# Supplementary Information

# *Peltaster fructicola* genome reveals evolution from an invasive phytopathogen to an ectophytic parasite

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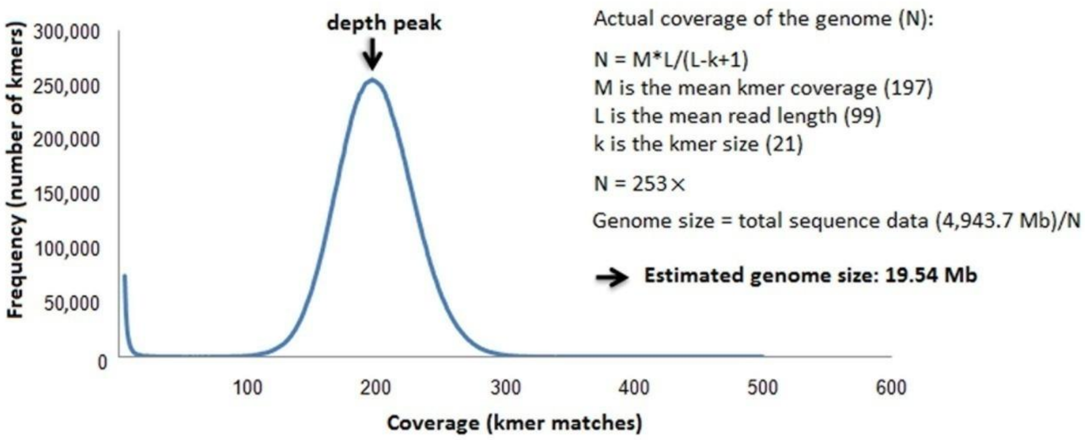
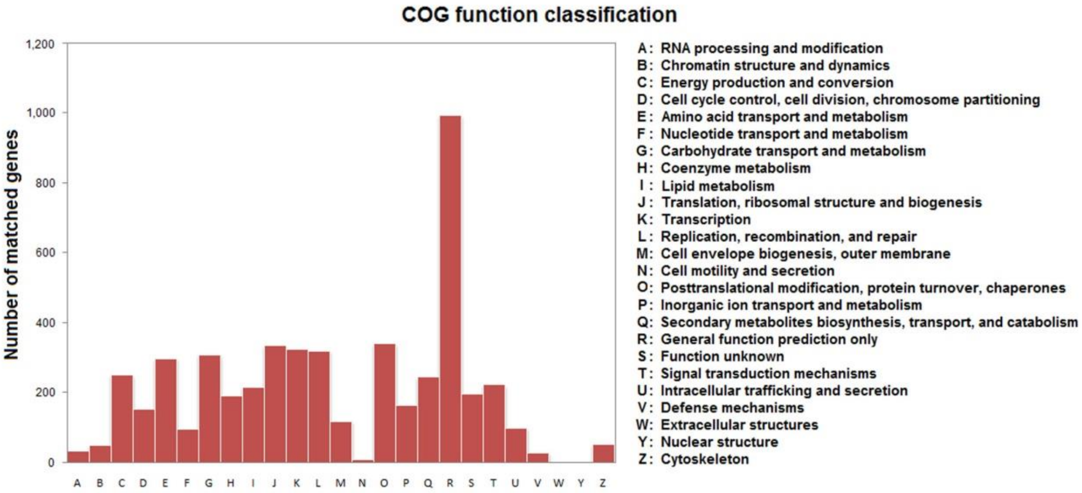
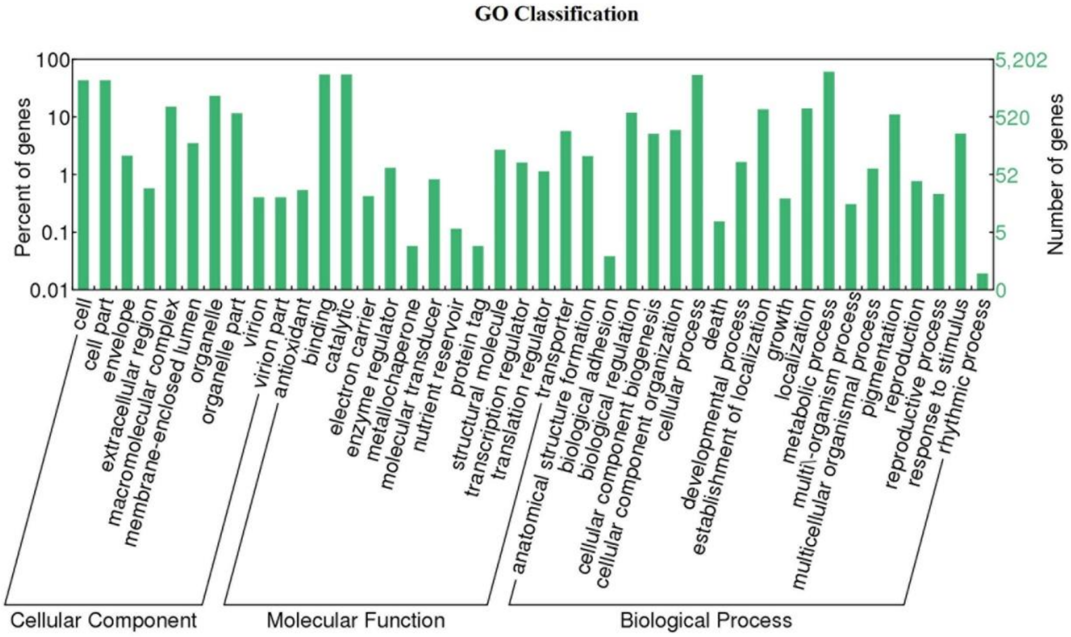
## Supplementary Figures



