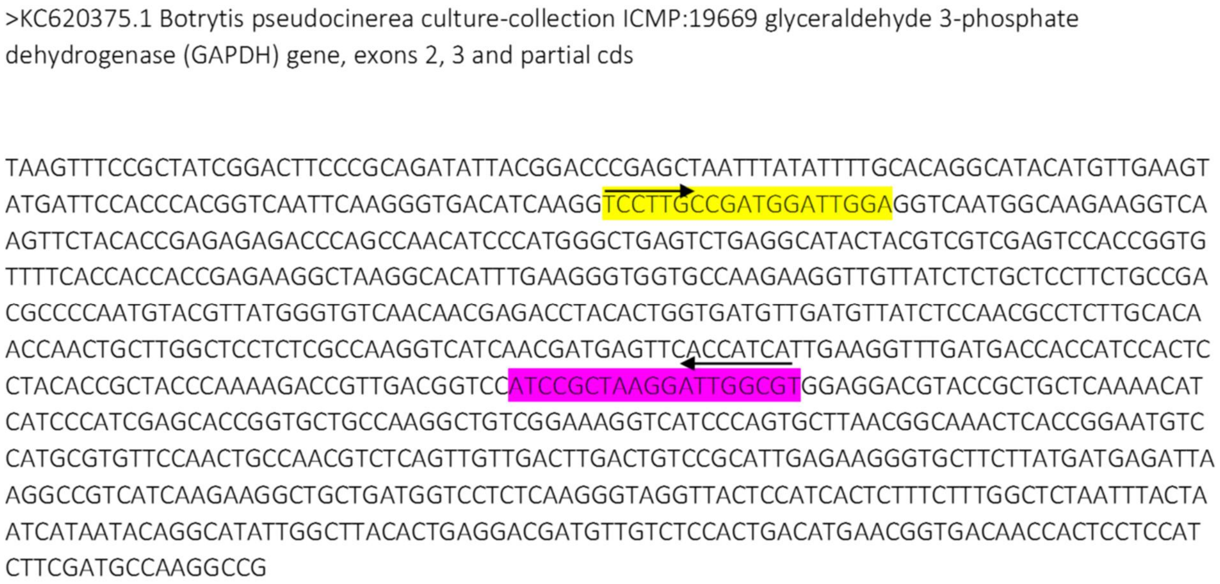
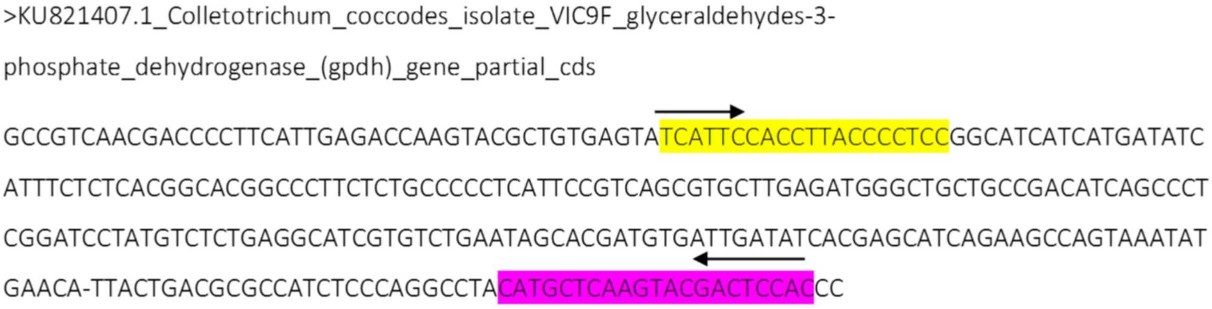


```
>KC620375.1 Botrytis pseudocinerea culture-collection ICMP:19669 glyceraldehyde 3-phosphate
dehydrogenase (GAPDH) gene, exons 2, 3 and partial cds

TAAGTTTCCGCTATCGGACTTCCCGCAGATATTACGGACCCGAGCTAATTTATATTTTGCACAGGCATACATGTTGAAGT
ATGATTCCACCCACGGTCAATTCAAGGGTGACATCAAGGTCCTTGCCGATGGATTGGAGGTCAATGGCAAGAAGGTCA
AGTTCTACACCGAGAGAGACCCAGCCAACATCCCATGGGCTGAGTCTGAGGCATACTACGTCGTCGAGTCCACCGGTG
TTTTCACCACCACCGAGAAGGCTAAGGCACATTTGAAGGGTGGTGCCAAGAAGGTTGTTATCTCTGCTCCTTCTGCCGA
CGCCCCAATGTACGTTATGGGTGTCAACAACGAGACCTACACTGGTGATGTTGATGTTATCTCCAACGCCTCTTGCACA
ACCAACTGCTTGGCTCCTCTCGCCAAGGTCATCAACGATGAGTTCACCATCATTGAAGGTTTGATGACCACCATCCACTC
CTACACCGCTACCCAAAAGACCGTTGACGGTCCATCCGCTAAGGATTGGCGTGGAGGACGTACCGCTGCTCAAAACAT
CATCCCATCGAGCACCGGTGCTGCCAAGGCTGTCGGAAAGGTCATCCCAGTGCTTAACGGCAAACTCACCGGAATGTC
CATGCGTGTTCCAACTGCCAACGTCTCAGTTGTTGACTTGACTGTCCGCATTGAGAAGGGTGCTTCTTATGATGAGATTA
AGGCCGTCATCAAGAAGGCTGCTGATGGTCCTCTCAAGGGTAGGTTACTCCATCACTCTTTCTTTGGCTCTAATTTACTA
ATCATAATACAGGCATATTGGCTTACACTGAGGACGATGTTGTCTCCACTGACATGAACGGTGACAACCACTCCTCCAT
CTTCGATGCCAAGGCCG
```

Figure S1. Position of the specific primer for *Botrytis cinerea*. The positioning of the forward and revers primer for drawing primer of *Botrytis cinerea* within the nucleotide sequence of the DNA glyceraldehyde 3-phosphate dehydrogenase (GAPDH) of *Botrytis pseudocinerea* (GenBank accession n. KC620375).

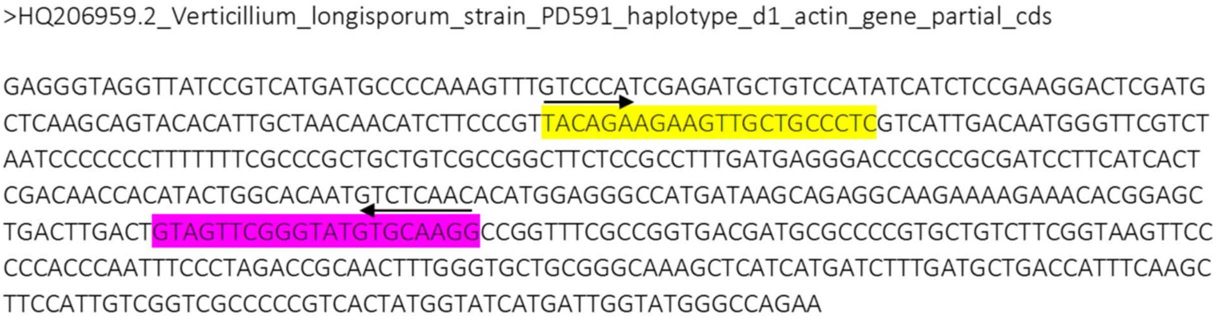


```
>KU821407.1_Colletotrichum_coccodes_isolate_VIC9F_glyceraldehydes-3-
phosphate_dehydrogenase_(gpdh)_gene_partial_cds

GCCGTCAACGACCCCTTCATTGAGACCAAGTACGCTGTGAGTATCATTCCACCTTACCCCTCCGGCATCATCATGATATC
ATTTCTCTCACGGCACGGCCCTTCTCTGCCCCCTCATTCCGTCAGCGTGCTTGAGATGGGCTGCTGCCGACATCAGCCCT
CGGATCCTATGTCTCTGAGGCATCGTGTCTGAATAGCACGATGTGATTGATATCACGAGCATCAGAAGCCAGTAAATAT
GAACA-TTACTGACGCGCCATCTCCCAGGCCTACATGCTCAAGTACGACTCCACCC
```

Figure S2. Position of the specific primer for *Colletotrichum* sp.. The positioning of the forward and revers primer for drawing primer of *Colletotrichum* sp. within the nucleotide sequence of the DNA glyceraldehyde 3-phosphate dehydrogenase (GAPDH) of *Colletotrichum coccodes* (GenBank accession n. KU821407).

```
>MF326807.1_Phytophthora_balyanboodja_strain_VHS25675R3_beta-tubulin_(TUB)_gene_partial_cds

TACCACGGCGACTCGGACCTGCAGCTGGAGCGCATCAATGTTTACTACAACGAGGCCACCGGCGGCCGATACGTGCCC
CGCGCCATCCTCATGGACCTTGAGCCCGGCACGATGGACTCGGTGCGCGCCGGCCCGTACGGCCAGCTCTTCCGCCCG
GACAACTTCGTGTTCGGCCAGACCGGCGCCGGTAACAACTGGGCCAAGGGACACTACACCGAAGGCGCCGAGCTCAT
TGACTCGGTGCTTGACGTCGTCCGCAAGGAGGCTGAAAGCTGTGACTGTCTGCAGGGGTTCCAGATCACGCACTCGCT
TGGTGGTGGTACCGGCTCCGGTATGGGCACGCTTCTTATTTCGAAGATCCGTGAAGAGTACCCGGACCGTATCATGTG
CACGTATTCGGTGTGCCCGTCGCCCAAGGTGTCGGACACCGTCGTGGAGCCGTACAACGCTACACTGTCGGTGCACCA
GCTGGTCGAGAACGCCGACGAGGTCATGTGCTTGGATAACGAGGCCCTGTACGACATTTGCTTCCGTACGTTGAAGCT
CACGACCCCCACCTACGGCGACCTGAACCACCTGGTATGCGCCGCCATGTCGGGTATCACCACGTGCCTGCGTTTCCCC
GGTCAGCTGAACTCGGACCTGCGTAAGCTGGCAGTGAATCTGATCCCGTTCCCGCGTCTTCACTTCTTCATGATCGGTTT
CGCCCCGCTGACGTCGCGTGGCTCGCAGCAGTACCGGGCCCTGACGGTGCCTGAGCTGACGCAGCAGCAGTTTGACG
CCAAGAACATGATGTGCGCCGCYGACCCGCGCCACGGCCGCTATTTAACTGCCGCGTGTATGTTCCGCGGACGTATGA
GCACGAAGGAGGTGGATGAGCAAATGCTGAATGTGCAGAACAAGAACTCGTCATACTTCGTCGAGTGGATCCCCAACA
ACATCAAGGCCAGCGTGTGCGACATCCCGCCCAAGGGACTCAAGATGAGCACCACGTTCATCGGTAACTCGACCGCCA
TCCAGGAGATGTTTAAGCGCGTGTCCGAGCAGTTCACGGCAATGTTCCGCCGTAAGGCTTTCTTGCACTGGTACACTGG
TGAGGGTATGGATGAGATGGAGTTCACTGGA
```

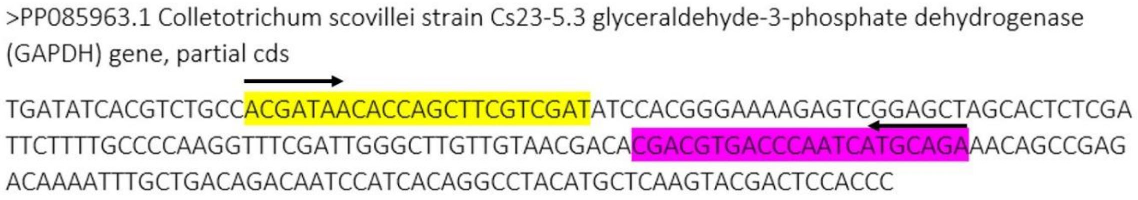
Figure S3. Position of the specific primer for *Phytophthora* sp.. The positioning of the forward and revers primer for drawing primer of *Phytophthora* sp. within the nucleotide sequence of the DNA β-tubulin (TUB) of *Phytophthora balyanboodja* (GenBank accession n. MF326807).



>HQ206959.2_Verticillium_longisporum_strain_PD591_haplotype_d1_actin_gene_partial_cds

GAGGGTAGGTTATCCGTCATGATGCCCCAAAGTTTGTCCCATCGAGATGCTGTCCATATCATCTCCGAAGGACTCGATG
CTCAAGCAGTACACATTGCTAACAACATCTTCCCGTTACAGAAGAAGTTGCTGCCCTCGTCATTGACAATGGGTTCGTCT
AATCCCCCCCTTTTTTTCGCCCGCTGCTGTCGCCGGCTTCTCCGCCTTTGATGAGGGACCCGCCGCGATCCTTCATCACT
CGACAACCACATACTGGCACAATGTCTCAACACATGGAGGGCCATGATAAGCAGAGGCAAGAAAAGAAACACGGAGC
TGACTTGACTGTAGTTCGGGTATGTGCAAGGCCGGTTTCGCCGGTGACGATGCGCCCCGTGCTGTCTTCGGTAAGTTCC
CCCACCCAATTTCCCTAGACCGCAACTTTGGGTGCTGCGGGCAAAGCTCATCATGATCTTTGATGCTGACCATTTCAAGC
TTCCATTGTCGGTCGCCCCCGTCACTATGGTATCATGATTGGTATGGGCCAGAA

Figure S4. Position of the specific primer for *Verticillium* sp.. The positioning of the forward and revers primer for drawing primer of *Verticillium* sp. within the nucleotide sequence of the DNA actin (ACT) of *Verticillium longisporum* (GenBank accession n. HQ206959).



>PP085963.1 Colletotrichum scovillei strain Cs23-5.3 glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, partial cds

TGATATCACGTCTGCCACGATAACACCAGCTTCGTCGATATCCACGGGAAAAGAGTCGGAGCTAGCACTCTCGA
TTCTTTTGCCCCAAGGTTTCGATTGGGCTTGTTGTAACGACACGACGTGACCCAATCATGCAGAAACAGCCGAG
ACAAAATTTGCTGACAGACAATCCATCACAGGCCTACATGCTCAAGTACGACTCCACCC

Figure S5. Position of the specific primer for *Colletotrichum acutatum*. The positioning of the forward and revers primer for drawing primer of *C. acutatum* within the nucleotide sequence of the DNA glyceraldehyde 3-phosphate dehydrogenase (GAPDH) of *Colletotrichum scovillei* (GenBank accession n. PP0859631) because the *C. scovillei* belongs to the *Colletotrichum acutatum* species complex (Damm *et al.*, 2012).

