

Supplementary Table 1. List of *Colletrotrichum* species and genes used for identification and phylogenetic study

Species	Isolates	GenBank accession No. ^a					
		ITS	TUB2	ACT	CHS-1	GAPDH	HIS3
<i>C. scovillei</i>	CBS 126529	JQ948267	JQ949918	JQ949588	JQ948928	JQ948597	JQ949258
<i>C. simmondsii</i>	CBS 122122	JQ948276	JQ949927	JQ949597	JQ948937	JQ948606	JQ949267
<i>C. fioriniae</i>	CBS 128517	JQ948292	JQ949943	JQ949613	JQ948953	JQ948622	JQ949283
<i>C. acutatum</i>	CBS 112996	JQ005776	JQ005860	JQ005839	JQ005797	JQ948677	JQ005818
<i>C. graminicola</i>	CBS 130826, M1.001	JQ005767	JQ005851	JQ005830	JQ005788	XM_008095871	JQ005809
<i>C. higginsianum</i>	IMI 349063	JQ005760	JQ005844	JQ005823	JQ005781	KM105536	JQ005802
<i>C. gloeosporioides</i>	CBS 112999	JQ005152	JQ005587	JQ005500	JQ005326	JQ005239	JQ005413
<i>C. orbiculare</i>	104-T, CBS 107.17	JQ005778	JQ005862	JQ005841	JQ005799	KF178489	JQ005820

^aITS, internal transcribed spacer; TUB2, β -tubulin; ACT, actin; CHS-1, chitin synthase 1; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; HIS3, histone 3.

Supplementary Table 2. Primers used in this study

Name	Primer sequence 5' to 3'
HPH_F	GGCTTGGCTGGAGCTAGTGGAGG
HPH_R	CTCCGGAGCTGACATCGACACCAAC
CSP_000836_5F	CCCAAGAGAACCAGTCACAAA
CSP_000836_5R	CCTCCACTAGCTCCAGCCAAGCCCGAAAGAGCTGCTGCAAATG
CSP_000836_3F	GTTGGTGTGCGATGTCAGTCCGGAGGTCTCAATCCACCACCGTATC
CSP_000836_3R	CGGATGAATAGCTTGCCTACTG
CSP_000836_NF	TTGCATTTCCTCGGAGCTATC
CSP_000836_NR	CCGACCTGAAAGCCACATAA
CSP_000836_SF	GGAGAACGTCACCTCCTGTATC
CSP_000836_SR	TCGATTCAATCACGCCCTATC
CSP_000836_PF	CGTGTTTCTGCCGTATCCA
CSP_000836_PR	GGGTCTCCAATCTTGTCTCTTC
CSP_001376_5F	ACATGAACAGGCTCCAAGAT
CSP_001376_5R	CCTCCACTAGCTCCAGCCAAGCCCAAAGTCAAAGAAGCCCTCAC
CSP_001376_3F	GTTGGTGTGCGATGTCAGTCCGGAGGTCTCTCCCGTTGAATGA
CSP_001376_3R	CTGCGCTCATGGTCAAGATA
CSP_001376_NF	ACTCTGCACTTTCTCAACTACC
CSP_001376_NR	GAAGATCAAGACCGAGCGTATC
CSP_001376_SF	GGATGTTGTTGCAGTTGAGATTG
CSP_001376_SR	ACTAACTTCGGCCAACTTCAC
CSP_001376_PF	CTAAGGCCACGGACAATGAA
CSP_001376_PR	CGCCTCATTCGACTGACTAAA
CSP_000583_5F	ATAGCCGAAGCTTAGCACTG
CSP_000583_5R	CCTCCACTAGCTCCAGCCAAGCCGGCGGAGGACAATATCATGG
CSP_000583_3F	GTTGGTGTGCGATGTCAGTCCGGAGGTATATGGTGATGCGGGTGAA
CSP_000583_3R	CTAATGACTGTCTGTCTCTGTGG
CSP_000583_NF	CCACCACTAAAGAACCTCACAG
CSP_000583_NR	GTCTCTTGAAGTGTCGAGAAGG