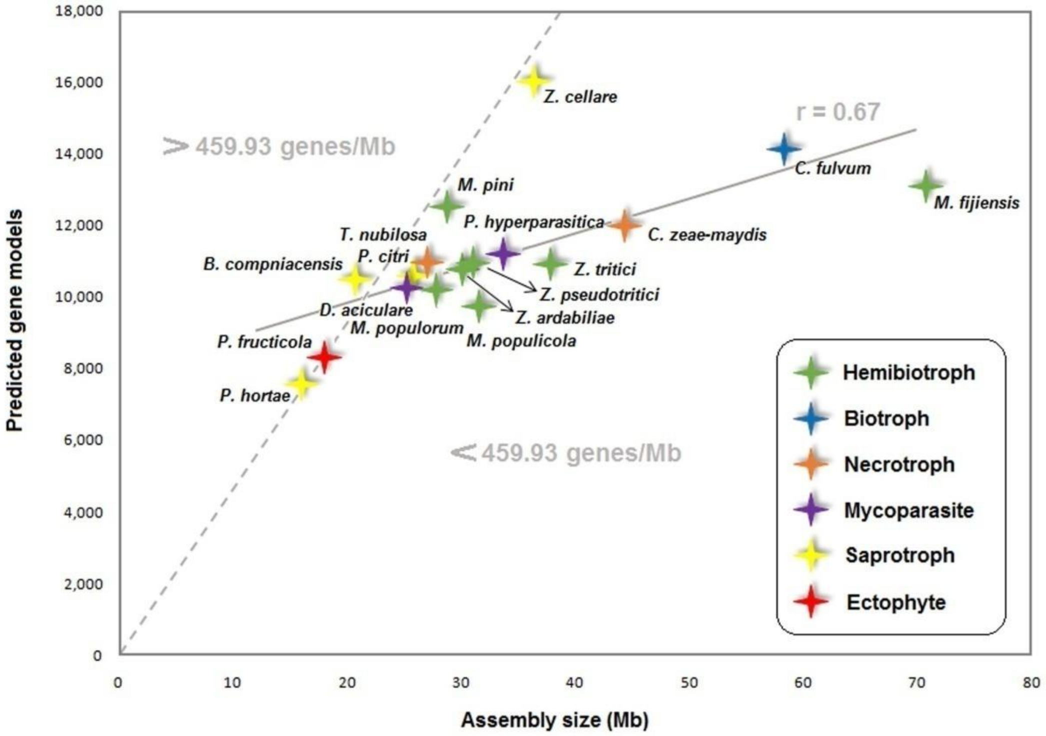
**Supplementary Figure 1. Distribution of 21-mer frequency in the raw Illumina genomic reads of *P. fructicola*.** The peak depth is at 197X. The peak of 21-mer frequency (M) in reads is correlated with the real sequencing depth (N), read length (L), and kmer length (K); their relationships can be expressed in the experienced formula: M = N * (L – K + 1) / L. We then divided the total sequence length by the real sequencing depth and obtained an estimated genome size of 19.54 Mb.



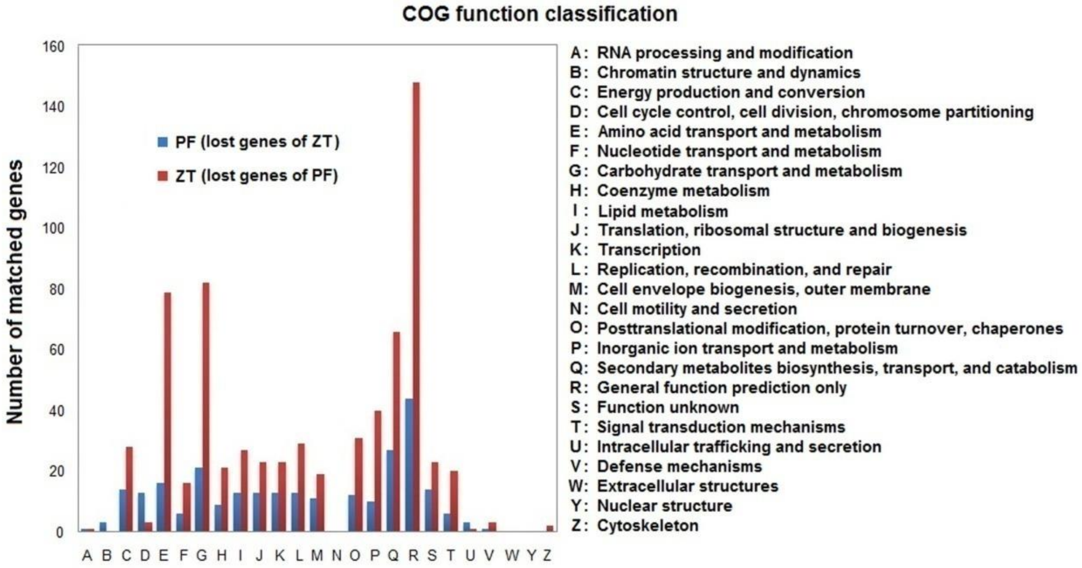
**Supplementary Figure S2. Distribution of COG function annotation of the *P. fructicola* genome.** In total, there are 3,856 genes (46.3%) that have functional assignments.



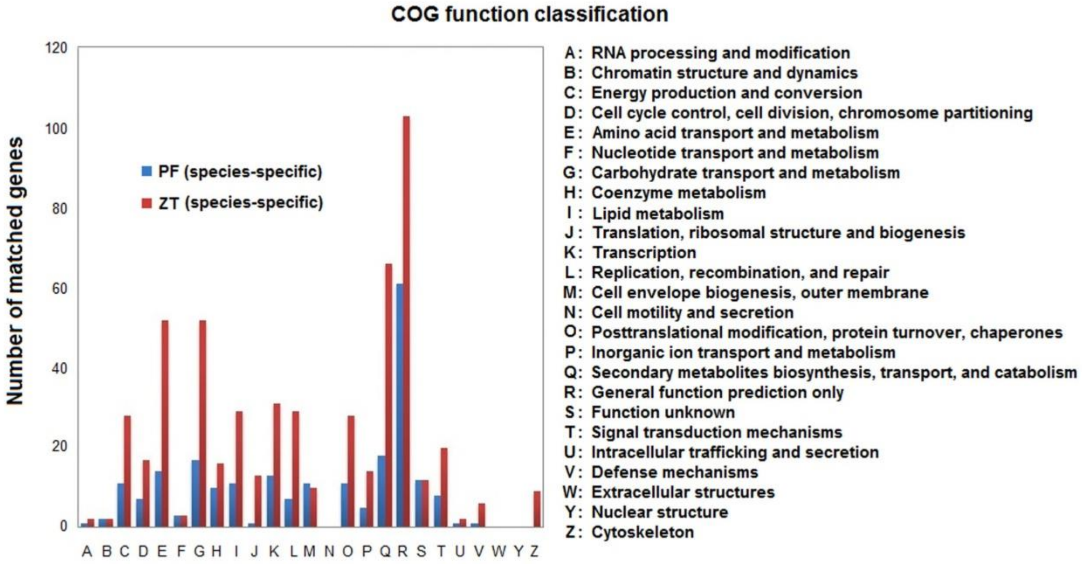
**Supplementary Figure S3. GO functional classification of the *P. fructicola* genome.** In total, there are 5202 genes (62.4%) that have functional assignments.



