

**Appendix 2.0** Alignment of the ITS region for 16 taxa of lignicolous mangrove fungi using Clustal W (Higgins et al., 1994) in MEGA 4 (Tamura et al., 2007)

	1	11	21	31	41	51	
'Phoma sp. HQ608114'	TGAACCTGCG	GAAGGATCAT	TACAATTTTG	GTACATTGGG	TCGCCTCCCG	GGCGGGCTCC	
0658	.T.CTG.ATC	TGGC.G.AGC	A.ATG.C.C.	C.CTT.GCA.	C.....GA.	ATAGAA.C..	
2954	.T.CTG.ATC	TGGC.G.AGC	A.ATG.C.C.	C.CTT.GCA.	C.....GA.	ATAGAA.C..	
2953	.T.CTG.ATC	TGGC.G.AGC	A.ATG.C.C.	C.CTT.GCA.	C.....GA.	ATAGAA.C..	
2952	.T.CTG.ATC	TGGC.G.AGC	A.ATG.C.C.	C.CTT.GCA.	C.....GA.	ATAGAA.C..	
0362	.T.CTG.ATC	TGGC.G.AGC	A.ATG.C.C.	C.CTT.GCA.	C.....GA.	ATAGAA.C..	
0361	.T.CTG.ATC	TGGC.G.AGC	A.ATG.C.C.	C.CTT.GCA.	C.....GA.	ATAGAA.C..	
5059	.T.CTG.ATC	TGGC.G.AGC	A.ATG.C.C.	C.CTT.GCA.	C.....GA.	ATAGAA.C..	
1350	.T.CTG.ATC	TGGC.G.AGC	A.ATG.C.C.	C.CTT.GCA.	C.....GA.	ATAGAA.C..	
3533	.T.CTG.ATC	TGGC.G.AGC	A.ATG.C.C.	C.CTT.GCA.	C.....GA.	ATAGAA.C..	
3532	.T.CTG.ATC	TGGC.G.AGC	A.ATG.C.C.	C.CTT.GCA.	C.....GA.	ATAGAA.C..	
1349	.T.CTG.ATC	TGGC.G.AGC	A.ATG.C.C.	C.CTT.GCA.	C.....GA.	ATAGAA.C..	
0301	.T.CTG.ATC	TGGC.G.AGC	A.ATG.C.C.	C.CTT.GCA.	C.....GA.	ATAGAA.C..	
0201	.T.CTG.ATC	TGGC.G.AGC	A.ATG.C.C.	C.CTT.GCA.	C.....GA.	ATAGAA.C..	
0657	.T.CTG.ATC	TGGC.G.AGC	A.ATG.C.C.	C.CTT.GCA.	C.....GA.	ATAGAA.C..	
GQ203796	-----	-----	-----	--CTT.GCA.	C.....GA.	ATAGAA.C..	
	61	71	81	91	101	111	
'Phoma sp. HQ608114'	GGTGTACCA	ATCGAGATAC	CAACCCATGT	CTTTTGAGCA	CCTCACGTTT	CCTCGGCA-G	
0658	ATACCTTG..	CA.CTCT.GT	TTT..TCG.C	AGGCCC.T.C	G.CTG.CAG.	AG.T....C.	
2954	ATACCTTG..	CA.CTCT.GT	TTT..TCG.C	AGGCCC.T.C	G.CTG.CAG.	AG.T....C.	
2953	ATACCTTG..	CA.CTCT.GT	TTT..TCG.C	AGGCCC.T.C	G.CTG.CAG.	AG.T....C.	
2952	ATACCTTG..	CA.CTCT.GT	TTT..TCG.C	AGGCCC.T.C	G.CTG.CAG.	AG.T....C.	
0362	ATACCTTG..	CA.CTCT.GT	TTT..TCG.C	AGGCCC.T.C	G.CTG.CAG.	AG.T....C.	
0361	ATACCTTG..	CA.CTCT.GT	TTT..TCG.C	AGGCCC.T.C	G.CTG.CAG.	AG.T....C.	
5059	ATACCTTG..	CA.CTCT.GT	TTT..TCG.C	AGGCCC.T.C	G.CTG.CAG.	AG.T....C.	
1350	ATACCTTG..	CA.CTCT.GT	TTT..TCG.C	AGGCCC.T.C	G.CTG.CAG.	AG.T....C.	
3533	ATACCTTG..	CA.CTCT.GT	TTT..TCG.C	AGGCCC.T.C	G.CTG.CAG.	AG.T....C.	
3532	ATACCTTG..	CA.CTCT.GT	TTT..TCG.C	AGGCCC.T.C	G.CTG.CAG.	AG.T....C.	
1349	ATACCTTG..	CA.CTCT.GT	TTT..TCG.C	AGGCCC.T.C	G.CTG.CAG.	AG.T....C.	
0301	ATACCTTG..	CA.CTCT.GT	TTT..TCG.C	AGGCCC.T.C	G.CTG.CAG.	AG.T....C.	
0201	ATACCTTG..	CA.CTCT.GT	TTT..TCG.C	AGGCCC.T.C	G.CTG.CAG.	AG.T....C.	
0657	ATACCTTG..	CA.CTCT.GT	TTT..TCG.C	AGGCCC.T.C	G.CTG.CAG.	AG.T....C.	
GQ203796	ATACCTTG..	CA.CTCT.GT	TTT..TCG.C	AGGCCC.T.C	G.CTG.CAG.	AG.T....C.	
	121	131	141	151	161	171	
'Phoma sp. HQ608114'	GCTCGCCTGC	CAA-TGGGG-	ACCCCTTTA-	-AAACCTTT-	TTGTGTATGC	AGTAAACGTC	
0658	C.CGC.....	..GC.....G	...T.A.CT	T....AC.A.	.CAAAAGCAG	.AACCGTAC.	
2954	C.CGC.....	..GC.....G	...T.A.CT	T....AC.A.	.CAAAAGCAG	.AACCGTAC.	
2953	C.CGC.....	..GC.....G	...T.A.CT	T....AC.A.	.CAAAAGCAG	.AACCGTAC.	
2952	C.CGC.....	..GC.....G	...T.A.CT	T....AC.A.	.CAAAAGCAG	.AACCGTAC.	
0362	C.CGC.....	..GC.....G	...T.A.CT	T....AC.A.	.CAAAAGCAG	.AACCGTAC.	
0361	C.CGC.....	..GC.....G	...T.A.CT	T....AC.A.	.CAAAAGCAG	.AACCGTAC.	
5059	C.CGC.....	..GC.....G	...T.A.CT	T....AC.A.	.CAAAAGCAG	.AACCGTAC.	
1350	C.CGC.....	..GC.....G	...T.A.CT	T....AC.A.	.CAAAAGCAG	.AACCGTAC.	
3533	C.CGC.....	..GC.....G	...T.A.CT	T....AC.A.	.CAAAAGCAG	.AACCGTAC.	
3532	C.CGC.....	..GC.....G	...T.A.CT	T....AC.A.	.CAAAAGCAG	.AACCGTAC.	
1349	C.CGC.....	..GC.....G	...T.A.CT	T....AC.A.	.CAAAAGCAG	.AACCGTAC.	
0301	C.CGC.....	..GC.....G	...T.A.CT	T....AC.A.	.CAAAAGCAG	.AACCGTAC.	
0201	C.CGC.....	..GC.....G	...T.A.CT	T....AC.A.	.CAAAAGCAG	.AACCGTAC.	
0657	C.CGC.....	..GC.....G	...T.A.CT	T....AC.A.	.CAAAAGCAG	.AACCGTAC.	
GQ203796	C.CGC.....	..GC.....G	...T.A.CT	T....AC.AA	.CAAAAGCAG	.AACCGTAC.	
	181	191	201	211	221	231	
'Phoma sp. HQ608114'	TACAAAATAA	AT--TAAATC	AAAACCTTCA	ACAACGGATC	TCTTGGTTCT	GGCATCGATG	
0658	C.A..C..T.	..TACTTT.A	.....	.....	.....	.....	
2954	C.A..CC.T.	..ACTTT.A	.....	.....	.....	.....	
2953	C.A..CC.T.	..ACTTT.A	.....	.....	.....	.....	
2952	C.A..CC.T.	..ACTTT.A	.....	.....	.....	.....	
0362	C.A..CC.T.	..ACTTT.A	.....	.....	.....	.....	
0361	C.A..CC.T.	..ACTTT.A	.....	.....	.....	.....	
5059	C.A..CC.T.	..ACTTT.A	.....	.....	.....	.....	
1350	C.A..CC.T.	..ACTTT.A	.....	.....	.....	.....	
3533	C.A..CC.T.	..ACTTT.A	.....	.....	.....	.....	
3532	C.A..CC.T.	..ACTTT.A	.....	.....	.....	.....	
1349	C.A..CC.T.	..ACTTT.A	.....	.....	.....	.....	

