

Morphology Characterization, Molecular Phylogeny, and Pathogenicity of *Diaporthe passifloricola* on *Citrus reticulata* cv. *Nanfengmiju* in Jiangxi Province, China

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Supplementary Material

Table S1. nucleotide substitution models, MP and ML alignment properties.

Region/gene ^a		ITS	TUB	TEF	HIS	CAL
No. of taxa analyzed		101	88	89	58	58
AIC nucleotide substitution model		HKY+I+G	HKY+I+G	HKY+I+G	GTR+I+G	HKY+I+G
MP	Characters included (with gaps)	611	868	527	581	578
	Invariable characters	375	456	221	371	275
	Parsimony informative characters	130	286	249	147	224
	Uninformative variable characters	106	126	57	63	79
	MP Tree length	763	1,236	1428	831	813
	Consistency index (CI)	0.446	0.513	0.432	0.569	0.450
	Retention index (RI)	0.687	0.764	0.819	0.795	0.662
	Rescaled consistency index (RC)	0.306	0.392	0.354	0.453	0.298
	Homoplasy index (HI)	0.554	0.487	0.568	0.431	0.550
ML	Matrix data distinct alignment patterns	305	533	406	268	359
	Proportion of gaps and completely undetermined characters (%)	11.00	31.29	35.05	19.62	13.21
	Final ML optimization likelihood value	−4488.074972	−7609.877475	−7162.092053	−4451.580737	−5109.256642
	ML Tree Length	7.522317	2.205523	5.012763	3.123529	1.855683
	Gamma distribution shape parameter α	0.332481	1.513512	2.776265	1.070465	2.831607
	Estimated base frequencies					
	: A	0.246158	0.194971	0.220438	0.185957	0.196481
	: C	0.268463	0.362216	0.324573	0.393657	0.306183
	: G	0.256610	0.227951	0.206457	0.225053	0.266316
	: T	0.228769	0.214862	0.248531	0.195334	0.231020
	: A-C	1.099693	0.844106	1.626526	1.407074	1.255762
	: A-G	5.529640	4.296600	3.886337	3.716687	4.167474
	: A-T	1.419461	0.921182	1.332342	1.708299	1.076839
	: C-G	0.955221	0.970776	1.347249	1.234273	1.143587
	: C-T	9.669130	3.773201	5.002268	6.366428	4.537714
	: G-T	1.000000	1.000000	1.000000	1.000000	1.000000

^a ITS: nuclear ribosomal internal transcribed spacer regions; TUB: beta-tubulin gene; TEF: translation elongation factor 1- α gene; HIS: histone-3 gene; and CAL: calmodulin gene.

Table S2. Polymorphic nucleotides in ITS, TUB, TEF, and CAL sequences of *D. passifloricola*, *D. durionigene*, and *D. rosae*.

Species	Isolates ^a	ITS													
		13	52	91	105	106	117	119	120	121	124	125	138	203	416
<i>D. passifloricola</i>	CBS 141329	C	C	T	C	C	T	G	T	G	A	A	G	–	G
	NFIF-3-11	–	T	•	T	A	•	•	•	•	•	•	A	–	•
	NFIF-3-19	–	T	•	T	A	•	•	•	•	•	•	A	–	•