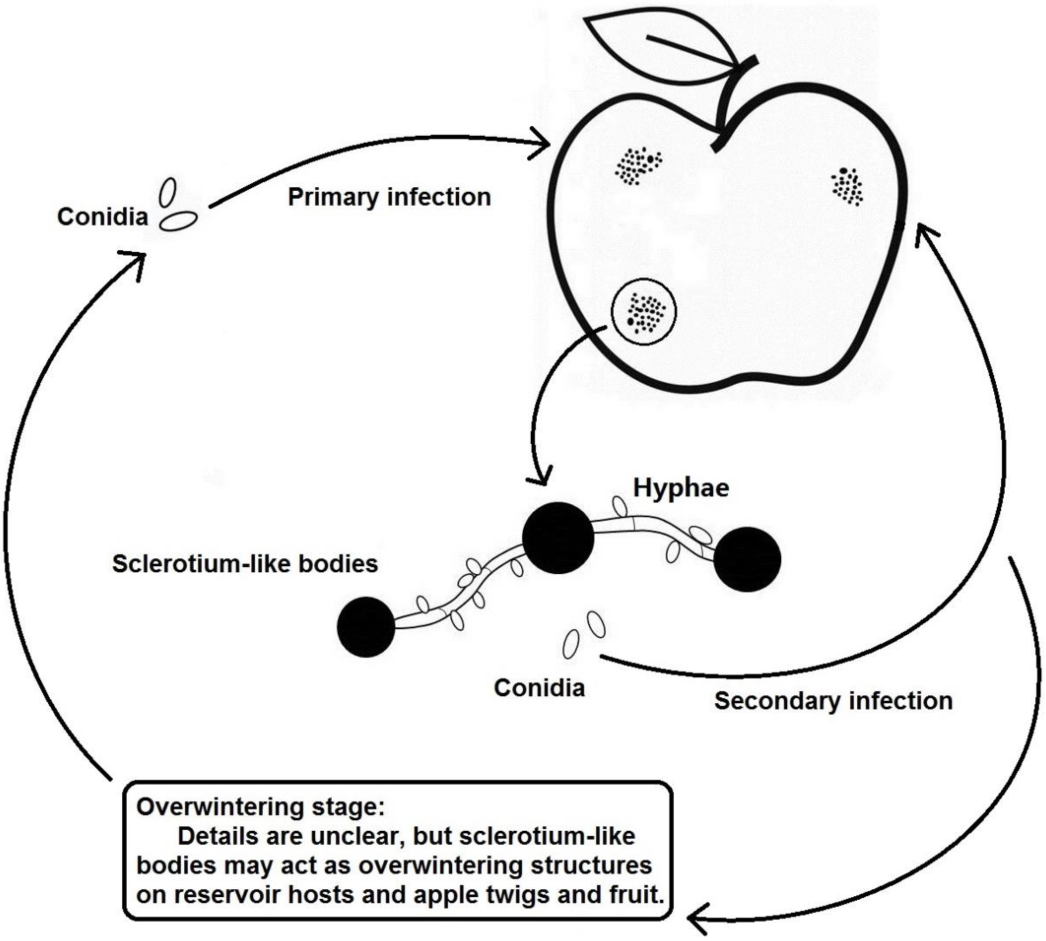
**Supplementary Figure S4. Distribution of total gene contents and assembly sizes of sequenced fungi with various lifestyles in Capnodiales.** The dashed line discriminates between fungi that have larger and smaller gene densities than *P. fructicola* (459.93 genes/Mb). The solid line indicates the linear trend with the linear correlation coefficient r (0.67). Hemibiotrophs: *Dothistroma septosporum*, *Mycosphaerella fijiensis*, *Zymoseptoria tritici*, *Mycosphaerella populorum*, *Mycosphaerella populicola*, *Zymoseptoria ardabiliae*, *Zymoseptoria pseudotritici*. Biotroph: *Cladosporium fulvum*. Necrotrophs: *Cercospora zeae-maydis*, *Teratosphaeria nubilosa*. Mycoparasites: *Dissoconium aciculare*, *Pseudovirgaria hyperparasitica*. Saprotrophs: *Baudoinia compniacensis*, *Piedraia hortae*, *Polychaeton citri*, *Zasmidium cellare.* Ectophyte: *Peltaster fructicola*.



**Supplementary Figure S5. Distribution of COG function annotation of the lost genes in *P. fructicola* and *Z. tritici*.** In total, 215 genes (38.4%) and 527 genes (45.9%) were annotated in *P. fructicola* (PF) and *Z. tritici* (ZT), respectively.



**Supplementary Figure S6. Distribution of COG function annotation of species-specific genes in *P. fructicola* and *Z. tritici*.** In total, 168 genes (10.3%) and 409 genes (11.7%) were annotated in *P. fructicola* (PF) and *Z. tritici* (ZT), respectively.



**Supplementary Figure S7. The life cycle of *P. fructicola*.** In this diagram, only the asexual stage of *P. fructicola* is described because its sexual stage has not been found in either nature or culture.

# Supplementary Tables

## Supplementary Table S1. Up-regulated and/or highly expressed secreted protein-coding genes *in vivo* in *P. fructicola*.

| Gene ID | Pfam annotation | E-value | Nr annotation | E-value | Expression *in vivo*[1] |
|---|---|---|---|---|---|
| Pelfr_1250 | Glyco_hydro_30 (PF02055) | 5.4e-29 | Beta-1,6-glucanase | 3e-177 | Up-regulated & highly expressed |
| Pelfr_1126 | COesterase (PF00135) | 6.7e-74 | Carboxylesterase type B | 0.0 | Up-regulated & highly expressed |
| Pelfr_6771 | Metallophos (PF00149) | 5.8e-29 | Acid phosphatase AphA | 0.0 | Up-regulated & highly expressed |
| Pelfr_3889 | Metallophos (PF00149) | 4.6e-07 | Metallo-phosphoesterase | 0.0 | Up-regulated |
| Pelfr_4114 | Phosphoesterase (PF04185) | 9.5e-70 | Phospholipase C | 0.0 | Up-regulated |
| Pelfr_5583 | GDPD (PF03009) | 6.6e-07 | Glycerophosphoryl diester phosphodiesterase | 0.0 | Up-regulated |
| Pelfr_3400 | Peroxidase_2 (PF01328) | 3.2e-13 | Cloroperoxidase | 0.0 | Up-regulated |
| Pelfr_2011 | FAD_binding_4 (PF01565) | 2.5e-25 | Secreted FAD-dependent oxidoreductase | 4e-96 | Up-regulated |
| Pelfr_5553 | Tyrosinase (PF00264) | 1.5e-49 | Tyrosinase | 4e-135 | Up-regulated |
| Pelfr_2833 | Arginase (PF00491) | 4.2e-83 | Arginase/deacetylase | 0.0 | Up-regulated |
| Pelfr_4025 | Cu-oxidase (PF00394);<br>Cu-oxidase_2 (PF07731);<br>Cu-oxidase_3 (PF07732) | 1.1e-44 | Multicopper oxidase type 1 | 0.0 | Up-regulated & highly expressed |
| Pelfr_4790 | S1-P1_nuclease (PF02265) | 3.2e-96 | Nuclease PA3 | 2e-144 | Up-regulated & highly expressed |
| Pelfr_1369 | - | - | Hypothetical protein | 4e-57 | Up-regulated |
| Pelfr_2143 | DUF1996 (PF09362) | 1.2e-59 | WSC domain-containing protein | 1e-70 | Up-regulated |
| Pelfr_7312 | - | - | Hypothetical protein | 1e-24 | Up-regulated & highly expressed |
| Pelfr_7724 | - | - | Hypothetical protein | 1e-10 | Up-regulated & highly expressed |
| Pelfr_3633 | Glyco_hydro_17 (PF00332) | 6.6e-33 | Exo-beta-1,3-glucanase | 1e-140 | Highly expressed |
| Pelfr_1460 | Peptidase_M28 (PF04389) | 1.9e-29 | Zinc-metallopeptidase | 0.0 | Highly expressed |
| Pelfr_0316 | FKBP_C (PF00254) | 2.3e-41 | FKBP-type peptidyl-prolyl cis-trans isomerase | 5e-60 | Highly expressed |

[1] Up-regulated: expression quantity (RPKM) of in vivo is more than that of in vitro (>=2-fold); Highly expressed: expression quantity (RPKM) of in vivo is more than 80.