CSP_000583_SF	AAGTCTGCGCCAAACCA
CSP_000583_SR	GCTACAGCAAACCAACCAAC
CSP_000583_PF	GTACAACCACACTCTCACAC
CSP_000583_PR	CGATGAGGATGAGGGATACT
CSP_001741_5F	CGACCGTAAACTTGGCTGATA
CSP_001741_5R	CCTCCACTAGCTCCAGCCAAGCCGCTATCGACACACCTCTCAATTA
CSP_001741_3F	GTTGGTGTGCGATGTCAGCTCCGGAGGCACTGAGCCTGTCATTCTA
CSP_001741_3R	GACTTTGTACACCGCAATCATATC
CSP_001741_NF	GCTGTTACGAGCCTCTTCTT
CSP_001741_NR	TCATAGATGCTTGTGGGTTCC
CSP_001741_SF	CCGGTGATGCGGAATTCTAT
CSP_001741_SR	CTAGGGCGGCATTTCTATCAA
CSP_001741_PF	CTAGTCGTGTGCAGAGTATTAGAG
CSP_001741_PR	GGGATCGAGCTCGTGTTTAT
CSP_002212_5F	CATCGCCATCGCTCACAGG
CSP_002212_5R	CCTCCACTAGCTCCAGCCAAGCCGCTTTCGGTCTGCTATGTA
CSP_002212_3F	GTTGGTGTGCGATGTCAGCTCCGGAGGGCGAGGGTCAAGATATAGATG
CSP_002212_3R	TTCGTGGCTCTTGACTTAGG
CSP_002212_NF	AGCAGATGCTGGGTCACTA
CSP_002212_NR	AGGAACCTGAGGTCGGTTAT
CSP_002212_SF	TTGAAGAACGGTCAGGTCAAG
CSP_002212_SR	GCTGATGCAATGAGGATGAGA
CSP_002212_PF	GGCTGTTTGTGTCTTCA
CSP_002212_PR	TTGGTGGCTCTTGACTTA
CSP_004175_5F	GTGTGTCAATTGTCTGGCTTTC
CSP_004175_5R	CCTCCACTAGCTCCAGCCAAGCCGCTGAGGGAGTCTCGGTATTAGTC
CSP_004175_3F	GTTGGTGTGCGATGTCAGCTCCGGAGCTAGGACATGGCGTACATACAAA
CSP_004175_3R	TCCTCCTCTGAACTAGGCTAAA
CSP_004175_NF	GGGAAAGTGCAAGAGCAAGA
CSP_004175_NR	GGCGCACACTCTCGTAAATA
CSP_004175_SF	CATACCTGTTACCACCCAATTACA
CSP_004175_SR	CTGGTATATGTCAAGCGCCTAAA
CSP_004175_PF	TCGTTTCGTTCTGTTCTG
CSP_004175_PR	ATGCGGTACTAGGTGTAATTGG
CSP_003850_5F	GATATACCCACTGCCTACTTACTT
CSP_003850_5R	CCTCCACTAGCTCCAGCCAAGCCCACAAATCTCATGTGGACCATAC
CSP_003850_3F	GTTGGTGTGCGATGTCAGCTCCGGAGGTGTGGTGGTTTCGGTTTATG
CSP_003850_3R	ACTGGAAGAGGAGGAGTAGTAG
CSP_003850_NF	CTTGACAGCTCCCGTGATT
CSP_003850_NR	AGAGCAACGGCTGGTATTAG
CSP_003850_SF	GTTTGTCTCTTCCTCCCTTCC
CSP_003850_SR	CCTTTCCCATCTGTCCTAGATTC
CSP_003850_PF	GGAGTGTTTGGAGGGATTGT
CSP_003850_PR	TTCTTACAAGACCGCCTTATT
CSP_003491_5F	GGCAATGTCGTCAAGGTAGT

