

Table S1. GenBank accessions of representative taxa from *Bionectriaceae*, *Cordycipitaceae* and outgroups included in the phylogenetic analyses.

Species	Strain number	GenBank accession numbers ¹			Citation
		ITS	LSU	<i>tef1</i>	
<i>Acremonium alternatum</i>	CBS 407.66 ^T	NR_144913.1	MH870479.1	NA	[1,2]
<i>Ac. behniae</i>	CBS 146824 ^T	NR_171996.1	NG_074497.1	NA	[3]
<i>Ac. curvum</i>	GZUIFR 22.035 ^T	ON041034	ON041050	ON494579	[4]
<i>Ac. egyptiacum</i>	CBS 303.64	MH858438.1	MH870069.1	NA	[1]
<i>Ac. globosporium</i>	GZUIFR 22.036 ^T	ON041035	ON041051	ON494580	[4]
<i>Ac. sclerotigenum</i>	A101	KC987139	KC987215	KC998961	[5]
<i>Ac. sordidulum</i>	CBS 385.73 ^T	NR_159618.1	MH872418.1	NA	[1]
<i>Beauveria bassiana</i>	ARSEF 1564 ^T	NR_111594.1	-	NA	[6]
<i>B. caledonica</i>	ARSEF 2567 ^T	HQ880817.1	NG_058620.1	NA	[6]
<i>Clonostachys buxi</i>	CBS 696.93	KM231840.1	KM231721.1	NA	[7]
<i>C. grammiscospora</i>	CBS 209.93 ^T	NR_137650.1	MH874052.1	NA	[1,8]
<i>C. leucaenae</i>	MFLU 19-0970 ^T	ON230050.1	ON230058.1	NA	[9]
<i>C. rosea</i>	CBS 710.86	MH862010.1	MH873700.1	NA	[1]
<i>C. spinulosa</i>	MFLU 18-2730 ^T	ON230049.1	ON230057.1	NA	[9]
<i>Cordyceps javanica</i>	CBS 134.22 ^T	MH854719.1	MG665231.1	NA	[1,10]
<i>Emericellopsis salmosynnemata</i>	CBS 182.56 ^T	MH857571.1	MH869115.1	NA	[1]
<i>E. terricola</i>	CBS 120.40 ^T	MH856058.1	MH867553.1	NA	[1]
<i>Fusariella atrovirens</i>	CBS 311.73	MH860688.1	MH872395.1	NA	[1]
<i>F. curvata</i>	MFLUCC 15.0844	KX025152.1	KX025154.1	NA	[11]
<i>Geosmithia brunnea</i>	CBS 142633 ^T	NR_158517.1	-	NA	[12]
<i>G. lavendula</i>	CBS 582.67	MH859054.1	MH870774.1	NA	[1]
<i>G. microcorthyli</i>	CCF 3861 ^T	NR_137566.1	NG_067560.1	NA	[13]
<i>Gliomastix murorum</i>	CBS 154.25	MH854827.1	MH866327.1	NA	[1]
<i>Gl. polychroma</i>	CBS 181.27 ^T	NR_119408.1	MH866417.1	NA	[14]
<i>Gl. roseogrisea</i>	CBS 134.56 ^T	MH857544.1	MH869081.1	NA	[1]
<i>Hapsidospora irregularis</i>	CBS 510.70 ^T	MH859824.1	MH871595.1	NA	[1]
<i>Heleococcum aurantiacum</i>	CBS 201.35	MH855645.1	MH867154.1	NA	[1]
<i>H. japonense</i>	CBS 397.67	JX158420.1	JX158442.1	NA	[5]
<i>Lasionectria germanica</i>	CBS 143538 ^T	-	NG_073659.1	NA	[15]
<i>L. marigotensis</i>	CBS 131606 ^T	KR105612.1	KR105613.1	NA	[16]
<i>Lasionectriopsis pteridii</i>	CBS 782.69 ^T	MH859425.1	MH871198.1	NA	[1]
<i>Metapochonia suchlasporia</i>	CBS 251.83 ^T	MH861580.1	MH873311.1	NA	[1]
<i>Nectriopsis fuliginicola</i>	CBS 400.82 ^T	NR_154234.1	-	NA	[17]
<i>N. lindauiana</i>	CBS 897.70 ^T	NR_154235.1	-	NA	[17]
<i>Nigrosabulum globosum</i>	CBS 512.70 ^T	MH859825.1	MH871597.1	NA	[1]
	CBS 514.70	MH859826.1	MH871598.1	NA	[1]
<i>Ochronectria calami</i>	CBS 125.87	-	AY489717.1	NA	[18]
<i>O. thailandica</i>	MFLUCC 15-0140 ^T	NR_168756.1	KU564069.1	NA	[1]
<i>Paracylindrocarpon aloicola</i>	CBA 141300 ^T	NR_154346.1	NG_058238.1	NA	[19]
<i>P. pandanicola</i>	KUMCC 17-0272 ^T	NR_168197.1	NG_068837.1	NA	[20]
<i>Pochonia chlamydospora</i>	CBS 504.66	MH858871.1	MH870512.1	NA	[1]
<i>Septofusidium berolinense</i>	CBS 731.70	KM231841.1	KM231722.1	NA	[7]
<i>Simplicillium lamellicola</i>	CBS 116.25 ^T	MH854806.1	MH866307.1	NA	[1]
<i>S. lanosoniveum</i>	CBS 123.42 ^T	MH856100.1	MH867593.1	NA	[1]
<i>Stephanonectria chromolaenae</i>	MFLUCC 18-0589 ^T	ON230051.1	ON230059.1	NA	[9]
<i>St. keithii</i>	CBS 100005	AF210671.1	-	NA	[8]

