hypoxylon guilanense</i>	MUCL 57726 T	MT214997	MT214992	MT212235	MT212239
<i>Hypoxylon haematostroma</i>	MUCL 53301	KC968911	KY610484	KY624301	KC977291
<i>Hypoxylon hepaticolor</i>	ILLS:00121426 T	MT799854	MT799853	/	/
<i>Hypoxylon hinnuleum</i>	DSM:107926	MK287532	MK287544	MK287557	MK287570
<i>Hypoxylon hinnuleum</i>	MUCL:3621 T	MK287537	MK287549	MK287562	MK287575
<i>Hypoxylon hongheensis</i>	KUMCC 21-0452	OM001333	OM001334	ON39008	ON468655
<i>Hypoxylon hongheensis</i>	HKAS 122663 T	OM001336	OM001339	ON392009	ON468656
<i>Hypoxylon howeanum</i>	MUCL 47599	AM749928	KY610448	KY624258	KC977277
<i>Hypoxylon hypomiltum</i>	MUCL 51845	KY610403	KY610449	KY624302	KX271249
<i>Hypoxylon invadens</i>	MUCL 51475 T	MT809133	MT809132	MT813037	MT813038
<i>Hypoxylon investiens</i>	CBS 118183	KC968925	KY610450	KY624259	KC977270
<i>Hypoxylon isabellinum</i>	STMA 10247 T	KC968935	/	/	KC977295
<i>Hypoxylon jecorinum</i>	YMJ 39	JN979429	/	/	AY951731
<i>Hypoxylon jianfengense</i>	FACATAS845 T	MW984546	MZ029707	MZ047260	MZ047264
<i>Hypoxylon larissae</i>	FACATAS844 T	MW984548	MZ029706	MZ047258	MZ047262
<i>Hypoxylon lateripigmentum</i>	MUCL 53304 T	KC968933	KY610486	KY624304	KC977290
<i>Hypoxylon lenormandii</i>	CBS 119003	KC968943	KY610452	KY624261	KC977273
<i>Hypoxylon lienhwacheense</i>	MFLUCC 14-1231	KU604558	MK287550	MK287563	KU159522
<i>Hypoxylon lignicola</i>	MFLUCC 16-0926 T	MK828609	MK835808	/	/
<i>Hypoxylon liviae</i>	CBS 115282	NR155154	/	/	KC977265
<i>Hypoxylon lividicolor</i>	YMJ 70	JN979432	/	/	AY951734
<i>Hypoxylon lividipigmentum</i>	YMJ 233	JN979433	/	/	AY951735
<i>Hypoxylon macrosporum</i>	YMJ 47	JN979434	/	/	AY951736
<i>Hypoxylon mangrovei</i>	MFLU 18-0575 T	MN047117	MN017881	/	MN077054
<i>Hypoxylon medogense</i>	FCATAS4061 T	ON075425	ON075431	ON093249	ON093243
<i>Hypoxylon musceum</i>	MUCL 53765	KC968926	KY610488	KY624306	KC977280

<i>Hypoxylon notatum</i>	YMJ 250	JQ009305	/	/	AY951739
<i>Hypoxylon ochraceum</i>	MUCL 54625	KC968937	/	KY624271	KC977300
<b><i>Hypoxylon olivaceopigmentum</i></b>	<b>DSM 107924 T</b>	<b>MK287530</b>	<b>MK287542</b>	<b>MK287555</b>	<b>MK287568</b>
<b><i>Hypoxylon papillatum</i></b>	<b>ATCC 58729 T</b>	<b>KC968919</b>	<b>KY610454</b>	<b>KY624223</b>	<b>KC977258</b>
<i>Hypoxylon perforatum</i>	CBS 115281	KY610391	KY610455	KY624224	KX271250
<b><i>Hypoxylon petriniae</i></b>	<b>CBS 114746 T</b>	<b>KY610405</b>	<b>KY610491</b>	<b>KY624279</b>	<b>KX271274</b>
<i>Hypoxylon pilgerianum</i>	STMA 13455	KY610412	KY610412	KY624308	KY624315
<i>Hypoxylon porphyreum</i>	CBS 119022	KC968921	KY610456	KY624225	KC977264
<i>Hypoxylon pseudofendleri</i>	MFLUCC 11-0639	KU940156	KU863144	/	/
<i>Hypoxylon pseudofuscum</i>	DSM 112035	MW367858	MW367849	MW373859	MW373868
<i>Hypoxylon pseudofuscum</i>	DSM 112036	MW367859	MW367850	MW373860	MW373869
<b><i>Hypoxylon pseudofuscum</i></b>	<b>DSM 112038 T</b>	<b>MW367857</b>	<b>MW367848</b>	<b>MW373858</b>	<b>MW373867</b>
<b><i>Hypoxylon pulicicidum</i></b>	<b>CBS 122622 T</b>	<b>JX183075</b>	<b>KY610492</b>	<b>KY624280</b>	<b>JX183072</b>
<i>Hypoxylon rickii</i>	MUCL 53309	KC968932	KY610416	KY624281	KC977288
<i>Hypoxylon rubiginosum</i>	MUCL 52887	KC477232	KY610469	KY624266	KY624311
<i>Hypoxylon rutilum</i>	YMJ 181	/	/	/	AY951752
<i>Hypoxylon samuelsii</i>	MUCL 51843	KC968916	KY610466	KY624269	KC977286
<i>Hypoxylon shearii</i>	YMJ 29	EF026142	/	/	AY951753
<b><i>Hypoxylon spagazzinianum</i></b>	<b>STMA 14082 T</b>	<b>KU604573</b>	/	/	<b>KU604582</b>
<b><i>Hypoxylon sporistriatatum</i></b>	<b>UCH9542 T</b>	<b>MN056426</b>	/	/	<b>MK908140</b>
<i>Hypoxylon subgilvum</i>	YMJ 88113007	JQ009315	/	/	AY951755
<b><i>Hypoxylon sublenormandii</i></b>	<b>JF 13026 T</b>	<b>KM610291</b>	/	/	<b>KM610303</b>
<i>Hypoxylon teeravasati</i>	PUFD4	KY863509	MF385274	MG986895	MG986894
<i>Hypoxylon texense</i>	DSM:107928	MK287527	MK287538	MK287551	MK287564
<b><i>Hypoxylon texense</i></b>	<b>DSM 107933 T</b>	<b>MK287536</b>	<b>MK287548</b>	<b>MK287561</b>	<b>MK287574</b>
<i>Hypoxylon ticinense</i>	CBS 115271	JQ009317	KY610471	KY624272	AY951757