CSP_003491_5R	CCTCCACTAGCTCCAGCCAAGCCATCGTTCACCCTCAGCTTTC
CSP_003491_3F	GTTGGTGTGCGATGTCAGCTCCGGAGGAGCTGGCGAGATGTTCTAAA
CSP_003491_3R	CATGCCCAGAGAGTGACAAA
CSP_003491_NF	GCCGGGAAATTTGCAACC
CSP_003491_NR	GCAGTCACCTAAGCACCTTAT
CSP_003491_SF	TGCCTTTCTGTCTCCATAAACT
CSP_003491_SR	GATGTTGTACTACGCGGAGATG
CSP_003491_PF	CTCGTAACTTCAGGTCGCTAAC
CSP_003491_PR	CGACACAGAATAGACCCATCAG
CSP_005482_5F	AGGTGGAATGCCAGATCAAA
CSP_005482_5R	CCTCCACTAGCTCCAGCCAAGCCCGGCCGTGGACTTAACTAAT
CSP_005482_3F	GTTGGTGTGCGATGTCAGCTCCGGAGAGAGTGTCTGGCTCACA
CSP_005482_3R	TGGACAAGCCTGTGGAGA
CSP_005482_NF	GCCAGCCCATTTCTACCAC
CSP_005482_NR	GCCTCACCTAGGTATCGCTT
CSP_005482_SF	GATACTTGTGCTCTCGGTCAG
CSP_005482_SR	CTTTCGTAGAGACCACCCATC
CSP_005482_PF	TCCCTCCACTCATCCTTCTC
CSP_005482_PR	GTCTTGGGCTGGTACTTGTT
CSP_005764_5F	TGTGTCGTAGGAGATGTCAAAG
CSP_005764_5R	CCTCCACTAGCTCCAGCCAAGCCCGGGTGTTCAGGTAGAAT
CSP_005764_3F	GTTGGTGTGCGATGTCAGCTCCGGAGCTGGTTCAGGTGTCATGGTT
CSP_005764_3R	GATGTCCAAAGGGAACAGGATAG
CSP_005764_NF	TGCGGAGTGAGAGAACCTA
CSP_005764_NR	CACGTACCAAGTGGGAAGAAA
CSP_005764_SF	CAGACGCCACTACGATTTCTAC
CSP_005764_SR	GCCCACGAGCATCACATT
CSP_005764_PF	GGTTTACCCGAGTCTACCTACT
CSP_005764_PR	GTGTAITGTCCTGCACTCTTG
CSP_006569_5F	GAAGGGTTCAC TTCAATTCAGG
CSP_006569_5R	CCTCCACTAGCTCCAGCCAAGCCCTGATGTGACAAAGTTGGCTAAG
CSP_006569_3F	GTTGGTGTGCGATGTCAGCTCCGGAGTGTATCGCAGCAGTCAAA
CSP_006569_3R	TGAAAGGAGCCAGCAGATAAG
CSP_006569_NF	GCTGCTCACTGCACAAATC
CSP_006569_NR	CCTCACCTTACCTTAGTATGAGAAA
CSP_006569_SF	ACTCGCTCTGCACACATT
CSP_006569_SR	GGCCCAGTGATAAAGCAAATC
CSP_006569_PF	CGTTCATCTTCCAGCGATCTAC
CSP_006569_PR	CTCGCCTCCAAACACTCATT
CSP_006607_5F	GATCTACACCGTCACCACAAA
CSP_006607_5R	CCTCCACTAGCTCCAGCCAAGCCGGTAGATGGGACGTTGCTTT
CSP_006607_3F	GTTGGTGTGCGATGTCAGCTCCGGAGCAACGACGACGACAGTATGG
CSP_006607_3R	GTGTCCTGCCATCTACTTG
CSP_006607_NF	GAGAACGGCGAAGACGAGTG
CSP_006607_NR	TTGCCCTGCTCTTTCAG