	CBS 434.70	MH859783.1	MH871546.1	NA	[1]
<i>Stl. colubrensis</i>	CBS 141857 [†]	NR_173884.1	NG_088099.1	NA	[21]
<i>Stl. gracilipes</i>	MFLUCC 17-2614	ON230052.1	ON230060.1	NA	[9]
<i>Stl. macrostoma</i>	CLLG18033	MN497402.1	MN497411.1	NA	[21]
<i>Stl. walteri</i>	CBS 144627	NR_160063.1	-	NA	[22]
<i>Synnemellisia aurantia</i>	COAD 2070 [†]	NR_154444.1	NG_059728.1	NA	[23]
<i>Sy. urenae</i>	BRIP 71652 [†]	NR_175758.1	OK342134.1	NA	
<i>Verrucostoma freycinetiae</i>	MAFF 240100 [†]	NR_137761.1	NG_059924.1	NA	[24,25]

ARSEF: Agricultural Research Service Collection of Entomopathogenic Fungal Cultures, USA; CBS: Culture Collection of the Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; CCF: Culture Collection of Fungi, Prague, Czech Republic; FMR: Facultat de Medicina i Ciències de la Salut, Reus, Spain; GZUIFR: Institute of Fungus Resources, Guizhou University, Guiyang City, Guizhou, China; MAFF: National Institute of Agrobiological Sciences, Ibaraki, Japan; MFLUCC: Mae Fah Luang University Culture Collection, Thailand. [†] indicates ex-type strains. “NA” indicates sequences not used in this study. “-” indicates the absence of that sequence. [†]ITS: Internal transcribed spacer region of the rDNA and 5.8S gene; LSU: 28S large ribosomal subunit; *tef1*: translation elongation factor 1 α .

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Table S2: Phylogenetic distance between *Amphichorda* species for the *BenA* region.

Strains																
<i>Amphichorda littoralis</i> FMR_19404																
FMR 17952	0,000															
FMR 19611	0,000	0,000														
FMR 20067	0,000	0,000	0,000													
FMR 20149	0,000	0,000	0,000	0,000												
<i>Amphichorda cavernicola</i> CGMCC 3.19571																
LC12674	0,076	0,076	0,076	0,076	0,076											
LC12560	0,076	0,076	0,076	0,076	0,076	0,000	0,000									
<i>Amphichorda guana</i> CGMCC 3.17908																
CGMCC 3.17909	0,095	0,095	0,095	0,095	0,095	0,038	0,038	0,038								
CBS 312.50	0,090	0,090	0,090	0,090	0,090	0,042	0,042	0,042	0,018	0,018						
<i>Amphichorda felina</i> CBS 250.34																
CBS 648.66	0,080	0,080	0,080	0,080	0,080	0,030	0,030	0,030	0,022	0,022	0,026					
CBS 110.08	0,080	0,080	0,080	0,080	0,080	0,034	0,034	0,034	0,026	0,026	0,030	0,007	0,007			
<i>Amphichorda coprophila</i> CBS 173.71																
CBS 424.88	0,041	0,041	0,041	0,041	0,041	0,058	0,058	0,058	0,080	0,080	0,076	0,066	0,066	0,067	0,000	
CBS 247.82	0,041	0,041	0,041	0,041	0,041	0,058	0,058	0,058	0,080	0,080	0,076	0,066	0,066	0,067	0,000	0,000