<i>D. durionigene</i>	<i>NFIF-3-21</i>	–	T	•	T	A	•	•	•	•	•	•	A	–	•
	VTCC 930005	–	–	C	T	A	C	C	–	–	T	G	A	–	•
	KCSR1906.7	–	–	C	T	A	C	C	–	–	T	G	A	–	•
<i>D. rosae</i>	MFLUCC 17-2658	T	T	C	•	A	C	C	–	–	T	G	A	A	A
	MFLUCC 17-2574	–	T	•	T	A	C	C	–	–	T	G	A	•	•
	MFLUCC 18-0354	–	T	•	T	A	C	C	–	–	T	G	A	•	•
Species	Isolates ^a	TUB				TEF									
		124	133	276	377	69	227	344	346						
<i>D. passifloricola</i>	CBS 141329	A	A	C	C	Sequence not available									
	<i>NFIF-3-11</i>	G	G	•	T	–	G	T	C						
	<i>NFIF-3-19</i>	G	G	•	T	A	•	•	•						
	<i>NFIF-3-21</i>	G	G	•	T	–	•	•	•						
<i>D. durionigene</i>	VTCC 930005	G	G	•	T	–	•	–	–						
	KCSR1906.7	–	•	•	•	–	•	–	–						
<i>D. rosae</i>	MFLUCC 17-2658	–	•	T	T	Sequence not available									
	MFLUCC 17-2574	–	•	T	T	–	C	C	A						
	MFLUCC 18-0354	–	•	T	T	–	C	C	A						
Species	Isolates ^a	CAL													
		67	198	205	208	217	225	251	395	443	446	503			
<i>D. passifloricola</i>	CBS 141329	Sequence not available													
	<i>NFIF-3-11</i>	C	T	A	A	T	A	G	C	T	T	A			
	<i>NFIF-3-19</i>	•	•	•	•	•	•	•	•	•	•	•			
	<i>NFIF-3-21</i>	•	•	•	•	•	•	•	•	•	•	•			
<i>D. durionigene</i>	VTCC 930005	Sequence not available													
	KCSR1906.7	Sequence not available													
<i>D. rosae</i>	MFLUCC 17-2658	T	C	C	G	C	G	A	T	C	–	G			
	MFLUCC 17-2574	Sequence not available													
	MFLUCC 18-0354	Sequence not available													

^a Isolates in this study are indicated in *italics*, Ex-type cultures are indicated in **bold**. Dashes (–) and dots (•) indicate the gaps and identical nucleotides in the sequences, respectively.

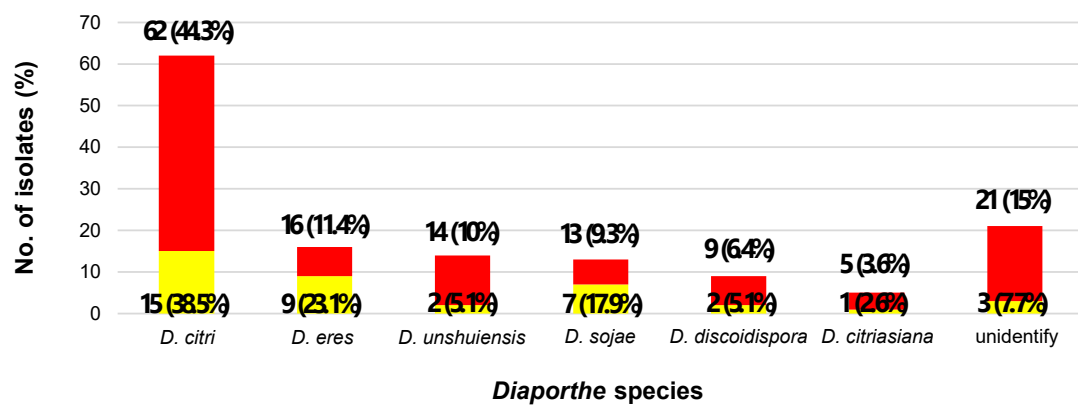


Figure S1. The prevalence of *Diaporthe* species on citrus in Jiangxi Province, China based on phylogenetic identification. Numbers (%) indicate the number of obtained isolates of certain species and the percentage among the total 140 isolates [1]. Yellow color indicate 39 isolates of *Diaporthe* sp. were found in this study.