Note: in vivo refers to *P. fructicola* infecting apple fruit about 1 month after inoculation; In vitro refers to *P. fructicola* growing on PDA at 22 °C for 15 days; RPKM, reads per kilobase per million mapped reads.

**Supplementary Table S2. Secreted peptidases in *P. fructicola*.**

| Gene ID | Pfam annotation | E-value | Nr annotation | E-value | MEROPS annotation | E-value |
|---|---|---|---|---|---|---|
| Pelfr_5071 | Asp (PF00026) | 2.6e-33 | Aspartic-type endopeptidase | 9e-73 | PepAc peptidase, subfamily A1A | 4.5e-76 |
| Pelfr_3148 | Asp (PF00026) | 2.0e-52 | Aspartic-type endopeptidase | 8e-77 | PepAc peptidase, subfamily A1A | 8.7e-96 |
| Pelfr_4918 | Pro-kuma_activ (PF09286) | 1.2e-46 | Tripeptidyl-peptidase | 0.0 | Grifolisin, subfamily S53 | 3.6e-113 |
| Pelfr_1460 | Peptidase_M28 (PF04389) | 1.9e-29 | Zinc-metallopeptidase | 0.0 | Mername-AA063 peptidase, subfamily M28E | 2.6e-110 |
| Pelfr_7574 | Peptidase_S8 (PF00082) | 1.2e-26 | Subtilisin-like protein | 5e-37 | Subtilisin-like peptidase 3, subfamily S8A | 2.3e-26 |
| Pelfr_0800 | Peptidase_S10 (PF00450) | 3.8e-104 | Serine carboxypeptidase | 0.0 | Carboxypeptidase OcpB, subfamily S10 | 7.2e-172 |
| Pelfr_6788 | Peptidase_S10 (PF00450) | 2.03e-82 | Serine carboxypeptidase | 0.0 | Carboxypeptidase O, subfamily S10 | 1.6e-165 |

**Supplementary Table S3. Small secreted proteins (SSPs) in *P. fructicola*.**

| Gene ID | Pfam annotation | E-value | Nr annotation | E-value | Cysteine[1] |
|---|---|---|---|---|---|
| Pelfr_0039 | - | - | Putative carbohydrate-binding protein | 7e-54 | 3.50% (high) |
| Pelfr_0316 | FKBP_C (PF00254) | 2.3e-41 | FKBP-type peptidyl-prolyl cis-trans isomerase | 5e-60 | 1.46% |
| Pelfr_1820 | His_Phos_1 (PF00300) | 1.2e-06 | Phosphoglycerate mutase family protein | 2e-83 | 2.87% (high) |
| Pelfr_3420 | - | - | Hypothetical protein | 5e-42 | 7.27% (high) |
| Pelfr_6255 | Ribonuclease (PF00545) | 1.3e-18 | Ribonuclease | 3e-41 | 2.99% (high) |
| Pelfr_2097 | - | - | Hypothetical protein | 4e-25 | 4.32% (high) |
| Pelfr_7294 | - | - | - | - | 1.87% |
| Pelfr_7319 | - | - | - | - | 0.00% |
| Pelfr_7431 | - | - | - | - | 0.00% |
| Pelfr_7511 | - | - | - | - | 0.72% |
| Pelfr_7794 | CVNH (PF08881) | 1.3e-07 | Cyanovirin-N | 9e-07 | 5.93% (high) |
| Pelfr_7907 | - | - | - | - | 4.55% (high) |

[1] Values were labeled "high" when the percentage of cysteine residues in the protein was at least twice as high as the average percentage of cysteine residues in all predicted proteins of *P. fructicola*.

**Supplementary Table S4. Distribution of putative PCWDEs in selected fungi according to the CAZy database.**

| Fungi | Total | CE5 | CE8 | PL1 | PL2 | PL3 | PL4 | PL9 | PL10 | PL11 | GH1 | GH2 | GH3 | GH5 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *Neurospora crassa* | 87 | 3 | 2 | 1 | 0 | 1 | 1 | 0 | 0 | 0 | 2 | 6 | 10 | 6 |
| *Laccaria bicolor* | 61 | 1 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 2 | 2 | 20 |
| *Rhizophagus irregularis* | 12 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 3 |
| *Rhizopus oryzae* | 61 | 0 | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 6 | 8 |
| *Saccharomyces cerevisiae* | 18 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 4 |
| *Puccinia graminis* | 97 | 9 | 8 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 7 | 2 | 28 |
| *Ustilago maydis* | 47 | 4 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 3 | 13 |
| *Botrytis cinerea* | 138 | 12 | 5 | 7 | 0 | 2 | 0 | 0 | 0 | 0 | 4 | 2 | 16 | 16 |
| *Colletotrichum higginsianum* | 226 | 14 | 10 | 16 | 0 | 14 | 6 | 4 | 0 | 0 | 1 | 6 | 22 | 18 |
| *Magnaporthe oryzae* | 156 | 19 | 1 | 2 | 0 | 1 | 1 | 0 | 0 | 0 | 2 | 8 | 18 | 13 |
| *Zymoseptoria tritici* | 90 | 6 | 1 | 2 | 0 | 1 | 0 | 0 | 0 | 0 | 2 | 8 | 16 | 9 |
| *Peltaster fructicola* | 38 | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 2 | 8 | 7 |

| Fungi | GH6 | GH7 | GH9 | GH10 | GH11 | GH12 | GH26 | GH27 | GH28 | GH29 | GH31 | GH35 | GH36 | GH43 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *Neurospora crassa* | 3 | 5 | 1 | 4 | 2 | 2 | 1 | 0 | 2 | 0 | 6 | 2 | 0 | 7 |
| *Laccaria bicolor* | 0 | 0 | 1 | 0 | 0 | 3 | 0 | 1 | 6 | 0 | 4 | 1 | 0 | 0 |
| *Rhizophagus irregularis* | 0 | 0 | 2 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 2 | 2 | 0 | 0 |
| *Rhizopus oryzae* | 0 | 0 | 3 | 0 | 0 | 0 | 1 | 0 | 18 | 0 | 3 | 1 | 1 | 2 |
| *Saccharomyces cerevisiae* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| *Puccinia graminis* | 0 | 10 | 0 | 5 | 0 | 3 | 6 | 7 | 1 | 0 | 2 | 1 | 0 | 2 |
| *Ustilago maydis* | 0 | 0 | 1 | 2 | 1 | 0 | 1 | 1 | 1 | 0 | 3 | 1 | 0 | 2 |
| *Botrytis cinerea* | 1 | 3 | 0 | 2 | 2 | 3 | 2 | 4 | 21 | 0 | 0 | 4 | 0 | 6 |
| *Colletotrichum higginsianum* | 3 | 7 | 0 | 7 | 5 | 10 | 1 | 1 | 13 | 1 | 7 | 4 | 1 | 21 |
| *Magnaporthe oryzae* | 3 | 7 | 0 | 6 | 5 | 3 | 0 | 3 | 3 | 4 | 6 | 0 | 0 | 20 |
| *Zymoseptoria tritici* | 0 | 1 | 1 | 2 | 1 | 1 | 0 | 1 | 2 | 1 | 7 | 2 | 1 | 9 |
| *Peltaster fructicola* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 5 | 1 | 0 | 1 |