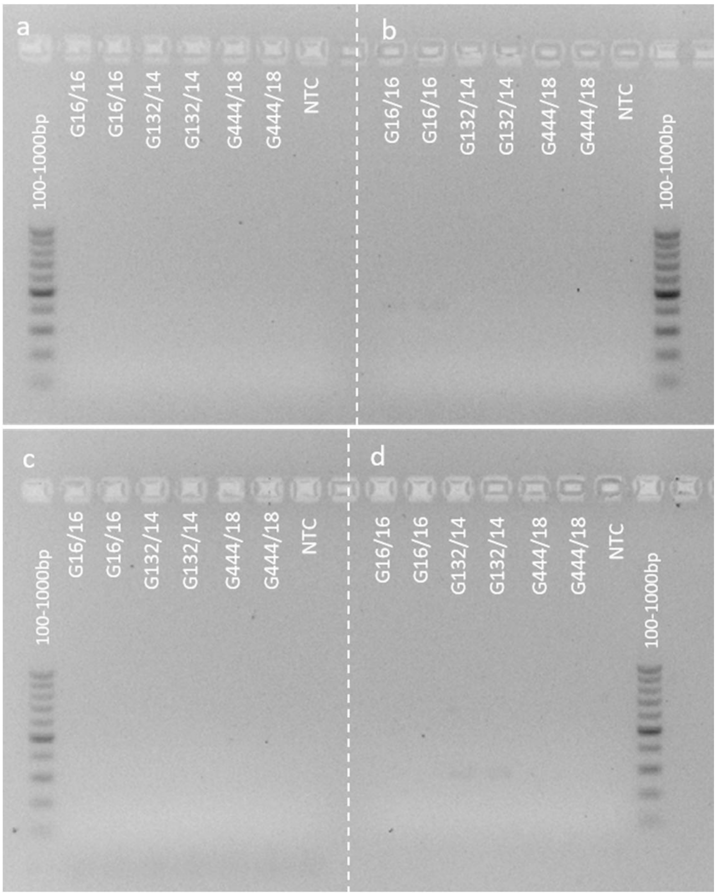


Figure S6. Specificity of the primer on pure fungal culture. PCR amplification using *B. cinerea* (a), *Colletotrichum* sp. (b), *Phytophthora* sp. (c), and *Verticillium* sp. (d) specific primers versus different fungi, as *Petriella setifera* (G16/16), *Neosartorya fischeri* (G132/14), *Gnomonia radicicola* (G444/18). Gel agarose 2% with 100-1,000 bp ladder. NTC means non-template control.

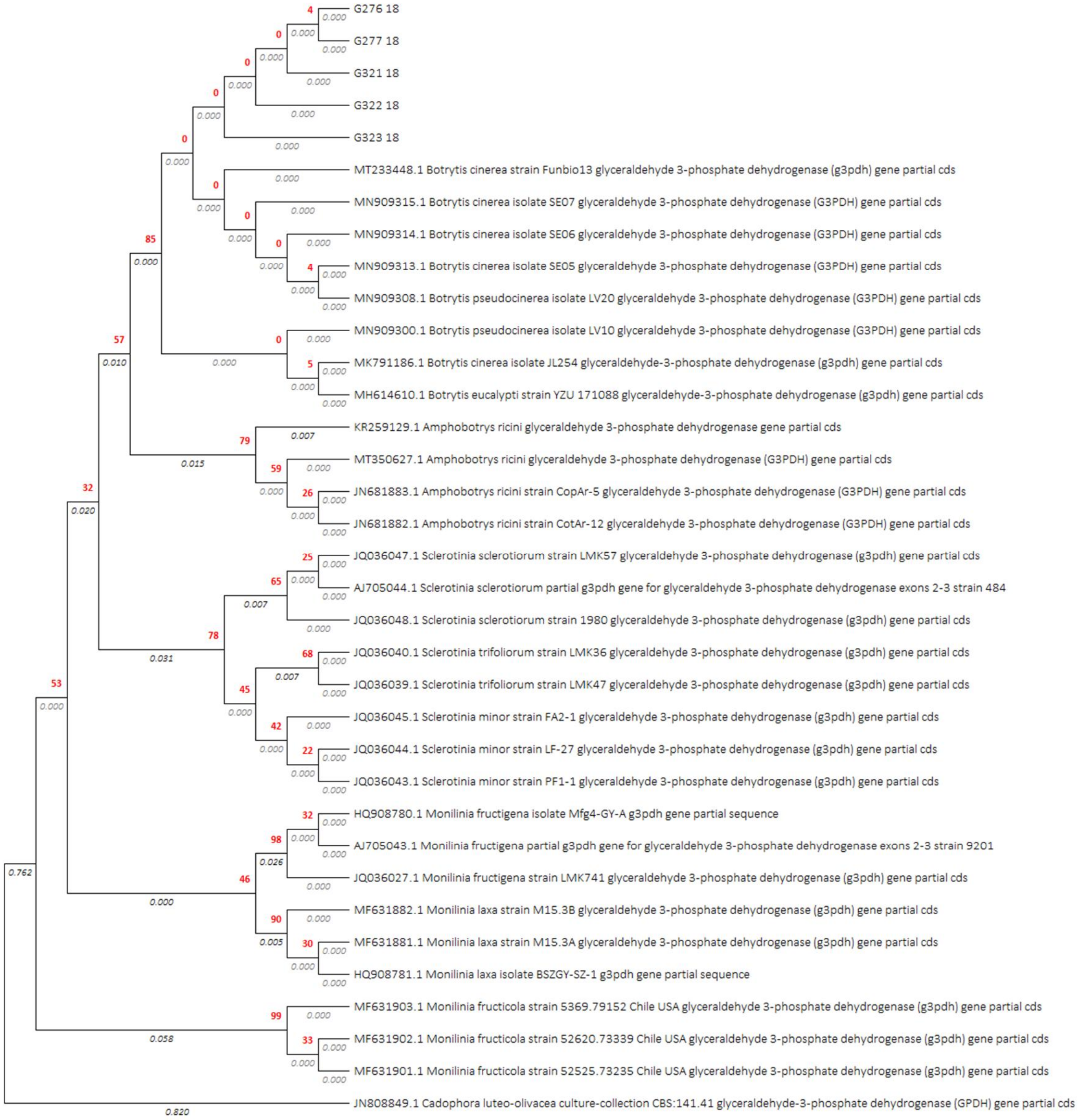


Figure S7. Phylogenetic analysis of *Botrytis cinerea* sequences based on glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene. Phylogenetic tree using the sequences obtained from tested pure strains of *Botrytis cinerea* (G276 18; G277 18; G321 18; G322 18; G323 18) and from environmental samples originating from National Center for Biotechnology Information (NCBI). The evolutionary history was inferred by using the Maximum Likelihood method and Kimura 2-parameter model with rate gamma distributed plus invariant sites. For this analysis was used the Bootstrap method (4000 number of Bootstrap replications). The percentage of trees in which the associated taxa clustered together is shown next to the branches in red bold, whereas in italic is written the branch lengths.

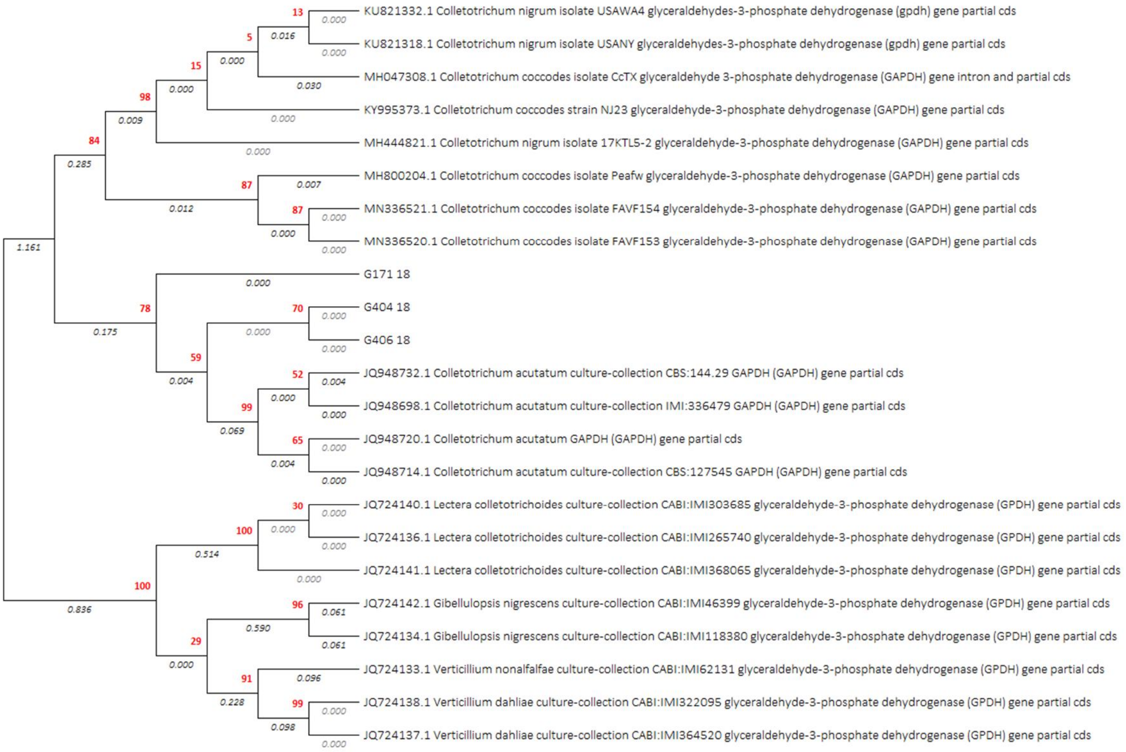


Figure S8. Phylogenetic analysis of *Colletotrichum* sp. sequences based on glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene. Phylogenetic tree using the sequences obtained from tested pure strains of *Colletotrichum* sp. (G171 18; G404 18; G406 18) and from environmental samples originating from National Center for Biotechnology Information (NCBI). The evolutionary history was inferred by using the Maximum Likelihood method and Kimura 2-parameter model with rate gamma distributed. For this analysis was used the Bootstrap method (4000 number of Bootstrap replications). The percentage of trees in which the associated taxa clustered together is shown next to the branches in red bold, whereas in italic is written the branch lengths.