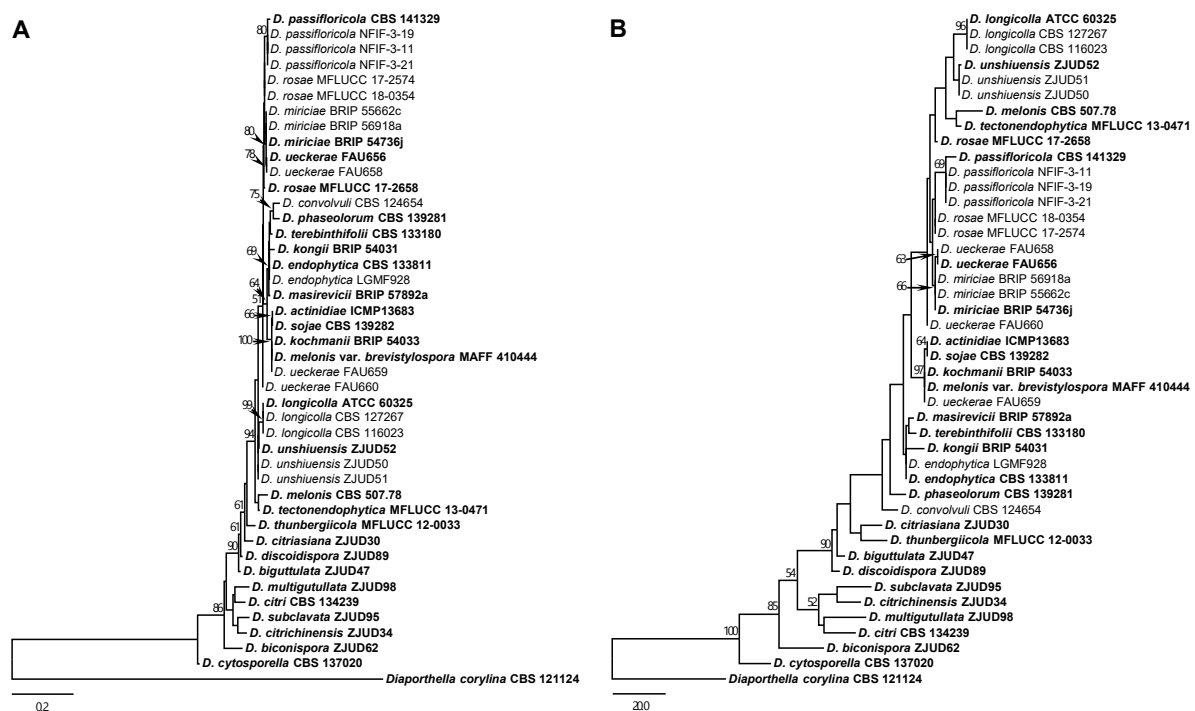


Figure S2. The phylogenetic tree is generated from the analysis of sequences of ITS locus. **A**, Maximum likelihood and **B**, Maximum parsimony. Bootstrap support values $\geq 50\%$, (MLBS/MPBS) are displayed at the nodes. The tree is rooted with *Diaporthe corylina* CBS 121124. Ex-type, ex-epitype and ex-isotype cultures are indicated in **bold**. The codes of isolates used for phylogenetic tree are given.

