Figure S1. Effect of deoxyphomenone on *Cladosporium fulvum* and tomato leaves.
Deoxyphomenone (120 μM) and 1% methanol (v/v) as a control were used. (**A**) Effect on spore germination. A filter paper containing deoxyphomenone was placed on the left on PDA, then a spore suspension of *C. fulvum* was dropped (arrowheads) at different distances from the paper and incubated at 25 °C for 2 weeks. (**B**) Effect on hyphal elongation. Spores were germinated in a sterile distilled water at 25 °C for 24 h. Germinated spores were treated with deoxyphomenone, then hyphal length was measured after 24 h using a light microscope. The line in the center of the box indicates the median; box margins represent the 25th and 75th percentiles. The length of the box is the interquartile range; whiskers indicate the minimum and maximum. Significant differences among treatments were determined using Tukey's test. (**C**) Fungistatic activity of deoxyphomenone. Spores of *C. fulvum* were suspended in distilled water (dH2O), deoxyphomenone (DP) or 100 μM fungicide captan for 24 h, then solutions were replaced with fresh solutions as shown, and treated for a further 24 h. Germinated spores were counted using a light microscope. Continuous treatment with dH2O or 1% methanol (v/v) was used as a positive control. Values are the means of three replicates (± SD). (**D**) Transmission electron micrographs of interior of *C. fulvum* spores 24 h after treatment with deoxyphomenone. Bars = 2 μm. (**E**) Evaluation of 20, 40 and 80 μM deoxyphomenone or 1% methanol (v/v) as a control for toxicity on tomato leaves 2 weeks after 1-month-old leaves were injected with the compound.

RYO74186.1_[Monosporascus_ibericus]

707

538 ELA24192.1_[Colletotrichum_fructicola_Nara_gc5]

Q9UR08.1_[Aspergillus_terreus]

642

364 1000 CDM31315.1_[Penicillium_roqueforti_FM164] **Ari1** ── PR toxin

XP_002557473.1_[Penicillium_rubens_Wisconsin_54-1255]

1000 KXH30086.1_[Colletotrichum_simmondsii]

955 KXH53729.1_[Colletotrichum_nymphaeae_SA-01]

906 KNG46670.1_[Stemphylium_lycopersici]

640 1000 ELA35498.1_[Colletotrichum_fructicola_Nara_gc5]

EQB49299.1_[Colletotrichum_gloeosporioides_Cg-14]

992 961 **DIP_001954p (HpDph1) [Hansfordia_pulvinata_414-3]** ── 13-Deoxyphomenone

1000 **XP_023093357.1 (AoDph1) [Aspergillus_oryzae_RIB40]**

XP_002377386.1_[Aspergillus_flavus_NRRL3357]

1,10-cyclization

1,11-cyclization

ELA33035.1_[Colletotrichum_fructicola_Nara_gc5]

1000 1000 EQB43642.1_[Colletotrichum_gloeosporioides_Cg-14]

ELA28458.1_[Colletotrichum_fructicola_Nara_gc5]

1000 KXH39379.1_[Colletotrichum_nymphaeae_SA-01]

AKE33935.1_[Colletotrichum_acutatum] ── α-Humulene

KXH53651.1_[Colletotrichum_simmondsii]

XP_018042396.1_[Paraphaeosphaeria_sporulosa]

XP_001795219.1_[Parastagonospora_nodorum_SN15]

1000 RAR15522.1_[Stemphylium_lycopersici]

982 **DIP_006271p [Hansfordia_pulvinata_414-3]**

849 RYP08311.1_[Monosporascus_ibericus]

KIJ41383.1_[Sphaerobolus_stellatus_SS14]

β-Caryophyllene

0.1

Figure S2. Phylogenetic tree of fungal sesquiterpene cyclases.
The phylogenetic tree was generated from amino acid sequences encoding sesquiterpene synthases by maximum likelihood phylogenetic analysis. Predicted aristolochene synthase-like proteins identified in *H. pulvinata* 414-3 and *A. oryzae* RIB40 genome sequences, and the aristolochene synthase Ari1 are shown in bold.
GenBank/EMBL/DDBJ accession numbers or unique numbers for *H. pulvinata*are are indicated. *Sphaerobolus stellatus* (*Basidiomycota*) was used as an outgroup. Numbers beside the branches represent bootstrap values based on 1000 replicates. The scale bar corresponds to 0.1 estimated amino acid substitutions per site. Representative metabolites and proteins associated with their cyclization are connected by lines.

```
DIP-001954p(HpDPH1)    1 MLSTLRSFELHKLLGLTGSSSNDSTTTTTTTITTTAASAAPQPKAQQQPQP    AYPSESEDMARDRRRFPSLAATTDTASPSPSAFAPEIHPAADRVSREVAE    100
                         .........::|:|.....||.:....|:.                       ..  :.:|||..|.||   ..:.|.|||:..|||.:|.||.||..
XP_023093357(AoDPH1)   1 -----------------------MLQRLWALSTSAIKLPFQPFSFGAPRD    LL------IEKDRRSMPCLA----KEAPPPSAFSATIHPLSDSVSTEVDN    67


DIP-001954p(HpDPH1)  101 AFLARWPFRGEAERRRFRAADFPRVTCLYFPHARAERIGFACRLLTLLFL    VDDLLEEMGLEEGSAYNERLISISKGDEEPEPDKPAEVLTRELWEDMRAC    200
                         .|||..|||.|.|.|.|.|.|.||.||.|||:.|..:||||||:..:||:  :||||||:.|..:||:...|:|||||.|:..:.|.:.....|:|..|.||:|.
XP_023093357(AoDPH1)  68 YFLQNWPFRTDNERARFHAAGFSRVTCLYFPMAMDDRIGFACRMLTILFL    IDDLLEEMSLDEGSTYNEKLISISRGDVAPDRTIPAQWIMYDLWEDMRAC    167


DIP-001954p(HpDPH1)  201 DARLAGEIKEPVFTFMRAQTDGSRLTLRELGAYFEYREKDVGQA------    ----LLSALMRFSMALHLTPAQLRLAQPLERNCARHISVVNDIYSWRKEV    290
                         |..|.|.|:.||||||||||:|||||:..|.:.|.:||||||||        |||.|.::|.:|.|...|:|.|.||||||:|||.|||||||:
XP_023093357(AoDPH1) 168 DHVLADELLEPVFTFMRAQTDKTRLTIHQFGEYLDYREKDVGQAIKAQTK    CIRSLLSGLQRYTMKLYLTEEDLRMAAPAERNCAKHIAILNDIYSWRKEL    267


DIP-001954p(HpDPH1)  291 RASETLHEEGAALCSSVAVLAAEASVPASGARRVLWALCREWEAEHRRME    GDLLRRLVEEEEEEGDQGGQVLRVYVRGLESQMSGNERWSESTPRYHKVK*    391
                         .||:||||.||||:||||:||||.||:...:::.:...:||||.:||||:.|.:::                ..|....|.:.|..|:.|||.||||||||||||||||..
XP_023093357(AoDPH1) 268 LASKTLHHEGAAICSSVQVLSEVTALSHAATQRVLWTMCREWESVHKQL-    ----------VTEVAGTGSRDLLDYIHGLEFQMSGNERWSESTPRYHF*--    355

Identity: 197/401 (49.1%) / Similarity: 247/401 (61.6%) / Gaps: 56/401 (14.0%)


DIP-001954p(HpDPH1)    1 -----------MLSTLRSFELHKLLGLTGSSS-----NDSTTTTTTTITTT    AASAAPQPKAQQQPQPAYPSESEDMARDRRRFPSLAATTDTASPSPSAFA    84
                         .|||:.| |.:|.::.:.||    |.|:...|..||               |.:.|.|.:..|:|                      |...|.:...
DIP-006271p            1 MASALLSLPTAALSTILS--LVRLSSVVSPSSTITTKNPSSNASATEETT    ATTPPPVPENSQRP-------------------------AGLRPTRLT    71


DIP-001954p(HpDPH1)   85 PEIHPAADRVSREVAEAFLARWPFRGEAERRRFRAADFPRVTCLYFPHAR    AERIGFACRLLTLLFLVDDLLEEMGLEEGSAYNERLISISKGDEEPEPDK    184
                         ...|...::..:.|:.||..|||:..||||...|||....|:...:.    .|||.:.||||||.:||:||||::.|.:.||:|:|.....:..|.:.|.|.
DIP-006271p           72 ARKHRLTEQTVEQVNDFFLRNWPFKTDKHRRRFVDEGYAFFVCVLVPESL    DERIHWGCRLLTVGFLIDDLVDNMNVAEGAAFNAAVVECCRGTQLPDRDV    171


DIP-001954p(HpDPH1)  185 PAEVLTRELWEDMRACDARLAGEIKEPVFTFMRAQTDGSRLTLRELGAYF    EYREKDVGQALLSALMRFSMALHLTPAQLRLAQPLERNCARHISVVNDIY    284
                         |:::...|:|.||||.||:|||.|||.:.|||||||:|.:.|||||.||    ||||.:.:|:.:|.:||:.:|||.|:|.....::.:|.|:|||::..:||
DIP-006271p          172 PSQWIMYDLFEAMRAVDRRLADELLQPTIDFLLAQVDGSRRRPMNLAEYF    EYRDADLGKGLISGIMRFCGGLSMTTAELDVVRPVDENVMKHITFVNDVC    271


DIP-001954p(HpDPH1)  285 SWRKEVRASETLHEEGAALCSSVAVLAAEASVPASGARRVLWALCREWEA    EHRRMEGDLLRRLVEEEEEEGDQG-GQVLRVYVRGLESQMSGNERWSEST    383
                         |:.||..:|..:|.:.:.|  .:|||||.::.||:....:|:|:|.|.||.    .|..|:.:|                .|..| ...||.|:|.:.:.|||||.||||:..|.|
DIP-006271p          272 SYEKERLAAEAGYELG-EICSSVPIVAAWLGVGEDDAKRVMWQAARGWED    RHLAMKRDIL---------AGPLGASSALRTYLRWVEYQASGNELWSLLT    361


DIP-001954p(HpDPH1)  384 PRYHKVK*------------     391
                         |||::...
DIP-006271p          362 PRYNRFGALGFTEGRPEAQ*     381

Identity: 140/420 (33.3%)  / Similarity: 207/420 (49.3%)  / Gaps: 68/420 (16.2%)


XP_023093357(AoDPH1)   1 MLQRLWALSTSA-------IKLPFQPFSFGAPRDLLIEKDRRSMPCLAKE    ----APP-------------PSAFSATIHPLSDSVSTEVDNYFLQNWPFR    76
                         |...|.:|.|:|       ::|.    |...|:.:::....|...|::   .||              |:.:.|.|::::....|:::.||:.|::
DIP-006271p            1 MASALLSLPTAALSTILSLVRLS----SVVSPSSTITTKNPSSNASATEE    TTATTPPPVPENSQRPAGLRPTRLTARKHRLTEQTVEQVNDFFLRNWPFK    96


XP_023093357(AoDPH1)  77 TDNERARFHAAGFSRVTCLYFPMAMDDRIGFACRMLTILFLIDDLLEEMS    LDEGSTYNEKLISISRGDVAPDRTIPAQWIMYDLWEDMRACDHVLADELL    176
                         ||..|.|...|:...|:.|:..|.:..|:||:.|:|.|:||||||:.:    :.||:.:.:.:....|...||:|:||||||||||.|||.:.||||||
DIP-006271p           97 TDKHRRRFVDEGYAFFVCVLVPESLDERIHWGCRLLTVGFLIDDLVDNMN    VAEGAAFNAAVVECCRGTQLPDRDVPSQWIMYDLFEAMRAVDRRLADELL    196


XP_023093357(AoDPH1) 177 EPVFTFMRAQTDKTRLTIHQFGEYLDYREKDVGQAIKAQTKCIRSLLSGL    QRYTMKLYLTEEDLRMAAPAERNCAKHIAILNDIYSWRKELLASKTLHHE    276
                         :|....|:.||.|.:|.......||.:|:.|.:|    :.|:||:       :.|:|||:    .|:....|.:|..:.:..:.:.|||.::.:|.:|||::. .:|
DIP-006271p          197 QPTIDFLLAQVDGSRRRPMNLAEYFEYRDADLG----------KGLISGI    MRFCGGLSMTTAELDVVRPVDENVMKHITFVNDVCSYEKERLAAEA-GYE    285


XP_023093357(AoDPH1) 277 GAAICSSVQVLSEVTALSHAATQRVLWTMCREWESVHKQLVTEV-AGT--    GSRDLLDYIHGLEFQMSGNERWSESTPRYHF*--------------     355
                         ...|||||.:::..::::.......||:|...:.||||:|.:.::: ||.                 .|..|..|:..:|:||||||.|..|||::.
DIP-006271p          286 LGEICSSVPIVAAWLGVGEDDAKRVMWQAARGWEDRHLAMKRDILAGPLG    ASSALRTYLRWVEYQASGNELWSLLTPRYNRFGALGFTEGRPEAQ*     381

Identity: 134/396 (33.8%) / Similarity: 205/396 (51.8%)  / Gaps: 56/396 (14.1%)
```

Figure S3. Alignment and homology of the amino acid sequences of the predicted sesquiterpene cyclases identified in *Hansfordia pulvinata* and *Aspergillus oryzae* genome sequences.
Amino acid sequences of two candidates of *H. pulvinata* 414-3, DIP_001954 (HpDph1) and DIP_006271, and one of *A. oryzae* RIB40 XP_023093357 (AoDph1) were compared.

Figure S4. Dot plot analysis of the deoxyphomenone biosynthesis (*DPH*) gene clusters from *Hansfordia pulvinata* 414-3 and *Aspergillus oryzae* RIB40.