<i>Hypoxylon trugodes</i>	MUCL 54794	KF234422	KY610493	KY624282	KF300548
<i>Hypoxylon ulmophilum</i>	YMJ 350	JQ009320	/	/	AY951760
<i>Hypoxylon vogesiacum</i>	CBS 115273	KC968920	KY610417	KY624283	KX271275
<b><i>Hypoxylon wujiangense</i></b>	<b>GMBC0213 T</b>	<b>MT568854</b>	<b>MT568853</b>	<b>MT585802</b>	<b>MT572481</b>
<b><i>Hypoxylon wuzhishanense</i></b>	<b>FCATAS2708 T</b>	<b>OL467292</b>	<b>OL615104</b>	<b>OL584220</b>	<b>OL584227</b>
<b><i>Hypoxylon zangii</i></b>	<b>FCATAS4029 T</b>	<b>ON075423</b>	<b>ON075429</b>	<b>ON093247</b>	<b>ON093241</b>
<i>Jackrogersella cohaerens</i>	CBS 119126	KY610396	KY610497	KY624270	KY624314
<i>Jackrogersella multiformis</i>	CBS 119016	KC477234	KY610473	KY624290	KX271262
<i>Pyrenopolyporus hunteri</i>	MUCL 52673	KY610421	KY610472	KY624309	KU159530
<b><i>Pyrenopolyporus laminosus</i></b>	<b>MUCL 53305 T</b>	<b>KC968934</b>	<b>KY610485</b>	<b>KY624303</b>	<b>KC977292</b>
<i>Rhopalostroma angolense</i>	CBS 126414	KY610420	KY610459	KY624228	KX271277
<b><i>Rostrohypoxylon terebratum</i></b>	<b>CBS 119137 T</b>	<b>DQ631943</b>	<b>DQ840069</b>	<b>DQ631954</b>	<b>DQ840097</b>
<b><i>Ruwenzoria pseudoannulata</i></b>	<b>MUCL 51394 T</b>	<b>KY610406</b>	<b>KY610494</b>	<b>KY624286</b>	<b>KX271278</b>
<b><i>Thamnomycetes dendroidea</i></b>	<b>CBS 123578 T</b>	<b>FN428831</b>	<b>KY610467</b>	<b>KY624232</b>	<b>KY624313</b>
<i>Xylaria hypoxylon</i>	CBS 122620	KY610407	KY610495	KY624231	KX271279



**Table S3.** The names, isolate numbers, and corresponding GenBank accession numbers of the taxa used in Figure 5. The taxa produced in this study are indicated in red, and the type strains are indicated in bold with “T”.

Species name	Isolate No.	GenBank accession No.			
		ITS	<i>tefl-α</i>	<i>tub2</i>	CAL
<i>Diaporthe acuta</i>	PSCG 046	MK626958	/	MK691224	MK691125
<i>Diaporthe acutispora</i>	LC6161 T	KX986764	KX999155	KX999195	KX999274
<i>Diaporthe arecae</i>	CBS 161.64 T	KC343032	KC343758	KC344000	KC343274
<i>Diaporthe arengae</i>	CBS 114979 T	NR_111843	KC343760	KC344002	KC343276
<i>Diaporthe aseana</i>	MFLUCC 12-0299a T	NR_154920	KT459448	KT459432	KT459464
<i>Diaporthe australiana</i>	BRIP 66145 T	MN708222	MN696522	MN696530	/
<i>Diaporthe biconispora</i>	ZJUD62	KJ490597	KJ490476	KJ490418	MT898460
<i>Diaporthe ceratozambiae</i>	CBS 131306 T	JQ044420	/	/	/
<i>Diaporthe cercidis</i>	TJX65	MW341306	MW362968	MW491981	MW491970
<i>Diaporthe endocitricola</i>	ZHKUCC20-0013 T	MT355683	MT409337	MT409291	MT409313
<i>Diaporthe eucalyptorum</i>	MFLUCC 12-0306	KT459419	KT459453	KT459437	/
<i>Diaporthe eugeniae</i>	ASHM302	MK110368	MK117249	MK122781	/
<i>Diaporthe eugeniae</i>	ASHM298	MK110346	MK117246	MK122779	/
<i>Diaporthe eugeniae</i>	CBS 444.82 T	KC343098	KC343824	KC344066	KC343340
<i>Diaporthe fraxini-angustifoliae</i>	MFLUCC 15-0748	KT459428	KT459446	KT459430	KT459462
<i>Diaporthe fujianensis</i>	JZB320152	MW010215	MW205233	MW056011	/
<i>Diaporthe fusiformis</i>	JZB320157	MW010219	/	MW056015	/
<i>Diaporthe ganzhouensis</i>	CFCC 53087	MK432665	MK578139	MK578065	MK442985

<i>Diaporthe guangxiensis</i>	JZB320094 T	MK335772	MK523566	MK500168	MK736727
<i>Diaporthe heveae</i>	LGMF1631	MG976433	MK007529	MK007530	/
<i>Diaporthe hongheensis</i>	KUMCC 21-0458	OM001330	ON468650	ON468659	ON715009
<i>Diaporthe hongheensis</i>	KUMCC 21-0457 T	OM001331	ON468649	ON468658	ON715010
<i>Diaporthe hongkongensis</i>	ZJ10B1	KY433562	KY433571	/	/
<i>Diaporthe limonicola</i>	ZHKUCC20-0005	MT355675	MT409329	MT409283	MT409306
<i>Diaporthe limonicola</i>	ZHKUCC20-0006	MT355676	MT409330	MT409284	MT409307
<i>Diaporthe limonicola</i>	CPC 28200 T	MF418422	MF418501	MF418582	MF418256
<i>Diaporthe litchicola</i>	BRIP 54900 T	JX862533	JX862539	KF170925	/
<i>Diaporthe lithocarpus</i>	CGMCC:3.15175 T	KC153104	KC153095	KF576311	KF576236
<i>Diaporthe melitensis</i>	CPC 27873 T	MF418424	MF418503	MF418584	MF418258
<i>Diaporthe millettia</i>	GUCC 9167 T	MK303387	MK480609	MK460488	MK502086
<i>Diaporthe multigutullata</i>	CFCC 53095	MK432645	MK578121	MK578048	MK442967
<i>Diaporthe multigutullata</i>	CFCC 53096	MK432646	MK578122	MK578049	MK442968
<i>Diaporthe multigutullata</i>	ZJUD98 T	NR_158389	KJ490512	KJ490454	/
<i>Diaporthe musigena</i>	CBS 129519 T	KC343143	KC343869	KC344111	KC343385
<i>Diaporthe osmanthusis</i>	GUCC9165	MK398675	MK480610	MK502091	MK502087
<i>Diaporthe pandanicola</i>	MFLU 17-0607 T	NR_172400	/	MG646930	/
<i>Diaporthe pascoei</i>	BPPCA147	MK111091	MK117255	MK122790	/
<i>Diaporthe pascoei</i>	PBMR343	MK111092	MK117274	MK122808	/
<i>Diaporthe pascoei</i>	BRIP 54847 T	JX862532	JX862538	KF170924	/
<i>Diaporthe perijuncta</i>	CBS 109745 T	NR_147527	KC343898	KC344140	KC343414
<i>Diaporthe perseae</i>	CBS 151.73 T	KC343173	KC343899	KC344141	KC343415