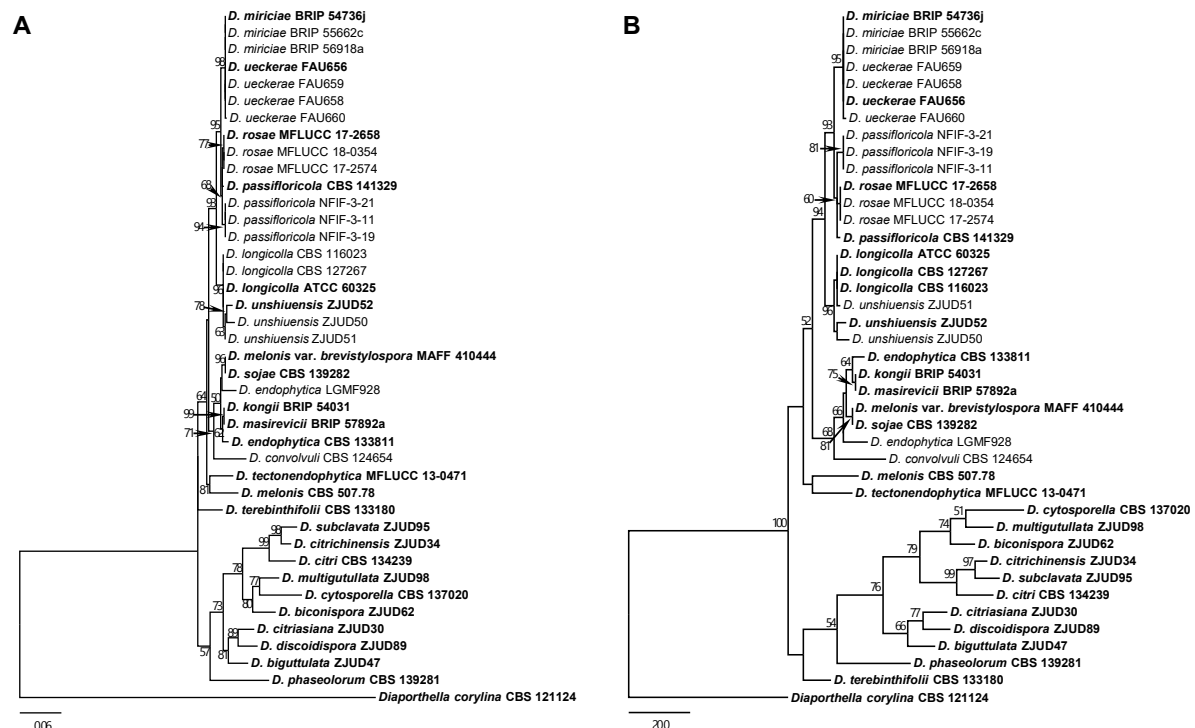


Figure S3. The phylogenetic tree is generated from the analysis of sequences of *TUB* locus. **A**, Maximum likelihood and **B**, Maximum parsimony. Bootstrap support values $\geq 50\%$, (MLBS/MPBS) are displayed at the nodes. The tree is rooted with *Diaporthe corylina* CBS 121124. Ex-type, ex-epitype and ex-isotype cultures are indicated in **bold**. The codes of isolates used for phylogenetic tree are given.