Fig. S5. Exon-intron structures of deoxyphomenone biosynthetic (*DPH*) genes.
Colored boxes: exon regions; boxes with dashed line: intron regions in *DPH* genes; gray shading: similarity of amino acid sequences.

```
H. pulvinata          MATEKHPA----------SLPGSQDAPPKTEAPPQGVERDSDAYGSDGEHGGGSSITEN TDADQKGGGLVLVITVAALAMGMFLVSLDMTIVATAIPRITDEFGQIELVGWYGAAFFTT
A. oryzae             MSTKTRSSQTGETAVSSRISTPATLEKPNKDALPSH----DPQVMEVRNKEDSGSGVDDA PTEEPSTGGFTLLMTVTALAMSMFLVSLDMTIVATAIPKITDEFGGIEDEGWYGSAFFIT
A. parvisclerotigenus MSTKTRSSQTGETAVSSRISTPATLEKPNKDALPSH----DPQVMEVRNKEDSGSGVDDA PTEEPSTGGFTLLMTVTALAMSMFLVSLDMTIVATAIPKITDEFGGIEDEGWYGSAFFIT
A. flavus             MSTKTRSSQTGETAVSSRISTPATLEKPNKDASPSH----DPQVMEVRNKEDSGSGVDDA PTEEPSTGGFTLLMTVTALAMSMFLVSLDMTIVATAIPKITDEFGGIEDEGWYGSAFFIT
A. minisclerotigenes  MSTKTRSSHTGETAVSSRISTPATPEKPNKDASPSH----DPQVMEVRNKEETGSGVDDA PTDEPSTGGFTLFMTVTALAMSMFLVSLDMTIVATAIPKITDEFGGIEDEGWYGSAFFIT
A. caelatus           MSTKTRSSQTGETAVSSGTSTPATLEKSNKDVSPSH----ETPVVGDREKEERGSGVDDA PTDKPSTGGFTFLMTVTALAMSMFLVSLDMTIVATAIPKITDEFGGIEDEAWYGSAFFIT
A. pseudocaelatus     MSTKTRSSQTGETAVSSGTSTHATLEKSNKDVSPSH----ETPVMGDREKEERGSGVDDA PTDKPSTGGFTFLMTVTALAMSMFLVSLDMTIVATAIPKITDEFGGIEDEAWYGSAFFIT
                      *:*:.:.:         *   .:: .*  *.:   :.   .:. **.:.  .  . .**:.:.**:****.**************:****** **  .***:*** *


H. pulvinata          LGGFQAAWGKAYKYFPLKITFLLSIFLFGVGSLICGVAPNSLTLIVGRAITGVGGAGVSC GCFTIIALSAPPKQQPAYIGILGASYGIAAAIGPLLGGAFTDKVTWRWCFYINLPIGAVT
A. oryzae             LGSFQAAWGKAYKYFPLKTSFLLSIFLFEVGSLICGVAPNSLALCIGRAITGVGGAGISS GAFTIIALSAPPKQRPAYIGILGASYGVAAIGPLVGGAFTTNITWRWCFYINLPIGGLA
A. parvisclerotigenus LGSFQAAWGKAYKYFPLKTSFLLSIFLFEVGSLICGVAPNSLALCIGRAITGVGGAGISS GAFTIIALSAPPKQRPAYIGILGASYGVAAIGPLVGGAFTTNITWRWCFYINLPIGGLA
A. flavus             LGSFQAAWGKAYKYFPLKTSFLLSIFLFEVGSLICGVAPNSLALCIGRAITGVGGAGISS GAFTIIALSAPPKQRPAYIGILGASYGVAAIGPLVGGAFTTNITWRWCFYINLPIGGLA
A. minisclerotigenes  LGSFQAAWGKAYKYFPLKTSFLLSIFLFEVGSLICGVAPNSLALCIGRAITGVGGAGISS GAFTIIALSAPPKQRPAYIGILGASYGVAAIGPLVGGAFTTNITWRWCFYINLPIGGLA
A. caelatus           LGSFQAAWGKAYKYFPLKISFLLSILLFEIGSLICGVAPNSLALCIGRAITGVGGAGISS GAFTIIALSAPPKQRPAYIGILGASYGVAAIGPLVGGAFTTNITWRWCFYINLPIGGLA
A. pseudocaelatus     LGSFQAAWGKAYKYFPLKISFLLSILLFEIGSLICGVAPNSIALCIGRAITGVGGAGISS GAFTIIALSAPPKQRPAYIGILGASYGVAAIGPLVGGAFTTNITWRWCFYINLPIGGLA
                      **.*************** :*****:** :**********::* :***********:*. *.*************:***********:******:**** ::**********.:


H. pulvinata          VAVIAFFYKPPPPLPSLNEPLREKLLQLDIPGTLLLTAALVCFVLSLQWAGVSRPWSDST VIGTLVGFGVLLIAYAVVQWLQGPRAAMVGHLLQRNVVIAMVYIHLIAGSFFLLVYYLPI
A. oryzae             AGIILFFYRPPPPLPFLDTPLKEKLLQMDLVGTLILVSALVCYVLALQWGGISLSWGDSK VIGTLVGFVVLLAVYAIVQWVQKERAAMIGRLFRRNVVVMMIYIDLLAGTFFLLVYYLPI
A. parvisclerotigenus AGIILFFYRPPPPLPFLDTPLKEKLLQMDLVGTLILVSALVCYVLALQWGGISLSWGDSK VIGTLVGFVVLLAVYAIVQWVQKERAAMIGRLFRRNVVVMMIYIDLLAGTFFLLVYYLPI
A. flavus             AGIILFFYRPPPPLPFLDTPLKEKLLQMDLVGTLILVSALVCYVLALQWGGISLSWGDSK VIGTLVGFVVLLAVYAIVQWVQKERAAMIGRLFRRNVVVMMIYIDLLAGTFFLLVYYLPI
A. minisclerotigenes  AGIILFFYRPPPPLPFLDTPLKEKLLQMDLVGTLILVSALVCYVLALQWGGISLSWGDSK VVGTLVGFVVLLAVYAIVQWVQKERAAMIGRLFRRNVLVMMIYIDLLAGTFFLLVYYLPI
A. caelatus           GGIILFFYRPPPPLPFLDTPLTEKLLQMDLPGTLILVSALVCYVLALQWGGVSLSWGDSK VVGTLVGFGVLLVVYAIVQRAQKERAAMIGRLFRRNVVIMMIYIDLLAGTFFLLVYYLPI
A. pseudocaelatus     GGIILFFYRPPPPLPFLDTPLTEKLLQMDLPGTLILVSALVCYVLALQWGGVSLSWGDSK IVGTLVGFGVLLVVYAIVQRAQKERAAMIGRLFRRNVVIMMIYIDLLAGTFFLLVYYLPI
                      .:* ***:****** *: ** *****:*: ***:*.:****:**:***.:* .*.**. ::****** *** .**:** *  ****:*:*:**:: *:**.*:**:**********


H. pulvinata          YFQVVNGVSAAQSGIRNLPLILGQSVFATISGVLLSKFERPQPFLIAGATLVTISSGLLY TLDVDTEPGKWIGYQLLAGVGVGWCFQVPVVTAQSTVQPEHVSSVTAMVLTVQTIGGSIF
A. oryzae             YFQVVSGVSAAQSGIRNLPLILAQSVSTVISGVTLSKFGYPQPFLLVGGVLTAIGSGLLY TLEVNTGSGKWIGYQLLAGIGIGWCFQIPVVTAQASVAPEDLPSVTAMVLTVQTLGGSVF
A. parvisclerotigenus YFQVVSGVSAAQSGIRNLPLILAQSSTVISGVTLSKFGYPQPFLLVGGVLTAIGSGLLY TLEVNTGSGKWIGYQLLAGIGIGWCFQIPVVTAQASVAPEDLPSVTAMVLTVQTLGGSVF
A. flavus             YFQVVSGVSAAQSGIRNLPLILAQSVSTVISGVTLSKFGYPQPFLLVGGVLTAIGSGLLY TLEVNTGSGKWIGYQLLAGIGIGWCFQVPVVTAQASVAPEDLPSVTAMVLTVQTLGGSVF
A. minisclerotigenes  YFQVVSGVSAAQSGIRNLPLILAQSVSTVISGVTLSKFGYPQPFLLVGGVLTAIGSGLLY TLEVNTGSGKWIGYQLLAGIGIGWCFQVPVVTAQASVAPEDLPSVTAMVLTVQTLGGSVF
A. caelatus           YFQVVSGVSAAQSGIRNLPLILAQSASTVISGVTLSKFGYPQPFLLVGGVLTAVGSGLLY TLEVNTGSGKWIGYQLLAGIGIGWCFQVPLVTAQASVAPEDLPSVTAMVLTVQTLGGSVF
A. pseudocaelatus     YFQVVSGVSAAQSGIRNLPLILAQSASTVISGVTLSKFGYPQPFLLVGGVLTAIGSGLLY TLEVNTGSGKWIGYQLLAGIGIGWCFQVPLVTAQASVAPEDLPSVTAMVLTVQTLGGSVF
                      *****.************.**. :.**** **** *****:*.:..*.:: .***.**:*  .*:*::*.*************:*:****:*:****::* **.:.**********:***:*


H. pulvinata          VSAGQSALVNILFKSLPAGFSDSDAAAVANTAGEKLRETVSPEHFPAVLRAYMDGIRGAL LIAVVASGLAFVASLLLRSTKLRTGNSAAAV
A. oryzae             VSAGQSAMVNVLLKNLRSETSTVDAVKVAMTGATELRQKFSSAQMPFILTAYMNGLQAAF LVAVVASSVATVVCLATRWIKFSGQTTAVAAA
A. parvisclerotigenus VSAGQSAMVNVLLKNLRSETSTVDAVKVAMTGATELRQKFSSAQMPFILTAYMNGLQAAF LVAVVASSVATVVCLATRWIKFSGQTTAVAAA
A. flavus             VSAGQSAMVNVLLKNLRSETSTVDAVKVAMTGATELRQKFSSAQMPFILTAYMNGLQAAF LVAVVASSVATVVCLATRWIKFSGQTTAVAAA
A. minisclerotigenes  VSAGQSAMVNVLLKNLRSETSTVDAVKVAMTGATELRQKFSSAQMPFILTAYMNGLQAAF LVAVVASSVATVVCLATRWIKFSGKTTAAAAA
A. caelatus           VSAGQSAMVNVLLKNLRSETSTIDAVKVAMTGATELRQKFSSTQMPFILTSYMEGLQATF LVAVIASSVATVVCLATRWVKFSGQTTAAAAA
A. pseudocaelatus     VSAGQSAMVNVLLKNLRSETSTIDAVKVAMTGATELRQKFSSTQMPFILTSYMEGLQATF LVAVIASSVATVVCLATRWVKFSGQTTAAAAA
                      *******:**:*:.* :  *  **. ** *.. :**:..*. ::* :* :**:*::.:: *:**:**.:* *..*  * *:   .:*.**.
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Figure S6. Alignment of deduced amino acid sequences of *HpDPH6* homologs from *Hansfordia pulvinata* and six *Aspergillus* species. The substrate binding pocket conserved in the transporters of the major facilitator superfamily is indicated in bold. Accession numbers and sequences are listed in Supplementary Table S2.
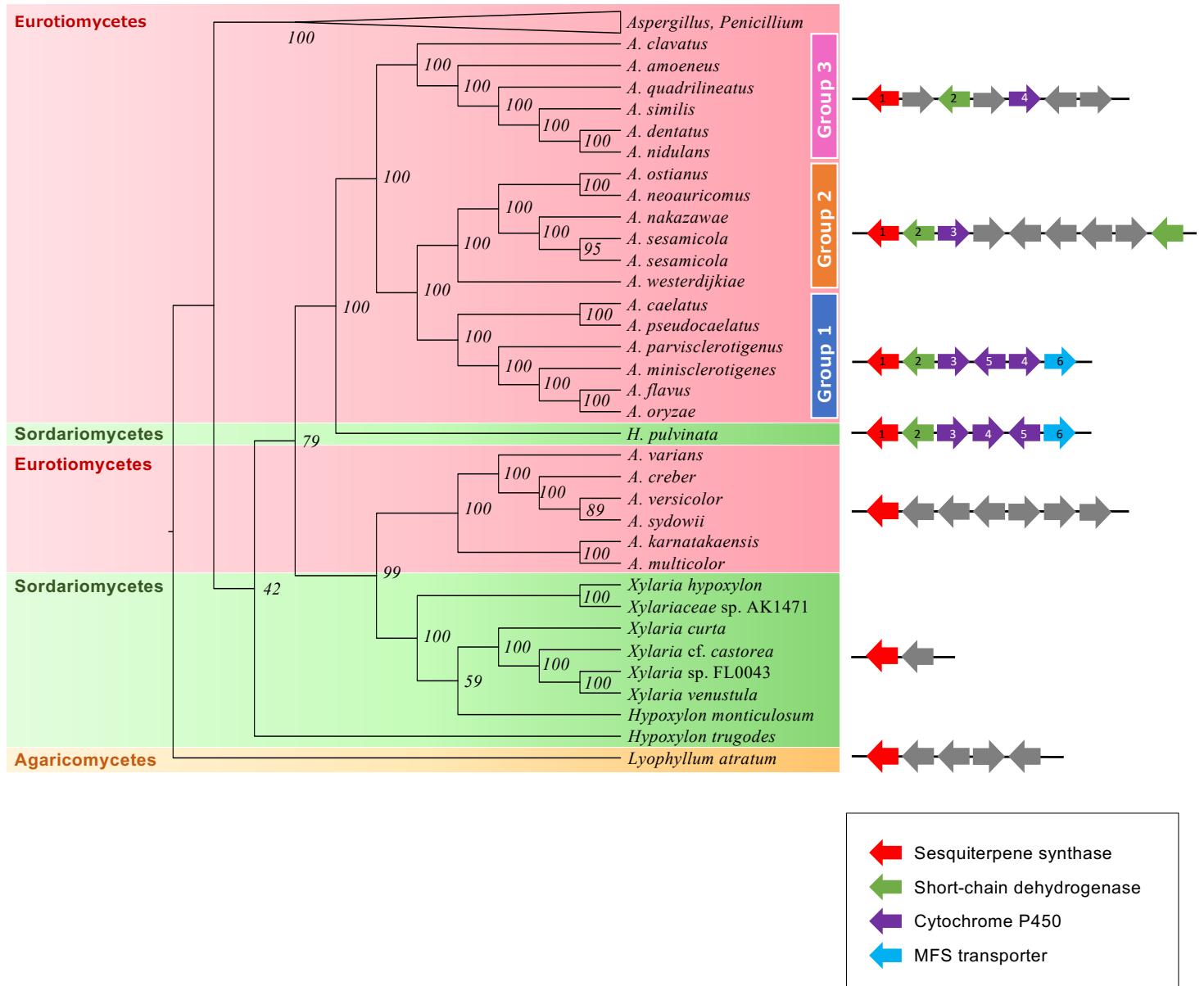
 Figure S7. Phylogenetic analysis of genomic sequences containing *HpDPH1* homologous genes and the upstream region using the maximum likelihood method.

The 60 fungal genome sequences (approximately 15 kb) used in the phylogenetic analysis are listed in Supplementary Table S1. Numbers at branches represent bootstrap percentages (1000 replicates). The sequence of *Lyophyllum atratum* belonging to *Agaricomycetes* was used as an outgroup. Schematic diagrams of genomic structures on the right indicate gene orientation with annotation information in color; numbers in the arrows indicate genes that are more than 50% homologous to HpDph1 to HpDph6 proteins of *H. pulvinata*.
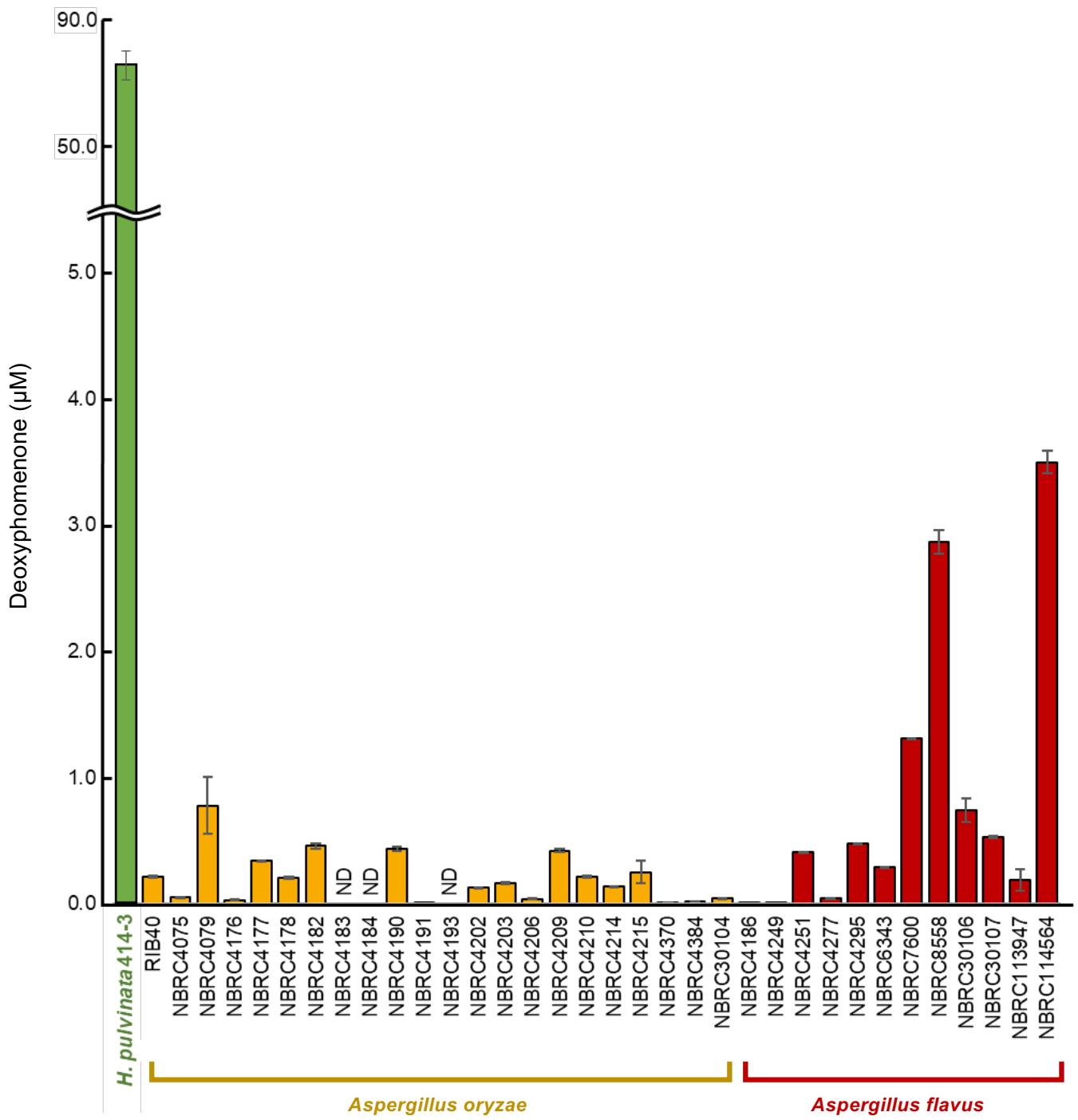
Figure S8. Deoxyphomenone produced by *Hansfordia pulvinata* 414-3 and strains of *Aspergillus oryzae* and *A. flavus*.