0301 C.A..CC.T. ...ACTTT.A .....  
0201 C.A..CC.T. ...ACTTT.A .....  
0657 C.A..C..T. .TACTTT.A .....  
GQ203796 C.A..CC.T. ...ACTTT.A .....

241 251 261 271 281 291  
| | | | | |  
'Phoma sp. HQ608114' AAGAACGCAG CGAAATGCGA TAAGTAGTGT GAATTGCAGA ATTCAGTGAA TCATCGAATC  
0658 .....  
2954 .....  
2953 .....  
2952 .....  
0362 .....  
0361 .....  
5059 .....  
1350 .....  
3533 .....  
3532 .....  
1349 .....  
0301 .....  
0201 .....  
0657 .....  
GQ203796 .....

301 311 321 331 341 351  
| | | | | |  
'Phoma sp. HQ608114' TTGAACGCA CATTGCGCCC TTTGGTATTC CTTAGGGCAT GCCTGTTCGA GCGTCATCTA  
0658 .....TA.  
2954 .....TA.  
2953 .....TA.  
2952 .....TA.  
0362 .....TA.  
0361 .....TA.  
5059 .....TA.  
1350 .....TA.  
3533 .....TA.  
3532 .....TA.  
1349 .....TA.  
0301 .....TA.  
0201 .....TA.  
0657 .....TA.  
GQ203796 .....TA.