<b><i>Diaporthe pescicola</i></b>	<b>MFLUCC 16-0105 T</b>	<b>KU557555</b>	<b>KU557623</b>	<b>KU557579</b>	<b>KU557603</b>
<i>Diaporthe phoenicicola</i>	CBS 161.64	MH858400	GQ250349	X275440	JX197432
<b><i>Diaporthe phragmitis</i></b>	<b>CBS 138897 T</b>	<b>KP004445</b>	<b>/</b>	<b>KP004507</b>	<b>/</b>
<i>Diaporthe podocarpi-macrophylli</i>	LC6197	KX986777	KX999170	KX999210	KX999279
<i>Diaporthe podocarpi-macrophylli</i>	CQJY3-1	MT877048	MT917080	MT874966	MT917067
<b><i>Diaporthe pseudomangiferae</i></b>	<b>CBS 101339 T</b>	<b>NR_111858</b>	<b>KC343907</b>	<b>KC344149</b>	<b>KC343423</b>
<b><i>Diaporthe pseudophoenicicola</i></b>	<b>CBS 462.69 T</b>	<b>KC343184</b>	<b>KC343910</b>	<b>KC344152</b>	<b>KC343426</b>
<b><i>Diaporthe pterocarp</i></b>	<b>MFLUCC 10-0571 T</b>	<b>JQ619899</b>	<b>JX275416</b>	<b>JX275460</b>	<b>JX275416</b>
<b><i>Diaporthe pterocarpicola</i></b>	<b>MFLUCC 10-0580a T</b>	<b>NR_111713</b>	<b>JX275403</b>	<b>JX275441</b>	<b>JX197433</b>
<i>Diaporthe salsuginosa</i>	NFCCI 4385	MN061372	MN184789	MN431500	/
<i>Diaporthe schimae</i>	CFCC 53103	MK432640	MK578116	MK578043	MK442962
<i>Diaporthe schimae</i>	CFCC 53104	MK432641	MK578117	MK578044	MK442963
<b><i>Diaporthe sennae</i></b>	<b>CFCC 51636 T</b>	<b>NR_152499</b>	<b>KY228885</b>	<b>KY228891</b>	<b>KY228875</b>
<i>Diaporthe sennae</i>	ZHKUCC20-0011	/	MT409335	MT409289	MT409311
<i>Diaporthe</i> sp.	MFLUCC 19-0102	MW192408	MW173088	/	MW294202
<i>Diaporthe taiwanensis</i>	NTUCC 18-105.2	MT241259	MT251201	MT251204	MT251198
<i>Diaporthe taiwanensis</i>	NTUCC 18-105.1	MT241257	MT251199	MT251202	MT251196
<b><i>Diaporthe taoicola</i></b>	<b>MFLUCC 16-0117 T</b>	<b>NR_154923</b>	<b>KU557635</b>	<b>KU557591</b>	<b>/</b>
<b><i>Diaporthe tectonigena</i></b>	<b>MFLUCC 12-0767 T</b>	<b>NR_147589</b>	<b>KU749371</b>	<b>KU743976</b>	<b>KU749358</b>
<b><i>Diaporthe undulata</i></b>	<b>LC8111 T</b>	<b>KY491546</b>	<b>KY491556</b>	<b>KY491566</b>	<b>/</b>
<b><i>Diaporthe vawdreyi</i></b>	<b>BRIP 57887a T</b>	<b>KR936126</b>	<b>KR936129</b>	<b>KR936128</b>	<b>/</b>
<i>Diaporthe viniferae</i>	JZB320072	MK341551	MK500108	MK500113	MK500120
<b><i>Diaporthe viniferae</i></b>	<b>JZB320071 T</b>	<b>MK341550</b>	<b>MK500107</b>	<b>MK500112</b>	<b>MK500119</b>

<i>Diaporthe xishuangbanica</i>	LC6707 T	KX986783	KX999175	KX999216	/
<i>Diaporthe xunwuensis</i>	CFCC 53085	MK432663	MK578137	MK578063	MK442983
<i>Diaporthe xunwuensis</i>	CFCC 53086	MK432664	MK578138	MK578064	MK442984
<i>Diaporthella corylina</i>	CBS 121124	KC343004	KC343730	KC343972	KC343246

Table S4. The names, isolate numbers, and corresponding GenBank accession numbers of the taxa used in Figure 7. The taxa produced in this study are indicated in red, and the type strains are indicated in bold with “T”.

Speciesname	Isolate No.	GenBank Accession No			
		ITS	LSU	SSU	<i>rpb1</i>
<i>Cyphellophora aestiva</i>	CBS 227.86	JQ766425	JQ766474	/	JQ766380
<i>Cyphellophora aestiva</i>	<b>CBS 228.86 T</b>	<b>MH861947</b>	<b>MH873637</b>	<b>NG_062863</b>	<b>JQ766381</b>
<i>Cyphellophora ambigua</i>	CMRP2859	MT075638	/	/	/
<i>Cyphellophora artocarpi</i>	CHCJHBJBLM	KP010367	KP122930	/	KP122920
<i>Cyphellophora attinorum</i>	<b>CBS 131958 T</b>	<b>KF928463</b>	<b>KF928527</b>	/	/
<i>Cyphellophora capiguarae</i>	<b>CBS 132767 T</b>	<b>KF928464</b>	<b>KF928528</b>	/	/
<i>Cyphellophora clematidis</i>	<b>CBS 144983 T</b>	<b>MK442577</b>	<b>MK442519</b>	/	/
<i>Cyphellophora eucalypti</i>	<b>CBS 124764 T</b>	<b>KC455238</b>	<b>KC455254</b>	<b>KC455297</b>	/
<i>Cyphellophora europaea</i>	CBS 101466	KC455246	KC455259	KC455303	/
<i>Cyphellophora filicis</i>	DP002A	MK404056	MK404052	MK404054	/
<i>Cyphellophora filicis</i>	<b>DP002B T</b>	<b>MK404057</b>	<b>MK404053</b>	<b>MK404055</b>	/
<i>Cyphellophora fusarioides</i>	CBS 130291	JQ766439	JQ766486	/	JQ766391