| **Fungi** | **GH45** | **GH51** | **GH53** | **GH54** | **GH62** | **GH67** | **GH74** | **GH78** | **GH88** | **GH93** | **GH95** | **GH105** | **GH115** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *Neurospora crassa* | 1 | 1 | 1 | 1 | 0 | 1 | 6 | 2 | 0 | 3 | 0 | 2 | 2 |
| *Laccaria bicolor* | 0 | 0 | 0 | 0 | 0 | 0 | 5 | 0 | 1 | 0 | 1 | 9 | 0 |
| *Rhizophagus irregularis* | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| *Rhizopus oryzae* | 5 | 0 | 0 | 0 | 0 | 0 | 7 | 0 | 0 | 0 | 0 | 0 | 0 |
| *Saccharomyces cerevisiae* | 0 | 0 | 0 | 0 | 0 | 0 | 12 | 0 | 0 | 0 | 0 | 0 | 0 |
| *Puccinia graminis* | 0 | 0 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 0 | 0 | 2 | 0 |
| *Ustilago maydis* | 3 | 2 | 0 | 0 | 1 | 0 | 2 | 0 | 0 | 0 | 0 | 2 | 1 |
| *Botrytis cinerea* | 2 | 2 | 2 | 1 | 1 | 0 | 2 | 7 | 1 | 1 | 3 | 2 | 2 |
| *Colletotrichum higginsianum* | 1 | 2 | 2 | 0 | 1 | 1 | 9 | 5 | 1 | 1 | 1 | 6 | 4 |
| *Magnaporthe oryzae* | 1 | 3 | 1 | 1 | 4 | 1 | 6 | 3 | 1 | 1 | 2 | 3 | 4 |
| *Zymoseptoria tritici* | 1 | 2 | 2 | 1 | 1 | 0 | 1 | 3 | 0 | 1 | 0 | 3 | 1 |
| *Peltaster fructicola* | 0 | 2 | 0 | 1 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |

**Supplementary Table S5. Manually annotated PCWDE-coding genes in *P. fructicola*.**

| Gene ID | Substrate | Enzyme activity | Abbreviation | EC number | CAZyme family | Secretion signal |
|---|---|---|---|---|---|---|
| Pelfr_4541 | Pectin (backbone chain) | Exopolygalacturonase | PGX | 3.2.1.67 | GH28 | Y |
| Pelfr_4343 | Pectin (backbone/side chain) | α-L-rhamnosidase | RHA | 3.2.1.40 | GH78 | N |
| Pelfr_0259 | Pectin (side chain)/Hemicellulose (Xyloglucan, side chain) | β-1,4-Galactosidase | LAC | 3.2.1.23 | GH2 | N |
| Pelfr_4976 | Pectin (side chain)/Hemicellulose (Xyloglucan, side chain) | β-1,4-Galactosidase | LAC | 3.2.1.23 | GH35 | Y |
| Pelfr_3609 | Pectin (side chain) | Endoarabinase | ABN | 3.2.1.99 | GH43 | N |
| Pelfr_2065 | Pectin (side chain)/Hemicellulose (Xylan, side chain) | α-Arabinofuranosidase | ABF | 3.2.1.55 | GH51 | N |
| Pelfr_1270 | Pectin (side chain)/Hemicellulose (Xylan, side chain) | α-Arabinofuranosidase | ABF | 3.2.1.55 | GH51 | N |
| Pelfr_5292 | Pectin (side chain)/Hemicellulose (Xylan, side chain) | α-Arabinofuranosidase | ABF | 3.2.1.55 | GH54 | N |
| Pelfr_6616 | Pectin (side chain)/Hemicellulose (Xylan, backbone chain) | β-1,4-Xylosidase | BXL | 3.2.1.37 | GH3 | Y |
| Pelfr_2228 | Cellulose (backbone chain)/Hemicellulose (Xyloglucan, backbone chain) | β-1,3-Glucosidase | BGL | 3.2.1.21 | GH3 | N |
| Pelfr_2067 | Cellulose (backbone chain)/Hemicellulose (Xyloglucan, backbone chain) | β-1,4-Glucosidase | BGL | 3.2.1.21 | GH3 | N |
| Pelfr_1452 | Cellulose (backbone chain)/Hemicellulose (Xyloglucan, backbone chain) | β-1,4-Glucosidase | BGL | 3.2.1.21 | GH3 | N |
| Pelfr_4358 | Cellulose (backbone chain)/Hemicellulose (Xyloglucan, backbone chain) | β-1,4-Glucosidase | BGL | 3.2.1.21 | GH3 | N |
| Pelfr_3458 | Cellulose (backbone chain)/Hemicellulose (Xyloglucan, backbone chain) | β-1,4-Glucosidase | BGL | 3.2.1.21 | GH3 | Y |
| Pelfr_6030 | Cellulose (backbone chain)/Hemicellulose (Xyloglucan, backbone chain) | β-1,4-Glucosidase | BGL | 3.2.1.21 | GH3 | Y |
| Pelfr_6282 | Cellulose (backbone chain)/Hemicellulose (Xyloglucan, backbone chain) | β-1,4-Glucosidase | BGL | 3.2.1.21 | GH1 | N |
| Pelfr_6050 | Hemicellulose (Galactomannan, side chain) | α-1,4-Galactosidase | BGL | 3.2.1.22 | GH27 | N |
| Pelfr_0281 | Hemicellulose (Galactomannan, backbone chain) | β-1,4-Mannosidase | MND | 3.2.1.25 | GH2 | Y |
| Pelfr_2106 | Cutin | Cutinase | - | 3.1.1.74 | CE5 | N |
| Pelfr_1390 | Cutin | Cutinase | - | 3.1.1.74 | CE5 | N |
| Pelfr_5491 | Cutin | Cutinase | - | 3.1.1.74 | CE5 | N |
| Pelfr_3966 | Cutin | Cutinase | - | 3.1.1.74 | CE5 | N |
| Pelfr_3219 | Cutin | Cutinase | - | 3.1.1.74 | CE5 | Y |
| Pelfr_1915 | Cutin | Cutinase | - | 3.1.1.74 | CE5 | Y |