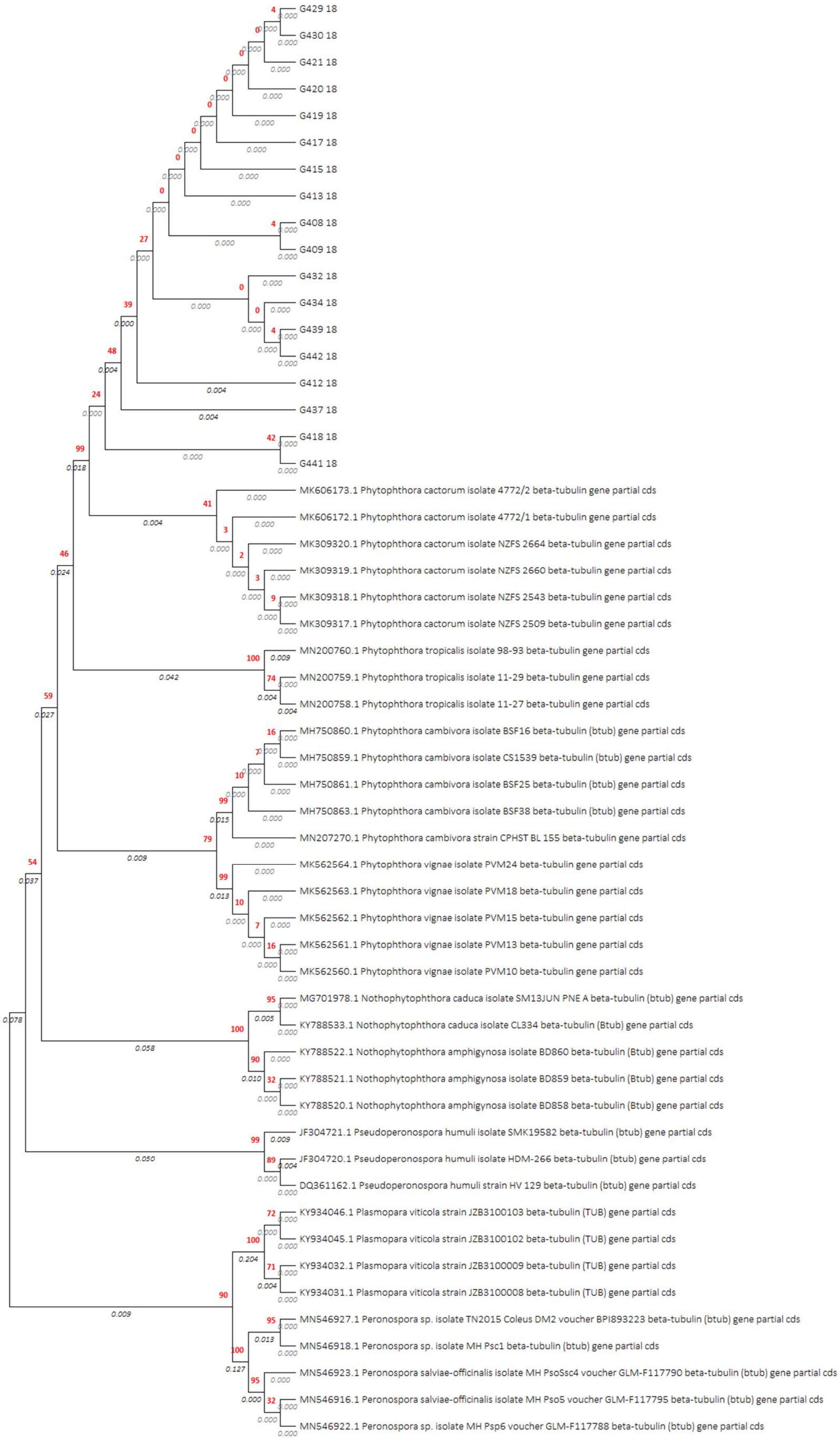

G429 18
G430 18
G421 18
G420 18
G419 18
G417 18
G415 18
G413 18
G408 18
G409 18
G432 18
G434 18
G439 18
G442 18
G412 18
G437 18
G418 18
G441 18
MK606173.1 Phytophthora cactorum isolate 4772/2 beta-tubulin gene partial cds
MK606172.1 Phytophthora cactorum isolate 4772/1 beta-tubulin gene partial cds
MK309320.1 Phytophthora cactorum isolate NZFS 2664 beta-tubulin gene partial cds
MK309319.1 Phytophthora cactorum isolate NZFS 2660 beta-tubulin gene partial cds
MK309318.1 Phytophthora cactorum isolate NZFS 2543 beta-tubulin gene partial cds
MK309317.1 Phytophthora cactorum isolate NZFS 2509 beta-tubulin gene partial cds
MN200760.1 Phytophthora tropicalis isolate 98-93 beta-tubulin gene partial cds
MN200759.1 Phytophthora tropicalis isolate 11-29 beta-tubulin gene partial cds
MN200758.1 Phytophthora tropicalis isolate 11-27 beta-tubulin gene partial cds
MH750860.1 Phytophthora cambivora isolate BSF16 beta-tubulin (btub) gene partial cds
MH750859.1 Phytophthora cambivora isolate CS1539 beta-tubulin (btub) gene partial cds
MH750861.1 Phytophthora cambivora isolate BSF25 beta-tubulin (btub) gene partial cds
MH750863.1 Phytophthora cambivora isolate BSF38 beta-tubulin (btub) gene partial cds
MN207270.1 Phytophthora cambivora strain CPHST BL 155 beta-tubulin gene partial cds
MK562564.1 Phytophthora vignae isolate PVM24 beta-tubulin gene partial cds
MK562563.1 Phytophthora vignae isolate PVM18 beta-tubulin gene partial cds
MK562562.1 Phytophthora vignae isolate PVM15 beta-tubulin gene partial cds
MK562561.1 Phytophthora vignae isolate PVM13 beta-tubulin gene partial cds
MK562560.1 Phytophthora vignae isolate PVM10 beta-tubulin gene partial cds
MG701978.1 Nothophytophthora caduca isolate SM13JUN PNE A beta-tubulin (btub) gene partial cds
KY788533.1 Nothophytophthora caduca isolate CL334 beta-tubulin (Btub) gene partial cds
KY788522.1 Nothophytophthora amphigynosa isolate BD860 beta-tubulin (Btub) gene partial cds
KY788521.1 Nothophytophthora amphigynosa isolate BD859 beta-tubulin (Btub) gene partial cds
KY788520.1 Nothophytophthora amphigynosa isolate BD858 beta-tubulin (Btub) gene partial cds
JF304721.1 Pseudoperonospora humuli isolate SMK19582 beta-tubulin (btub) gene partial cds
JF304720.1 Pseudoperonospora humuli isolate HDM-266 beta-tubulin (btub) gene partial cds
DQ361162.1 Pseudoperonospora humuli strain HV 129 beta-tubulin (btub) gene partial cds
KY934046.1 Plasmopara viticola strain JZB3100103 beta-tubulin (TUB) gene partial cds
KY934045.1 Plasmopara viticola strain JZB3100102 beta-tubulin (TUB) gene partial cds
KY934032.1 Plasmopara viticola strain JZB3100009 beta-tubulin (TUB) gene partial cds
KY934031.1 Plasmopara viticola strain JZB3100008 beta-tubulin (TUB) gene partial cds
MN546927.1 Peronospora sp. isolate TN2015 Coleus DM2 voucher BPI893223 beta-tubulin (btub) gene partial cds
MN546918.1 Peronospora sp. isolate MH Psc1 beta-tubulin (btub) gene partial cds
MN546923.1 Peronospora salviae-officinalis isolate MH PsoSsc4 voucher GLM-F117790 beta-tubulin (btub) gene partial cds
MN546916.1 Peronospora salviae-officinalis isolate MH Pso5 voucher GLM-F117795 beta-tubulin (btub) gene partial cds
MN546922.1 Peronospora sp. isolate MH Psp6 voucher GLM-F117788 beta-tubulin (btub) gene partial cds

Figure S9. Phylogenetic analysis of *Phytophthora* sp. sequences based on β-tubulin (TUB) gene. Phylogenetic tree using all the sequences obtained from tested pure strains (G429 18; G430 18; G421 18; G420 18; G419 18; G417 18; G415 18; G413 18; G408 18; G409 18; G432 18; G434 18; G439 18; G442 18; G412 18; G437 18; G418 18; G441 18) and from environmental samples originating from National Center for Biotechnology Information (NCBI). The evolutionary history was inferred by using the Maximum Likelihood method and Tamura-Nei model with invariant sites. For this analysis was used the Bootstrap method (4000 number of Bootstrap replications). The percentage of trees in which the associated taxa clustered together is shown next to the branches in red bold, whereas in italic is written the branch lengths.

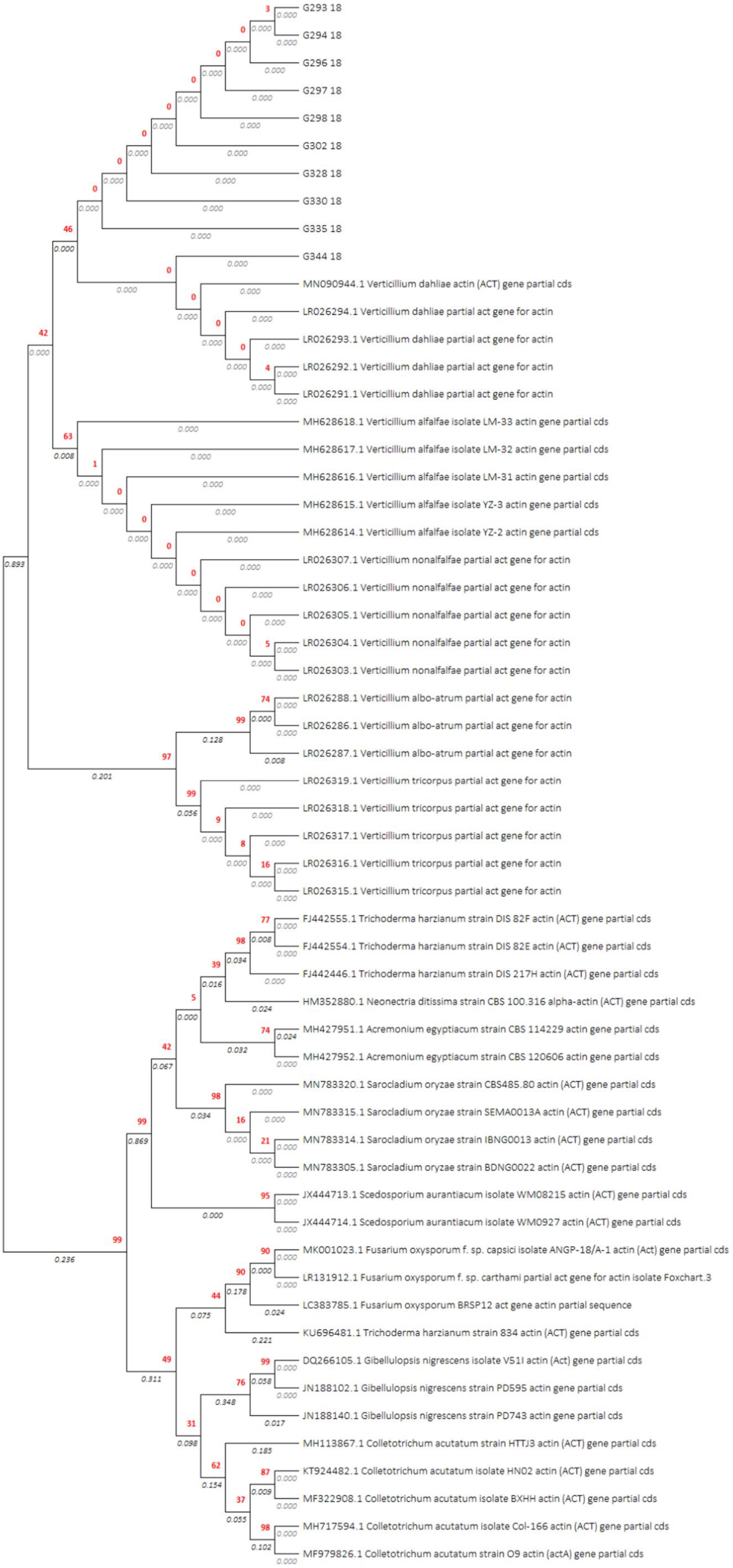

G293 18
G294 18
G296 18
G297 18
G298 18
G302 18
G328 18
G330 18
G335 18
G344 18
MN090944.1 Verticillium dahliae actin (ACT) gene partial cds
LR026294.1 Verticillium dahliae partial act gene for actin
LR026293.1 Verticillium dahliae partial act gene for actin
LR026292.1 Verticillium dahliae partial act gene for actin
LR026291.1 Verticillium dahliae partial act gene for actin
MH628618.1 Verticillium alfalfae isolate LM-33 actin gene partial cds
MH628617.1 Verticillium alfalfae isolate LM-32 actin gene partial cds
MH628616.1 Verticillium alfalfae isolate LM-31 actin gene partial cds
MH628615.1 Verticillium alfalfae isolate YZ-3 actin gene partial cds
MH628614.1 Verticillium alfalfae isolate YZ-2 actin gene partial cds
LR026307.1 Verticillium nonalfalfae partial act gene for actin
LR026306.1 Verticillium nonalfalfae partial act gene for actin
LR026305.1 Verticillium nonalfalfae partial act gene for actin
LR026304.1 Verticillium nonalfalfae partial act gene for actin
LR026303.1 Verticillium nonalfalfae partial act gene for actin
LR026288.1 Verticillium albo-atrum partial act gene for actin
LR026286.1 Verticillium albo-atrum partial act gene for actin
LR026287.1 Verticillium albo-atrum partial act gene for actin
LR026319.1 Verticillium tricorpus partial act gene for actin
LR026318.1 Verticillium tricorpus partial act gene for actin
LR026317.1 Verticillium tricorpus partial act gene for actin
LR026316.1 Verticillium tricorpus partial act gene for actin
LR026315.1 Verticillium tricorpus partial act gene for actin
FJ442555.1 Trichoderma harzianum strain DIS 82F actin (ACT) gene partial cds
FJ442554.1 Trichoderma harzianum strain DIS 82E actin (ACT) gene partial cds
FJ442446.1 Trichoderma harzianum strain DIS 217H actin (ACT) gene partial cds
HM352880.1 Neonectria ditissima strain CBS 100.316 alpha-actin (ACT) gene partial cds
MH427951.1 Acremonium egyptiacum strain CBS 114229 actin gene partial cds
MH427952.1 Acremonium egyptiacum strain CBS 120606 actin gene partial cds
MN783320.1 Sarocladium oryzae strain CBS485.80 actin (ACT) gene partial cds
MN783315.1 Sarocladium oryzae strain SEMA0013A actin (ACT) gene partial cds
MN783314.1 Sarocladium oryzae strain IBNG0013 actin (ACT) gene partial cds
MN783305.1 Sarocladium oryzae strain BDNG0022 actin (ACT) gene partial cds
JX444713.1 Scedosporium aurantiacum isolate WM08215 actin (ACT) gene partial cds
JX444714.1 Scedosporium aurantiacum isolate WM0927 actin (ACT) gene partial cds
MK001023.1 Fusarium oxysporum f. sp. capsici isolate ANGP-18/A-1 actin (Act) gene partial cds
LR131912.1 Fusarium oxysporum f. sp. carthami partial act gene for actin isolate Foxchart.3
LC383785.1 Fusarium oxysporum BRSP12 act gene actin partial sequence
KU696481.1 Trichoderma harzianum strain 834 actin (ACT) gene partial cds
DQ266105.1 Gibellulopsis nigrescens isolate V51I actin (Act) gene partial cds
JN188102.1 Gibellulopsis nigrescens strain PD595 actin gene partial cds
JN188140.1 Gibellulopsis nigrescens strain PD743 actin gene partial cds
MH113867.1 Colletotrichum acutatum strain HTTJ3 actin (ACT) gene partial cds
KT924482.1 Colletotrichum acutatum isolate HN02 actin (ACT) gene partial cds
MF322908.1 Colletotrichum acutatum isolate BXHH actin (ACT) gene partial cds
MH717594.1 Colletotrichum acutatum isolate Col-166 actin (ACT) gene partial cds
MF979826.1 Colletotrichum acutatum strain O9 actin (actA) gene partial cds

Figure S10. Phylogenetic analysis of *Verticillium* sp. sequences based on the actin (ACT) gene . Phylogenetic tree using all the sequences obtained from tested pure strains of *Verticillium* sp. (G293 18; G294 18; G296 18; G297 18; G298 18; G302 18; G328 18; G330 18; G335 18; G344 18) and from environmental samples originating from National Center for Biotechnology Information (NCBI). The evolutionary history was inferred by using the Maximum Likelihood method and Tamura-Nei model with rate gamma distributed. For this analysis was used the Bootstrap method (4000 number of Bootstrap replications). The percentage of trees in which the associated taxa clustered together is shown next to the branches in red bold, whereas in italic is written the branch lengths.