<i>Cyphellophora fusarioides</i>	MUCL 44033 T	KC455239	KC455252	KC455298	/
<i>Cyphellophora gamsii</i>	CPC 25867 T	KX228255	NG_067308	/	/
<i>Cyphellophora goniomatis</i>	CPC 37032 T	NR_166332	NG_068669	/	/
<i>Cyphellophora guyanensis</i>	CBS 124764	KF928477	KF928541	/	JQ766387
<i>Cyphellophora guyanensis</i>	CBS 125756	JQ766433	JQ766482	/	JQ766388
<i>Cyphellophora guyanensis</i>	CBS 126014	JQ766434	JQ766483	/	JQ766389
<i>Cyphellophora guyanensis</i>	CBS 126020	KF928475	KF928539	/	JQ766390
<i>Cyphellophora hongheensis</i>	KUMCC 21-0456	OM001332	OM001329	OM001337	ON468647
<i>Cyphellophora hongheensis</i>	KUMCC 21-0455 T	OM001338	OM001335	OM001340	ON468646
<i>Cyphellophora jingdongensis</i>	IFRDCC 2659 T	MF285234	MF285236	MF285235	/
<i>Cyphellophora laciniata</i>	CBS 190.61 T	MH858019	FJ358239	FJ358307	FJ358370
<i>Cyphellophora livistoniae</i>	CPC 19433 T	NR_111824	NG_042752	/	/
<i>Cyphellophora ludoviensis</i>	CMRP1317	KX434722	KX583708	/	/
<i>Cyphellophora musae</i>	GLGZXJ9B	/	KP122931	/	KP122923
<i>Cyphellophora musae</i>	GLZJXJ41 T	/	KP122932	/	KP122922
<i>Cyphellophora olivacea</i>	CBS 123.74 T	KC455248	NG_067280	NG_062865	/
<i>Cyphellophora oxyspora</i>	CBS 416.89	MH862181	MH873869	KF155208	/
<i>Cyphellophora oxyspora</i>	CBS 698.73 T	MH860790	NG_067405	NG_062866	/
<i>Cyphellophora pauciseptata</i>	CBS 284.85	MH861880	MH873568	/	JQ766421
<i>Cyphellophora phyllostachydis</i>	HLHNZWYZZ08 T	KP010371	KP122933	/	KP122924
<i>Cyphellophora pluriseptata</i>	CBS 109633	JQ766430	JQ766479	/	/
<i>Cyphellophora pluriseptata</i>	CBS 286.85 T	NR_111431	NG_067429	NG_062861	JQ766384
<i>Cyphellophora reptans</i>	CBS 113.85 T	NR_121346	NG_067426	NG_062867	/

<i>Cyphellophora sambuci</i>	CPC 39957 T	OK664711	OK663750	/	/
<i>Cyphellophora sessilis</i>	CBS 238.93	KF928459	KC455264	KC455309	KC455289
<i>Cyphellophora sessilis</i>	CBS 243.85 T	MH861875	MH873561	KC455308	KC455288
<i>Cyphellophora suttonii</i>	CBS 449.91 T	KC455243	KC455256	KC455300	JQ922030
<i>Cyphellophora vermispora</i>	CBS 228.86 T	KC455244	KC455257	KC455301	JQ766381
<i>Cyphellophora vietnamensis</i>	CBS 146924 T	LR814107	LR814108	/	/
<i>Exophiala equina</i>	CBS 127579	MH864585	MH876027	/	/
<i>Exophiala salmonis</i>	CBS 157.67 T	MH858932	MH870616	JN856020	/

Table S5. The names, isolate numbers, and corresponding GenBank accession numbers of the taxa used in Figure 9. The taxa produced in this study are indicated in red, and the type strains are indicated in bold with “T”.

Species	Isolate No.	GenBank Accession No		
		ITS	<i>tef-a</i>	<i>tub2</i>
<i>Botryosphaeria stevensii</i>	CMW 7060	AY236955	AY236904	AY236933
<i>Botryosphaeria obtusa</i>	CBS 112555 T	AY259094	AY573220	/
<i>Lasiodiplodia acaciae</i>	CBS:136434 T	MT587421	MT592133	MT592613
<i>Lasiodiplodia americana</i>	CFCC50065 T	KP217059	KP217067	KP217075
<i>Lasiodiplodia aquilariae</i>	CGMCC 3.18471	KY783442	KY848600	/
<i>Lasiodiplodia avicenniae</i>	CMW41467 T	KP860835	KP860680	KP860758
<i>Lasiodiplodia avicenniae</i>	LAS199	KU587957	KU587868	KU587868
<i>Lasiodiplodia avicenniarum</i>	MFLUCC17-2591 T	MK347777	MK340867	/
<i>Lasiodiplodia brasiliensis</i>	CBS:120395	MT587423	MT592135	MT592615
<i>Lasiodiplodia brasiliensis</i>	CBS:115447	MT587422	MT592134	MT592614

<i>Lasiodiplodia bruguierae</i>	CMW42480	KP860832	KP860677	KP860755
<b><i>Lasiodiplodia bruguierae</i></b>	<b>CMW 41470 T</b>	<b>KP860833</b>	<b>KP860678</b>	<b>KP860756</b>
<i>Lasiodiplodia caatinguensis</i>	IBL381	KT154757	KT154751	KT154764
<b><i>Lasiodiplodia caatinguensis</i></b>	<b>CMM 1325 T</b>	<b>KT154760</b>	<b>KT008006</b>	<b>KT154767</b>
<i>Lasiodiplodia chinensis</i>	CGMCC 3.18044	KX499875	KX499913	KX499988
<i>Lasiodiplodia chinensis</i>	CGMCC3.18066	KX499899	KX499937	KX500012
<i>Lasiodiplodia cinnamomi</i>	CFCC 51998	MG866029	MH236800	MH236798
<i>Lasiodiplodia cinnamomi</i>	CFCC 51997	MG866028	MH236799	MH236797
<i>Lasiodiplodia citricola</i>	IRAN1521C	GU945353	GU945339	KU887504
<b><i>Lasiodiplodia citricola</i></b>	<b>IRAN1522C T</b>	<b>GU945354</b>	<b>GU945340</b>	<b>KU887505</b>
<i>Lasiodiplodia clavispora</i>	CGMCC 3.19595	MK802165	/	MK816338
<b><i>Lasiodiplodia clavispora</i></b>	<b>CGMCC 3.19594 T</b>	<b>MK802166</b>	/	<b>MK816339</b>
<i>Lasiodiplodia crassisporea</i>	WAC12533	DQ103550	DQ103557	KU887506
<i>Lasiodiplodia crassisporea</i>	CMM 4583	MG954353	MG979519	MG979551
<b><i>Lasiodiplodia crassisporea</i></b>	<b>CMW 13488 T</b>	<b>DQ103552</b>	<b>DQ103559</b>	<b>KU887507</b>
<i>Lasiodiplodia curvata</i>	CGMCC 3.18456	KY783437	KY848596	KY848529
<i>Lasiodiplodia curvata</i>	CGMCC 3.18476	KY783443	KY848601	KY848532
<i>Lasiodiplodia egyptiaca</i>	CBS:167.28	MT587425	MT592136	MT592618
<b><i>Lasiodiplodia endophytica</i></b>	<b>MFLUCC 18-1121 T</b>	<b>MK501838</b>	<b>MK584572</b>	<b>MK550606</b>
<i>Lasiodiplodia euphorbicola</i>	CMW33353	KU887152	KU887028	KU887456
<i>Lasiodiplodia euphorbicola</i>	CMW36077	KU887157	KU887035	KU887473
<i>Lasiodiplodia euphorbicola</i>	CMM 3609	KU887149	KU887026	KU887455
<i>Lasiodiplodia euphorbicola</i>	CMW 33350	KU887187	KU887063	KU887494
<i>Lasiodiplodia exigua</i>	BL184	KJ638318	KJ638337	/
<b><i>Lasiodiplodia exigua</i></b>	<b>CBS 137785 T</b>	<b>NR_147353</b>	<b>KJ638336</b>	<b>KU887509</b>
<b><i>Lasiodiplodia fujianensis</i></b>	<b>CGMCC 3.19593 T</b>	<b>MK802164</b>	<b>MK887178</b>	<b>MK816337</b>