361 371 381 391 401 411  
| | | | | |  
'Phoma sp. HQ608114' AACCTTCAAG CACTGCTTGG TGTGGGGCGT CCTTGTCCCG CCTCCTGGCG CGGACTCGCC  
0658 .T....G.. .....A .....T.C TT.GTC.... ..C.TG..TA G.....  
2954 .T....G.. .....A .....T.C TT.GTC.... ..C.TG..TA G.....  
2953 .T....G.. .....A .....T.C TT.GTC.... ..C.TG..TA G.....  
2952 .T....G.. .....A .....T.C TT.GTC.... ..C.TG..TA G.....  
0362 .T....G.. .....A .....T.C TT.GTC.... ..C.TG..TA G.....  
0361 .T....G.. .....A .....T.C TT.GTC.... ..C.TG..TA G.....  
5059 .T....G.. .....A .....T.C TT.GTC.... ..C.TG..TA G.....  
1350 .T....G.. .....A .....T.C TT.GTC.... ..C.TG..TA G.....  
3533 .T....G.. .....A .....T.C TT.GTC.... ..C.TG..TA G.....  
3532 .T....G.. .....A .....T.C TT.GTC.... ..C.TG..TA G.....  
1349 .T....G.. .....A .....T.C TT.GTC.... ..C.TG..TA G.....  
0301 .T....G.. .....A .....T.C TT.GTC.... ..C.TG..TA G.....  
0201 .T....G.. .....A .....T.C TT.GTC.... ..C.TG..TA G.....  
0657 .T....G.. .....A .....T.C TT.GTC.... ..C.TG..TA G.....  
GQ203796 .T....G.. .....A .....T.C TT.GTC.... ..C.TG..TA G.....

421 431 441 451 461 471  
| | | | | |  
'Phoma sp. HQ608114' TTAATAATCAT TGGCGGCCTG TGTATTGGCT TCGAGCGCAG CAGACTCGCG CTTTCGTCTC  
0658 C....C... .....C. ....T. ....C.A.... ACCCTCGA..  
2954 C....C... .....C. ....T. ....C.A.... ACCCTCGA..  
2953 C....C... .....C. ....T. ....C.A.... ACCCTCGA..  
2952 C....C... .....C. ....T. ....C.A.... ACCCTCGA..  
0362 C....C... .....C. ....T. ....C.A.... ACCCTCGA..  
0361 C....C... .....C. ....T. ....C.A.... ACCCTCGA..  
5059 C....C... .....C. ....T. ....C.A.... ACCCTCGA..  
1350 C....C... .....C. ....T. ....C.A.... ACCCTCGA..  
3533 C....C... .....C. ....T. ....C.A.... ACCCTCGA..  
3532 C....C... .....C. ....T. ....C.A.... ACCCTCGA..  
1349 C....C... .....C. ....T. ....C.A.... ACCCTCGA..  
0301 C....C... .....C. ....T. ....C.A.... ACCCTCGA..

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0201      C.....C... ..C. .... .T..... ..C.A..... ACCCTCGA..
0657      C.....C... ..C. .... .T..... ..C.A..... ACCCTCGA..
GQ203796  C.....C... ..C. .... .T..... ..C.A..... ACCCTCGA..

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                                481      491      501      511
                                |         |         |         |
'Phoma sp. HQ608114' CTTTAGCATA GCGTCCAGT AAGCCTCACC CACTAAGTTT
0658      .AG..TACCG .CATC.A..A .GCTGAA.A. A.ACCCTC..
2954      .AG..TACCG .CGTC.A..A .GCTGAA.A. A.ACCCTC..
2953      .AG..TACCG .CGTC.A..A .GCTGAA.A. A.ACCCTC..
2952      .AG..TACCG .CGTC.A..A .GCTGAA.A. A.ACCCTC..
0362      .AG..TACCG .CGTC.A..A .GCTGAA.A. A.ACCCTC..
0361      .AG..TACCG .CGTC.A..A .GCTGAA.A. A.ACCCTC..
5059      .AG..TACCG .CGTC.A..A .GCTGAA.A. A.ACCCTC..
1350      .AG..TACCG .CGTC.A..A .GCTGAA.A. A.ACCCTC..
3533      .AG..TACCG .CGTC.A..A .GCTGAA.A. A.ACCCTC..
3532      .AG..TACCG .CGTC.A..A .GCTGAA.A. A.ACCCTC..
1349      .AG..TACCG .CGTC.A..A .GCTGAA.A. A.ACCCTC..
0301      .AG..TACCG .CGTC.A..A .GCTGAA.A. A.ACCCTC..
0201      .AG..TACCG .CGTC.A..A .GCTGAA.A. A.ACCCTC..
0657      .AG..TACCG .CATC.A..A .GCTGAA.A. A.ACCCTC..
GQ203796  .AG..TACCG .CGCC.A..A .GCTGAA.A. A.-CCCT---

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