Strains were cultured in MM broth at 25 ºC. Deoxyphomenone in the culture filtrate was quantified using LC-MS/MS. Values are the means of three replicates ($\pm$ SD). ND, not detected.
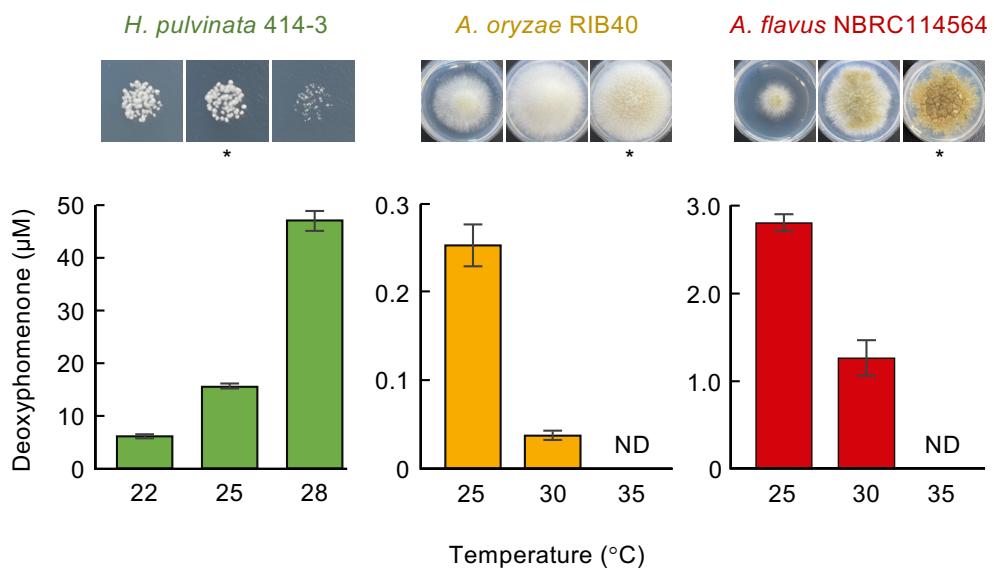
Figure S9. Deoxyphomenone production by *Hansfordia pulvinata* 414-3, *Aspergillus oryzae* RIB40 and *A. flavus* NBRC114564 on MM agar or in broth at different temperatures.
Deoxyphomenone in the culture filtrate of the broth was quantified by LC-MS/MS. The optimum temperature for growth on agar is indicated by the asterisk. Values are the means of three replicates (± SD). ND, not detected.
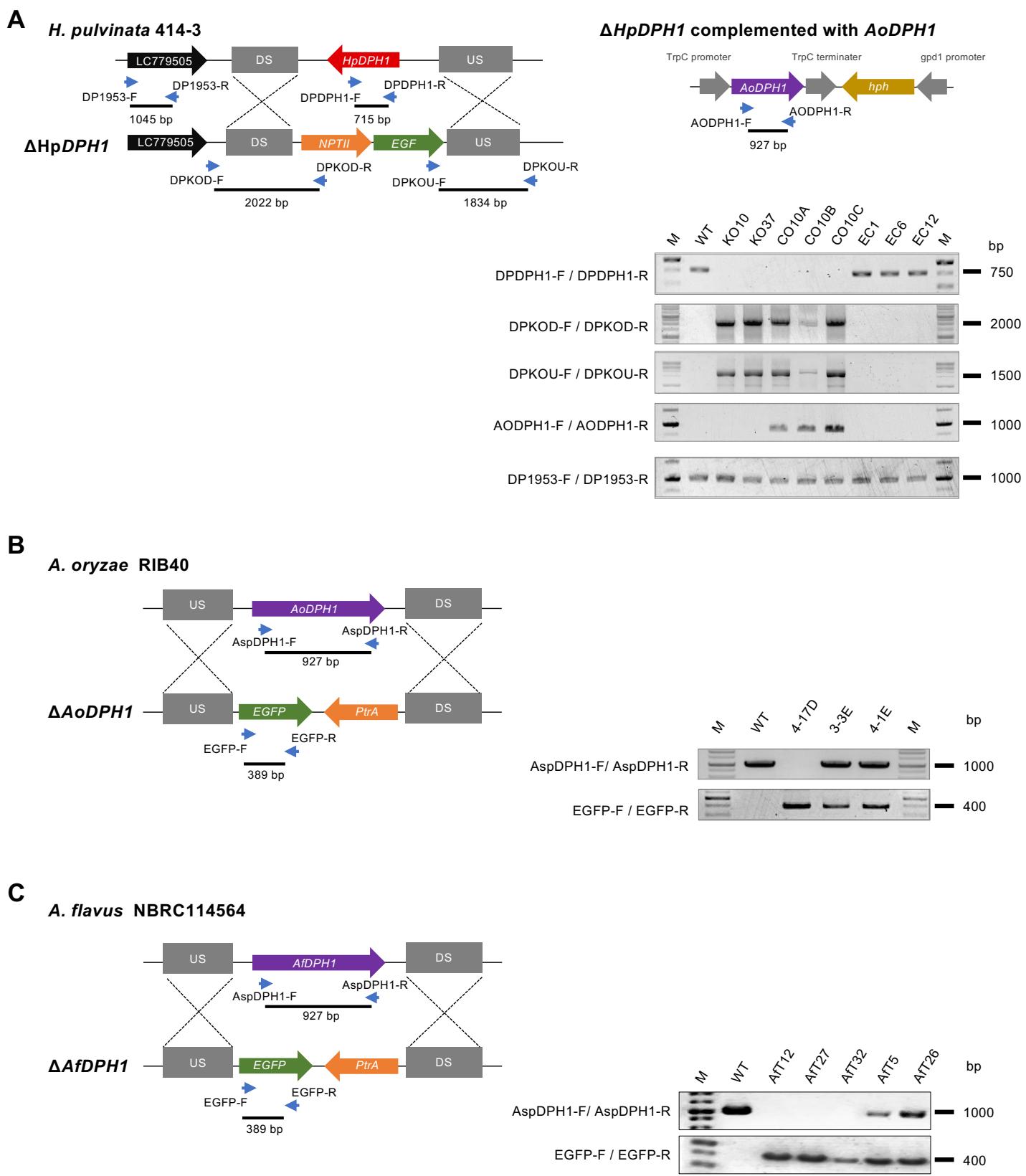
Figure S10. PCR detection of the inserted cassettes in transformants and wild-type strains.
Representation of the locus of *HpDPH1* homologous genes in wild-type strains of *Hansfordia pulvinata* 414-3 (A), *Aspergillus oryzae* RIB40 (B), *A. flavus* NBRC114564 (C) and transformants. Target genes were replaced by homologous recombination of the downstream (DS) and upstream (US) regions. *HpDPH1* knock-out mutant strain KO10 of *H. pulvinata* was complemented with functional *AoDPH1*. Large arrows: gene sequence; small blue arrows: primer sequence. The expected sizes of the amplicons are indicated under the primers. Each amplicon is shown on the right.
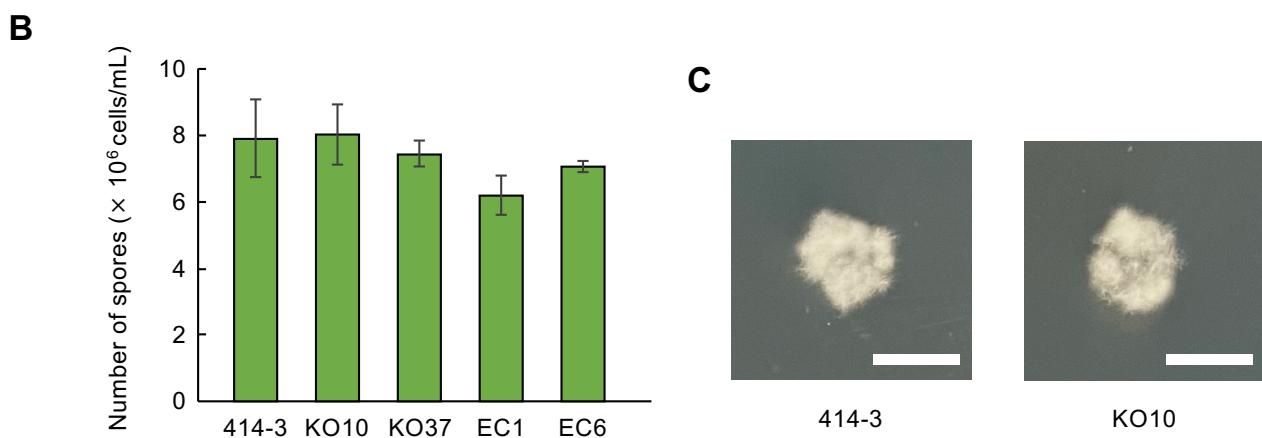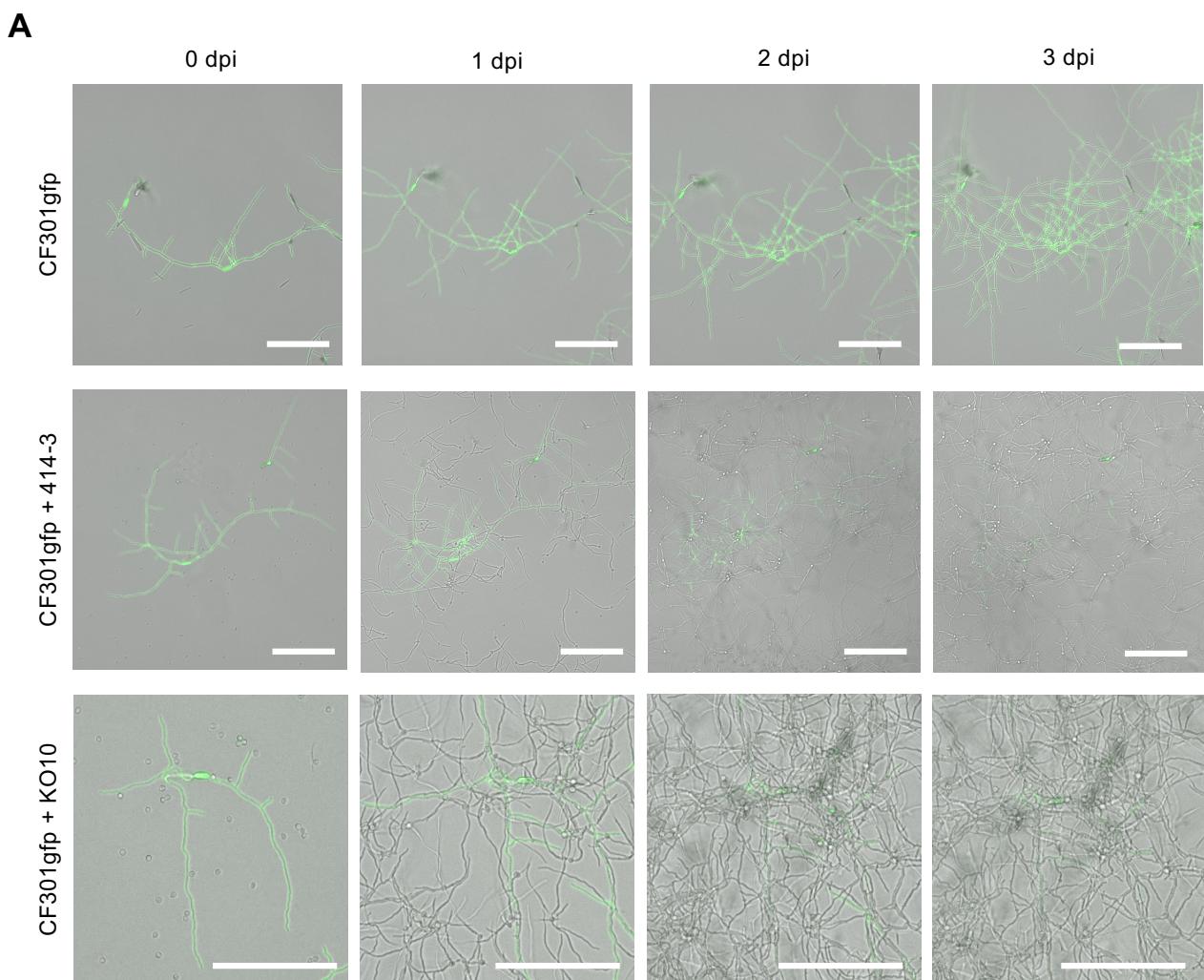
Figure S11. *In vitro* **assay of** *Hansfordia pulvinata* **mycoparasitic activity against GFP-expressing** *Cladosporium fulvum.*

(A) *H. pulvinata* wild-type 414-3 or Δ*HpDPH1* mutant strain KO10 were cocultured with *C. fulvum* CF301gfp, which constitutively expresses GFP, in MM broth without a carbon source at 25 ºC. The parasitized *C. fulvum* cells lost GFP fluorescence. Bars indicate 100 μm. (B) Number of spores of 414-3, Δ*HpDPH1* mutants (KO10 and KO37) and ectopic strains (EC01 and EC06). Values are means of three biological replicates. Error bars indicate the standard deviation. (C) Mycelial growth of *H. pulvinata* 414-3 and KO10 strains on PDA.
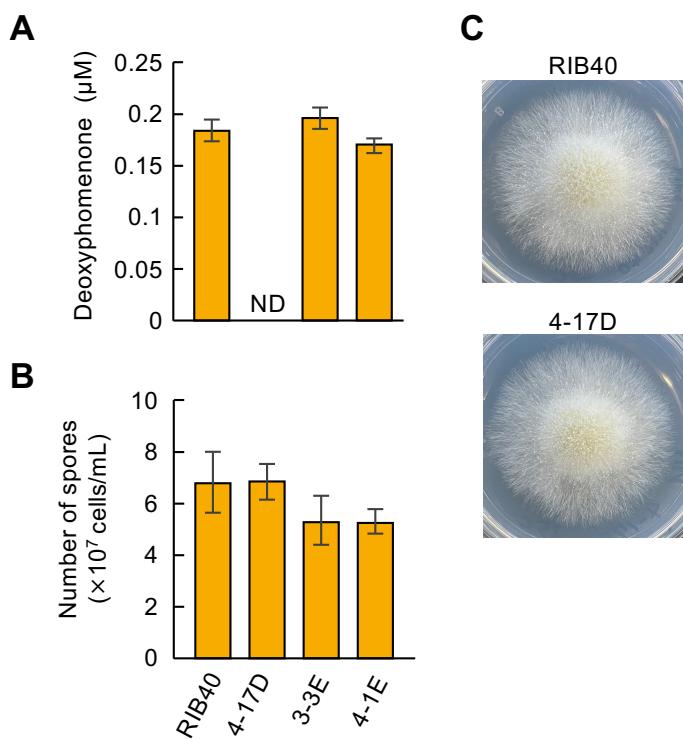
Figure S12. Deoxyphomenone production and sporulation of *A. oryzae* RIB40 and transformants. Wild-type RIB40, Δ*AoDPH1* mutant 4-17D, and ectopic strains 3-3E and 4-1E were cultured in MM broth or agar. Values in A and B are means of three replicates. Error bars indicate the standard deviation. (**A**) LC-MS/MS quantification of deoxyphomenone in culture filtrates. ND, not detected. (**B**) Number of spores formed on agar. (**C**) Colony morphology of wild-type RIB40 and Δ*AoDPH1* mutant 4-17D on MM agar 25°C.
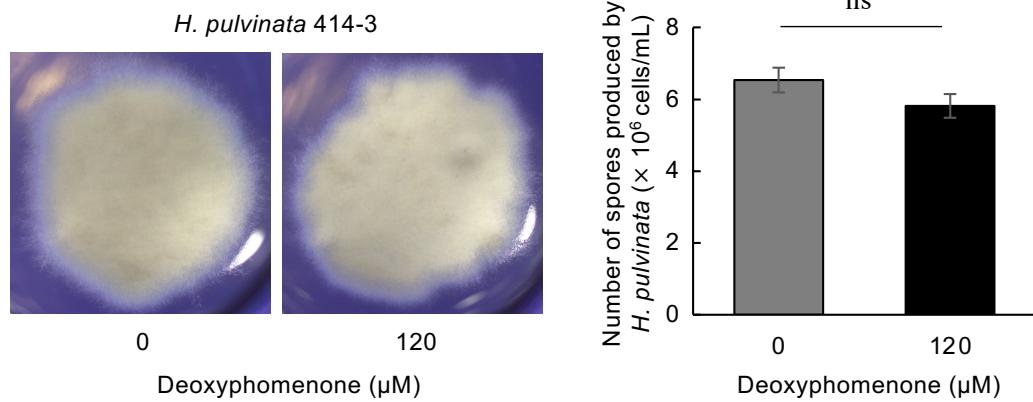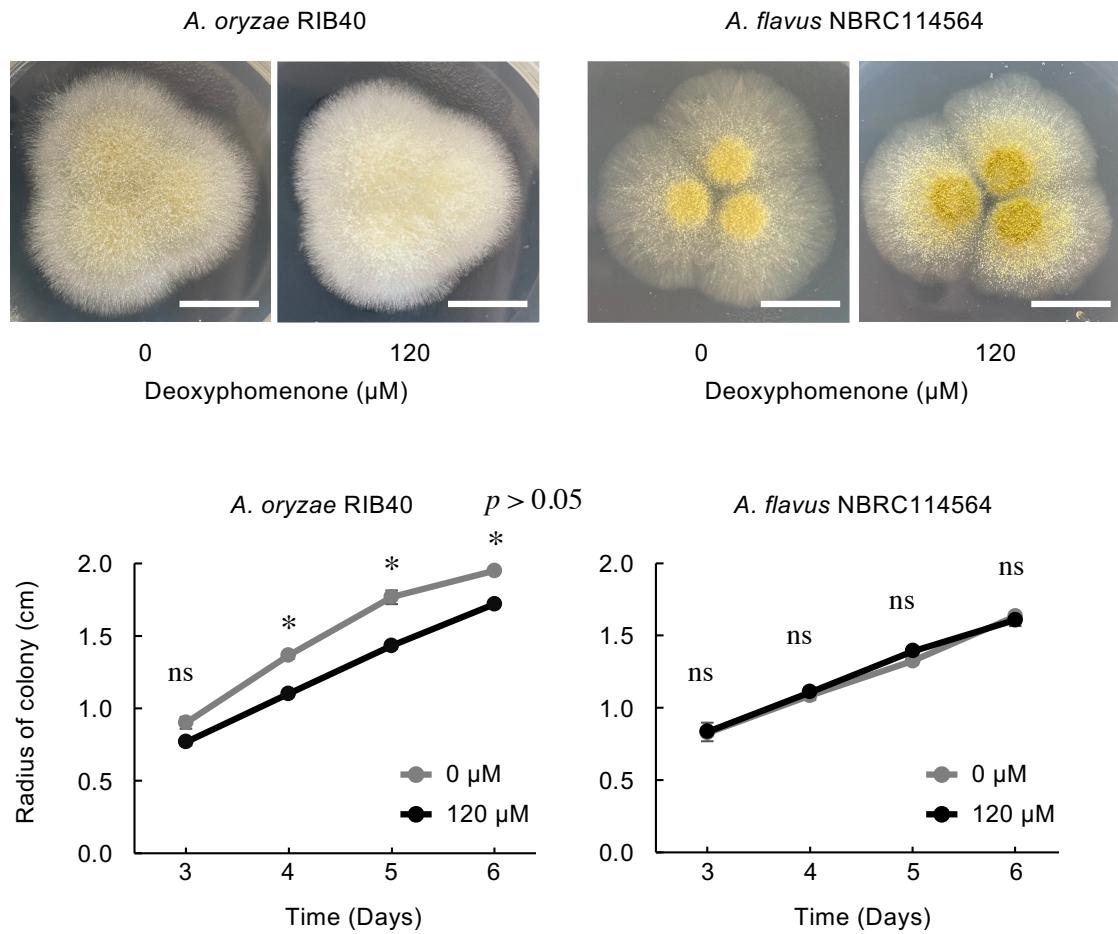
Figure S13. Effect of deoxyphomenone on mycelial growth of *Hansfordia pulvinata*, *Aspergillus oryzae* and *A. flavus*.
Strains were grown on MM agar with 1% methanol (0 μM) or 120 μM deoxyphomenone. Values are means of three biological replicates (± SD). Means were compared for significant differences amount treatments using Tukey's test. ns, no significance. (**A**) Colony morphology and number of spores produced by *H. pulvinata* 414-3. (**B**) Colony of *A. oryzae* RIB40 and *A. flavus* NBRC114564. Bars = 1 cm. Fewer ocherous spores were produced by RIB40 in the presence of deoxyphomenone but more were produced by NBRC114564.
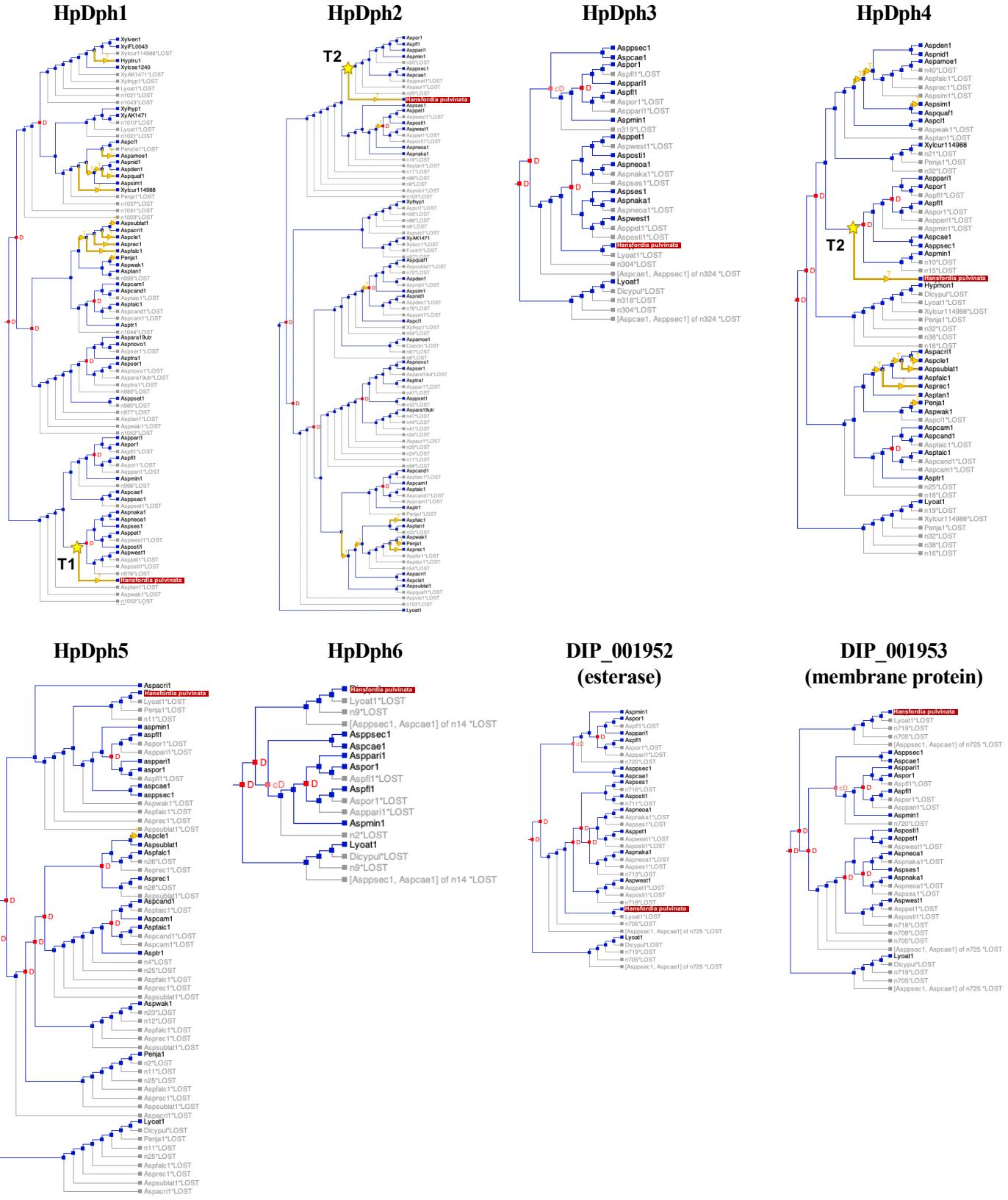
Figure S14. Reconciliation of gene trees with species tree based on *DPH* nucleotide and amino acid sequences.
Phylogenetic protein trees were compared with the species tree using NOTUNG v.2.9 to infer duplications, losses, and horizontal transfer events for the HpDPH amino acid sequences. Duplication nodes are marked by red squares with a red D; losses are in grey; migrations are indicated with yellow arrows. Horizontal gene transfer events for the HpDph1 (T1) and HpDph2/HpDph4 (T2) proteins are indicated by yellow stars. *Hansfordia pulvinata* is highlighted by a red box. Event scores were calculated as total cost of duplications, transfers and losses. Costs/weights were set as duplications (D), 1.5; transfers (T), 8.0; losses (L), 1.0 (ratio D:T:L is 1:5.3:0.67).
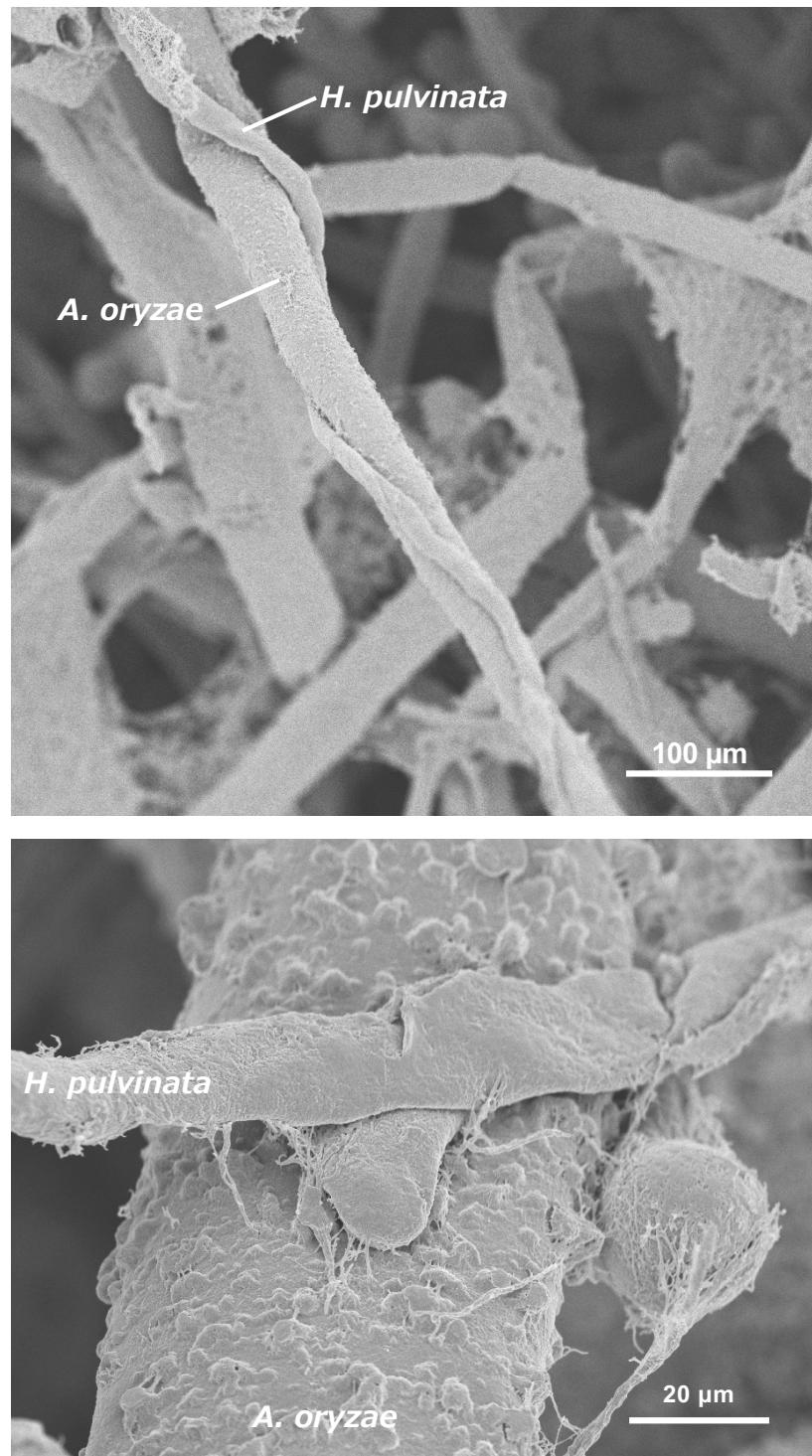
Figure S15. **Hyphal contact between the mycoparasite *Hansfordia pulvinata* 414-3 and *Aspergillus oryzae* RIB40.**
Coiling of hyphae of 414-3 around the thick, rough hyphae of RIB40 was rarely found.

Supplemental table S1. Fungal genomic sequences used in this study

| Species name [a]	Abbreviation name in JGI	Class (kingdom)	Database	Nucleotide sequence
* *Hansfordia pulvinata* 414-3	-	Sordariomycetes (Ascomycota)	NCBI (ncbi.nlm.nih.gov/)	TCACTTGACCTTGTGGTACCGCGGCGTGGACTCGCTCCACCTCTCGTTGCCGCTCATCTG
* *Aspergillus acristatulus* CBS 119.55 v1.0	Aspacri1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAGCGCTGATTCGGCGAGTTGTAGCGCTGGGTCGTCAGACTCCATAACTCATTTCCACT
* *Aspergillus amoeneus* CBS 111.32 v1.0	Aspamoe1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTACGCGCTGGCGGTTGCCTCCTTTTCAACATAACGCAGGGTCGTACGACTCCACAGCTG
* *Aspergillus arachidicola* v1.0	Aspara19utr	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAGGCAGCACCAGGCGAATTGTATCGCAAAGTAGTCACACTCCACAGCTCATTACCAG
* *Aspergillus caelatus* CBS 763.97 v1.0	Aspcae1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAAAAATGATAACGAGAAGTTGATTCACTCCAGCGCTCATTTCCGCTCATCTGAAACTG
* *Aspergillus campestris* IBT 28561 v1.0	Aspcam1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	GTTATATCGAAGAGTAGTCAAACTCCACAACTCATTCCCACTAATTTGTAATTCCAACCC
* *Aspergillus candidus* CBS 102.13 v1.0	Aspcand1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAGTTAGGCGAGTTATAGCGAAGAGTAGTCAAACTCCACAACTCATTCCCACTAATCTC
* *Aspergillus clavatus* NRRL 1 from AspGD	Aspcl1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTACGCACTAGCGGCTGCCTCTTTTTCAACATAGCGCAGGGTTGTCCGACTCCACAGCTC
* *Aspergillus cleistominutus* CBS 200.75 v1.0	Aspcle1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAGCGCTGATTCGGCGAGTTGTAGCGCTGAGTCGTCAGACTCCATAACTCATTTCCACT
* *Aspergillus creber* IBT 32277 v1.0	Aspcreb1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TTAATATATCTTATACCGGCTTGTTGTGCCGGACCACTGCTCATTTCCACTTGCCATATAT
* *Aspergillus dentatus* CBS 114.63 v1.0	Aspden1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTACGCGCTAGCGGTTGCCTCCTTTTCAACATAGCGCAGGGTCGTACGACTCCACCGCTG
* *Aspergillus falconensis* CBS 271.91 v1.0	Aspfalc1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	GGAAGAAGCAGTAACAATCTATCACATTCCATATGAGCGCATTCTAGCCTTGATTCGGC
* *Aspergillus flavus* NRRL3357	Aspfl1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TATATCCTGCATGTGTTGGCATCGGAGGATAATCGTCTACCTGATGCCCCGAGGTCAGAG
* *Aspergillus karnatakaensis* CBS 102800 v1.0	Aspkar1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TTCAACCCACCTAACTTCACGACACCCTGCTAAACCCAGCCCCCCTCCCGCTACATACCA
* *Aspergillus minisclerotigenes* CBS 117635 v1.0	Aspmin1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAAAAATGATAACGAGGAGTAGATTCACTCCAGCGCTCATTTCCACTCATCTGAAACTG
* *Aspergillus multicolor* v1.0	Aspmul1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTACTCAATTTGATACCGACTTGTCGTCCGACACCCACTCCTCATTCCCACTAGCCAGATAG