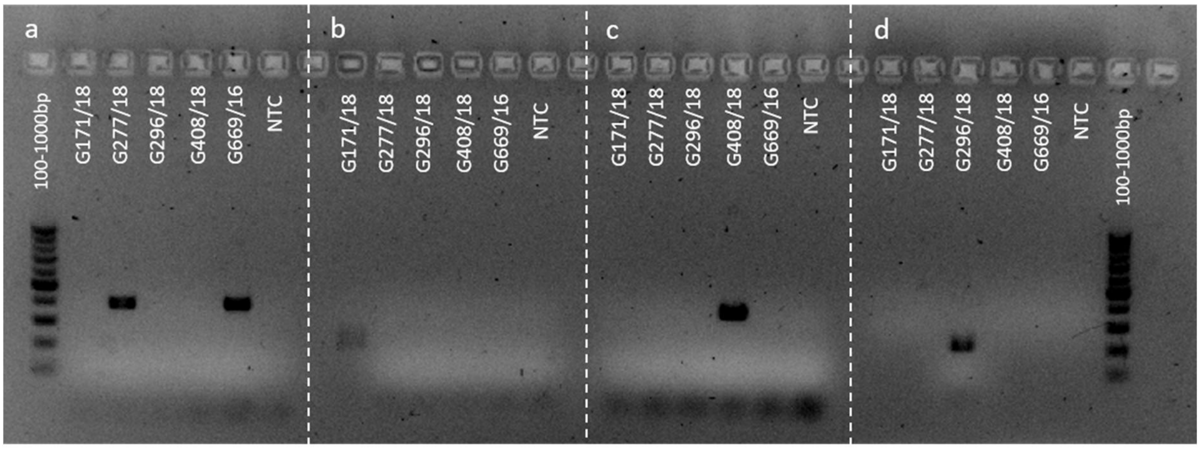


Figure S11. Specificity of the primer on pure fungal culture. PCR replication of the amplification using *B. cinerea* (a), *Colletotrichum* sp. (b), *Phytophthora* sp. (c), and *Verticillium* sp. (d) specific primers in pure cultures. Gel agarose 2% with 100-1,000 bp ladder. NTC means non-template control. The strains are *Colletotrichum* sp. (G171/18), *Botrytis* sp. (G277/18, G699/16), *Verticillum* sp. (G296/18), and *Phytophthora* sp. (G406/19).

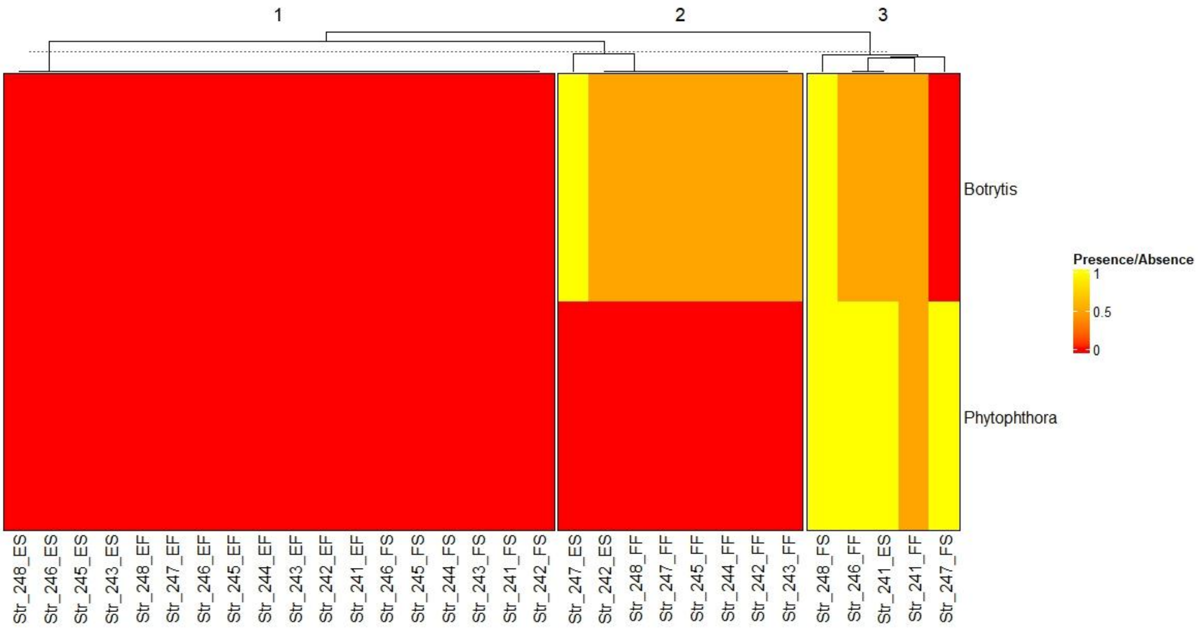


Figure S12. Specificity of the primer on naturally infected strawberry fruit. Heatmaps of the presence or absence of the phytopathogens *B. cinerea* and *Phytophthora* sp. using the specific primers in strawberry naturally infected working with 4 different kits of DNA extraction. The samples 244/19 and 245/19 came from a healthy plant; whereas 241/19-243/19 and 246/19 and 247/19 came from a plant that showed symptoms of the presence of the pathogens that we analysed.

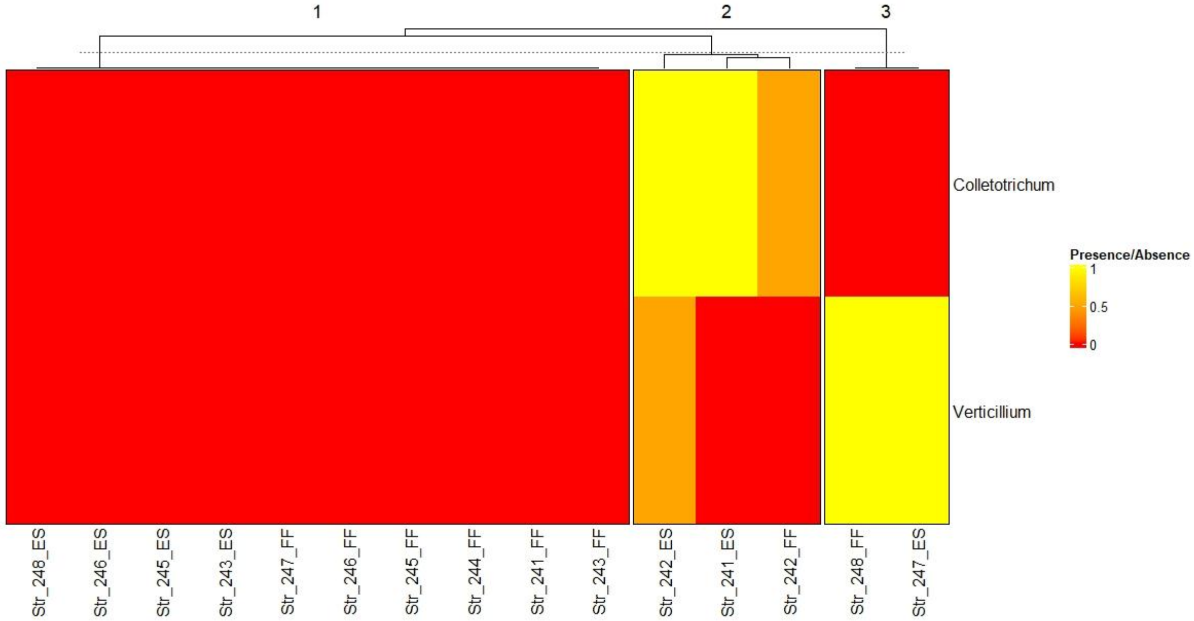


Figure S13. Specificity of the primer on naturally infected strawberry fruit. Heatmaps of the presence or absence of the phytopathogens *Colletotrichum* sp. and *Verticillium* sp. using the specific primers in strawberry naturally infected working with 2 different kits of DNA extraction. The samples 244/19 and 245/19 came from a healthy plant; whereas 241/19-243/19 and 246/19 and 247/19 came from a plant that showed symptoms of the presence of the pathogens that we analysed.

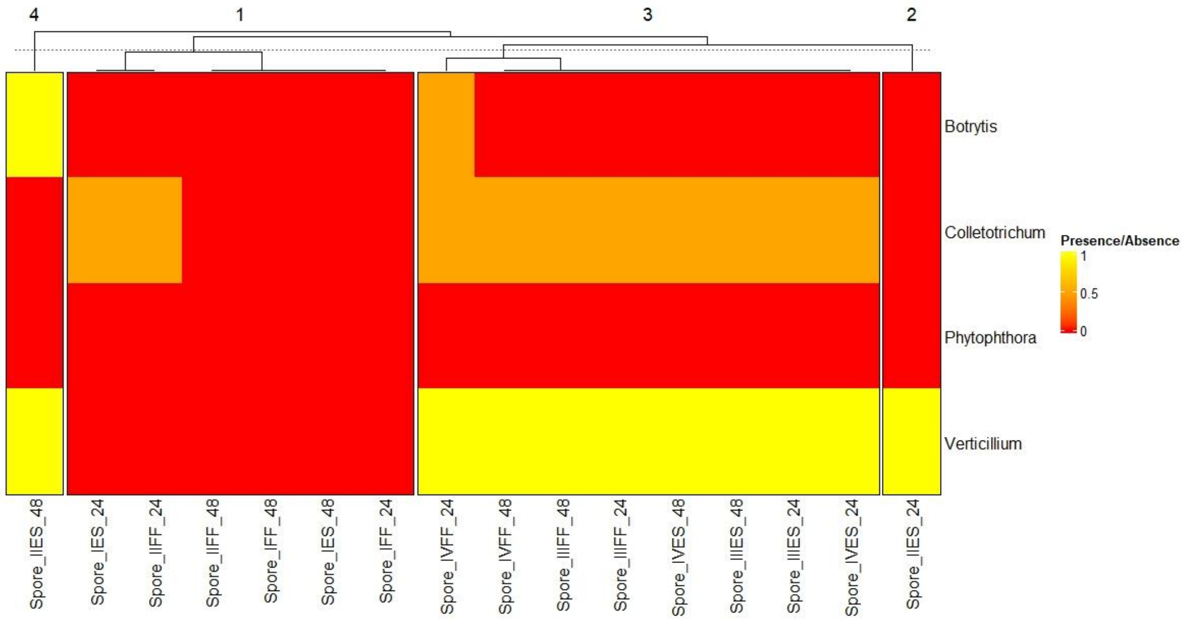


Figure S14. Specificity of the primer on soil artificially contaminated. Heatmaps of the presence or absence of *B. cinerea*, *Colletotrichum* sp., *Phytophthora* sp., and *Verticillium* sp. Using specific primers in soil artificial contaminated incubated at 24°C for 24, and 48 hours using two different kits of DNA extraction (FastDNA™ SPIN kit for Feces, FF; Soil DNA Purification kit, ES). The roman numerals indicate the concentration of pathogen spores per gram of soil (I – 500; II – 1,000; III – 5,000; IV – 10,000 spores g^{-1}). The increase in roman numerals indicates the increase in spores of each pathogen inside the soil.

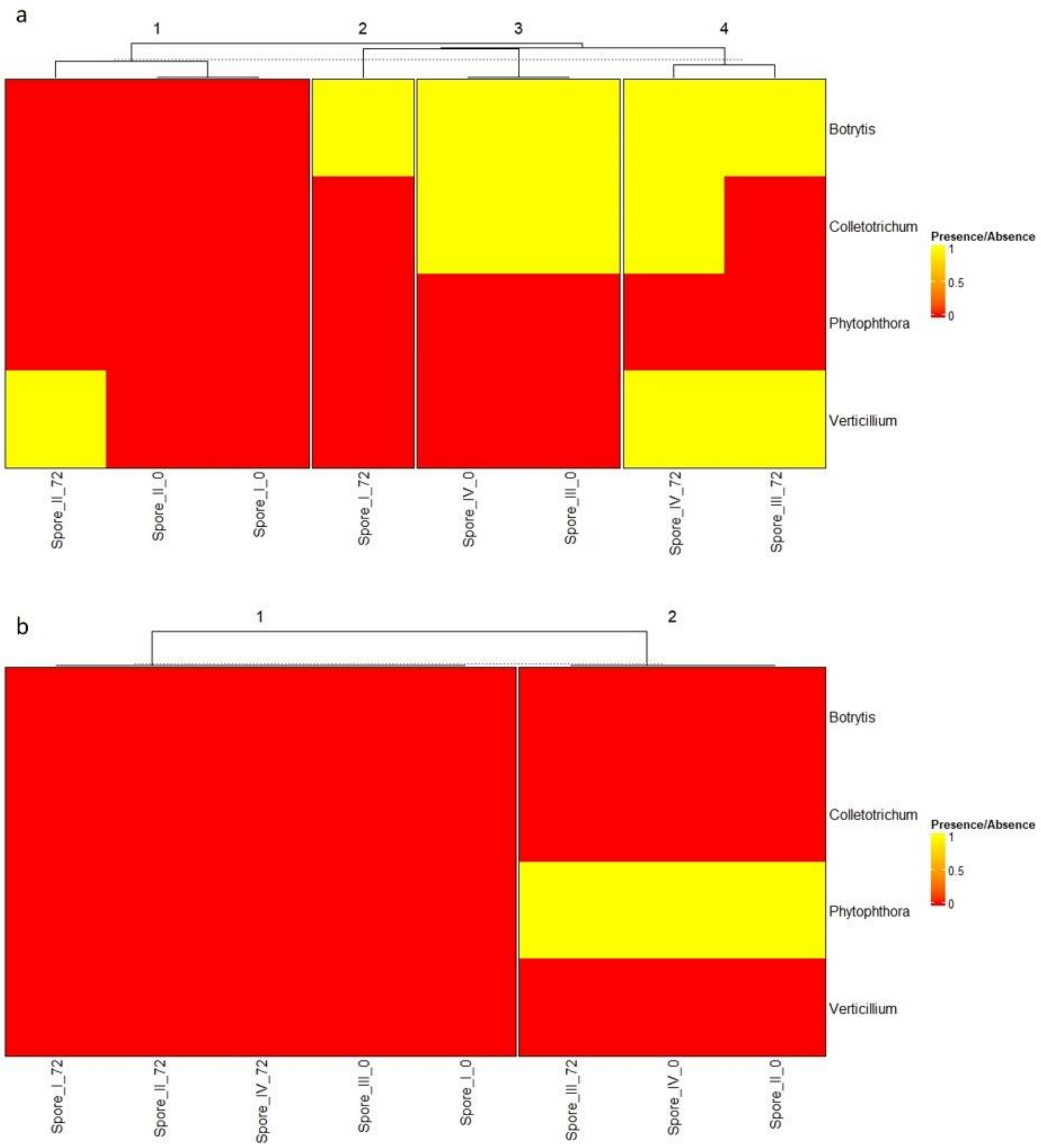


Figure S15. Specificity of the primer on soil artificially contaminated. Heatmaps of the presence or absence of *B. cinerea*, *Colletotrichum* sp., *Phytophthora* sp., and *Verticillium* sp. in soil (a) and strawberry (b) artificial contaminated incubated at 24°C for 0 and 72 hours extracted with the Soil DNA Purification kit (ES). The roman numerals indicate the concentration of pathogen spores per gram of soil (I – 100; II – 1,000; III – 10,000; IV – 100,000 spores g^{-1}). The increase in roman numerals indicates the increase in spores of each pathogen inside the soil.