<i>Lasiodiplodia gilanensis</i>	IRAN 1523C	GU945352	GU945341	KU887510
<b><i>Lasiodiplodia gilanensis</i></b>	<b>IRAN 1501C T</b>	<b>GU945351</b>	<b>GU945342</b>	<b>KU887511</b>
<i>Lasiodiplodia gonubiensis</i>	CMW43763	KU587955	KU587944	KU587865
<i>Lasiodiplodia gonubiensis</i>	CMW43762	KU587954	KU587943	KU587864
<i>Lasiodiplodia gonubiensis</i>	CMW 14078	AY639594	DQ103567	EU673126
<b><i>Lasiodiplodia gonubiensis</i></b>	<b>CMW 14077 T</b>	<b>AY639595</b>	<b>DQ103566</b>	<b>DQ458860</b>
<i>Lasiodiplodia gravistriata</i>	CMM 4565	KT250947	KT266812	/
<i>Lasiodiplodia gravistriata</i>	CMM 4564	KT250949	KT250950	/
<i>Lasiodiplodia henanica</i>	CGMCC 3.19176	MH729351	MH729357	MH729360
<i>Lasiodiplodia hormozganensis</i>	CBS:133510	MT587426	MT592137	MT592620
<i>Lasiodiplodia hormozganensis</i>	CBS:177.89	KX464134	KX464627	KX464898
<i>Lasiodiplodia hormozganensis</i>	IRAN 1498C	GU945356	GU945344	KU887514
<i>Lasiodiplodia hyalina</i>	BJFU DZP160121-9	/	KY751302	KY751299
<b><i>Lasiodiplodia hyalina</i></b>	<b>CGMCC3.17975 T</b>	<b>KX499879</b>	<b>KX499917</b>	<b>KX499992</b>
<b><i>Lasiodiplodia indica</i></b>	<b>IBP 01 T</b>	<b>KM376151</b>	/	/
<i>Lasiodiplodia iraniensis</i>	IRAN 1502C	GU945347	GU945335	KU887517
<i>Lasiodiplodia iraniensis</i>	IRAN 1520C	GU945348	GU945336	KU887516
<b><i>Lasiodiplodia irregularis</i></b>	<b>GuoLD01673 T</b>	<b>KY783472</b>	<b>KY848610</b>	<b>KY848553</b>
<i>Lasiodiplodia jatrophiicola</i>	CMW 36237	KU887121	KU886998	KU887499
<i>Lasiodiplodia jatrophiicola</i>	CMW 36239	KU887123	KU887000	KU887501
<i>Lasiodiplodia jatrophiicola</i>	CBS:111005	MT587430	MT592142	MT592624
<i>Lasiodiplodia jatrophiicola</i>	CBS:111008	MT587431	MT592143	MT592625
<b><i>Lasiodiplodia krabiensis</i></b>	<b>MFLU 17-2617 T</b>	<b>MN047093</b>	<b>MN077070</b>	/
<i>Lasiodiplodia laeliocattleyae</i>	BOT 29	JN814401	JN814428	/
<i>Lasiodiplodia laeliocattleyae</i>	CMW35895	KU887095	KU886973	KU887467
<b><i>Lasiodiplodia laeliocattleyae</i></b>	<b>CBS 130992 T</b>	<b>JN814397</b>	<b>JN814424</b>	<b>KU887508</b>



<i>Lasiodiplodia laosensis</i>	CGMCC 3.18473	KY783450	KY848603	KY848536
<b><i>Lasiodiplodia laosensis</i></b>	<b>CGMCC 3.18464 T</b>	<b>KY783471</b>	<b>KY848609</b>	<b>KY848552</b>
<i>Lasiodiplodia lignicola</i>	CGMCC 3.18449	KY783466	KY848619	/
<i>Lasiodiplodia lignicola</i>	CBS 134112	/	KU887003	KT852958
<i>Lasiodiplodia lignicola</i>	MFLUCC 11-0656	JX646798	JX646863	JX646846
<b><i>Lasiodiplodia macroconidica</i></b>	<b>CGMCC 3.18479 T</b>	<b>KY783438</b>	<b>KY848597</b>	<b>KY848530</b>
<b><i>Lasiodiplodia macrospora</i></b>	<b>CMM 3833 T</b>	<b>KF234557</b>	<b>KF226718</b>	<b>KF254941</b>
<i>Lasiodiplodia magnoliae</i>	MFLUCC 18-0948	MK499387	MK568537	MK521587
<i>Lasiodiplodia mahajangana</i>	CMW 27818	FJ900596	FJ900642	FJ900631
<b><i>Lasiodiplodia mahajangana</i></b>	<b>CMW 27801 T</b>	<b>FJ900595</b>	<b>FJ900641</b>	<b>FJ900630</b>
<i>Lasiodiplodia margaritacea</i>	CBS 138291	KP872322	KP872351	KP872381
<i>Lasiodiplodia margaritacea</i>	CBS 138289	KP872320	KP872349	KP872379
<b><i>Lasiodiplodia margaritacea</i></b>	<b>CBS 122519 T</b>	<b>EU144050</b>	<b>EU144065</b>	<b>KU887520</b>
<i>Lasiodiplodia mediterranea</i>	CBS 137784	KJ638311	KJ638330	KU887522
<b><i>Lasiodiplodia mediterranea</i></b>	<b>CBS 137783 T</b>	<b>KJ638312</b>	<b>KJ638331</b>	<b>KU887521</b>
<b><i>Lasiodiplodia microcondia</i></b>	<b>CGMCC 3.18485 T</b>	<b>KY783441</b>	<b>KY848614</b>	/
<i>Lasiodiplodia missouriana</i>	UCD 2193MO	HQ288225	HQ288267	HQ288304
<b><i>Lasiodiplodia missouriana</i></b>	<b>UCD 2199MO T</b>	<b>HQ288226</b>	<b>HQ288268</b>	<b>HQ288305</b>
<b><i>Lasiodiplodia mitidjana</i></b>	<b>ALG111 T</b>	<b>MN104115</b>	/	/
<i>Lasiodiplodia nanpingensis</i>	CGMCC 3.19596	MK802167	/	MK816340
<i>Lasiodiplodia nanpingensis</i>	CGMCC 3.19597	MK802168	/	MK816341
<b><i>Lasiodiplodia pandanicola</i></b>	<b>MFLUCC 16-0265 T</b>	<b>MH275068</b>	<b>MH412774</b>	/
<i>Lasiodiplodia paraphysoides</i>	CGMCC 3.19174	MH729349	MH729355	MH729358
<i>Lasiodiplodia paraphysoides</i>	CGMCC 3.19175	MH729350	MH729356	MH729359
<i>Lasiodiplodia parva</i>	CBS 494.78	EF622084	EF622064	EU673114
<b><i>Lasiodiplodia parva</i></b>	<b>CBS 456.78 T</b>	<b>EF622083</b>	<b>EF622063</b>	<b>KU887523</b>