* *Aspergillus nakazawae* v1.0	Aspnaka1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TCAACGGTGGTAGCGAGGGGTCGATTCACTCCACCGCTCGTTGCCACTCATTTGGTCTTC
* *Aspergillus neoauricomus* CBS112787 v1.0	Aspneoa1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TCAACGGTGGTAGCGAGGGGTCGATTCACTCCACCGCTCGTTGCCACTCATTTGGTCTTC
* *Aspergillus nidulans*	Aspnid1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTACGCGCTAGCGGTTGCCTCCTTTTCAACATAGCGCAGGGTCGTACGACTCCACCGCTC
* *Aspergillus novoparasiticus* CBS 126849 v1.0	Aspnovo	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAGGCAGCACCAGGCGAATTGTATCGCAAAGTAGTCACACTCCACAGCTCATTACCAG
* *Aspergillus oryzae* RIB40	Aspor1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAAAAATGATAACGAGGAGTAGATTCACTCCAGCGCTCATTTCCACTCATCTGAAACTG
* *Aspergillus ostianus* v1.0	Asposti1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TCAACGGTGGTAGCGAGGGGTCGATTCACTCCACCGCTCGTTGCCACTCATTTGGTCTTC
* *Aspergillus parvisclerotigenus* CBS 121.62 v1.0	Asppari1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAAAAATGATAACGAGGAGTAGATTCACTCCAGCGCTCATTTCCACTCATCTGAAACTG
* *Aspergillus petrakii* CBS 105.57 v1.0	Asppet1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TATCTCGGCGATTCCTGAAATGGCAAGAGTTGACGCTGCCTAGACGGCCCCAAGGAACC
* *Aspergillus pseudocaelatus* CBS 117616 v1.0	Asppsec1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAAAAATGATAACGAGAAGTTGATTCACTCCAGCGCTCATTTCCGCTCATCTGAAACTG
* *Aspergillus pseudotamarii* CBS 117625 v1.0	Asppset1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAGGTCGCACTAGGCGAATTGTACCGTAAAGTGTACCACTCCACAGCTCATTGCCGG
* *Aspergillus quadrilineatus (floriformis)* CBS 937.73 v1.0	Aspquaf1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTACGCGCTAGCGGTTGCCTCCTTTTCAACATAGCGCAGGGTCGTACGACCCCACAGCTG
* *Aspergillus recurvatus* v1.0	Asprec1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAGCGCTGATTCGGCGAGTTGTAGCGCTGAGTCGTCAGACTCCATAACTCATTTCCACT
* *Aspergillus sergii* CBS 130017 v1.0	Aspser1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAGGCAGCAGTAGGCGAATTGTATCGCAAAGTAGTCACACTCCACAGCTCATTACCAG
* *Aspergillus sesamicola* CBS 137324 v1.0	Aspses1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TCAGGCTGCAATTGAGCATAGATGGACGCTACTATTGCTACTAGTACTCCGGAGTAGA
* *Aspergillus similis* v1.0	Aspsim1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	GGGTTGACGTCGGGAGGAGAACAAGAAACACCTTTTGGTTTGCAACCACGTAGCTAGC
* *Aspergillus sublatus* IBT 19356 v1.0	Aspsublat1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAGCGCTGATTCGGCGAGTTGTAGCGCTGAGTCGTCAGACTCCATAACTCATTTCCACT
* *Aspergillus sydowii* CBS 593.65 v1.0	Aspsy1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	ATACCGGCTCGTAGTCCGAGACCACTGCTCATTCCCACTCGGCCATATATTTCAAGGCCTG
* *Aspergillus taichungensis* IBT 19404 v1.0	Asptaic1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TTAGTTAGGCGAGTTATAGCGAAGAGTAGTCAAACTCCACAACTCATTCCCACTAATCTG
* *Aspergillus tanneri* DTO 303-18 v1.0	Asptan1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TTATGAGGTGACTCCTATTTGAGCTGGCTCTGCTCGGTACGAGATGAATTTGCATAGTAG
* *Aspergillus transmontanensis* CBS 130015 v1.0	Asptra1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAGGCAGCACTAGGCGAATTGTATCGCAAAGTAGTCACACTCCACAGCTCATTACCAG
* *Aspergillus triticus* CBS266.81 v1.0	Asptr1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAGTTAGGCGAGTTATAGCGAAGTGTAGTCAAGCTCCACAACTCATTCCCACTAATCTC
* *Aspergillus varians* CBS 505.65 v1.0	Aspvar1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	AGACTGCTAAGAGAGAGAATAGGATCTGTAGTCTAGGTATCCATGGATCTATATATTTA
* *Aspergillus versicolor* v1.0	Aspve1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CAACTTCCCCGACTCGCGCGAGTTCATCCCCGAGCGATGGCTAGACCCGGAAAAGCGTA
* *Aspergillus waksmanii* IBT 31900 v1.0	Aspwak1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CCCATATGAACGCATCCTAGCGTTGATTCGGCGAGTTGTAGCGCTGAGTCGTCAGACTCC
* *Aspergillus westerdijkiae* CBS 112803 v1.0	Aspwest1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TCAACGATGGTAGCGAGGGGTCGATTCACTCCACCGCTCGTTGCCACTCATTTGGTCTTC
* *Penicillium antarcticum* DTO 356-E5 v1.0	Penanta1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TTATTGCCGATATCTTGGAGTCCACTGACTCCATAGCTCATTTCCACGCATAAAACTTTCC
* *Penicillium atramentosum* RS17 v1.0	Penatra1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TTATTGCCGATATCTTGGAGTCCACTGACTCCATAGCTCATTTCCACGCATAAAACTTTCC
* *Penicillium brasilianum* MG11	Penbra1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TTACTTTTGGTAGCGAGGAGTCCACTGAGTCCATGTCTCCATTCCACTCATAGTATTCC
* *Penicillium coprophilum* IBT 31321	Pencop1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	GTCAGTCTCTTATTCGAGCAAAATGTTCATCGTGAGAGCGAAAGGTCAGGTTACTAATG
* *Penicillium decumbens* IBT 11843	Pendec1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CGGAAAACCAGGAGTCAGCTTCGTCGGATAGCTGAGTTTGTTAGATTGATGTGCATAGT
* *Penicillium flavigenum* IBT 14082	Penfla1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTCCTGGTTGATATAGCGTCCATGCAGGTGACTACTCGTCGGCGACTCTTGTTGATATAA
* *Penicillium janthinellum* ATCC 10455 v1.0	Penja1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	GTCCATTCCACCTCTTGGTATAGAGGCAGTTTGTGTATGCCTAGAGTGCAACTCAATCAT
* *Penicillium nalgiovense* FM193	Pennal1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	GCATATAACTCATTCACTTCTATTGTAAAAAGTTCGTTGGACCAAAGAGGATTGCCTATA
* *Penicillium steckii* IBT 24891	Penste1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	GGCCAGCATACTGTACATCGCCGTTGCGCAGCGCTATACCATCTTGGTGGAAACCAAAA
* *Penicillium swiecickii* 182 6C1 v1.0	Penswi1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	GAGCTTTCAGCTCAAAAAGTGTTGGGACTAAAGTTTGATGACGGCTTGGTCAAAATCCT
* *Hypoxylon monticulosum* FL0542 v1.0	Hypmon1	Sordariomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TCAACGACCTTCTGTAAAAGCAAGACCCCCACTCCTATTGTACCGTGGCGTTAGAAGAC
* *Hypoxylon trugodes* CBS 135444 v1.0	Hyptru1	Sordariomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	AATACCATACTTTCGGATTTCTACGCCATATTGTACTCTCTCGCATTGATAAACTTCTAGA
* *Xylaria cf. castorea* CBS 124033 v1.0	Xylcas1240	Sordariomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAGGGGTAGGGGAGGTTAAATGCGGTGAAATCTTAATTTTCGTAGCGACCTCCGTAGA
* *Xylaria curta* CBS 114988 v1.0	Xylcur1149	Sordariomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTGTTATATGGTGTATATAAAAAGGCATGGTAATTATGCATGATCAGATACCTAAATACGA
* *Xylaria hypoxylon* OSC100004 v1.0	Xylhyp1	Sordariomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TCAGTTAACACTAGAGTAGCGAAGCGTGGTCTTGCTCCAAAGTTCATTACCACTCATCTC
* *Xylaria sp.* FL0043 v1.0	XylFL0043	Sordariomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAATAGCGAATAGAGCCCAGGCTATGCACATCTGCAGACGCCTCTTCCGGTGCCAGGT
* *Xylariaceae sp.* AK1471 v1.0	XyAK1471	Sordariomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TCAGCTAACCTTAGAGTATCGAAGGGTGGTCTTGCTCCAGAGCTCATTGCCGCTCATCTG

*	*Xylaria venustula* FL0490 v1.0	Xylven1	Sordariomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TTCCGGTGCCAAGTATCGCAGGGTAGTCCTGCTCCAGAGTTCATTTCCACACATTTGTAG
*	*Lyophyllum atratum* CBS 144462 v1.0	Lyoat1	Eubasidiomycetes (Basidiomycota)	JGI (mycocosm.jgi.doe.gov)	TCTCTATCTTTGCGTCAAATAGACATTGATCGCTAGCGTCACGGGCTACTACACAACCCG