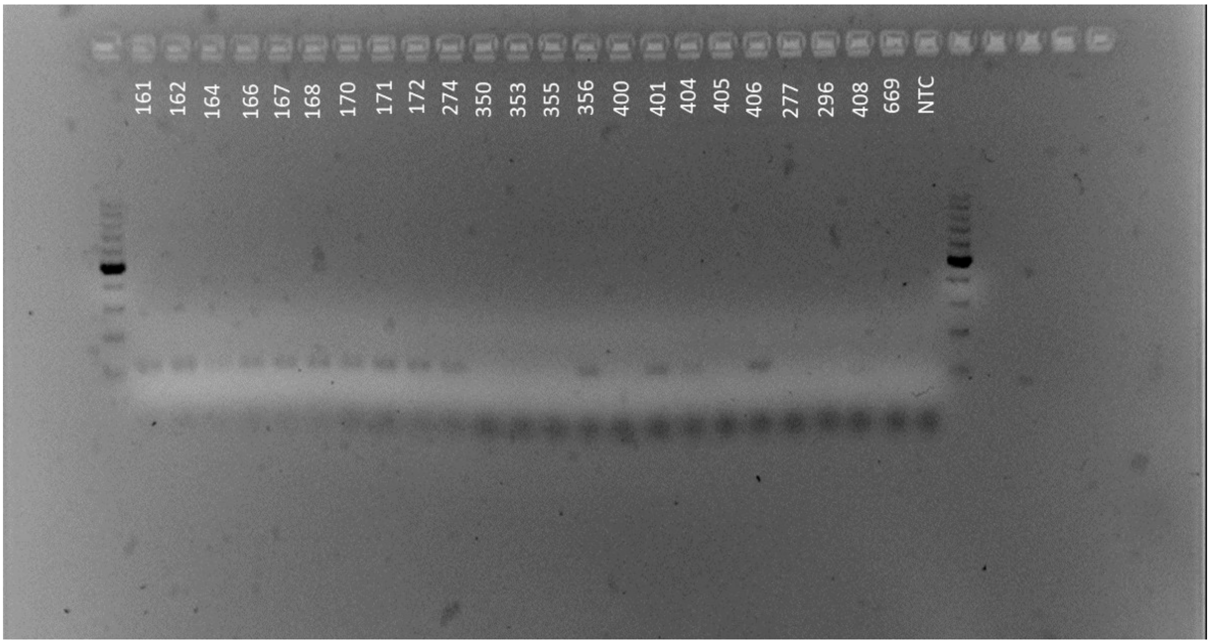
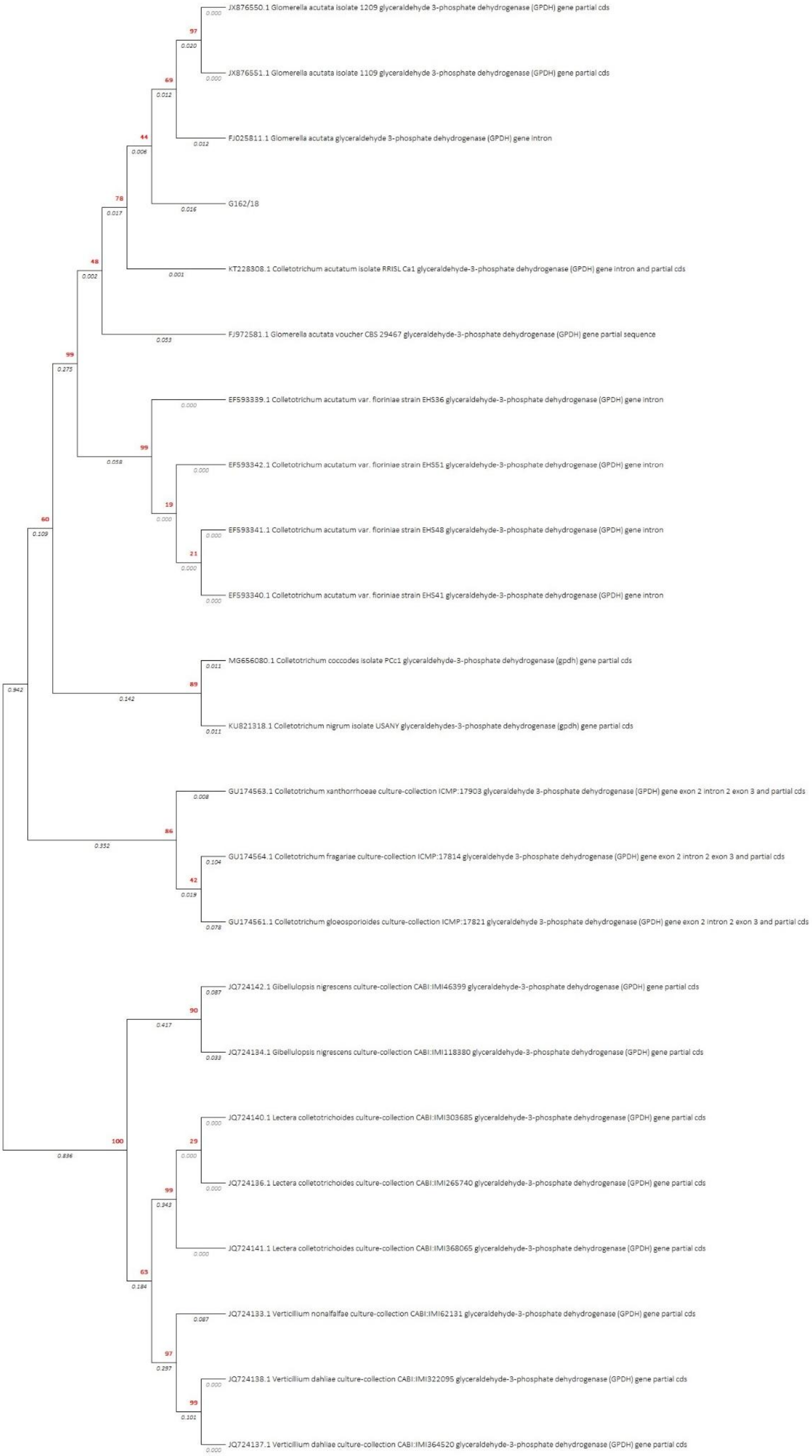


Figure S16. PCR amplification using *Colletotrichum acutatum* specific primer in pure culture. Gel agarose 2% with 100-1,000 bp ladder. NTC means non-template control. The replications are presented in the Figure S10. The number means: *Colletotrichum* sp.: 161, 162, 164, 166, 168, 170, 171, 172, 274, 350, 355, 356, 400, 401, 404, 405, 406; *Botrytis* sp.: 277, 669; *Verticillium* sp.: 296; *Phytophthora* sp.: 408.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0.000
97
0.020
JX876551.1 Glomerella acutata isolate 1109 glyceraldehyde 3-phosphate dehydrogenase (GPDH) gene partial cds
0.000
69
0.012
44
0.006
FJ025811.1 Glomerella acutata glyceraldehyde 3-phosphate dehydrogenase (GPDH) gene intron
0.012
78
G162/18
0.017
0.016
48
0.002
KT228308.1 Colletotrichum acutatum isolate RRISL Ca1 glyceraldehyde-3-phosphate dehydrogenase (GPDH) gene intron and partial cds
0.001
FJ972581.1 Glomerella acutata voucher CBS 29467 glyceraldehyde-3-phosphate dehydrogenase (GPDH) gene partial sequence
0.053
99
0.275
EF593339.1 Colletotrichum acutatum var. fioriniae strain EHS36 glyceraldehyde-3-phosphate dehydrogenase (GPDH) gene intron
0.000
99
0.058
EF593342.1 Colletotrichum acutatum var. fioriniae strain EHS51 glyceraldehyde-3-phosphate dehydrogenase (GPDH) gene intron
0.000
19
0.000
60
0.109
EF593341.1 Colletotrichum acutatum var. fioriniae strain EHS48 glyceraldehyde-3-phosphate dehydrogenase (GPDH) gene intron
0.000
21
0.000
EF593340.1 Colletotrichum acutatum var. fioriniae strain EHS41 glyceraldehyde-3-phosphate dehydrogenase (GPDH) gene intron
0.000
MG656080.1 Colletotrichum coccodes isolate PCc1 glyceraldehyde-3-phosphate dehydrogenase (gpdh) gene partial cds
0.011
89
0.942
0.142
KU821318.1 Colletotrichum nigrum isolate USANY glyceraldehydes-3-phosphate dehydrogenase (gpdh) gene partial cds
0.011
GU174563.1 Colletotrichum xanthorrhoeae culture-collection ICMP:17903 glyceraldehyde 3-phosphate dehydrogenase (GPDH) gene exon 2 intron 2 exon 3 and partial cds
0.008
86
0.352
GU174564.1 Colletotrichum fragariae culture-collection ICMP:17814 glyceraldehyde 3-phosphate dehydrogenase (GPDH) gene exon 2 intron 2 exon 3 and partial cds
0.104
42
0.019
GU174561.1 Colletotrichum gloeosporioides culture-collection ICMP:17821 glyceraldehyde 3-phosphate dehydrogenase (GPDH) gene exon 2 intron 2 exon 3 and partial cds
0.078
JQ724142.1 Gibellulopsis nigrescens culture-collection CABI:IMI46399 glyceraldehyde-3-phosphate dehydrogenase (GPDH) gene partial cds
0.087
90
0.417
JQ724134.1 Gibellulopsis nigrescens culture-collection CABI:IMI118380 glyceraldehyde-3-phosphate dehydrogenase (GPDH) gene partial cds
0.033
JQ724140.1 Lectera colletotrichoides culture-collection CABI:IMI303685 glyceraldehyde-3-phosphate dehydrogenase (GPDH) gene partial cds
0.000
100
29
0.836
0.000
JQ724136.1 Lectera colletotrichoides culture-collection CABI:IMI265740 glyceraldehyde-3-phosphate dehydrogenase (GPDH) gene partial cds
0.000
99
0.343
JQ724141.1 Lectera colletotrichoides culture-collection CABI:IMI368065 glyceraldehyde-3-phosphate dehydrogenase (GPDH) gene partial cds
0.000
63
0.184
JQ724133.1 Verticillium nonalfalfae culture-collection CABI:IMI62131 glyceraldehyde-3-phosphate dehydrogenase (GPDH) gene partial cds
0.087
97
0.297
JQ724138.1 Verticillium dahliae culture-collection CABI:IMI322095 glyceraldehyde-3-phosphate dehydrogenase (GPDH) gene partial cds
0.000
99
0.101
JQ724137.1 Verticillium dahliae culture-collection CABI:IMI364520 glyceraldehyde-3-phosphate dehydrogenase (GPDH) gene partial cds
0.000

Figure S17. Phylogenetic analysis of *Colletotrichum acutatum* sequences based on glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene. Phylogenetic tree using the sequence obtained from tested pure strain (G162 18) of *Colletotrichum acutatum* and from environmental samples originating from National Center for Biotechnology Information (NCBI). The evolutionary history was inferred by using the Maximum Likelihood method and Kimura 2-parameter model with rate gamma distributed. For this analysis was used the Bootstrap method (4000 number of Bootstrap replications). The percentage of trees in which the associated taxa clustered together is shown next to the branches in red bold, whereas in italic is written the branch lengths.

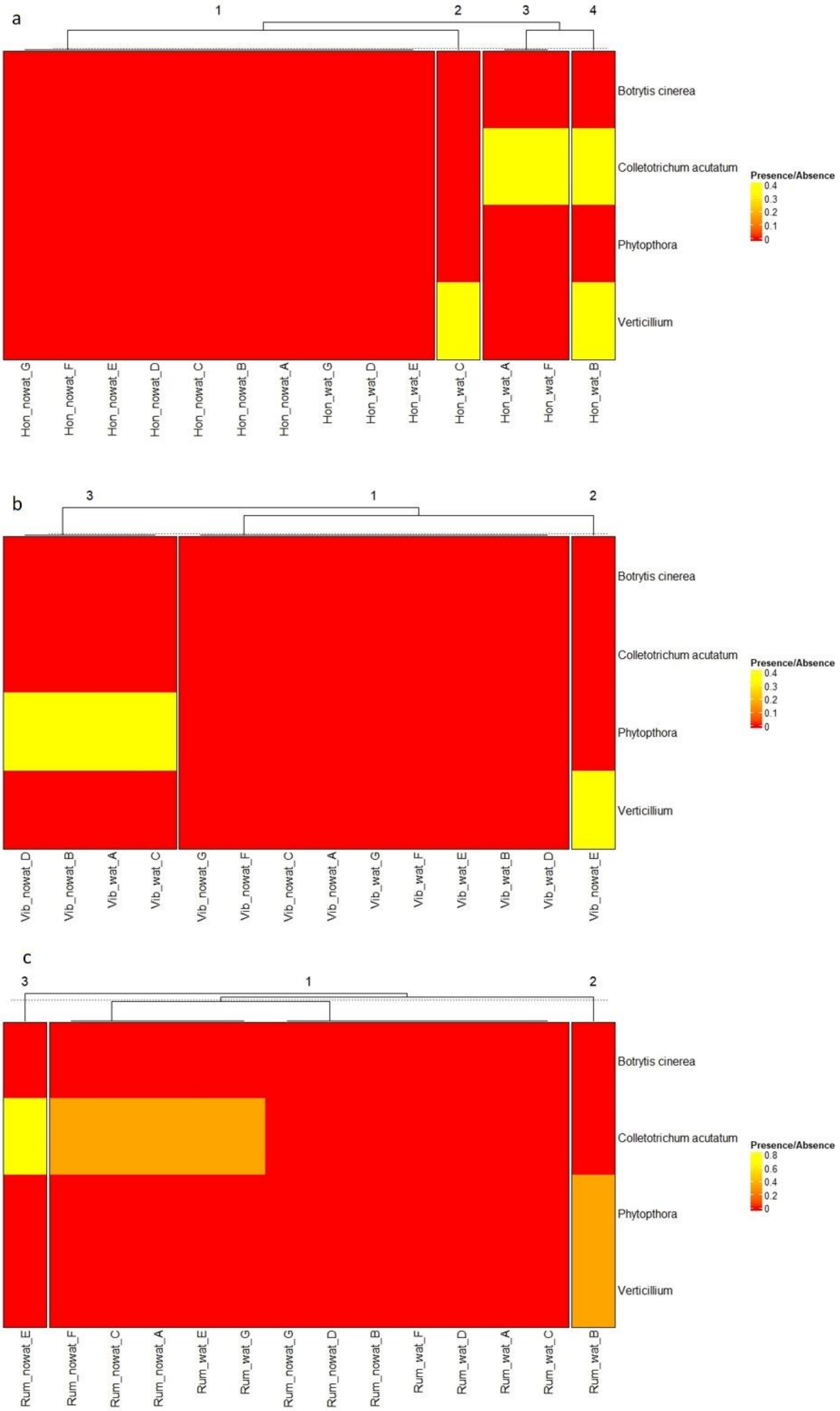a
1
2
3
4
Botrytis cinerea
Colletotrichum acutatum
Phytopthora
Verticillium
Presence/Absence
0.4
0.3
0.2
0.1
0
Hon_nowat_G
Hon_nowat_F
Hon_nowat_E
Hon_nowat_D
Hon_nowat_C
Hon_nowat_B
Hon_nowat_A
Hon_wat_G
Hon_wat_D
Hon_wat_E
Hon_wat_C
Hon_wat_A
Hon_wat_F
Hon_wat_B
b
3
1
2
Botrytis cinerea
Colletotrichum acutatum
Phytopthora
Verticillium
Presence/Absence
0.4
0.3
0.2
0.1
0
Vib_nowat_D
Vib_nowat_B
Vib_wat_A
Vib_wat_C
Vib_nowat_G
Vib_nowat_F
Vib_nowat_C
Vib_nowat_A
Vib_wat_G
Vib_wat_F
Vib_wat_E
Vib_wat_B
Vib_wat_D
Vib_nowat_E
c
3
1
2
Botrytis cinerea
Colletotrichum acutatum
Phytopthora
Verticillium
Presence/Absence
0.8
0.6
0.4
0.2
0
Rum_nowat_E
Rum_nowat_F
Rum_nowat_C
Rum_nowat_A
Rum_wat_E
Rum_wat_G
Rum_nowat_G
Rum_nowat_D
Rum_nowat_B
Rum_wat_F
Rum_wat_D
Rum_wat_A
Rum_wat_C
Rum_wat_B