**Supplementary Table S6. Manually annotated PCWDE-coding genes in *Z. tritici*.**

| Gene ID | Substrate | Enzyme activity | Abbreviation | EC number | CAZyme family | Secretion signal |
|---|---|---|---|---|---|---|
| Mycgr3_66866 | Pectin (side chain) | Pectin methyl esterase | PME | 3.1.1.11 | CE8 | Y |
| Mycgr3_85457 | Pectin (backbone chain) | Pectate lyase | PLY | 4.2.2.2 | PL1 | Y |
| Mycgr3_42327 | Pectin (backbone chain) | Pectate lyase | PLY | 4.2.2.2 | PL1 | Y |
| Mycgr3_27839 | Pectin (backbone chain) | Pectate lyase | PLY | 4.2.2.2 | PL3 | N |
| Mycgr3_86032 | Pectin (backbone chain) | Exopolygalacturonase | PGX | 3.2.1.67 | GH28 | N |
| Mycgr3_77196 | Pectin (backbone chain) | Rhamnogalacturonase | RHG | 3.2.1.171 | GH28 | Y |
| Mycgr3_51381 | Pectin (side chain) | β-1,4-Endogalactanase | GAL | 3.2.1.89 | GH53 | N |
| Mycgr3_25958 | Pectin (side chain) | β-1,4-Endogalactanase | GAL | 3.2.1.89 | GH53 | N |
| Mycgr3_33711 | Pectin (backbone/side chain) | α-L-rhamnosidase | RHA | 3.2.1.40 | GH78 | N |
| Mycgr3_69329 | Pectin (backbone/side chain) | α-L-rhamnosidase | RHA | 3.2.1.40 | GH78 | N |
| Mycgr3_95102 | Pectin (side chain) | Exoarabinanase | ABX | 3.2.1.- | GH93 | Y |
| Mycgr3_57259 | Pectin (backbone chain) | Unsaturated glucuronyl hydrolase | UGH | 3.2.1.179 | GH105 | N |
| Mycgr3_50077 | Pectin (backbone chain) | Unsaturated rhamnogalacturonyl hydrolase | URH | 3.2.1.172 | GH105 | N |
| Mycgr3_68586 | Pectin (side chain)/Hemicellulose (Xyloglucan, side chain) | β-1,4-Galactosidase | LAC | 3.2.1.23 | GH2 | N |
| Mycgr3_43384 | Pectin (side chain)/Hemicellulose (Xyloglucan, side chain) | β-1,4-Galactosidase | LAC | 3.2.1.23 | GH2 | N |
| Mycgr3_87705 | Pectin (side chain)/Hemicellulose (Xyloglucan, side chain) | β-1,4-Galactosidase | LAC | 3.2.1.23 | GH2 | Y |
| Mycgr3_51250 | Pectin (side chain)/Hemicellulose (Xyloglucan, side chain) | β-1,4-Galactosidase | LAC | 3.2.1.23 | GH2 | N |
| Mycgr3_86272 | Pectin (side chain)/Hemicellulose (Xyloglucan, side chain) | β-1,4-Galactosidase | LAC | 3.2.1.23 | GH2 | N |
| Mycgr3_42647 | Pectin (side chain)/Hemicellulose (Xyloglucan, side chain) | β-1,4-Galactosidase | LAC | 3.2.1.23 | GH2 | N |
| Mycgr3_75961 | Pectin (side chain)/Hemicellulose (Xyloglucan, side chain) | β-1,4-Galactosidase | LAC | 3.2.1.23 | GH35 | N |
| Mycgr3_101693 | Pectin (side chain)/Hemicellulose | β-1,4-Galactosidase | LAC | 3.2.1.23 | GH35 | N |

| | | | | | | |
|---|---|---|---|---|---|---|
| | (Xyloglucan, side chain) | | | | | |
| Mycgr3_105728 | Pectin (side chain)/Hemicellulose (Xylan, backbone chain) | β-1,4-Xylosidase | BXL | 3.2.1.37 | GH43 | Y |
| Mycgr3_75584 | Pectin (side chain)/Hemicellulose (Xylan, backbone chain) | β-1,4-Xylosidase | BXL | 3.2.1.37 | GH43 | Y |
| Mycgr3_73095 | Pectin (side chain)/Hemicellulose (Xylan, backbone chain) | β-1,4-Xylosidase | BXL | 3.2.1.37 | GH43 | N |
| Mycgr3_105323 | Pectin (side chain) | Endoarabinase | ABN | 3.2.1.99 | GH43 | Y |
| Mycgr3_30121 | Pectin (side chain)/Hemicellulose (Xylan, backbone chain) | β-1,4-Xylosidase | BXL | 3.2.1.37 | GH43 | Y |
| Mycgr3_98714 | Pectin (side chain)/Hemicellulose (Xylan, backbone chain) | β-1,4-Xylosidase | BXL | 3.2.1.37 | GH43 | N |
| Mycgr3_84076 | Pectin (side chain)/Hemicellulose (Xylan, backbone chain) | β-1,4-Xylosidase | BXL | 3.2.1.37 | GH43 | N |
| Mycgr3_96505 | Pectin (side chain)/Hemicellulose (Xylan, backbone chain) | β-1,4-Xylosidase | BXL | 3.2.1.37 | GH43 | Y |
| Mycgr3_40215 | Pectin (side chain)/Hemicellulose (Xylan, side chain) | α-Arabinofuranosidase | ABF | 3.2.1.55 | GH51 | N |
| Mycgr3_111130 | Pectin (side chain)/Hemicellulose (Xylan, side chain) | α-Arabinofuranosidase | ABF | 3.2.1.55 | GH51 | Y |
| Mycgr3_70396 | Pectin (side chain)/Hemicellulose (Xylan, side chain) | α-Arabinofuranosidase | ABF | 3.2.1.55 | GH54 | Y |
| Mycgr3_68922 | Pectin (side chain)/Hemicellulose (Xylan, side chain) | α-Arabinofuranosidase | ABF | 3.2.1.55 | GH62 | Y |
| Mycgr3_71284 | Pectin (side chain)/Hemicellulose (Xylan, backbone chain) | β-1,4-Xylosidase | BXL | 3.2.1.37 | GH3 | Y |
| Mycgr3_38178 | Pectin (side chain)/Hemicellulose (Xylan, backbone chain) | β-1,4-Xylosidase | BXL | 3.2.1.37 | GH3 | N |
| Mycgr3_85505 | Cellulose (backbone chain)/Hemicellulose (Xyloglucan, backbone | β-1,4-Glucosidase | BGL | 3.2.1.21 | GH3 | Y |

| | | | | | | |
|---|---|---|---|---|---|---|
| | chain) | | | | | |
| Mycgr3_41307 | Cellulose (backbone chain)/Hemicellulose (Xyloglucan, backbone chain) | β-1,4-Glucosidase | BGL | 3.2.1.21 | GH3 | N |
| Mycgr3_99970 | Cellulose (backbone chain)/Hemicellulose (Xyloglucan, backbone chain) | β-1,4-Glucosidase | BGL | 3.2.1.21 | GH3 | Y |
| Mycgr3_45540 | Cellulose (backbone chain)/Hemicellulose (Xyloglucan, backbone chain) | β-1,4-Glucosidase | BGL | 3.2.1.21 | GH3 | N |
| Mycgr3_107206 | Cellulose (backbone chain)/Hemicellulose (Xyloglucan, backbone chain) | β-1,4-Glucosidase | BGL | 3.2.1.21 | GH3 | N |
| Mycgr3_20995 | Cellulose (backbone chain)/Hemicellulose (Xyloglucan, backbone chain) | β-1,4-Glucosidase | BGL | 3.2.1.21 | GH3 | N |
| Mycgr3_54587 | Cellulose (backbone chain)/Hemicellulose (Xyloglucan, backbone chain) | β-1,4-Glucosidase | BGL | 3.2.1.21 | GH3 | N |
| Mycgr3_38222 | Cellulose (backbone chain)/Hemicellulose (Xyloglucan, backbone chain) | β-1,4-Glucosidase | BGL | 3.2.1.21 | GH3 | N |
| Mycgr3_42620 | Cellulose (backbone chain)/Hemicellulose (Xyloglucan, backbone chain) | β-1,4-Glucosidase | BGL | 3.2.1.21 | GH3 | N |
| Mycgr3_42323 | Cellulose (backbone chain)/Hemicellulose (Xyloglucan, backbone chain) | β-1,4-Glucosidase | BGL | 3.2.1.21 | GH3 | Y |
| Mycgr3_64142 | Cellulose (backbone chain)/Hemicellulose (Xyloglucan, backbone chain) | β-1,4-Glucosidase | BGL | 3.2.1.21 | GH3 | Y |
| Mycgr3_77647 | Cellulose (backbone chain)/Hemicellulose (Xyloglucan, backbone | β-1,4-Glucosidase | BGL | 3.2.1.21 | GH3 | N |