	Aspergillus albertensis v1.0	aspalbe	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	GGACAACGAACTTAAGTCGACATGAGGTGGACGGGAGGCTGAAGAAGAAATGATCAG
	Aspergillus alliaceus CBS 536.65 v1.0	Aspalli1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAGTCAACTACCACGCTATACCGCAACGTTGTCTGACTCCACAGCTCATTGCCACTCAT
	Aspergillus amylovorus CBS 600.67 v1.0	Aspamy1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TCAGTCAGTCACCACGCTGTATCGCTGGGTTGTCCGACTCCAGAGCTCATTACCGCTCAT
	Aspergillus assulatus CBS 27911 v1.0	Aspass1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TCATTTCCACTCATCTGGTATTCCAAGCCCTTGATATATAGCCTCAGATTCTCACTGCATG
	Aspergillus aureoterreus v1.0	Aspaur1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TTCGTCGATCATCCAGTGCCACGAATGGATATACGCCATGGATGAATTCAGTTGGCTCGG
	Aspergillus bertholletius IBT 29228 v1.0	Aspber1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAATCCACCAATAAATACCTCGGCGTTGTCTTACTCCACAGTTCGTTCCCGCTCATTTG
	Aspergillus biplanus CBS 468.65 v1.0	Aspbip1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TCATGCCTTGACAGCATAACGACCAGTAAGCTTGCTCCAAACCTCGTGACCGCTAGCGC
	Aspergillus californicus CBS 123895 v1.0	Aspcalif1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TGTTTTGGTAAGTTAGAAAATGCATTCTTTGGTTCACGGTAGATGATATATCTAGAGTCC
	Aspergillus crustosus CBS 478.65 v1.0	Aspcru1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	ATGATCTCTTTCTCCCCTTTGCCAAGGAGGGGAGGAAGGGCGTCCGTGTTCTAATTCGAT
	Aspergillus desertorum CBS 653.73 v1.0	Aspdese1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAGTCAACTACCACGCTATAACGCAACGTTGTCTGACTCCACAGCTCATTGCCACTCAT
	Aspergillus dromiae CBS 140633 v1.0	Aspdro1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	GTGCGATTCTTCCCTCTTCTACTGTTCAATTCAAGCAGAAACGAAAAGAGGAACTACAG
	Aspergillus duricaulis CBS 481.65 v1.0	Aspdur1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TCAATCCGTACCCCGGCCATATCGCTCCGTGGTCCTGCTCCACAGCTCATTTCCGCTCATG
	Aspergillus elegans CBS 116.39 v1.0	Aspele1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TCAACCGTGGTAGCGAGGGGTCGATTCGCTCCACCGCTCGTTGCCACTCATTTGATACTG
	Aspergillus ferenczii CBS 121594 v1.0	Aspfer1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	ACTGCTTACTGCTTACTGCTTCATAGTGGACAGGGGCAATCCCGCCACGTACATCCTGAA
	Aspergillus flocculosus v1.0	Aspfloc1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TCAACAATGGTAGCGAGGAGTGCGATTCACTCCACCGCTCATTGCCACTCATGTGGTACTG
	Aspergillus foveolata CBS 279.81 v1.0	Aspfove1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAGTCAACTACCGCGCTATAACGCAACGTTTTCCGACTCCACTGCTCATTGCCACTCATG
	Aspergillus fructiculosus v1.0	Aspfru1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	AAAAAAAAAAAGGAAATAGGAAGAAGCAGTAACAATCTATCACATTCCATATGAGCG
	Aspergillus galapagensis CBS 117522 v1.0	Aspgal1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TGCCGCCCAGTGTGGTATTTGAAGTGTTAACACCCCTCACTGGAGGGATGCGTAATTCCC
	Aspergillus granulosus CBS 588.65 v1.0	Aspgra1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAGACGGCAGCGCCAACCAAATTATTATAGCGCAGCGTCGTTCTACTCCACTCTTCATT
	Aspergillus hiratsukae CBS 294.93 v1.0	Asphir1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TTAGAAACTCATTCTCTTGTATGGAAACACCTGCCGCTTGATTACTGCTTCATTATGCTAT
	Aspergillus implicatus CBS 484.95 v1.0	Aspimp1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTACAAGTCAAGATACAGCTCCGGATGATACCGGCGGCAGGCTGCCTGCCACAGCTCAT
	Aspergillus indicus v2.0	Aspind2	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAGTCAACTACCACGCTATACCGCAACGTTGTCTGACTCCACAGCTCATTGCCACTCAT
	Aspergillus lucknowensis CBS 449.75 v1.0	Aspluc1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	GGATCGCACATATATAGCCTGCACGCCGTGACAACCATCCCCCCGCCAAGGGAAGGCT
	Aspergillus muricatus v1.0	Aspmuri1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TTAAATATGGTACCGTGGAGTACTTTCGCTCCATCGCTCGTTTCCACTCATTTGAGCTTCC
	Aspergillus neoechinulatus CBS120.55 v1.0	Aspne1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	GAAGCAAGGGTGTTCGCGTTTTGATCCGGTAGGAGACCCGATCCCGAAGAGCAGACTT
	Aspergillus neoindicus CBS 444.75 v1.0	Aspneoi1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAGCTGGGACGATCAAAATTGTATCGCTGGGTGATCTTGCTCCAGAGCTCATTACCAG
	Aspergillus parasiticus CBS 117618 v1.0	Asppar1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAGGCAGCACTAGGCGAATTGTATCGTAAAGTAGTGACACTCCACAGCTCATTACCAG
	Aspergillus pseudofelis IBT 34107 v1.0	Asppsf1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTCAAAACAATACATGTGTCCGCCTATGTATTTCTTTAGTTATGGTTCGAGGCTACTTAAC
	Aspergillus pseudoustus CBS 123904 v1.0	Asppust1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TTAGCCGACAACGCTATATCGCAACGTAGTCCGACTCCAGAGCTCATTCCCACTCATCTC
	Aspergillus pulvericola CBS 137327 v1.0	Asppul1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	GGTCAGGCTCTGACCGAAATTAGGTGCGAATATGACATCAGGGAGCTCAAGGGAT
	Aspergillus puulaauensis IBT 32284 v1.0	Asppuu1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TTAATAAATCTTATACCGGCTTGTTGTGCCGGACCACTGCTCATTTCCACTTGCCATATAT
	Aspergillus roseoglobulosus CBS112800 v1.0	Aspros1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTATTCTGACTGTAGCGATCGGCTATGATAACGAGGCGTAGATTCACTCCACCGCTCATT
	Aspergillus siamensis CBS 137452 v1.0	Aspsia1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TTAAAGACTACTCTAAGTATGTCAATGGTTTAAAACTCCACAACATACCTCCCTGACTCG
	Aspergillus silvaticus CBS 128.55 v1.0	Aspsil1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	GGTCCAGTAGCTTAGGTAGGGAATCATGTTCAGGTACGAATTTGATATCTCGTTGTCGTG
	Aspergillus spectabilis CBS 429.77A v1.0	Aspspe1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTACTCAACCCGGTACCGGCTCGTTGTCCTTGACCACTCCTCATTTCCACTCGCCAGATAG
	Aspergillus steynii IBT 23096 v1.0	Aspste1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTACTCCAAATGATGATACCTCAAGGTAGTCTGGCTCCATCGCTCATTCCCACTCATCTG
	Aspergillus stercoraria CBS 428.93 v1.0	Aspstec1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAGTCAACTACCACGCTATAACGCAACGTTGTCTGACTCCACAGCTCATTGCCACTCAT
	Aspergillus stella-maris CBS 113639 v1.0	Aspstell1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	GTGGTAGCGAGGGGTCGATTCGCTCCACCGCTCGTTGCCACTCATTTGATACTCAAGTCC
	Aspergillus subauricomus CBS 638.78 v1.0	Aspsub1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TCAGACATGATACCGCGGAGTGGATTCGCTCCAGAGTTCGTTCCCACTCATTTGATATTC
	Aspergillus tennesseensis IBT 32283 v1.0	Aspten1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CCACATACTTAATATATCTTATACCGGCTTGTTGTGCCGGACCACTGCTCATTTCCACTTG
	Aspergillus tetrazonus CBS 591.65A v1.0	Asptetr1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTACTCAACCCGGTACCGGCTCGTTGTCCGACTCCACTCTTCATTCCCACTGGCCAGGTA
	Aspergillus thermomutatus v1.0	Aspthe1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TGTCGTGGTCGACTGTAGCATCTATCGGGAAGTCTTCGTATTCTGCCAGCAAGTCAGGA
	Aspergillus venezuelensis CBS 868.97 v1.0	Aspven1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CAACTTCCCCGACTCGCGCGAGTTCATCCCCGAGCGATGGCTAGACCCGGAAAAGCGTA
	Aspergillus violaceofuscus CBS 115571 v1.0	Aspvio1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTACAAGCTAGAGTCAGGCTCAGGCTTGATCGACATAGCGCAGGGTTGTCCGACTCCACAGCT