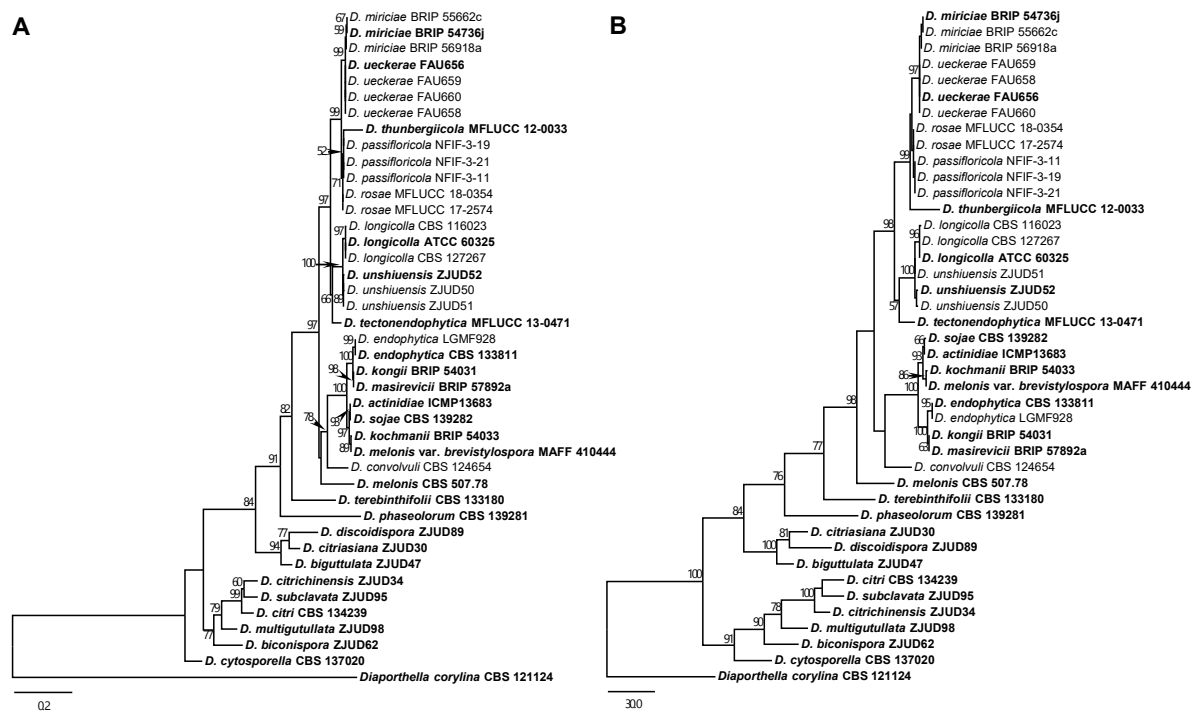


Figure S4. The phylogenetic tree is generated from the analysis of sequences of *TEF* locus. **A**, Maximum likelihood and **B**, Maximum parsimony. Bootstrap support values $\geq 50\%$, (MLBS/MPBS) are displayed at the nodes. The tree is rooted with *Diaporthe corylina* CBS 121124. Ex-type, ex-epitype and ex-isotype cultures are indicated in **bold**. The codes of isolates used for phylogenetic tree are given.

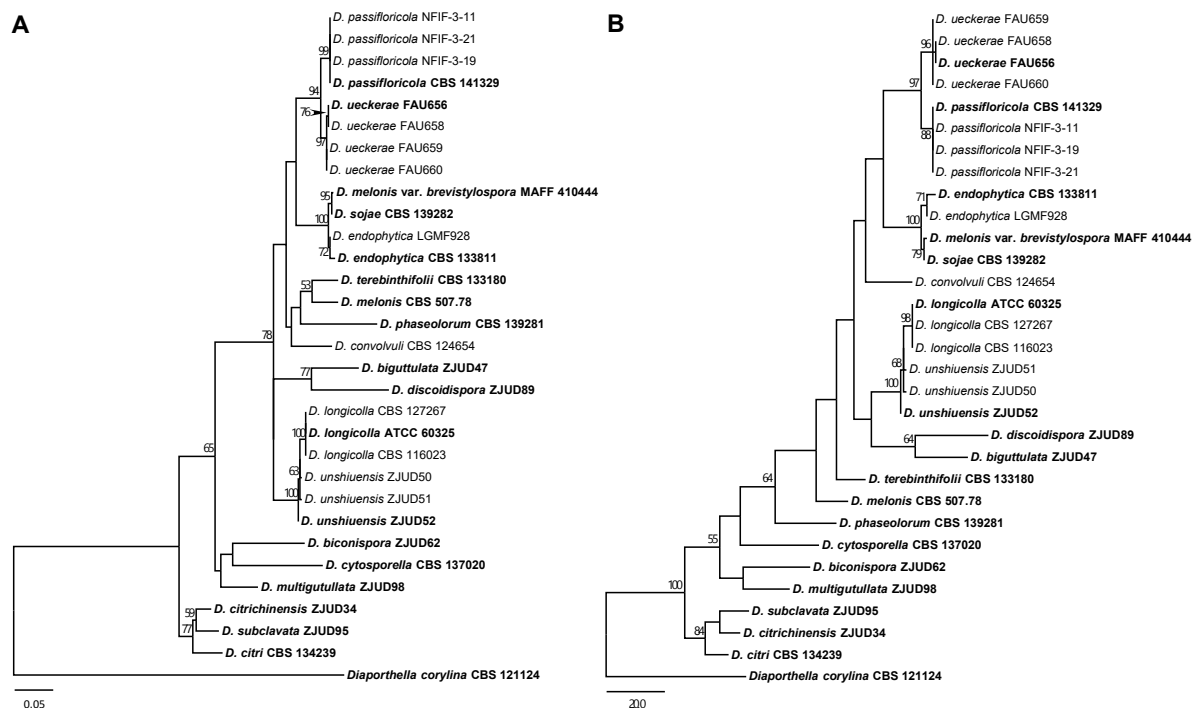


Figure S5. The phylogenetic tree is generated from the analysis of sequences of *HIS* locus. **A**, Maximum likelihood and **B**, Maximum parsimony. Bootstrap support values $\geq 50\%$, (MLBS/MPBS) are displayed at the nodes. The tree is rooted with *Diaporthe corylina* CBS 121124. Ex-type, ex-epitype and ex-isotype cultures are indicated in **bold**. The codes of isolates used for phylogenetic tree are given.