| | | | | | | |
|---|---|---|---|---|---|---|
| | chain) | | | | | |
| Mycgr3_70973 | Cellulose (backbone chain)/Hemicellulose (Xyloglucan, backbone chain) | β-1,4-Glucosidase | BGL | 3.2.1.21 | GH1 | N |
| Mycgr3_49899 | Cellulose (backbone chain)/Hemicellulose (Xyloglucan, backbone chain) | β-1,4-Glucosidase | BGL | 3.2.1.21 | GH1 | Y |
| Mycgr3_100252 | Cellulose (backbone chain)/Hemicellulose (Xyloglucan, backbone chain) | Cellobiohydrolase I | CBHI | 3.2.1.176 | GH7 | N |
| Mycgr3_76589 | Cellulose (backbone chain)/Hemicellulose (Xyloglucan, backbone chain) | β-1,4-Endoglucanase | EG | 3.2.1.4 | GH45 | Y |
| Mycgr3_71664 | Cellulose (backbone chain)/Hemicellulose (Xyloglucan, backbone chain) | β-1,4-Endoglucanase | EG | 3.2.1.4 | GH5 | N |
| Mycgr3_105871 | Cellulose (backbone chain)/Hemicellulose (Xyloglucan, backbone chain) | β-1,4-Endoglucanase | EG | 3.2.1.4 | GH12 | Y |
| Mycgr3_94846 | Hemicellulose (Xylan, backbone chain) | β-1,4-Endoxylanase | XLN | 3.2.1.8 | GH10 | Y |
| Mycgr3_61141 | Hemicellulose (Xylan, backbone chain) | β-1,4-Endoxylanase | XLN | 3.2.1.8 | GH10 | Y |
| Mycgr3_60105 | Hemicellulose (Xylan, backbone chain) | β-1,4-Endoxylanase | XLN | 3.2.1.8 | GH11 | Y |
| Mycgr3_107208 | Hemicellulose (Galactomannan, side chain) | α-1,4-Galactosidase | AGL | 3.2.1.22 | GH27 | N |
| Mycgr3_110289 | Hemicellulose (Galactomannan, side chain) | α-1,4-Galactosidase | AGL | 3.2.1.22 | GH36 | Y |
| Mycgr3_68054 | Hemicellulose (Galactomannan, backbone chain) | β-1,4-Mannosidase | MND | 3.2.1.25 | GH2 | N |
| Mycgr3_107565 | Hemicellulose (Galactomannan, backbone chain) | β-1,4-Mannosidase | MND | 3.2.1.25 | GH2 | Y |
| Mycgr3_92097 | Hemicellulose | β-1,4-Endomannanase | MAN | 3.2.1.78 | GH5 | Y |

| | | | | | | |
|---|---|---|---|---|---|---|
| | (Galactomannan, backbone chain) | | | | | |
| Mycgr3_38237 | Hemicellulose (Xyloglucan, side chain) | α-Fucosidase | AFC | 3.2.1.51 | GH29 | N |
| Mycgr3_68483 | Cutin | Cutinase | - | 3.1.1.74 | CE5 | Y |
| Mycgr3_99331 | Cutin | Cutinase | - | 3.1.1.74 | CE5 | Y |
| Mycgr3_18212 | Cutin | Cutinase | - | 3.1.1.74 | CE5 | N |
| Mycgr3_43394 | Cutin | Cutinase | - | 3.1.1.74 | CE5 | Y |
| Mycgr3_35055 | Cutin | Cutinase | - | 3.1.1.74 | CE5 | N |
| Mycgr3_77282 | Cutin | Cutinase | - | 3.1.1.74 | CE5 | Y |

**Supplementary Table S7. Secondary metabolism (SM) key genes in *P. fructicola*.**

| **Gene ID** | **SM cluster** | **SM class** | **Nr annotation** | **E-value** |
|---|---|---|---|---|
| Pelfr_2368 | Cluster1 | PKS | Conidial pigment biosynthesis polyketide synthase | 0.0 |
| Pelfr_4242 | Cluster2 | PKS | Conidial yellow pigment biosynthesis polyketide synthase | 0.0 |
| Pelfr_6860 | Cluster3 | PKS | Lovastatin nonaketide synthase | 0.0 |
| Pelfr_1160 | Cluster4 | PKS-NRPS | Hybrid PKS-NRPS enzyme | 0.0 |
| Pelfr_0875 | Cluster5 | PKS-NRPS | Lovastatin nonaketide synthase | 0.0 |
| Pelfr_0462 | Cluster6 | NRPS | HC-toxin synthetase-like protein | 1e-151 |
| Pelfr_0485 | Cluster6 | NRPS | HC-toxin synthetase-like protein | 0.0 |
| Pelfr_0978 | Cluster7 | NRPS | Linear gramicidin synthase subunit D | 0.0 |
| Pelfr_6327 | Cluster8 | NRPS | Nonribosomal siderophore peptide synthase | 0.0 |
| Pelfr_6213 | Cluster9 | NRPS | Linear gramicidin synthetase subunit C | 0.0 |
| Pelfr_6610 | Cluster10 | NRPS | Peroxisomal-coenzyme A synthetase | 0.0 |
| Pelfr_3849 | Cluster11 | NRPS | Acetyl-CoA synthetase-like protein | 0.0 |
| Pelfr_1264 | Cluster12 | TS | Squalene synthase | 0.0 |
| Pelfr_6032 | Cluster13 | TS | Geranylgeranyl diphosphate synthase | 0.0 |
| Pelfr_4219 | Cluster14 | TS | Lycopene beta-cyclase | 0.0 |

**Supplementary Table S8. DHN-melanin biothythesis-related genes in *P. fructicola*.**

| **Gene ID** | **Gene name** | **Description** | **GenBank number of reference gene[1]** | **Identity** | **Similarity** |
|---|---|---|---|---|---|
| Pelfr_2368 | PKS18 | Polyketide synthase | AY495659 | 65% | 76% |
| Pelfr_6774 | BRN2 | T4HN reductase | EF060260 | 82% | 91% |
| Pelfr_0341 | SCD1 | Scytalone dehydratase | EF060261 | 69% | 83% |
| Pelfr_2393 | BRN1 | T3HN reductase | AB001564 | 78% | 87% |

[1] GenBank numbers of the referenced gene models are from *Cochliobolus heterostrophus*.