	Aspergillus viridinutans CBS 127.56 v1.0	Aspvir1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TCAGCTCAGAACGAACTTTTGGAATTTAACCATACCTAAGGATAAAGCACCATACACGG
	Aspergillus westlandensis CBS 123905 v1.0	Aspwes1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TTACACATGATAGCGCGGGGTGGATTCGCTCCACAGCTCGTTCCCAATCATTTGACATTC
	Cladophialophora carrionii CBS 160.54	Claca1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAACCCACAGTCACGTCGTTATATCGCGGCGTAATGAGACTCCAGACTTCATTCCCGGC
	Cladophialophora yegresii CBS 114405	Claye1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAGCCAACAGTCGCGTCATTATATCGTGGCGTGATGAGACTCCAGACTTCATTCCCGGC
	Penicillium canescens ATCC 10419 v1.0	Penca1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	GATATTCGGTGAGAAATATAGCGCAGTGAGATGTTTCTTTCCATAACAATTACATGGTT
	Penicillium chrysogenum v1.0	Pench1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TTAAAGGACGGGCTCATCTGAGACAGAATGGTATCTGAGTGTCGTCTGGCTCCACCTCT
	Penicillium digitatum Pd1	Pendig1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAGACCAGATTATTATATCGCAACGTGGTCTTACTCCACTCCTCGTTGCCACTCATCTG
	Penicillium expansum d1	Penexp1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAGACCACATTGTTATATCGTAAAGTGGTCTTACTCCACTCCTCGTTACCACTCATCTG
	Penicillium fellutanum ATCC 48694 v1.0	Penfe1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	GTTGGTGAGGTCTATATCATGAGGAGTGACAAGCCATATATCGTATGAGGCAGGCTATC
	Penicillium glabrum DAOM 239074 v1.0	Pengl1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TCATCGATAGCGTGGCGTCCATTGACTCCATAGCTCTATCCCGCTCATGAGATACTCAAG
	Penicillium italicum PHI-1	Penita1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TCATTGTCGATACCCGGGAGTGGTCCACTGACTCCATAACTCGATGCCGGCACATAAAGTATT
	Penicillium polonicum IBT 4502	Penpol1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TCATTGTCGATATCGTGGAGTCCACTGACTCCATAACTCGATGCCGCACATAAAGTATT
	Penicillium raistrickii ATCC 10490 v1.0	Penra1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	GTCATTCAAGCAGATGTATTGAAGAAAAACTCTTATCAAAGGCCTTCATCACGGATTCC
	Penicillium solitum IBT 29525	Pensol1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TTAGTTGTATCGACGCGTGGCCTTACTCCACTGCTCATTGCCGCTCATCTGGTGCTCTAGC
	Penicillium sp.	Pensp1	Eurotiomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTCGTAAATAGATGGTATTTCTATGACTCTCTGTGTGCTTCTTGGATATCCTTCTCGGTAC
	Alternaria alternata SRC1lrK2f v1.0	Altal1	Dothideomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTACATCTGTACAGGATGGTACCTCGAAGTCGTCGAGCTCCACACTTCATTCCCACTCAT
	Alternaria sp. UNIPAMPA012 v1.0	Altsp012	Dothideomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTACATCTGTACAGGATGGTACCTCGAAGTCGTCGAGCTCCACACTTCATTCCCACTCAT

Cercospora berteroae CBS 538.71	Cerbe1	Dothideomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TTATGATCCAACTGCACCACCCAGCAGCTCTGGATGACCAGAATTGAACTCCTCCGCAT
Cercospora zeae-maydis v1.0	Cerzm1	Dothideomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TTATGATCCAACATTACCACTCAGCAGCCGCGGGATTCGCGTAATTAAACTCCTCCTCATC
Phyllosticta capitalensis CBS 173.77 v2.0	Phycapi2	Dothideomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTACCGGTCGCTTGACTCCGAAAATCCATAGCGGGGAGTGGTGATGCTCCAATGCAAAT
Phyllosticta citriasiana CBS 120486 v1.0	Phycit1	Dothideomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CACCTTTCCCTGTCCCGCGCCCCGTCCACCACTTTTATCAAGCATCGCTTGCCCGTGCTGT
Phyllosticta citricarpa CBS 141352 v1.0	Pcit141352	Dothideomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TTACCCCCTCGACTCTGAAAATCCGTAGCGCGGAGTCGTGATGCTCCAATGCAAGTGGC
Phyllosticta citricarpa CBS 127454 v1.0	Phycitr1	Dothideomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TTACATGCCGGCAAAGGACGAACTGCTGCTCGACTCCGAAAATCCGTACCGCGGAGTT
Phyllosticta sp. CPC 27913 v1.0	Phycpc1	Dothideomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TGAAAATCCGTAGCGCGGAGTCGTGATGCTCCAATGCAAGTGGCCGCTCATGAGATCCT
Colletotrichum cereale CBS 129662 v1.0	Colce1	Sordariomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAAGCCGTCGAAGGTGCGTTGTAGCGCAGTGTCGTCTTGCTCCAAAGCTCGTTCCCGCT
Colletotrichum eremochloae CBS129661 v1.0	Coler1	Sordariomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TTTGAAGGCAGACTCAAATTCAAAATAAAAATAAAAACATCGTGAAGTGACCAGTCTT
Colletotrichum godetiae CBS 193.32 v1.0	Colgo1	Sordariomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAGACAGAGTGATATCTTGGAGTAATGCTGCTCCATGCCTCATTCCCACTCATTTGATA
Colletotrichum orbiculare 104-T	Colorb1	Sordariomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTAAGCGGTGGGAGGAGCATTGTACCGCAACGTGGTCTTGCTCCAAAGCTCGTTGCCGC
Colletotrichum sublineola CBS 131301 v1.0	Colsu1	Sordariomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	ATACCGCGGAGTTGTCCGGCTCCAGAGCTCGTTTCCACTCATCTGGTACTCCAAGCCTTT
Colletotrichum zoysiae MAFF235873 v1.0	Colzo1	Sordariomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	GTTCAGCACATTACATACGCTTCCGGTAGTCTTGATCCGTATAACTTAATTGCTTTCAATT
Fusarium redolens MPI-CAGE-AT-0023 v1.0	Fusre1	Sordariomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTACTCAGAATAGCGACGTGTAGTCTTGCTCCAGAGCTCATTGCCACTCATCTGATACTC
Fusarium avenaceum MPI-SDFR-AT-0044 v1.0	Fustri1	Sordariomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	TTACACGTTGTTATACCGAGGTGTCAACCTGCTCCATGCTTCATTGCCGCTCATTTGATAC
Hypoxylon sp. FL1284 v2.0	HyFL1284	Sordariomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CTGCATAATAAGCCACTTGCATGTAGGTACCTCTCAATGTTTGCATTTATTGGTAAGCCT
Xylaria scruposa CBS 123580 v1.0	Xylscr1	Sordariomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	CGATGATACATGTACGATGCCCCTCATTACTCCAAAGGTGCTAGGTACCGCAATGTGGT
Xylariaceae sp. FL0662B v1.0	XylFL0662B	Sordariomycetes (Ascomycota)	JGI (mycocosm.jgi.doe.gov)	GTGTAGAGTAAAATCACATATGAAGTAAGTTAAATACTAAACTATGAATGACCAGACA

[a] Asterisks indicate sequences of 60 fungal species used in the phylogenetic analysis shown in supplemental figure S6.

Supplemental table S2. Amino acid sequences of deoxyphomenone biosynthesis (*DPH*) genes from *Hansfordia pulvinata* and *Aspergillus* species

Organism	Gene function	DDBJ accession number or JGI protein ID [a]	Protein sequence [b]	Database
Hansfordia pulvinata 414-3	Esterase (HP001952)	LC779504	MDASTALGLIPTISRSFYGVAAASA	DDBJ/NCBI/EMBL
Hansfordia pulvinata 414-3	Integral membrane ptorein (HP001953)	LC779505	MAGEENKGPGFTAACIIVTVAAVL	DDBJ/NCBI/EMBL
Hansfordia pulvinata 414-3	Sesquiterpene synthase (DPH1, HP001954)	LC779506	MLSTLRSFELHKLLGLTGSSSNDST	DDBJ/NCBI/EMBL
Hansfordia pulvinata 414-3	Short chain dehydrogenase (DPH2, HP001955)	LC779507	MTTLRLSQAAIPDCTGKTVVITGGS	DDBJ/NCBI/EMBL
Hansfordia pulvinata 414-3	CytochromeP450 (DPH3, HP001956)	LC779508	MALITLALLCVAAWVLRRLGLAVY	DDBJ/NCBI/EMBL
Hansfordia pulvinata 414-3	CytochromeP450 (DPH4, HP001957)	LC779509	MAPRPTSGFWVLVFAVSWLGQVV	DDBJ/NCBI/EMBL
Hansfordia pulvinata 414-3	CytochromeP450 (DPH5, HP001958)	LC779510	MSLTVDLEALRWKLVPVLLAFLSW	DDBJ/NCBI/EMBL
Hansfordia pulvinata 414-3	MFS transporter (DPH6, HP001959)	LC779511	MATEKHPASLPGSQDAPPKTEAPP	DDBJ/NCBI/EMBL
Aspergillus oryzae RIB40	Esterase	10092*	MAGLWLGLGFTAGKSIAITLWSAIT	JGI (mycocosm.jgi.doe.gov)
