

SUPPLEMENTARY TABLE 1. Accession number, percent identity, and query cover of the highest matches to isolate ITS and *TUB2* sequences obtained from NCBI's nucleotide database by BLAST searching.

Isolate	ITS				TUB				RDP Taxonomy
	Genbank Accession (this Study)	Most Similar Genbank Accession	% ID	Query Cover	Genbank Accession (this Study)	Most Similar Genbank Accession	% ID	Query Cover	
1.1	MH231193.1	KT265802.1	97%	91%	MH791992.1	EF551497.1	100%	50%	Ascomycota[100%] Peizomycotina[100%] Eurotiomycetes[100%] Chaetothryiomycetidae[100%] Chaetothryiales[100%] Herpotrichiellaceae[100%] Exophiala[100%] Exophiala bergeri[100%]
2.1	MH231185.1	KU683957.1	99%	92%	MH791984.1	KU684154.1	99%	65%	Ascomycota[100%] Peizomycotina[100%] Sordariomycetes[100%] Xylariomycetidae[100%] Xylariales[100%] Xylariaceae[96%] Anthostomella[84%] Anthostomella eucalyptorum[84%]
2.2	MH231184.1	EF419945.1	99%	97%	MH791982.1	KU684155.1	99%	99%	Ascomycota[100%] Peizomycotina[100%] Sordariomycetes[100%] Xylariomycetidae[100%] Xylariales[100%] Xylariaceae[94%] Xylaria[59%] Xylaria bambusicola[26%]
2.3	MH231189.1	JQ760469.1	99%	90%	MH791988.1	KU684154.1	99%	65%	Ascomycota[100%] Peizomycotina[100%] Sordariomycetes[100%] Xylariomycetidae[98%] Xylariales[98%] Xylariaceae[97%] Anthostomella[81%] Anthostomella eucalyptorum[81%]
2.4	MH231188.1	EF419945.1	99%	99%	MH791987.1	KU684158.1	95%	99%	Ascomycota[100%] Peizomycotina[100%] Sordariomycetes[100%] Xylariomycetidae[96%] Xylariales[96%] Xylariaceae[93%] Xylaria[50%] Xylaria bambusicola[30%]
2.5	MH231191.1	KX271300.1	98%	99%	MH791990.1	KU684158.1	97%	99%	Ascomycota[100%] Peizomycotina[100%] Sordariomycetes[100%] Xylariomycetidae[100%] Xylariales[100%] Xylariaceae[99%] Xylaria[74%] Xylaria bambusicola[32%]
3.1	MH231187.1	HM036631.1	99%	91%	MH791986.1	AY999154.1	80%	68%	Ascomycota[100%] Peizomycotina[100%] Sordariomycetes[96%] Sordariomycetidae[94%] Sordariales[93%] Lasiosphaeriaceae[49%] Podospora[28%] Podospora fimiseda[24%]

SUPPLEMENTARY TABLE 1 CONTINUED.

Isolate	ITS				TUB				RDP Taxonomy
	Genbank Accession (this Study)	Most Similar Genbank Accession	% ID	Query Cover	Genbank Accession (this Study)	Most Similar Genbank Accession	% ID	Query Cover	
4.1	MH231186.1	JQ759932.1	100%	92%	MH791985.1	JQ005670.1	87%	92%	Ascomycota[100%] Peizomycotina[100%] Sordariomycetes[100%] Sordariomycetidae[100%] Sordariomycetidae_Incertae sedis[100%] Glomerellaceae[100%] Glomerella[100%] Colletotrichum hippeastri[29%]
5.1	MH231183.1	JQ760788.1	99%	91%	MH791983.1	KU684158.1	97%	99%	Ascomycota[100%] Peizomycotina[100%] Sordariomycetes[100%] Xylariomycetidae[97%] Xylariales[97%] Xylariaceae[95%] Hypoxylon[88%] Hypoxylon sp H119[34%]
6.1	MH231190.1	KY124642.1	99%	97%	MH791989.1	AB539436.1	80%	84%	Ascomycota[100%] Peizomycotina[100%] Dothideomycetes[100%] Pleosporomycetidae[100%] Pleosporales[100%] Sporormiaceae[100%] Preussia[100%] Preussia minima[93%]
7.1	MH231192.1	KU702432.1	100%	91%	MH791991.1	KC977293.1	97%	98%	Ascomycota[100%] Peizomycotina[100%] Sordariomycetes[100%] Xylariomycetidae[100%] Xylariales[100%] Xylariaceae[100%] Hypoxylon[100%] Hypoxylon investiens[100%]

SUPPLEMENTARY TABLE 2. Estimates of evolutionary divergence between ITS sequences from morphologically similar isolates¹.

	2.4	2.5	2.2	2.1	2.3
2.4	0				
2.5	0.023	0			
2.2	0.003	0.020	0		
2.1	0.248	0.246	0.245	0	
2.3	0.254	0.251	0.250	0.013	0

¹The number of base substitutions per site from between sequences are shown. Analyses were conducted using the Maximum Composite Likelihood model. The rate variation among sites was modeled with a gamma distribution (shape parameter = 1). There were a total of 779 positions in the final dataset.