<i>Lasiodiplodia plurivora</i>	STE-U 4583	AY343482	EF445396	KU887525
<i>Lasiodiplodia pontae</i>	CMM 1277	KT151794	KT151791	KT151797
<i>Lasiodiplodia pontae</i>	CBS:117454	MT587432	MT592144	MT592626
<i>Lasiodiplodia pseudotheobromae</i>	CSF5802	MT028604	MT028770	MT028936
<i>Lasiodiplodia pseudotheobromae</i>	CGMCC 3.18068	KX499902	KX499940	KX500015
<i>Lasiodiplodia pseudotheobromae</i>	CSF6050	MT028603	MT028769	MT028935
<i>Lasiodiplodia pseudotheobromae</i>	HKAS 122658	OL989258	ON468648	ON468654
<b><i>Lasiodiplodia pseudotheobromae</i></b>	<b>CBS 116459 T</b>	<b>EF622077</b>	<b>EF622057</b>	<b>EU673111</b>
<i>Lasiodiplodia pyriformis</i>	CBS 121771	EU101308	EU101353	KU887528
<b><i>Lasiodiplodia pyriformis</i></b>	<b>CBS 121770 T</b>	<b>EU101307</b>	<b>EU101352</b>	<b>KU887527</b>
<i>Lasiodiplodia rubropurpurea</i>	WAC12536	DQ103554	DQ103572	KP872425
<b><i>Lasiodiplodia rubropurpurea</i></b>	<b>WAC12535 T</b>	<b>DQ103553</b>	<b>DQ103571</b>	<b>EU673136</b>
<i>Lasiodiplodia</i> sp.1	CBS 125266	MT587436	MT592148	KP872409
<i>Lasiodiplodia</i> sp.2	GuoLD01859	KY783469	KY848608	KY848550
<i>Lasiodiplodia sterculiae</i>	CBS:127106	MN555400	MT592146	MT592631
<b><i>Lasiodiplodia sterculiae</i></b>	<b>CBS 342.78 T</b>	<b>KX464140</b>	<b>KX464634</b>	<b>KX464908</b>
<i>Lasiodiplodia subglobosa</i>	CMM 4046	KF234560	KF226723	KF254944
<b><i>Lasiodiplodia subglobosa</i></b>	<b>CMM 3872 T</b>	<b>KF234558</b>	<b>KF226721</b>	<b>KF254942</b>
<b><i>Lasiodiplodia swieteniae</i></b>	<b>MFLUCC 18-0244 T</b>	<b>MK347789</b>	<b>MK340870</b>	<b>MK412877</b>
<i>Lasiodiplodia syzygii</i>	MFLUCC 19-0257	MT990531	MW016943	MW014331
<i>Lasiodiplodia syzygii</i>	GUCC 9719.2	MW081991	MW087101	MW087104
<i>Lasiodiplodia syzygii</i>	GUCC 9719.4	MW081993	MW087103	MW087106
<b><i>Lasiodiplodia tenuiconidia</i></b>	<b>CGMCC3.18061 T</b>	<b>KX499889</b>	<b>KX499927</b>	<b>KX500002</b>
<i>Lasiodiplodia thailandica</i>	CBS 138653	KM006433	KM006464	/
<i>Lasiodiplodia thailandica</i>	CBS 138760	KJ193637	KJ193681	/
<i>Lasiodiplodia thailandica</i>	DZP160119-9	KY676788	KY676797	KY676794

<i>Lasiodiplodia thailandica</i>	DZP160123-13	KY676789	KY676798	KY676795
<i>Lasiodiplodia theobromae</i>	CBS 111530	EF622074	EF622054	KU887531
<i>Lasiodiplodia theobromae</i>	HKAS 122660	OM030349	ON468652	ON468661
<i>Lasiodiplodia theobromae</i>	HKAS 122659	OM030345	ON468653	ON468662
<i>Lasiodiplodia theobromae</i>	CBS:339.90	KX464147	KX464641	KX464916
<b><i>Lasiodiplodia theobromae</i></b>	<b>CBS 164.96 T</b>	<b>AY640255</b>	<b>AY640258</b>	<b>KU887532</b>
<b><i>Lasiodiplodia tropica</i></b>	<b>CGMCC 3.18477 T</b>	<b>KY783454</b>	<b>KY848616</b>	<b>KY848540</b>
<i>Lasiodiplodia vaccinii</i>	CGMCC 3.19023	MH330319	MH330329	MH330326
<i>Lasiodiplodia vaccinii</i>	CGMCC3.19256	MK157139	MK157166	MK157157
<i>Lasiodiplodia vaccinii</i>	CGMCC3.19255	MK157138	MK157165	MK157156
<i>Lasiodiplodia venezuelensis</i>	WAC12540	DQ103548	DQ103569	KP872427
<b><i>Lasiodiplodia venezuelensis</i></b>	<b>WAC 12539 T</b>	<b>DQ103547</b>	<b>DQ103568</b>	<b>KU887533</b>
<i>Lasiodiplodia viticola</i>	UCD2604MO	HQ288228	HQ288270	HQ288307
<b><i>Lasiodiplodia viticola</i></b>	<b>UCD 2553AR T</b>	<b>HQ288227</b>	<b>HQ288269</b>	<b>HQ288306</b>
<i>Lasiodiplodia vitis</i>	CBS 124060	KX464148	KX464642	KX464917

**Table S6.** The names, isolate numbers, and corresponding GenBank accession numbers of the taxa used in Figure 12. The taxa produced in this study are indicated in red, and the type strains are indicated in bold with “T”.

