

Endophytes from medicinal plants and their potential for producing indole acetic acid, improving seed germination and mitigating oxidative stress

Table S1 Location and length of 18S, 25S, 5.8S and ITS1, ITS2 sequences of various fungal strains

Endophytes	Location					Length				
	18S	ITS1	5.8S	ITS2	28S	18S	ITS1	5.8S	ITS2	28S
<i>A. alternata</i> (AC4)	1 – 27	28 – 189	190 – 348	349 – 506	507 – 564	27	162	159	158	58
<i>Alternaria</i> sp. (RSL8.1)	1 – 25	26 – 188	189 – 347	348 – 504	505 – 563	25	163	159	157	59
<i>B. sorokiniana</i> (RSL1.2)	1 – 37	38 – 212	213 – 369	370 – 541	542 – 597	37	175	157	172	56
<i>C. sphaerosperumum</i> (MPB8.1)	1 – 25	26 – 178	179 – 336	337 – 487	488 – 546	25	153	158	151	59
<i>Phoma</i> sp. (RS-OS1.3)	1 – 24	25 – 163	164 – 320	321 – 475	476 – 538	24	139	157	155	63
<i>Phoma</i> sp. (CA2)	1 – 30	31 – 168	169 – 325	326 – 480	481 – 544	30	138	157	155	64
<i>Phoma</i> sp. (MPB5.2)	1 – 26	27 – 165	166 – 322	323 – 477	478 – 538	26	139	157	155	61
<i>Phoma</i> sp. (MPB6.2)	1 – 24	25 – 163	164 – 320	321 – 475	476 – 534	24	139	157	155	59
<i>Phoma</i> sp. (MPB6.1)	1 – 20	21 – 159	160 – 316	317 – 471	472 – 522	20	139	157	155	51
<i>Phoma</i> sp. (MPS10.1)	1 – 27	28 – 166	167 – 323	324 – 478	479 – 540	27	139	157	155	62

Table S2 Estimates of evolutionary divergence between sequences

	<i>A. alternata</i> (AC4)	<i>Alternaria</i> sp. (RSL 8.1)	<i>B. sorokiniana</i> (RSL 1.2)	<i>C. sphaer-</i> <i>osperumum</i> (MPB 8.1)	<i>Phoma</i> sp. (RS-OS 1.3)	<i>Phoma</i> sp. (CA2)	<i>Phoma</i> sp. (MPB 5.2)	<i>Phoma</i> sp. (MPB 6.2)	<i>Phoma</i> sp. (MPB 6.1)	<i>Phoma</i> sp. (MPS 10.1)
<i>A. alternata</i> (AC4)		0.002	0.086	0.368	0.166	0.166	0.168	0.169	0.179	0.168
<i>Alternaria</i> sp. (RSL 8.1)	0.002		0.084	0.365	0.168	0.163	0.166	0.171	0.182	0.166
<i>B. sorokiniana</i> (RSL 1.2)	0.086	0.084		0.324	0.157	0.152	0.152	0.154	0.168	0.152
<i>C. sphaerosperumum</i> (MPB 8.1)	0.368	0.365	0.324		0.372	0.369	0.361	0.363	0.383	0.361
<i>Phoma</i> sp. (RS-OS 1.3)	0.166	0.168	0.157	0.372		0.004	0.008	0.008	0.016	0.008
<i>Phoma</i> sp. (CA2)	0.166	0.163	0.152	0.369	0.004		0.008	0.012	0.020	0.008
<i>Phoma</i> sp. (MPB 5.2)	0.168	0.166	0.152	0.361	0.008	0.008		0.004	0.012	0.000
<i>Phoma</i> sp. (MPB 6.2)	0.169	0.171	0.154	0.363	0.008	0.012	0.004		0.012	0.004
<i>Phoma</i> sp. (MPB 6.1)	0.179	0.182	0.168	0.383	0.016	0.020	0.012	0.012		0.012
<i>Phoma</i> sp. (MPS 10.1)	0.168	0.166	0.152	0.361	0.008	0.008	0.000	0.004	0.012	

The number of base substitutions per site from between sequences are shown. Analyses were conducted using the Maximum Composite Likelihood model. The analysis involved 10 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing gaps and missing data were eliminated. There were a total of 499 positions in the final dataset. Evolutionary analyses were conducted in MEGA 5.1.

Table S3 Sequence homology matrix of fungal strains

	<i>A. alternata</i> (AC4)	<i>Alternaria</i> sp. (RSL 8.1)	<i>B. sorokiniana</i> (RS-L1.2)	<i>C. sphaer-</i> <i>osperumum</i> (MPB 8.1)	<i>Phoma</i> sp. (RS-OS 1.3)	<i>Phoma</i> sp. (CA2)	<i>Phoma</i> sp. (MPB 5.2)	<i>Phoma</i> sp. (MPB 6.2)	<i>Phoma</i> sp. (MPB 6.1)	<i>Phoma</i> sp. (MPS 10.1)
<i>A. alternata</i> (AC4)		99	88	93	86	86	86	86	86	86
<i>Alternaria</i> sp. (RSL 8.1)	99		86	93	86	86	86	86	86	86
<i>B. sorokiniana</i> (RS-L1.2)	88	86		93	85	85	85	85	84	85
<i>C. sphaerosperumum</i> (MPB 8.1)	93	93	93		93	93	93	93	93	93
<i>Phoma</i> sp. (RS-OS 1.3)	86	86	85	93		99	99	99	99	99
<i>Phoma</i> sp. (CA2)	86	86	85	93	99		99	99	99	99
<i>Phoma</i> sp. (MPB 5.2)	86	86	85	93	99	99		99	99	99
<i>Phoma</i> sp. (MPB 6.2)	86	86	85	93	99	99	99		99	99
<i>Phoma</i> sp. (MPB 6.1)	86	86	84	93	99	99	99	99		99
<i>Phoma</i> sp. (MPS 10.1)	86	86	85	93	99	99	99	99	99	