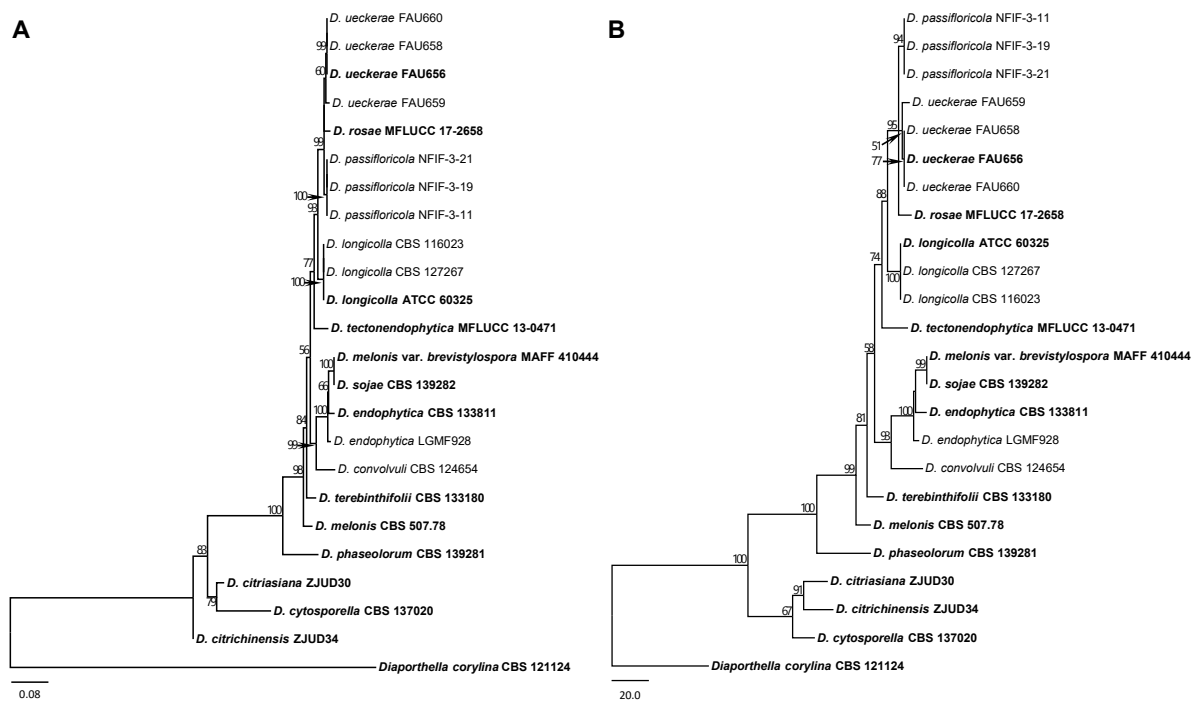


Figure S6. The phylogenetic tree is generated from the analysis of sequences of CAL locus. **A**, Maximum likelihood and **B**, Maximum parsimony. Bootstrap support values $\geq 50\%$, (MLBS/MPBS) are displayed at the nodes. The tree is rooted with *Diaporthe corylina* CBS 121124. Ex-type, ex-epitype and ex-isotype cultures are indicated in **bold**. The codes of isolates used for phylogenetic tree are given.