Species name	Isolate No.	GenBank Accession No.		
		ITS	LSU	<i>tef1-a</i>
<i>Aplosporella africana</i>	CBS 121777	EU101315	EU101380	EU101360
<i>Aplosporella africana</i>	CBS 121779	EU101317	EU101382	EU101362
<i>Aplosporella artocarpi</i>	KUMCC 21-0460	OL989220	OL989222	ON468651

<i>Aplosporella artocarp</i>	<b>B0391 T</b>	<b>KM006450</b>	/	<b>KM006481</b>
<i>Aplosporella chromolaenae</i>	<b>MFLUCC 17-1517 T</b>	<b>MT214340</b>	<b>NG_070506</b>	/
<i>Aplosporella ginkgonis</i>	CFCC 52442	MH133916	MH133933	MH133950
<i>Aplosporella ginkgonis</i>	CFCC 52443	MH133917	MH133934	MH133951
<i>Aplosporella ginkgonis</i>	CFCC 52444	MH133918	MH133935	MH133952
<i>Aplosporella ginkgonis</i>	<b>CFCC 89661 T</b>	<b>KM030583</b>	<b>KM030590</b>	<b>KM030597</b>
<i>Aplosporella ginkgonis</i>	CFCC 89660	KM030582	KM030589	KM030596
<i>Aplosporella hesperidica</i>	CBS 208.37	MH867398	/	KX464552
<i>Aplosporella hesperidica</i>	CBS:732.79	KX464083	KX464239	KX464553
<i>Aplosporella hesperidica</i>	<b>MFLUCC:17-1518 T</b>	<b>MT214341</b>	<b>MT214435</b>	/
<i>Aplosporella javeedii</i>	CFCC 50054	KP208840	KP208843	KP208846
<i>Aplosporella javeedii</i>	CFCC 50053	KP208839	KP208842	KP208845
<i>Aplosporella javeedii</i>	CFCC 50052	KP208838	KP208841	KP208844
<i>Aplosporella javeedii</i>	<b>CFCC 89657 T</b>	<b>KM030579</b>	<b>KM030586</b>	<b>KM030593</b>
<i>Aplosporella macropycnidia</i>	CGMCC3.17726	KT343649	/	KX011177
<i>Aplosporella macropycnidia</i>	CGMCC3.17727	KT343647	/	KX011175
<i>Aplosporella macropycnidia</i>	<b>CGMCC3.17725 T</b>	<b>KT343648</b>	/	<b>KX011176</b>
<i>Aplosporella papillata</i>	CBS 121781	EU101329	EU101384	EU101374
<i>Aplosporella papillata</i>	CBS 121782	EU101330	EU101385	EU101375
<i>Aplosporella papillata</i>	<b>CBS 121780 T</b>	<b>EU101328</b>	<b>NG_070359</b>	<b>EU101373</b>
<i>Aplosporella prunicola</i>	STE-U 6326	EF564375	EF564377	/
<i>Aplosporella prunicola</i>	STE-U 6327	EF564376	EF564378	/
<i>Aplosporella prunicola</i>	<b>CBS 121167 T</b>	<b>KF766147</b>	/	/
<i>Aplosporella thailandica</i>	<b>MFLU 16-0615 T</b>	<b>KX423536</b>	/	<b>KX423537</b>
<i>Aplosporella yalgorensis</i>	MUCC 511	EF591926	EF591943	EF591977
<i>Aplosporella yalgorensis</i>	<b>MUCC 512 T</b>	<b>EF591927</b>	<b>EF591944</b>	<b>EF591978</b>

<i>Saccharata proteae</i>	CBS 115206 T	KF766226	GU357753	GU349030
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Table S7. The names, isolate numbers, and corresponding GenBank accession numbers of the taxa used in Figure 16. The taxa produced in this study are indicated in red, and the type strains are indicated in bold with “T”.

Species name	Isolate No.	GenBank Accession No			
		ITS	LSU	SSU	<i>tub2</i>
<i>Jattaea Algeriensis</i>	STE-U 6201	EU367446	EU367456	EU367462	EU367466
<i>Pleurostoma hongkongense</i>	HKU 44 T	MT153150	NG_073830	MT158344	MT501300
<i>Pleurostoma ochraceum</i>	CBS 131321 T	MT153175	MT158397	MT158370	JX073271
<i>Pleurostoma ootheca</i>	HKAS 122679	OM017217	OM017219	OM017218	ON468660
<i>Pleurostoma ootheca</i>	CBS 115329	MH862984	MH874544	MT158369	MT501325
<i>Pleurostoma repens</i>	CBS 294.39 T	NR_135925	MT158398	NG_062675	MT501327
<i>Pleurostoma richardsiae</i>	UAMH 8654	MT153167	MT158388	MT158361	MT501317
<i>Pleurostoma richardsiae</i>	UAMH 8335	MT153166	MT158387	MT158360	MT501316
<i>Pleurostoma richardsiae</i>	UAMH 5056	MT153165	MT158386	MT158359	MT501315
<i>Pleurostoma richardsiae</i>	UAMH 5058	MT153164	MT158385	MT158358	MT501314
<i>Pleurostoma richardsiae</i>	UAMH 5052	MT153163	MT158384	MT158357	MT501313
<i>Pleurostoma richardsiae</i>	UAMH 4377	MT153162	MT158383	MT158356	MT501312
<i>Pleurostoma richardsiae</i>	UAMH 10452	MT153161	MT158382	MT158355	MT501311
<i>Pleurostoma richardsiae</i>	UAMH 10082	MT153160	MT158381	MT158354	MT501310
<i>Pleurostoma richardsiae</i>	NCPF 2752	MT153172	MT158393	MT158366	MT501322
<i>Pleurostoma richardsiae</i>	NCPF 7565	MT153171	MT158392	MT158365	MT501321

<i>Pleurostoma richardsiae</i>	NCPF 2707	MT153170	MT158391	MT158364	MT501320
<i>Pleurostoma richardsiae</i>	NCPF 2961	MT153169	MT158390	MT158363	MT501319
<i>Pleurostoma richardsiae</i>	NCPF 2765	MT153168	MT158389	MT158362	MT501318
<i>Pleurostoma richardsiae</i>	IFM 63541	MT153173	MT158395	MT158368	MT501324
<i>Pleurostoma richardsiae</i>	IFM 63001	MT153159	MT158380	MT158353	MT501309
<i>Pleurostoma richardsiae</i>	IFM 4926	MT153158	MT158379	MT158352	MT501308
<i>Pleurostoma richardsiae</i>	IFM 41579	MT153157	MT158378	MT158351	MT501307
<b><i>Pleurostoma richardsiae</i></b>	<b>CBS 270.33 T</b>	<b>MT153151</b>	<b>MH866889</b>	<b>NG_062674</b>	<b>MT501301</b>
<i>Pleurostoma richardsiae</i>	CBS 483.80	MT153155	MT158377	MT158349	MT501305
<i>Pleurostoma richardsiae</i>	CBS 506.90	MT153156	MT505716	MT505714	MT501306
<i>Pleurostoma richardsiae</i>	CBS 406.93	MT153154	MT158376	MT158348	MT501304
<i>Pleurostoma richardsiae</i>	CBS 271.66	NR_135933	MT158394	MT158367	MT501323