Figure S18. Heatmaps about the presence/absence of *B. cinerea*, *Colletotrichum acutatum*., *Phytophthora* sp., and *Verticillium* sp. in strawberry fruit from field experiment for Honeoye (a), Vibrant (b), and Rumba (c). Explanations: Honeoye (Hon), Vibrant (Vib), Rumba (Rum), irrigated (wat), no-irrigated (nowat), Control without carrier (A), Control with carrier (B), P3 (C), P3+P1 (D), P3+P2 (E), P3+P1+P2 (F), P1+P2 (G).

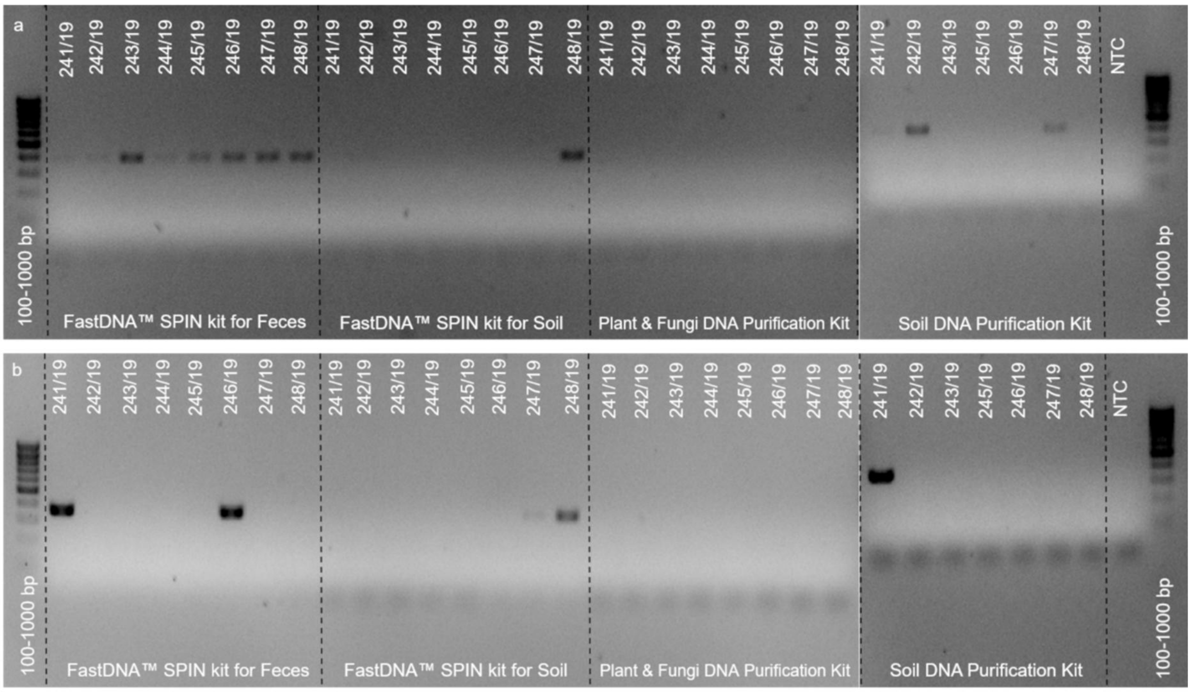

Figure S19. The specificity of the primer on naturally infected strawberry fruit. PCR amplification using *B. cinerea* (a) and *Phytophthora* sp. (b) specific primers in strawberry naturally infected using 4 different kits of DNA extraction. Gel agarose 2% with 100-1,000 bp ladder. NTC means non-template control. The samples 244/19 and 245/19 came from a healthy plant; whereas 241/19-243/19 and 246/19 and 247/19 were collected from sympthomatic plants diseased by pathogens. The replications are presented in the Figure S20.

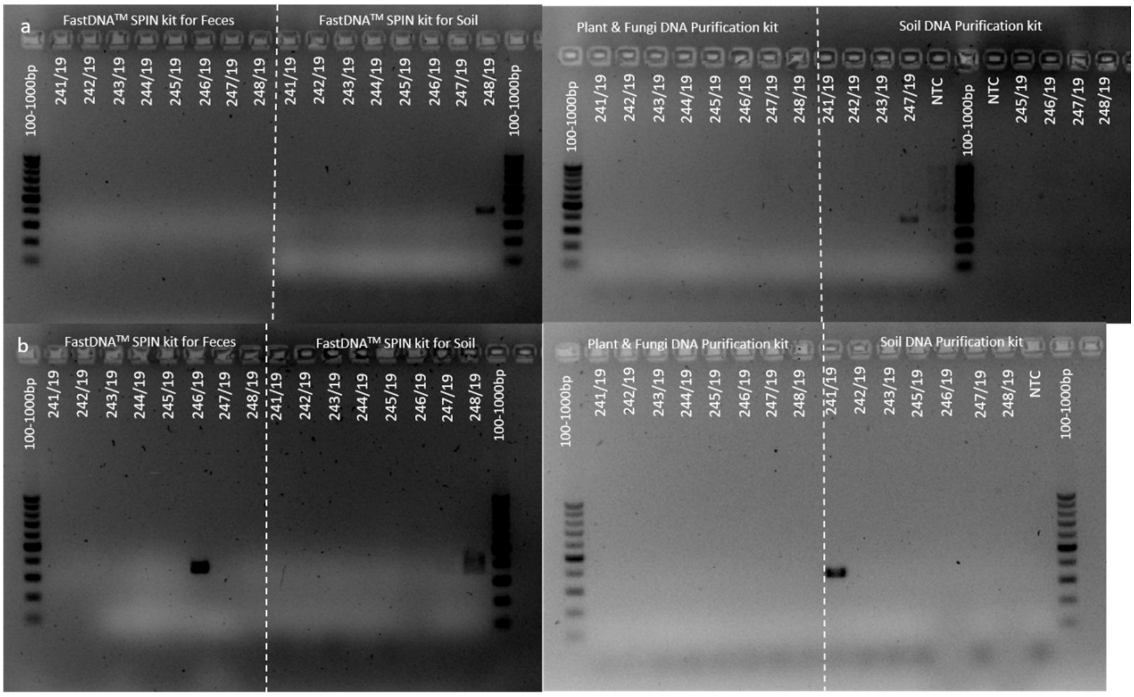

Figure S20. The specificity of the primer on naturally infected strawberry fruit. PCR replication of the amplification using *B. cinerea* (a) and *Phytophthora* sp. (b) specific primers in strawberry naturally infected using 4 different kits of DNA extraction. Gel agarose 2% with 100-1,000 bp ladder. NTC means non-template control. The samples 244/19 and 245/19 came from a healthy plant; whereas 241/19-243/19 and 246/19 and 247/19 were collected from sympthomatic plants diseased by pathogens.

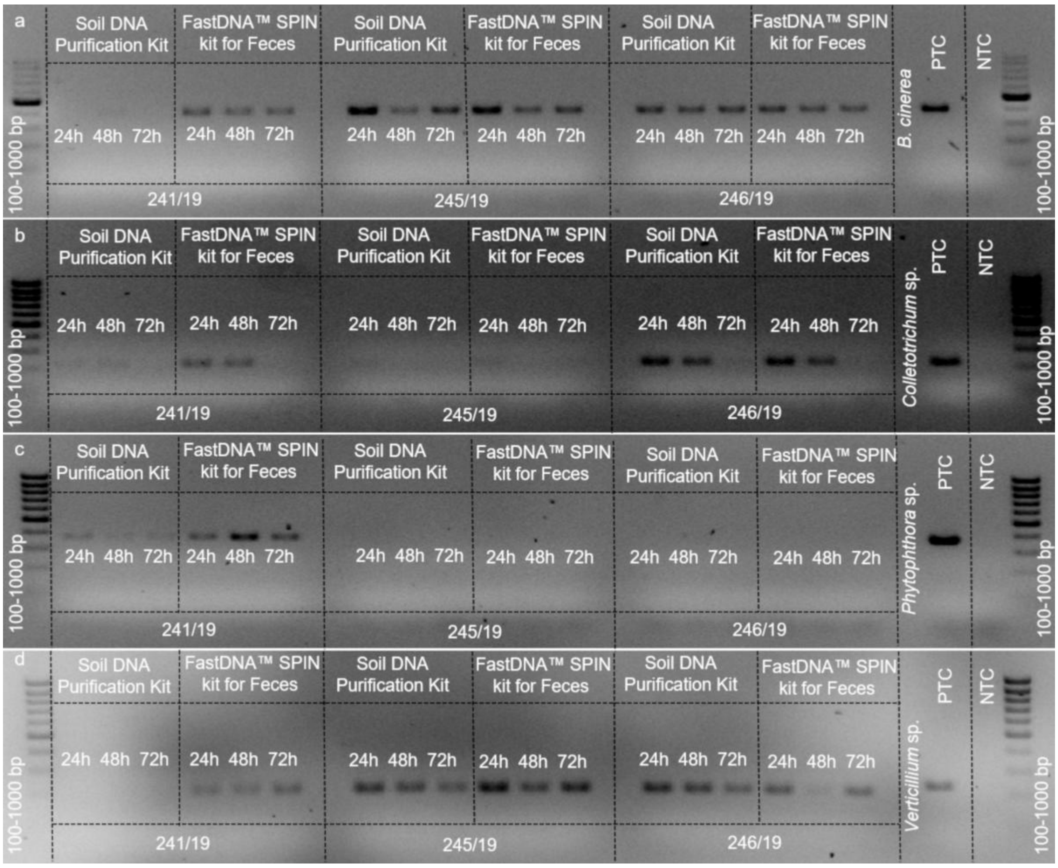

Figure S21. The specificity of the primer on naturally infected strawberry fruit. PCR amplification using B. *cinerea* (a), *Colletotrichum* sp. (b), *Phytophthora* sp. (c), and *Verticillium* sp. (d) specific primers in strawberry fruit (241/19; 245/19; 246/19) naturally infected incubated at 24°C for 24, 48, and 72 hours using 2 different kits of DNA extraction. Gel agarose 2% with 100-1,000 bp ladder. NTC means non-template control, and PTC is positive-template control (*B. cinerea* – G277/18; *Colletotrichum* sp. – G171/18; *Phytophthora* sp. – G408/18; *Verticillium* sp. – G296/18). The sample 245/19 came from a healthy plant; whereas 241/19 and 246/19 were collected from sympthomatic plants diseased by pathogens. The replications are presented in the Figure S22.