Aspergillus oryzae RIB40	Integral membrane ptorein	10091*	MGAKENKGPGMTAASIVLTVIAVV	JGI (mycocosm.jgi.doe.gov)
Aspergillus oryzae RIB40	Sesquiterpene synthase (AoDPH1)	10090	MLQRLWALSTSAIKLPFQPFSFGAP	JGI (mycocosm.jgi.doe.gov)
Aspergillus oryzae RIB40	Short chain dehydrogenase (AoDPH2)	10089*	MASMQLSDADIPSCAGKTVVITGG	JGI (mycocosm.jgi.doe.gov)
Aspergillus oryzae RIB40	CytochromeP450 (AoDPH3)	10088*	MTLISLSLLALSLWIIIRVLVIIYRLA'	JGI (mycocosm.jgi.doe.gov)
Aspergillus oryzae RIB40	CytochromeP450 (AoDPH5)	10086	MRSSTQLTALYWVHLVIYNVFFHP	JGI (mycocosm.jgi.doe.gov)
Aspergillus oryzae RIB40	CytochromeP450 (AoDPH4)	10087*	MDLFPRDYLFAGLAVFIFWWIIDHS	JGI (mycocosm.jgi.doe.gov)
Aspergillus oryzae RIB40	MFS transporter (AoDPH6)	10084	MSTKTRSSQTGETAVSSRISTPATLI	JGI (mycocosm.jgi.doe.gov)
Aspergillus flavus NRRL3357 v1.0	Esterase	2229159	MAGLWLGLGFTAGKSIAITLWSAIT	JGI (mycocosm.jgi.doe.gov)
Aspergillus flavus NRRL3357 v1.0	Integral membrane ptorein	2229158	MGAKENKGPGMTAASIVLTVIAVV	JGI (mycocosm.jgi.doe.gov)
Aspergillus flavus NRRL3357 v1.0	Sesquiterpene synthase	1834709	MLQRLWALSTSAIKLPFQPFSFGAP	JGI (mycocosm.jgi.doe.gov)
Aspergillus flavus NRRL3357 v1.0	Short chain dehydrogenase	2200580*	MASMQLSDADIPSCAGKTVVITGG	JGI (mycocosm.jgi.doe.gov)
Aspergillus flavus NRRL3357 v1.0	CytochromeP450	2200579	MTLISLSLLALSLWIIIRVLVIIYRLA'	JGI (mycocosm.jgi.doe.gov)
Aspergillus flavus NRRL3357 v1.0	CytochromeP450	2063894	MRSSTQLTALYWIHLAIYNVFFHPI	JGI (mycocosm.jgi.doe.gov)
Aspergillus flavus NRRL3357 v1.0	CytochromeP450	2062078	MDLFPRDYLFAGLAVFIFWWIIDHS	JGI (mycocosm.jgi.doe.gov)
Aspergillus flavus NRRL3357 v1.0	MFS transporter	2210056	MSTKTRSSQTGETAVSSRISTPATLI	JGI (mycocosm.jgi.doe.gov)
Aspergillus parvisclerotigenus CBS 121.62 v1.0	Esterase	166540	MAGLWLGLGFTAGKSIAITLWSAIT	JGI (mycocosm.jgi.doe.gov)
Aspergillus parvisclerotigenus CBS 121.62 v1.0	Integral membrane ptorein	166547	MGAKENKGPGMTAASIVLTVIAVV	JGI (mycocosm.jgi.doe.gov)
Aspergillus parvisclerotigenus CBS 121.62 v1.0	Sesquiterpene synthase	403455*	MLQRLWALSTSAIKLPFQPFSFGAP	JGI (mycocosm.jgi.doe.gov)
Aspergillus parvisclerotigenus CBS 121.62 v1.0	Short chain dehydrogenase		MASMQLSDADIPSCAGKTVVITGG	JGI (mycocosm.jgi.doe.gov)
Aspergillus parvisclerotigenus CBS 121.62 v1.0	CytochromeP450	403457	MTLISLSLLALSLWIIIRVLVIIYRLA'	JGI (mycocosm.jgi.doe.gov)
Aspergillus parvisclerotigenus CBS 121.62 v1.0	CytochromeP450	375701	MRSSTQLTALYWVHLVIYNVFFHP	JGI (mycocosm.jgi.doe.gov)
Aspergillus parvisclerotigenus CBS 121.62 v1.0	CytochromeP450	334960*	MDLFPRDYLFAGLAVFIFWWIIDHS	JGI (mycocosm.jgi.doe.gov)
Aspergillus parvisclerotigenus CBS 121.62 v1.0	MFS transporter	334970	MSTKTRSSQTGETAVSSRISTPATLI	JGI (mycocosm.jgi.doe.gov)
Aspergillus minisclerotigenes CBS 117635 v1.0	Esterase	229809*	MAGLWLGLGFTAGKSIAITLWSAIT	JGI (mycocosm.jgi.doe.gov)
Aspergillus minisclerotigenes CBS 117635 v1.0	Integral membrane ptorein	242403	MGAKENKGPGMTAASIVLTVIAVV	JGI (mycocosm.jgi.doe.gov)
Aspergillus minisclerotigenes CBS 117635 v1.0	Sesquiterpene synthase	229813*	MLQHLWAIATSAIKLPFQPFSFGAP	JGI (mycocosm.jgi.doe.gov)
Aspergillus minisclerotigenes CBS 117635 v1.0	Short chain dehydrogenase		MASMQLSDADIPSCAGKTVVITGG	JGI (mycocosm.jgi.doe.gov)
Aspergillus minisclerotigenes CBS 117635 v1.0	CytochromeP450	251374	MTLISLSLLALSLWIIIRVLVIIYRLA'	JGI (mycocosm.jgi.doe.gov)
Aspergillus minisclerotigenes CBS 117635 v1.0	CytochromeP450	229816	MDRVVWLSLAVALTALYWVHLVI	JGI (mycocosm.jgi.doe.gov)

Aspergillus minisclerotigenes CBS 117635 v1.0	CytochromeP450	229815*	MDLLPRDYLFAGLAVFIFWWIIDHS JGI (mycocosm.jgi.doe.gov)
Aspergillus minisclerotigenes CBS 117635 v1.0	MFS transporter	216838	MSTKTRSSHTGETAVSSRISTPATPI JGI (mycocosm.jgi.doe.gov)
Aspergillus caelatus CBS 763.97 v1.0	Esterase	160431	MAGLWLGLGLTASKSVAVALWSA JGI (mycocosm.jgi.doe.gov)
Aspergillus caelatus CBS 763.97 v1.0	Integral membrane ptorein	25776	MGAKENKGPGMTAASIVLTVIAVV JGI (mycocosm.jgi.doe.gov)
Aspergillus caelatus CBS 763.97 v1.0	Sesquiterpene synthase	147588*	MLQRLWSLSTSAIKLPFQPVSFGAF JGI (mycocosm.jgi.doe.gov)
Aspergillus caelatus CBS 763.97 v1.0	Short chain dehydrogenase		MAAIQLSDADIPSCAGKVVVITGG JGI (mycocosm.jgi.doe.gov)
Aspergillus caelatus CBS 763.97 v1.0	CytochromeP450	132601	MTLIYLSLLVLCLWIISRVLVIIYRLA JGI (mycocosm.jgi.doe.gov)
Aspergillus caelatus CBS 763.97 v1.0	CytochromeP450	147591*	MVDRVVWLSLAVALIALYWANLV JGI (mycocosm.jgi.doe.gov)
Aspergillus caelatus CBS 763.97 v1.0	CytochromeP450	132604	MDLFTRGYLLGGVVVCMFWWIVA JGI (mycocosm.jgi.doe.gov)
Aspergillus caelatus CBS 763.97 v1.0	MFS transporter	160439	MSTKTRSSQTGETAVSSGTSTPATL JGI (mycocosm.jgi.doe.gov)
Aspergillus pseudocaelatus CBS 117616 v1.0	Esterase	290130	MAGLWLGLGLTASKSVAVALWSA JGI (mycocosm.jgi.doe.gov)
Aspergillus pseudocaelatus CBS 117616 v1.0	Integral membrane ptorein	91998	MGAKENKGPGMTAASIVLTVIAVV JGI (mycocosm.jgi.doe.gov)
Aspergillus pseudocaelatus CBS 117616 v1.0	Sesquiterpene synthase	290130*	MLQRLWSLSTSAIKLPFQPVSFGAF JGI (mycocosm.jgi.doe.gov)
Aspergillus pseudocaelatus CBS 117616 v1.0	Short chain dehydrogenase		MAAIQLSDADIPSCAGKVVVITGG JGI (mycocosm.jgi.doe.gov)
Aspergillus pseudocaelatus CBS 117616 v1.0	CytochromeP450	305986	MTLIYLSLLVLCLWIISRVLVIIYRLA JGI (mycocosm.jgi.doe.gov)
Aspergillus pseudocaelatus CBS 117616 v1.0	CytochromeP450	278998*	MVDRVVWLSLAVALIALYWANLV JGI (mycocosm.jgi.doe.gov)
Aspergillus pseudocaelatus CBS 117616 v1.0	CytochromeP450	278999	MDLFTREYLLGGVVVCMFWWIVA JGI (mycocosm.jgi.doe.gov)
Aspergillus pseudocaelatus CBS 117616 v1.0	MFS transporter	290122	MSTKTRSSQTGETAVSSGTSTHATI JGI (mycocosm.jgi.doe.gov)
Aspergillus nakazawae v1.0	Esterase	234342	MDQIRIGATVGKAVAAGVWGGLA JGI (mycocosm.jgi.doe.gov)
Aspergillus nakazawae v1.0	Integral membrane ptorein	234343	MENKGPGMIAASIVLTTVAFLLFCI JGI (mycocosm.jgi.doe.gov)
Aspergillus nakazawae v1.0	Sesquiterpene synthase	234344	MLATIWTALSKASATPKSAELSPIEI JGI (mycocosm.jgi.doe.gov)
Aspergillus nakazawae v1.0	Short chain dehydrogenase	234345	MSSLTITDADIPDCSGKTVVITGGS JGI (mycocosm.jgi.doe.gov)
Aspergillus nakazawae v1.0	CytochromeP450	224099	MAWFIVPVALLLLPAVIAVYRLVLI JGI (mycocosm.jgi.doe.gov)
Aspergillus sesamicola CBS 137324 v1.0	Esterase	344839*	MEQIRIGATVGKAVAAGVWGGLA JGI (mycocosm.jgi.doe.gov)
Aspergillus sesamicola CBS 137324 v1.0	Integral membrane ptorein	301945	MENNGPGMIAASIVLTTVAFLLFCI JGI (mycocosm.jgi.doe.gov)
Aspergillus sesamicola CBS 137324 v1.0	Sesquiterpene synthase	301946	MLATIWAALSKASATPKSAEFSPIE JGI (mycocosm.jgi.doe.gov)
Aspergillus sesamicola CBS 137324 v1.0	Short chain dehydrogenase	344844	MSTLTITDADIPDCSGKTFVITGGS JGI (mycocosm.jgi.doe.gov)
Aspergillus sesamicola CBS 137324 v1.0	CytochromeP450	344846	MAWFIVPVALLLLPAVIAVYRLVLI JGI (mycocosm.jgi.doe.gov)
Aspergillus neoauricomus CBS112787 v1.0	Esterase	169847	MEQIRIGATVGKAVAAGVWGGLA JGI (mycocosm.jgi.doe.gov)
Aspergillus neoauricomus CBS112787 v1.0	Integral membrane ptorein	141434	MENKGPGMIAASIVLTTVAFLLFCI JGI (mycocosm.jgi.doe.gov)
Aspergillus neoauricomus CBS112787 v1.0	Sesquiterpene synthase	141433	MLATIWTALSKASATPKSAELSPIEI JGI (mycocosm.jgi.doe.gov)