## Supplementary information S1

The 97 strains are included in the combined gene analysis with 1157 total character including gaps (ITS: 1–678 bp,  $\beta$ -tubulin: 679–1157 bp). Tree topology of the ML analysis was similar to the BI. The matrix had distinct alignment patterns, with the final ML optimization likelihood value of -15128.940737 (ln). All free model parameters were estimated by the RAxML model, with 854 distinct alignment patterns and 34.25% of undetermined characteristics or gaps. Estimated base frequencies were as follows: A = 0.225249, C = 0.265998, G = 0.234520, T = 0.274233, with substitution rates AC = 1.081904, AG = 3.209457, AT = 1.396424, CG = 0.972402, CT = 4.022213, GT = 1.000000. The gamma distribution shape parameter alpha = 0.626180 and the Tree-Length = 6.028220. The final average standard deviation of split frequencies at the end of total MCMC generations was calculated as 0.009873 in BI analysis. (Figure 1).

## Supplementary information S2

The 114 strains are included in the combined gene analysis with 4343 total characters including gaps (LSU: 1–849 bp,  $\beta$ -tubulin: 850–2681 bp, ITS: 2682–3269 bp, *rpb2*: 3270–4343 bp). Tree topology of the ML analysis was similar to the BI. The matrix had distinct alignment patterns, with the final ML optimization likelihood value of -89990.012031 (ln). All free model parameters were estimated by RAxML model, with 2653 distinct alignment patterns and 32.57% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.239087, C = 0.268334, G = 0.251684, T = 0.240895, with substitution rates AC = 1.249855, AG = 4.147667, AT = 1.421319, CG = 0.936661, CT = 6.234325, GT = 1.000000. The gamma distribution shape parameter alpha = 0.899968 and the Tree-Length = 11.773179. The final average standard deviation of split frequencies at the end of total MCMC generations was calculated as 0.0098765 in BI analysis (Figure 3).

## Supplementary information S3

The 68 strains are included in the combined gene analysis with 2163 total characters including gaps (ITS: 1–574 bp, *tefl- $\alpha$* : 575–934 bp,  $\beta$ -tubulin: 935–1677 bp, CAL: 1678–2163 bp). The tree topology of the ML analysis was similar to the BI. The matrix had distinct alignment patterns, with the final ML optimization likelihood value of -18655.070841 (ln). All free model parameters were estimated by RAxML model, with 1207 distinct alignment patterns and 22.01% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.222883, C = 0.315096, G = 0.234336, T = 0.227685, with substitution rates AC = 1.504522, AG = 3.896321, AT = 1.359487, CG = 1.091388, CT = 5.495981, GT = 1.000000. The gamma distribution shape parameter alpha = 0.618776 and the Tree-Length = 3.289590. The final average standard deviation of split frequencies at the end of total MCMC generations was calculated as 0.009975 in BI analysis (Figure 5).

## Supplementary information S4

The 43 strains are included in the combined gene analysis with 3239 total characters including gaps (LSU: 1–899 bp, SSU: 900–1869 bp, ITS: 1870–2513 bp, *rpb1*: 2514–3239 bp). The tree topology of the ML analysis was similar to the BI. The matrix had distinct alignment patterns, with the final ML optimization likelihood value of -14760.740041 (ln). All free model parameters were estimated by the RAxML model, with 874 distinct alignment patterns and 36% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.248563, C = 0.239637, G = 0.277107, T = 0.234693, with substitution rates AC = 2.518026, AG = 3.753497, AT = 3.014914, CG = 1.974550, CT = 10.451143, GT = 1.000000. The gamma distribution shape parameter alpha = 0.142975 and the Tree-Length = 2.542539. The final average standard deviation of split frequencies at the end of total MCMC generations was calculated as 0.009941 in BI analysis (Figure 7).

### **Supplementary information S5**

The 129 strains are included in the combined gene analyses with 1280 total characters including gaps (ITS: 1–524 bp,  $\beta$ -tubulin: 525–948 bp, *tefl- $\alpha$* : 949–1280). The tree topology of the ML analysis was similar to the BI. The matrix had distinct alignment patterns, with the final ML optimization likelihood value of -6076.750023 (ln). All free model parameters were estimated by the RAxML model, with 459 distinct alignment patterns and 15.08% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.206462, C = 0.307393, G = 0.255825, T = 0.230320, with substitution rates AC = 0.884829, AG = 3.200275, AT = 1.096972, CG = 1.056166, CT = 4.178329, GT = 1.000000. The gamma distribution shape parameter alpha = 0.658513 and the Tree-Length = 0.992396. The final average standard deviation of split frequencies at the end of total MCMC generations was calculated as 0.009654 in BI analysis (Figure 9).

### **Supplementary information S6**

The 30 strains are included in the combined gene analyses with 1501 total characters including gaps (LSU: 1–857 bp, ITS: 858–1162 bp, *tefl- $\alpha$* : 1163–1501 bp). The tree topology of the ML analysis was similar to the BI. The matrix had distinct alignment patterns, with the final ML optimization likelihood value of -5432.091532 (ln). All free model parameters were estimated by the RAxML model, with 361 distinct alignment patterns and 24.98% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.222215, C = 0.258363, G = 0.272308, T = 0.247114, with substitution rates AC = 1.739870, AG = 4.289736, AT = 1.814791, CG = 2.163902, CT = 6.443658, GT = 1.000000. The gamma distribution shape parameter alpha = 0.462895 and the Tree-Length = 2.612554. The final average standard deviation of split frequencies at the end of total MCMC generations was calculated as 0.009881 in BI analysis (Figure 12).

### **Supplementary information S7**



The 28 strains are included in the combined gene analysis with 2648 total characters including gaps (LSU: 1–565 bp, SSU: 566–1593 bp, ITS: 1594–2175 bp,  $\beta$ -tubulin: 2176–2648 bp). The tree topology of the ML analysis was similar to the BI. The matrix had distinct alignment patterns, with the final ML optimization likelihood value of -7526.761364 (ln). All free model parameters were estimated by the RAxML model, with 412 distinct alignment patterns and 5.23% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.236380, C = 0.264724, G = 0.279019, T = 0.219877, with substitution rates AC = 1.753295, AG = 2.247977, AT = 1.304010, CG = 1.106293, CT = 6.505394, GT = 1.000000. The gamma distribution shape parameter alpha = 0.443058 and the Tree-Length = 0.653975. The final average standard deviation of split frequencies at the end of total MCMC generations was calculated as 0.009836 in BI analysis (Figure 16).