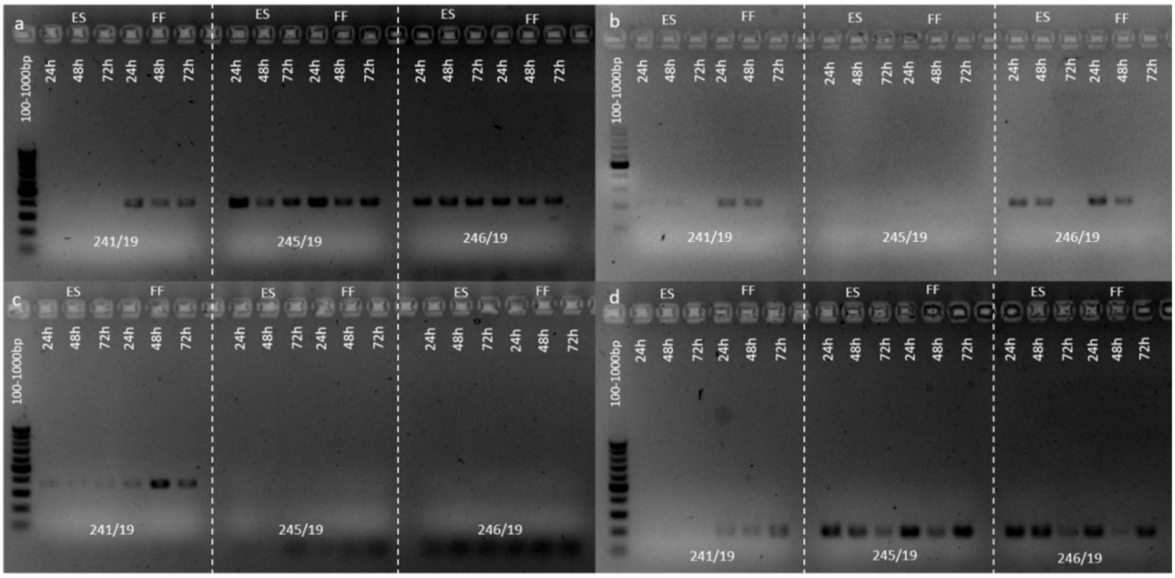

Figure S22. The specificity of the primer on naturally infected strawberry fruit. PCR replication of the amplification using *B. cinerea* (a), *Colletotrichum* sp. (b), *Phytophthora* sp. (c), and *Verticillium* sp. (d) specific primers in strawberry fruit naturally infected incubated at 24°C for 24, 48, and 72 hours using 2 different kits of DNA extraction. Gel agarose 2% with 100-1,000 bp ladder. NTC means non-template control, PTC is positive-template control, ES is Soil DNA purification kit, and FF is FastDNA™ SPIN kit for Feces. The sample 245/19 came from a healthy plant; whereas 241/19 and 246/19 were collected from sympthomatic plants diseased by pathogens.

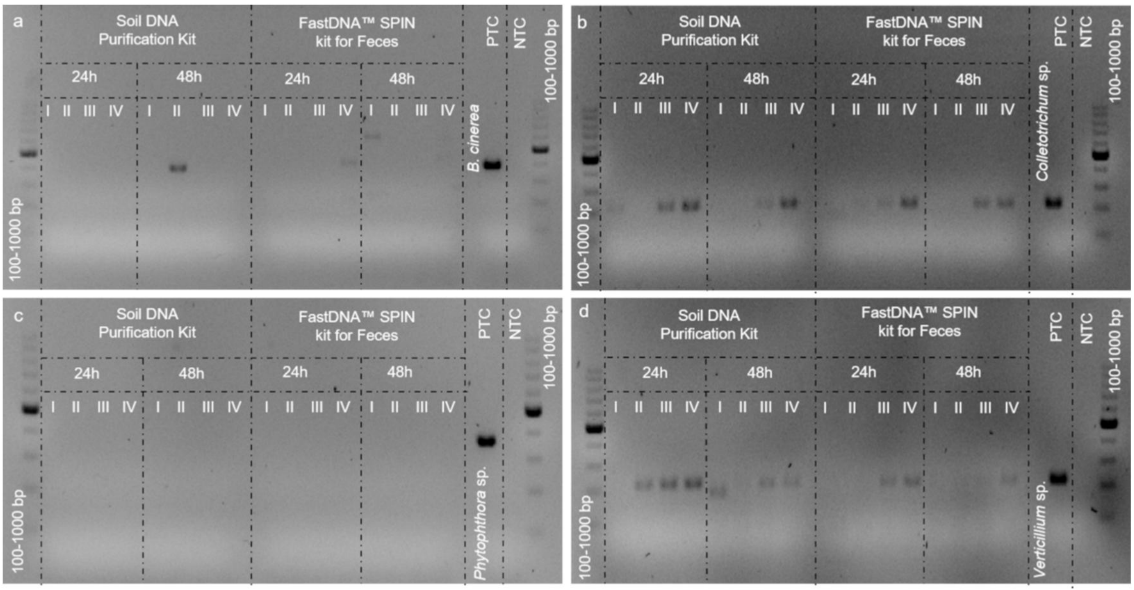

Figure S23. The specificity of the primer on artificially contaminated soil. PCR amplification using *B. cinerea* (a), *Colletotrichum* sp. (b), *Phytophthora* sp. (c), and *Verticillium* sp. (d) specific primers in soil artificially contaminated and incubated at 24°C for 24, and 48 hours using two different kits of DNA extraction. Gel agarose 2% with 100-1,000 bp ladder. NTC refers to non-template control, and PTC denotes positive-template control. The roman numerals indicate the concentration of pathogen spores per gram of soil (I – 500; II – 1,000; III – 5,000; IV – 10,000 spores g^{-1}). The increase in roman numerals indicates the increase in spores of each pathogen inside the soil. The replications are presented in Figure S24.

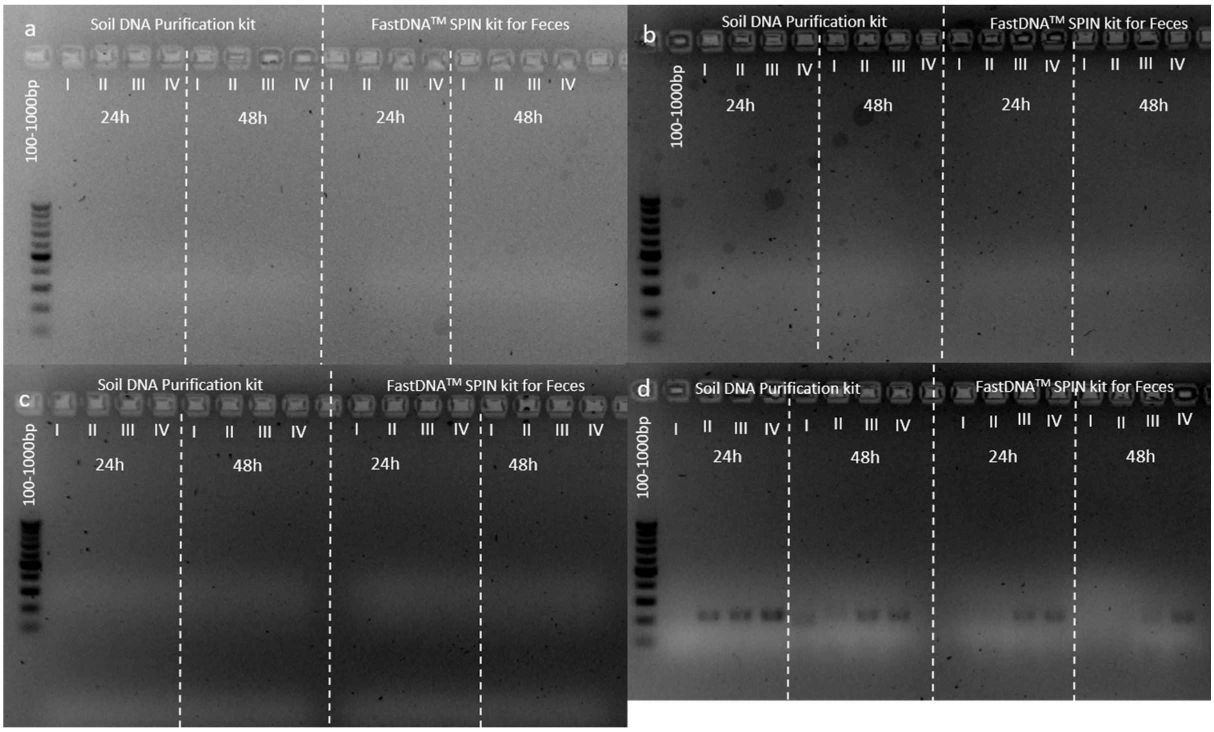

Figure S24. The specificity of the primer on artificially contaminated soil. PCR replication of the amplification using *B. cinerea* (a), *Colletotrichum* sp. (b), *Phytophthora* sp. (c), and *Verticillium* sp. (d) specific primers in soil artificial contaminated incubated at 24°C for 24, and 48 hours using two different kits of DNA extraction. Gel agarose 2% with 100-1,000 bp ladder. NTC means non-template control, and PTC is positive-template control. The roman numerals indicate the concentration of pathogen spores per gram of soil (I – 500; II – 1,000; III – 5,000; IV – 10,000 spores g^{-1}). The increase in roman numerals indicates the increase in spores of each pathogen inside the soil.

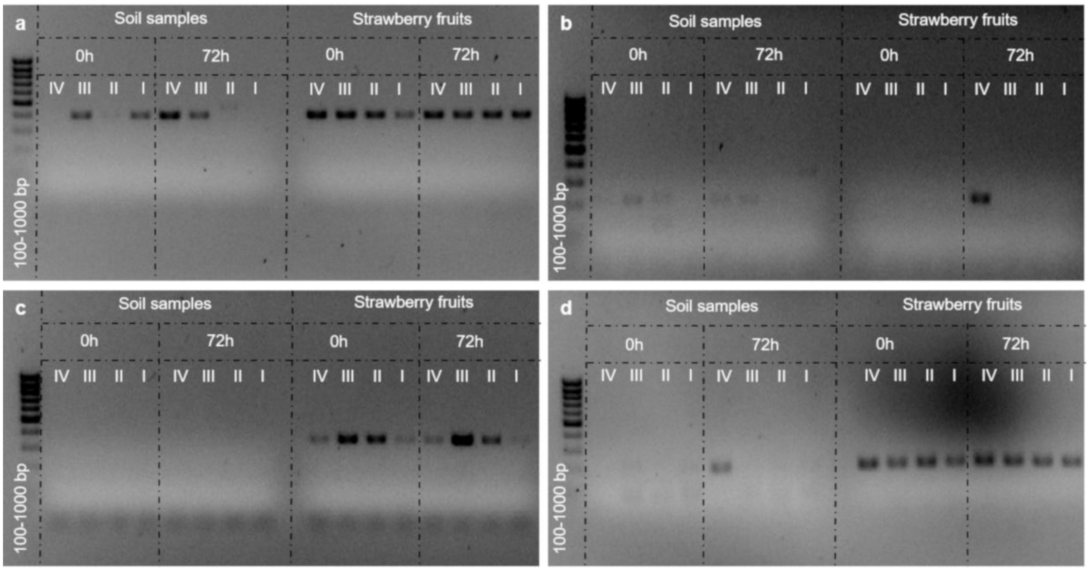

Figure S25. The specificity of the primer on artificially contaminated soil and strawberry fruit. PCR amplification using *B. cinerea* (a), *Colletotrichum* sp. (b), *Phytophthora* sp. (c), and *Verticillium* sp. (d) specific primers in artificially contaminated soil and strawberry, incubated at 24°C for 0 and 72 hours extracted with the FastDNA™ SPIN kit for Feces. Gel agarose 2% with 100-1,000 bp ladder. The roman numerals indicate the concentration of pathogen spores per gram of soil (I – 100; II – 1,000; III – 10,000; IV – 100,000 spores g^{-1}). The increase in roman numerals indicates the increase in spores of each pathogen inside the soil. The replications are presented in the Figure S26.

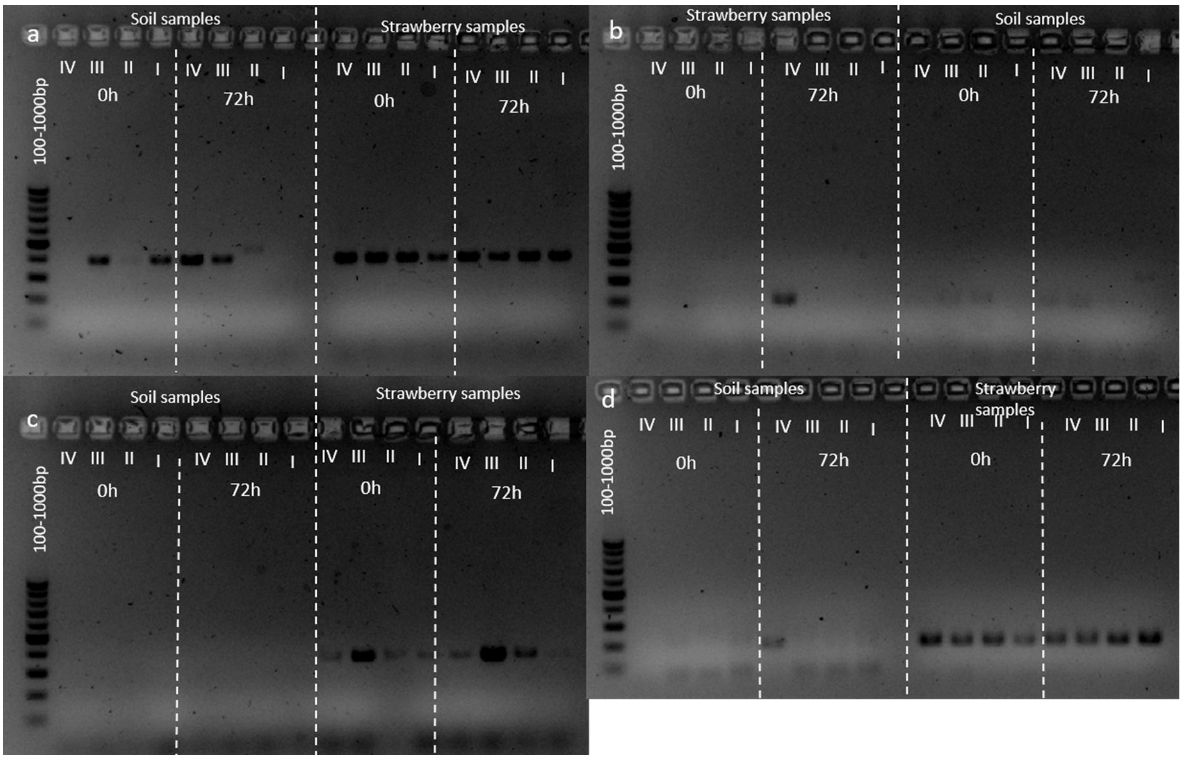

Figure S26. The specificity of the primer on artificially contaminated soil and strawberry fruit. PCR replication of the amplification using *B. cinerea* (a), *Colletotrichum* sp. (b), *Phytophthora* sp. (c), and *Verticillium* sp. (d) specific primers in artificially contaminated soil and strawberry, incubated at 24°C for 0 and 72 hours extracted with the FastDNA™ SPIN kit for Feces. Gel agarose 2% with 100-1,000 bp ladder. The roman numerals indicate the concentration of pathogen spores per gram of soil (I – 100; II – 1,000; III – 10,000; IV – 100,000 spores g^{-1}). The increase in roman numerals indicates the increase in spores of each pathogen inside the soil.