CSP_006607_SF	CACCAGGGACCTTTGGTAT
CSP_006607_SR	CATCGACGTGTGAACGAAAC
CSP_006607_PF	CCATTCCAGTTCAGGTCTA
CSP_006607_PR	TCGCTATCCAGACCATTCC
CSP_006607_5F	GTGTCCAAGCCTGCTTCTT
CSP_007586_5R	CCTCCACTAGCTCCAGCCAAGCCGGCCAAGGATGAAGGAGATG
CSP_007586_3F	GTTGGTGTCGATGTCAGCTCCGGAGAGAGTAGCTAAGCACCGAGT
CSP_007586_3R	CCTACCGTGGTCTCTTTGATTG
CSP_007586_NF	CGAATAGACCGGTATCCAGAAC
CSP_007586_NR	CCTTCCCAATGGCATTCTCTA
CSP_007586_SF	GGCTGAAAGGTACCCAGTATT
CSP_007586_SR	AGCCGTATTCGCCAGTTT
CSP_007586_PF	G TTCAGTTGACACGGGATGA
CSP_007586_PR	GACGACGATGACGATGATGAA
CSP_008738_5F	CTACTTACGACGAACCTCTGAC
CSP_008738_5R	CCTCCACTAGCTCCAGCCAAGCCGCTTCTATCCTTATCGCTCACT
CSP_008738_3F	GTTGGTGTCGATGTCAGCTCCGGAGGTTTGGGCAATATTCTCGCTAC
CSP_008738_3R	CTGGAGCATTTCGCTACTTTCG
CSP_008738_NF	CCACGAAGACCAATAGGAGAATA
CSP_008738_NR	CGCACTCTACCTGATGTTTGA
CSP_008738_SF	AACTCGAAGTCTCGCCAATAA
CSP_008738_SR	CGCTGAGATTGACCACTAGAA
CSP_008738_PF	TGAGAGCCAGAGCTTGTTTAG
CSP_008738_PR	CTACCGCCTTAGCCTTGATT
CSP_009802_5F	TTGACGAGTCTGTCCGTTTG
CSP_009802_5R	CCTCCACTAGCTCCAGCCAAGCCCGTGGTCTAGGGTATTGAATGAG
CSP_009802_3F	GTTGGTGTCGATGTCAGCTCCGGAGCGTACTTTAGTACCTATCAGTGAACCT
CSP_009802_3R	GACCATCTGGCGTGACTTATC
CSP_009802_NF	GGACAGGACCGGTGATACT
CSP_009802_NR	CAGCCAAATCTCCTTGGGTAG
CSP_009802_SF	GATCGCTCGCGTACTGAAATA
CSP_009802_SR	GACGAGAAACACAACCTCATAAATC
CSP_009802_PF	TGAAAGGTACCTGGCCAATC
CSP_009802_PR	CGGGCCATTGACTGTATTAGT
CSP_010617_5F	AGGAGGTAGCTGTCAGAGAA
CSP_010617_5R	CCTCCACTAGCTCCAGCCAAGCCCGACTTCAAGAGGGTCGATAA
CSP_010617_3F	GTTGGTGTCGATGTCAGCTCCGGAGCAGATGGGATTGCAGATCGATAG
CSP_010617_3R	CTAATTA CTGCTGGCTGGGTAG
CSP_010617_NF	GCTGACTGAGTTGTGGTCTAAC
CSP_010617_NR	GCAGAAGGCGGGTCAATTAT
CSP_010617_SF	CAGTGTCTTCCCTCTCATTGG
CSP_010617_SR	GATTCGTCGCCTGGAAC T
CSP_010617_PF	CCATGCACAGCGATTTCTTTC
CSP_009947_5F	AAGCTAGCTAGGTACGTATT
CSP_009947_5R	CCTCCACTAGCTCCAGCCAAGCCGTCAAAGCCTCAAAGTTGTGTTG
CSP_009947_3F	GTTGGTGTCGATGTCAGCTCCGGAGTGATGGGACATCATCTGAAAGGTAGG

CSP_009947_3R	GCTGTGGACTGTGTATACTGAT
CSP_009947_NF	CCTAACCCCTTTGGGCCTATATT
CSP_009947_NR	ACCCGTGTCTGAATCTGAATG
CSP_009947_SF	GGATCAGGTTAGTGCCATGAG
CSP_009947_SR	GACCACAGTATGCGGAGTTT
CSP_009947_PF	GCCTAACCCCTTTAGCCCTATATT
CSP_009947_PR	TACTGACGGCTAGGACGATAA
CSP_010985_5F	GGACGGCAAGGATGAAGAT
CSP_010985_5R	CCTCCACTAGCTCCAGCCAAGCCGGTAGCAACGGACAGATACAA
CSP_010985_3F	GTTGGTGTCTGATGTCAGCTCCGGAGGTCGAAGCTAGGAGTCGTAAAC
CSP_010985_3R	TTATGAGCTTGTATCCGGTATGT
CSP_010985_NF	CGCTCTGTTCAGTTCGACTATG
CSP_010985_NR	AACGAGGTGTGGAGGTAAGA
CSP_010985_SF	CCCATGTTGTTGGACTTGTATCT
CSP_010985_SR	CCCGTGTCTTGTCCAATCTTC
CSP_010985_PF	GGGACAGGCGTGACAATAAA
CSP_010985_PR	CACACTCACGACCAAATACGA
CSP_011033_5F	ACCTATCTTGTCCCTCGTTTG
CSP_011033_5R	CCTCCACTAGCTCCAGCCAAGCCGATGGTGTGGTCTGATGTGGAGA
CSP_011033_3F	GTTGGTGTCTGATGTCAGCTCCGGAGGAACAGAAGCAAGCGAGAGA
CSP_011033_3R	TACGCAGCACAGATACGAAG
CSP_011033_NF	CCTCACCTCACCTCACCTCA
CSP_011033_NR	GGAGACTGGGACTAGGCGTT
CSP_011033_SF	CGATCCCACCCTTCCTTTC
CSP_011033_SR	TCTCCTATCCGTCCCCTATG
CSP_011033_PF	CCTCTATTCTCTGGATGCTCTG
CSP_011033_PR	GCAGGTAATTTGTCTGGTTGAG