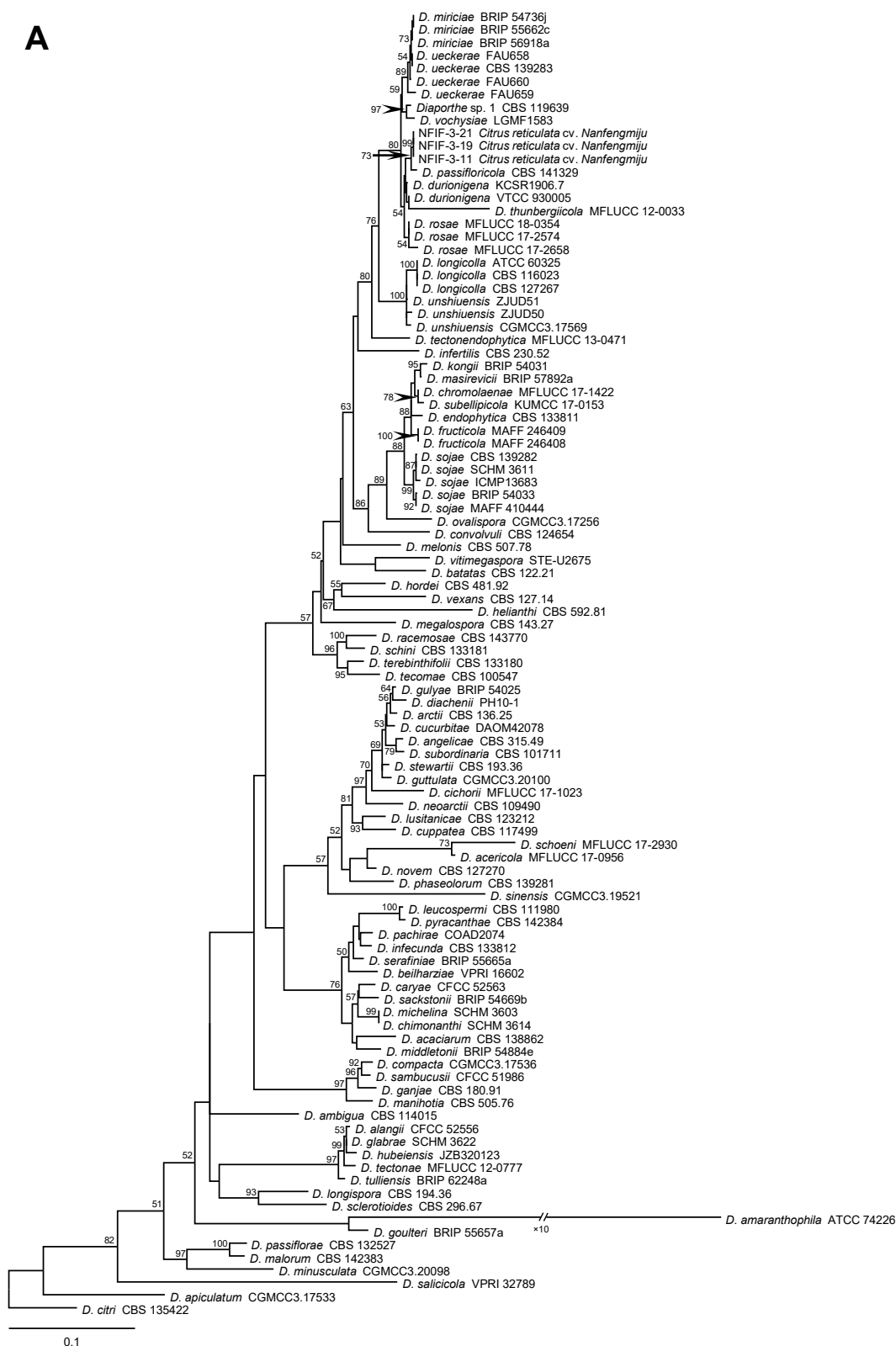


Figure S7. The phylogenetic tree is generated from the analysis of the combined sequences of five loci (ITS, *TUB*, *TEF*, *HIS*, and *CAL*). **A**, Maximum likelihood and **B**, Maximum parsimony, bootstrap support values $\geq 50\%$, (MLBS/MPBS) are displayed at the nodes. The tree is rooted with *D. citri* CBS 135422. Ex-type, ex-epitype and holotype cultures are indicated in **bold**. The codes of isolates used for phylogenetic tree are given.

B



Figure S7. (Continued).

Reference:

1. Chaisiri, C.; Liu, X.Y.; Lin, Y.; Li, J.B.; Xiong, B.; Luo, C.X. Phylogenetic analysis and development of molecular tool for detection of *Diaporthe citri* causing melanose disease of citrus. *Plants* **2020**, *9*, 329.