Table S1. List of the sequence obtained using the specific-primer designed on the functional genes.

Organism	Strain	Source	D2 LSU identification	Functional gene identification
Botrytis cinerea	G276/18	Root	MT154303.1	MW826561
	G277/18	Root	MT154304.1	MW826562
	G321/18	Root	MT154305.1	MW826563
	G322/18	Root	MT154306.1	MW826564
	G323/18	Root	MT154307.1	MW826565
Colletotrichum	G171/18	Fruit	MT126802.1	MW829155
	G404/18	Strawberry plant	MT126797.1	MW829156
	G406/18	Strawberry plant	MT126795.1	MW829157
Phytophthora	G408/18	Strawberry plant	MT126670.1	MW829168
	G409/18	Strawberry plant	MT126671.1	MW829169
	G412/18	Strawberry plant	MT126672.1	MW829170
	G413/18	Strawberry plant	MT126673.1	MW829171
	G415/18	Strawberry plant	MT126674.1	MW829172
	G417/18	Strawberry plant	MT126676.1	MW829173
	G418/18	Strawberry plant	MT126677.1	MW829174
	G419/18	Strawberry plant	MT126678.1	MW829175
	G420/18	Strawberry plant	MT126679.1	MW829176
	G421/18	Strawberry plant	MT126680.1	MW829177
	G429/18	Strawberry plant	MT126681.1	MW829178
	G430/18	Strawberry plant	MT126682.1	MW829179
	G432/18	Strawberry plant	MT126684.1	MW829180
	G434/18	Strawberry plant	MT126685.1	MW829181
	G437/18	Strawberry plant	MT126686.1	MW829182

	G439/18	Strawberry plant	MT126687.1	MW829183
	G441/18	Strawberry plant	MT126689.1	MW829184
	G442/18	Strawberry plant	MT126690.1	MW829185
Verticillium	G293/18	Root	MT133324.1	MW829158
	G294/18	Root	MT133317.1	MW829159
	G296/18	Root	MT133320.1	MW829160
	G297/18	Root	MT133316.1	MW829161
	G298/18	Root	MT133318.1	MW829162
	G302/18	Root	MT133314.1	MW829163
	G328/18	Root	MT133326.1	MW829164
	G330/18	Root	MT133315.1	MW829165
	G335/18	Root	MT133322.1	MW829166
	G344/18	Root	MT133321.1	MW829167
Colletotrichum acutatum	G162/18	Strawberry fruit	-	PV013547

Table S2. Description of the primer's concentration and PCR thermoprofile for detection in naturally and artificially contaminated environmental samples.

Fungal strain	**Final concentration primer**	**DNA**	**Thermoprofile**
Botrytis cinerea **(G669/16; G277/18)**	1 µM	3 µl of diluted eDNA (1:10)	94°C for 3 min; 35 cycles at 94°C for 15 sec, 50°C for 30 sec, 72°C for 45 sec; followed by 72°C for 10 min
Colletotrichum **sp. (G171/18)**	1 µM	4 µl diluted eDNA (1:10)	94°C for 3 min; 5 cycles at 94°C for 15 sec, 54°C (touchdown -1°C) for 15 sec, 72°C for 15 sec; followed by 35 cycles at 94°C for 15 sec, 48°C for 15 sec, 72°C for 15 sec; followed by 72°C for 7 min
Phytophthora **sp. (G408/18)**	1 µM	2 µl diluted eDNA (1:10)	94°C for 3 min; 35 cycles at 94°C for 15 sec, 60°C for 40 sec, 72°C for 45 sec; followed by 72°C for 10 min
Verticillium **sp. (G296/18)**	1 µM	4 µl diluted eDNA (1:10)	94°C for 3 min; 5 cycles at 94°C for 15 sec, 51°C (touchdown -1°C) for 15 sec, 72°C for 15 sec; followed by 40 cycles at 94°C for 15 sec, 46°C for 15 sec, 72°C for 15 sec; followed by 72°C for 7 min

Table S3. List of GenBank number of the sequences were used to draw the specific primer for *Colletotrichum acutatum*

Pathogen	Accession numbers of sequences used to design primers	Accession numbers of sequences used to check specificity of designed primers on the basis of in sillico analysis
Colletotrichum acutatum	KT228308.1 *Colletotrichum acutatum*	PP737585.1 *Colletotrichum nymphaeae*
	JX876552.1 *Glomerella acutata*	PP729319.1 *Colletotrichum cairnsense*
	JX876551.1 *Glomerella acutata*	PP729309.1 *Colletotrichum cairnsense*
	JX876550.1 *Glomerella acutata*	LC812073.1 *Colletotrichum nymphaeae*
	FJ972581.1 *Glomerella acutata*	PP565773.1 *Colletotrichum scovillei*
	FJ972580.1 *Glomerella acutata*	OR493925.1 *Colletotrichum* sp.
	FJ788418.1 *Glomerella acutata*	OR493924.1 *Colletotrichum* sp.
	FJ025811.1 *Glomerella acutata*	PP320349.1 *Colletotrichum scovillei*
	MG656080.1 *Colletotrichum coccodes*	PP320348.1 *Colletotrichum scovillei*
	KU821407.1 *Colletotrichum coccodes*	PP085963.1 *Colletotrichum scovillei*
	KU821332.1 *Colletotrichum nigrum*	PP085962.1 *Colletotrichum scovillei*
	KU821331.1 *Colletotrichum coccodes*	PP085961.1 *Colletotrichum scovillei*
	KU821318.1 *Colletotrichum nigrum*	PP085960.1 *Colletotrichum scovillei*
	KU821304.1 *Colletotrichum coccodes*	PP085958.1 *Colletotrichum scovillei*
	KT228301.1 *Colletotrichum gigasporum*	PP085957.1 *Colletotrichum scovillei*
	KJ781335.1 *Colletotrichum truncatum*	PP085954.1 *Colletotrichum scovillei*
	JX870646.1 *Colletotrichum capsici*	PP085953.1 *Colletotrichum scovillei*
	JQ400014.1 *Colletotrichum hemerocallidis*	PP085951.1 *Colletotrichum scovillei*
	JQ400011.1 *Colletotrichum liriopes*	PP085950.1 *Colletotrichum scovillei*
	JQ400010.1 *Colletotrichum spaethianum*	PP085949.1 *Colletotrichum scovillei*
	JN050232.1 *Colletotrichum thailandicum*	PP048929.1 *Colletotrichum nymphaeae*
	JN050230.1 *Colletotrichum tropicicola*	PP048922.1 *Colletotrichum nymphaeae*
	HM585383.1	PP048921.1

	Colletotrichum liriopes	*Colletotrichum nymphaeae*
	/	OQ511701.1 *Colletotrichum scovillei*
	/	OQ511698.1 *Colletotrichum nymphaeae*
	/	OR995765.1 *Colletotrichum nymphaeae*
	/	OR767823.1 *Colletotrichum nymphaeae*
	/	OR271561.1 *Colletotrichum nymphaeae*
	/	OR271560.1 *Colletotrichum nymphaeae*
	/	OR271559.1 *Colletotrichum nymphaeae*
	/	OR251073.1 *Colletotrichum nymphaeae*
	/	LC778045.1 *Colletotrichum* sp.
	/	OR043479.1 *Colletotrichum nymphaeae*
	/	OR043473.1 *Colletotrichum nymphaeae*
	/	OR043480.1 *Colletotrichum fruticola*
	/	OQ799892.1 *Colletotrichum scovillei*
	/	OQ799891.1 *Colletotrichum scovillei*
	/	OQ799890.1 *Colletotrichum scovillei*
	/	OQ799889.1 *Colletotrichum scovillei*
	/	OQ799888.1 *Colletotrichum scovillei*
	/	OQ613575.1 *Colletotrichum scovillei*
	/	OQ613574.1 *Colletotrichum scovillei*
	/	OQ613573.1 *Colletotrichum scovillei*
	/	OQ613572.1 *Colletotrichum scovillei*
	/	OQ613571.1 *Colletotrichum scovillei*
	/	OQ613570.1 *Colletotrichum scovillei*
	/	OQ613569.1 *Colletotrichum scovillei*
	/	OQ613568.1 *Colletotrichum scovillei*
	/	OQ613567.1 *Colletotrichum scovillei*

	/	OQ613566.1 *Colletotrichum scovillei*
	/	OQ613565.1 *Colletotrichum scovillei*
	/	OQ613564.1 *Colletotrichum scovillei*
	/	OP156923.1 *Colletotrichum scovillei*
	/	OP156922.1 *Colletotrichum scovillei*
	/	OP156921.1 *Colletotrichum scovillei*
	/	OP156920.1 *Colletotrichum scovillei*
	/	OP156919.1 *Colletotrichum scovillei*
	/	OP156918.1 *Colletotrichum scovillei*
	/	OQ874731.1 *Colletotrichum scovillei*
	/	OQ859040.1 *Colletotrichum scovillei*
	/	OP746004.1 *Colletotrichum nymphaeae*
	/	OP746003.1 *Colletotrichum nymphaeae*
	/	OP746002.1 *Colletotrichum nymphaeae*
	/	OP746001.1 *Colletotrichum nymphaeae*
	/	OP746000.1 *Colletotrichum nymphaeae*
	/	OP745999.1 *Colletotrichum nymphaeae*
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	/	OP745996.1 *Colletotrichum nymphaeae*
	/	OP745995.1 *Colletotrichum nymphaeae*
	/	OP745994.1 *Colletotrichum nymphaeae*
	/	OP745993.1 *Colletotrichum nymphaeae*
	/	OP745992.1 *Colletotrichum nymphaeae*
	/	OQ200436.1 *Colletotrichum nymphaeae*
	/	OQ200435.1 *Colletotrichum nymphaeae*
	/	OQ200434.1 *Colletotrichum nymphaeae*

	/	OQ200433.1 *Colletotrichum nymphaeae*
	/	OQ200432.1 *Colletotrichum nymphaeae*
	/	OQ127268.1 *Colletotrichum scovillei*
	/	ON457860.1 *Colletotrichum nymphaeae*
	/	ON457859.1 *Colletotrichum nymphaeae*
	/	LC742915.1 *Colletotrichum fioriniae*
	/	OP781555.1 *Colletotrichum nymphaeae*
	/	OP781547.1 *Colletotrichum nymphaeae*
	/	OP750572.1 *Colletotrichum nymphaeae*
	/	OP750571.1 *Colletotrichum nymphaeae*
	/	OP750552.1 *Colletotrichum nymphaeae*
	/	MZ999002.1 *Colletotrichum* sp.
	/	MZ999001.1 *Colletotrichum* sp.
	/	MZ999000.1 *Colletotrichum* sp.
	/	MZ998999.1 *Colletotrichum* sp.
	/	MZ998998.1 *Colletotrichum* sp.
	/	MZ998997.1 *Colletotrichum* sp.
	/	MZ998996.1 *Colletotrichum* sp.
	/	MZ998995.1 *Colletotrichum* sp.
	/	MZ998994.1 *Colletotrichum* sp.
	/	MZ998993.1 *Colletotrichum* sp.
	/	MZ998992.1 *Colletotrichum* sp.
	/	MZ998991.1 *Colletotrichum* sp.
	/	MZ998990.1 *Colletotrichum* sp.
	/	PP760163.1 *Colletotrichum fioriniae*
	/	PP729312.1 *Colletotrichum cairnsense*
	/	LC812093.1 *Colletotrichum fioriniae*

	/	PP576667.1 *Colletotrichum fioriniae*
	/	PP576664.1 *Colletotrichum fioriniae*
	/	PP576662.1 *Colletotrichum fioriniae*
	/	PP576655.1 *Colletotrichum fioriniae*
	/	PP576654.1 *Colletotrichum fioriniae*
	/	OR644992.1 *Colletotrichum* sp.
	/	OR596675.1 *Colletotrichum fioriniae*
	/	OR493928.1 *Colletotrichum* sp.
	/	OR493927.1 *Colletotrichum* sp.
	/	OR493926.1 *Colletotrichum* sp.
	/	PP085959.1 *Colletotrichum scovillei*
	/	PP085956.1 *Colletotrichum scovillei*
	/	PP085955.1 *Colletotrichum scovillei*
	/	PP085952.1 *Colletotrichum scovillei*
	/	LC797741.1 *Colletotrichum fioriniae*
	/	PP091748.1 *Colletotrichum cairnsense*
	/	PP048931.1 *Colletotrichum fioriniae*
	/	PP048922.1 *Colletotrichum nymphaeae*
	/	OR140163.1 *Colletotrichum fioriniae*
	/	OR140162.1 *Colletotrichum fioriniae*
	/	OR140161.1 *Colletotrichum fioriniae*
	/	OR140160.1 *Colletotrichum fioriniae*
	/	OR140159.1 *Colletotrichum fioriniae*
	/	OQ511700.1 *Colletotrichum nymphaeae*
	/	OR251071.1 *Colletotrichum fioriniae*
	/	OR251070.1 *Colletotrichum fioriniae*
	/	OR251069.1 *Colletotrichum fioriniae*

	/	OR238921.1 *Colletotrichum fioriniae*
	/	OR238920.1 *Colletotrichum fioriniae*
	/	OR842619.1 *Colletotrichum fioriniae*
	/	OR766557.1 *Colletotrichum fioriniae*
	/	OR282741.1 *Colletotrichum fioriniae*
	/	LC778049.1 *Colletotrichum fioriniae*
	/	OQ929149.1 *Colletotrichum* sp.
	/	OQ929148.1 *Colletotrichum* sp.
	/	OQ929147.1 *Colletotrichum* sp.
	/	OQ929146.1 *Colletotrichum* sp.
	/	OQ929145.1 *Colletotrichum* sp.
	/	OQ929144.1 *Colletotrichum* sp.
	/	OQ929126.1 *Colletotrichum* sp.
	/	OQ067617.1 *Colletotrichum fioriniae*
	/	OQ613605.1 *Colletotrichum fioriniae*
	/	OQ613604.1 *Colletotrichum fioriniae*
	/	OQ613603.1 *Colletotrichum fioriniae*
	/	LC722617.1 *Colletotrichum nymphaeae*
	/	LC722616.1 *Colletotrichum fioriniae*
	/	LC722612.1 *Colletotrichum fioriniae*
	/	LC722611.1 *Colletotrichum fioriniae*