Aspergillus neoauricomus CBS112787 v1.0	Short chain dehydrogenase	141432	MSSLTITDADIPDCSGKTVVITGGS JGI (mycocosm.jgi.doe.gov)
Aspergillus neoauricomus CBS112787 v1.0	CytochromeP450	141431	MKMAWFIVPVALLLLPAVIAVYRL JGI (mycocosm.jgi.doe.gov)
Aspergillus ostianus v1.0	Esterase	185058	MDQIRIGATVGKAVAIGVWGGLA JGI (mycocosm.jgi.doe.gov)
Aspergillus ostianus v1.0	Integral membrane ptorein	185057	MENKGPGMIAASIVLTTVAFLLFCI JGI (mycocosm.jgi.doe.gov)
Aspergillus ostianus v1.0	Sesquiterpene synthase	185056	MLATIWTALSKASVTPKSADLSPID JGI (mycocosm.jgi.doe.gov)
Aspergillus ostianus v1.0	Short chain dehydrogenase	185055	MASLTITDADIPDCSGKTVVITGGS JGI (mycocosm.jgi.doe.gov)
Aspergillus ostianus v1.0	CytochromeP450	185054	MQAGLGDGPKWSGPSIRLSARAIT JGI (mycocosm.jgi.doe.gov)
Aspergillus petrakii CBS 105.57 v1.0	Esterase	285361	MDQIRIGATVGKAVAAGVWGGLA JGI (mycocosm.jgi.doe.gov)
Aspergillus petrakii CBS 105.57 v1.0	Integral membrane ptorein	285360	MENKGPGMIAASIVLTTVAFLLFCI JGI (mycocosm.jgi.doe.gov)
Aspergillus petrakii CBS 105.57 v1.0	Sesquiterpene synthase	285359	MLATIWTALSKASATPKSADVSPIE JGI (mycocosm.jgi.doe.gov)
Aspergillus petrakii CBS 105.57 v1.0	Short chain dehydrogenase	285358	MASLTITDADIPDCSGKTVVITGGS JGI (mycocosm.jgi.doe.gov)
Aspergillus petrakii CBS 105.57 v1.0	CytochromeP450	296418	MTMAWFIVPVALLLLPVAIAVYRL JGI (mycocosm.jgi.doe.gov)

Aspergillus westerdijkiae CBS 112803 v1.0	Esterase	289693	MDQIRIGATVGKAVAAGVWGGLA JGI (mycocosm.jgi.doe.gov)
Aspergillus westerdijkiae CBS 112803 v1.0	Integral membrane ptorein	265657	MENKGPGMIAASIVLTTVAFILFCL JGI (mycocosm.jgi.doe.gov)
Aspergillus westerdijkiae CBS 112803 v1.0	Sesquiterpene synthase	265656	MLATIWTALSKASPTPKSAELSPIEF JGI (mycocosm.jgi.doe.gov)
Aspergillus westerdijkiae CBS 112803 v1.0	Short chain dehydrogenase	265655*	MASLTITDADIPDCSGKTVVITGGS JGI (mycocosm.jgi.doe.gov)
Aspergillus westerdijkiae CBS 112803 v1.0	CytochromeP450	289683	MAWLIVSVALLLLPVVIAVYRLVLl JGI (mycocosm.jgi.doe.gov)
Aspergillus amoeneus CBS 111.32 v1.0	Sesquiterpene synthase	227190	MPSAIDTDAISTQLLLNGVAKRHS(JGI (mycocosm.jgi.doe.gov)
Aspergillus amoeneus CBS 111.32 v1.0	Short chain dehydrogenase	227192	MTSLDLSADDIPRLEGRTAIITGGCS JGI (mycocosm.jgi.doe.gov)
Aspergillus amoeneus CBS 111.32 v1.0	CytochromeP450	227194	MSASWVEQPNSLLDISKVVVFVLTL' JGI (mycocosm.jgi.doe.gov)
Aspergillus dentatus CBS 114.63 v1.0	Sesquiterpene synthase	315840	MPSAIDTDAISTQLLLNGVGKSHSF JGI (mycocosm.jgi.doe.gov)
Aspergillus dentatus CBS 114.63 v1.0	Short chain dehydrogenase	315842	MTSLNLSVDDIPRLDGKTAIITGGC JGI (mycocosm.jgi.doe.gov)
Aspergillus dentatus CBS 114.63 v1.0	CytochromeP450	315844	MSASWVDEPSSLLGIFKVVFVLKK JGI (mycocosm.jgi.doe.gov)
Aspergillus nidulans	Sesquiterpene synthase	8825	MPSAIDTDAISTQLLLNGVAKSHSF JGI (mycocosm.jgi.doe.gov)
Aspergillus nidulans	Short chain dehydrogenase	8823	MYICPFRDTTNHRFLGGCSGIGWES JGI (mycocosm.jgi.doe.gov)
Aspergillus nidulans	CytochromeP450	8821	MSASWVDEPSSLLGIFEVVFVLKRl JGI (mycocosm.jgi.doe.gov)
Aspergillus similis v1.0	Sesquiterpene synthase	210129	MPSAIDTDAISTQLLLNGVAKSHSF JGI (mycocosm.jgi.doe.gov)
Aspergillus similis v1.0	Short chain dehydrogenase	175589	MTSLNLSVDDIPRLDGKTAIITGGC JGI (mycocosm.jgi.doe.gov)
Aspergillus similis v1.0	CytochromeP450	210125	MSASWVDEPSSLLGIFKVVFVLKK JGI (mycocosm.jgi.doe.gov)
Aspergillus quadrilineatus (*floriformis*) CBS 937.7.	Sesquiterpene synthase	144829	MPSAIDTDAISTQLLLNGVAKSHSF JGI (mycocosm.jgi.doe.gov)
Aspergillus quadrilineatus (*floriformis*) CBS 937.7.	Short chain dehydrogenase	144831	MTSLNLSVDDIPRLDGKTAIITGGC JGI (mycocosm.jgi.doe.gov)
Aspergillus quadrilineatus (*floriformis*) CBS 937.7.	CytochromeP450	145836	MSASWVDEPSSLLGIFKVVFVLKK JGI (mycocosm.jgi.doe.gov)
Aspergillus clavatus NRRL 1 from AspGD	Sesquiterpene synthase	3242	MPSAIDTGAISTQLLLNGAIKSHSG JGI (mycocosm.jgi.doe.gov)
Aspergillus clavatus NRRL 1 from AspGD	Short chain dehydrogenase	3244	MTSLNLSVDDIPRLEGKTAIITGIFY JGI (mycocosm.jgi.doe.gov)
Aspergillus clavatus NRRL 1 from AspGD	CytochromeP450	3246	MSASWGYEPTSWLDIFTVVFVLVT JGI (mycocosm.jgi.doe.gov)
Lyophyllum atratum CBS 144462 v1.0	Sesquiterpene synthase	1784547	MPEPPSSFIAHHPSTPQFNPLLDPPl JGI (mycocosm.jgi.doe.gov)

[a] Asterisks indicate that the sequence information was reanalyzed based on the sequence of *A. oryzae* and re-annotated as protein seqneces. 403455, 229813, 147588, and 290130 were registered as one amino acid sequece consisting of *DPH1* and *DPH2* homologous genes. *DPH5* homologous sequences of *Aspergillus* species registered in JGI were reannotated based on the DIP_001958 sequence.

Supplemental table S3. Primer sequences used in this study

Primer name	Primer sequence (5'-3')	Purpose
Dpprx2LF3	ACCATGATTACGCCAGGAAGGTGGTCGTTACGAGT	Amplification of the upstream of *DPH1* gene for pGW43_dpprx2ko
Dpprx2LR3	TAGGGAACTGCCAGGACTGTGCCTATGCCTGTGTG	
Dpprx2UF3	AGCTGTTTCCTGGCAGGATGTAAAGAGGGCAGTCG	Amplification of the downstream of *DPH1* gene for pGW43_dpprx2ko
Dpprx2UR3	GGCCAGTGAATTATCAAAGGCAATGCAATGCGAAG	
pRM254 attL1_F	CCTGGCAGTTCCCTACTCTC	Amplification of *gen* cassettes for pGW43_dpprx2ko
pRM254 attL2_R	TGCCAGGAAACAGCTATGAC	
pPM43GW_RB_F	TTGATAATTCACTGGCCGTC	Linearization of pPM43GW
pPM43GW_LB_R	TGGCGTAATCATGGTCATAG	
DPKOD-F	ACTACCACCACCACGACAGC	Screening for *DPH1* knocked-out mutants
DPKOD-R	AATTACACCCTTTGCGCCCT	
DPKOU-F	ATTGAATCCTGTTGCCGGTC	
DPKOU-R	ACGACATCGCCATCAACACG	
pPTREXeGFP_F	ATTCTAGAAGTCCTGAATAGTAGTTTGTGG	Amplification of *EGFP* cassettes
pPTREXeGFP_R	CCATTGGTAACGAAATGTAAAAGCTAGG	
AoDPH1_LB_F	CGAGCAGCTGAAGCTATCTCGGCGACACTCTCATTTGA	Amplification of *AoDPH1* gene
AoDPH1_LB_R	CAGGACTTCTAGAATTGTGAGCCTTGACAGCTGGATATC	
AoDPH1_RB_F	TTTCGTTACCAATGGCTCACACGCACCTCGTGCTGC	
AoDPH1_RB_R	GGAGACCGGCAGATCATTTAAATGATACGTGATATGCTCGTCGATCG	
AspDPH1_F	AACCTCAGCTATCAAGCTACCG	Detection of *AoDPH1/AfDPH1* gene
AspDPH1_R	GTCACGAGCTGTTTATGTACCG	
EGFP_F	TGACCCTGAAGTTCATCTGCAC	Detection of insertion sequence
EGFP_R	GATGTTGTGGCGGATCTTGAAG	
DP1953_F	AGAAGGGCTGAAACGGTAGCTT	Detection of DIP_001953
DP1953_R	GAATCCTGGAGATGCTGACGAT	
DPDPH1-F	AGCTGTAGATGTCGTTGACC	Detection of *DPH1* gene
DPDPH1-R	GCCTTCTCACGCTGCTGTTTCT	
DpACTrt_F1n	AGGACTCTTACGTCGGTGAC	qPCR detection of *H. pulvinata* actin gene
DpACTrt_R1n	TCCATGTCATCCCAGTTGGT	
Dp1952rt_F1i	GACAGCCCTGGGTCTTATCC	qPCR detection of DIP_001952
Dp1952rt_R1i	CCGGTGGGCTTTACCCATTA	
Dp1953rt_F1i	CTCGTGAACCAGCGCAAATA	qPCR detection of DIP_001953
Dp1953rt_R1i	GCGCACTTGATGAGGAACAT	
Dp1954rt_F1i	TTTGAGTACCGCGAGAAGGA	qPCR detection of DPH1
Dp1954rt_R1i	TCGTTGACCACCGAGATGT	
Dp1955rt_F1i	ATGACTACCCTTCGGCTGTC	qPCR detection of DPH2
Dp1955rt_R1i	CACGTCGAAGAGGAACACG	
Dp1956rt_F1i	GGAGGGCCAGATCATCATAGG	qPCR detection of DPH3
Dp1956rt_R1i	TGTCGAGGATGTGGAAGACG	
Dp1957rt_F1i	GATGAGCCTCGAGGAGCTG	qPCR detection of DPH4
Dp1957rt_R1i	GAGAGCAGGTGGTACGTCA	
Dp1958rt_F1i	CAGGGAGAACATCCAGCAGA	qPCR detection of DPH5
Dp1958rt_R1i	GGGACGTAGAACAGACTTCCA	
Dp1959rt_F1i	CGTTCTCGTCATCACTGTCG	qPCR detection of DPH6
Dp1959rt_R1i	TCGGTGATTCTAGGGATGGC	

[a] An overhang sequence in each primer for overlap with sequences at the ends of the linearized plasmid, *gen/gfp* cassettes, or genes is underlined.