**Supplementary Table S9. Genes and their expression, which involve in four major signal transduction pathways, autophagy and Ros in *P. fructicola* and related species.**

| Gene name | *M. oryzae* | *Z. tritici* | *P. fructicola* | *In vivo*[1] | *In vitro*[2] |
|---|---|---|---|---|---|
| **cAMP-PKA pathway: pathogenicity, surface recognition, and turgor generation** | | | | | |
| Cap1 | MGG_01722 | Mycgr3_76018 | Pelfr_1322 | 77.62 | 51.78 |
| Cpk2 | MGG_02832 | Mycgr3_38697 | Pelfr_6488 | 0 | 24.24 |
| CpkA | MGG_06368 | Mycgr3_99725 | Pelfr_2492 | 5.07 | 52.35 |
| Ctdf | MGG_11346 | Mycgr3_89219 | Pelfr_8173 | 0 | 0 |
| Mac1 | MGG_09898 | Mycgr3_86659 | Pelfr_5544 | 8.45 | 52.81 |
| MagA | MGG_01818 | Mycgr3_76503 | Pelfr_1576 | 12.05 | 191.43 |
| MagB | MGG_00365 | Mycgr3_52873 | Pelfr_5694 | 0.53 | 65.31 |
| Mgb1 | MGG_05201 | Mycgr3_68892 | Pelfr_6673 | 0 | 13.2 |
| Mgg1 | MGG_10193 | Mycgr3_102649 | Pelfr_0632 | 20.11 | 201.07 |
| Mstu1 | MGG_00692 | Mycgr3_93828 | Pelfr_4840 | 4.19 | 60.81 |
| PdeH | MGG_05664 | Mycgr3_33550 | Pelfr_0043 | 18.16 | 37.6 |
| Pth11 | MGG_05871 | Mycgr3_16078 | Pelfr_1389 | 12.48 | 48.99 |
| Pth12 | MGG_12865 | - | - | - | - |
| Rgs1 | MGG_14517 | Mycgr3_50182 | Pelfr_1219 | 0 | 11.19 |
| Som1 | MGG_04708 | Mycgr3_109061 | Pelfr_0213 | 11.44 | 31.45 |
| **Pmk1 pathway: appressorium formation, pathogenicity, and invasive growth** | | | | | |
| Cdc42 | MGG_00466 | Mycgr3_99553 | Pelfr_2379 | 0 | 155.43 |
| Gap1 | MGG_11062 | Mycgr3_86730 | Pelfr_1799 | 227.76 | 206.74 |
| Gas1 | MGG_12337 | - | - | - | - |
| Gas2 | MGG_04202 | - | - | - | - |
| Mcm1 | MGG_02773 | Mycgr3_31170 | Pelfr_2334 | 24.51 | 122.36 |
| Msb2 | MGG_06033 | - | Pelfr_2676 | 53.06 | 247.9 |
| Mst7 | MGG_00800 | Mycgr3_52389 | Pelfr_2369 | 0.41 | 104.79 |
| Mst11 | MGG_14847 | Mycgr3_71128 | Pelfr_0435 | 54.77 | 49.18 |
| Mst12 | MGG_12958 | Mycgr3_46840 | Pelfr_4757 | 12.95 | 212.64 |
| Mst50 | MGG_05199 | Mycgr3_91070 | Pelfr_6694 | 15.19 | 55.78 |
| Pic5 | MGG_08600 | Mycgr3_100168 | Pelfr_0651 | 37.83 | 19.23 |
| Pmk1 | MGG_09565 | Mycgr3_73071 | Pelfr_4994 | 0 | 96.23 |
| Ras1 | MGG_06154 | Mycgr3_75299 | Pelfr_4161 | 64.57 | 246.68 |
| Ras2 | MGG_09499 | Mycgr3_59862 | Pelfr_5632 | 0 | 58.67 |
| Rgf1 | MGG_03064 | Mycgr3_57099 | Pelfr_6633 | 99.02 | 59.32 |
| Sfl1 | MGG_06971 | Mycgr3_38379 | Pelfr_6316 | 18.59 | 42.51 |
| Sho1 | MGG_09125 | Mycgr3_108657 | Pelfr_6493 | 45.94 | 191.34 |
| **Mps1 pathway: pathogenicity, penetration, cell wall integrity, and conidiation** | | | | | |
| Cch1 | MGG_05643 | Mycgr3_32076 | Pelfr_3280 | 103.55 | 51.04 |
| Cna1 | MGG_07456 | Mycgr3_100967 | Pelfr_3472 | 28.61 | 90.75 |
| Cnb1 | MGG_06933 | Mycgr3_68731 | Pelfr_5246 | 13.52 | 260.24 |
| Crz1 | MGG_05133 | Mycgr3_117712 | Pelfr_1135 | 20.69 | 43.23 |
| Mck1 | MGG_00883 | - | Pelfr_2301 | 3.48 | 18.81 |
| Mig1 | MGG_01204 | Mycgr3_117729 | Pelfr_5664 | 2.89 | 36.74 |

| | | | | | |
|---|---|---|---|---|---|
| Mkk1 | MGG_06482 | Mycgr3_71299 | Pelfr_6025 | 9.15 | 213.35 |
| Mkk2 | MGG_00800 | Mycgr3_52389 | Pelfr_2369 | 0.41 | 104.79 |
| Mps1 | MGG_04943 | Mycgr3_102121 | Pelfr_1869 | 53.27 | 287.2 |
| Pkc1 | MGG_08689 | Mycgr3_87605 | Pelfr_4305 | 12.31 | 47.68 |
| Plc1 | MGG_02444 | Mycgr3_66273 | Pelfr_5462 | 0 | 14.59 |
| Pmc1 | MGG_02487 | Mycgr3_35226 | Pelfr_3000 | 19.93 | 55.7 |
| Rho1 | MGG_07176 | Mycgr3_106397 | Pelfr_0710 | 164.12 | 892.02 |
| Swi6 | MGG_09869 | Mycgr3_48696 | Pelfr_1581 | 2.82 | 16.89 |
| **Oms1 pathway: osmoregulation, stress response, and fungicide sensitivity** | | | | | |
| Ap1 | MGG_12814 | Mycgr3_35076 | Pelfr_3144 | 83.7 | 89.36 |
| Atf1 | MGG_08212 | Mycgr3_98304 | Pelfr_6217 | 45.26 | 127.81 |
| Hik1 | MGG_11174 | Mycgr3_35302 | Pelfr_0583 | 86 | 67.86 |
| Oms1 | MGG_01822 | Mycgr3_76502 | Pelfr_1558 | 1.87 | 534 |
| Pbs2 | MGG_10268 | Mycgr3_76249 | Pelfr_5316 | 65.72 | 121.39 |
| Skn7 | MGG_03516 | Mycgr3_109990 | Pelfr_3787 | 14.4 | 41.27 |
| Sln1 | MGG_07312 | Mycgr3_63909 | Pelfr_0738 | 18.23 | 47.59 |
| SSk1 | MGG_02897 | Mycgr3_70181 | Pelfr_5884 | 5.1 | 108.13 |
| Ssk2 | MGG_00183 | Mycgr3_67344 | Pelfr_3555 | 5.52 | 22.77 |
| Ypd1 | MGG_07173 | Mycgr3_32785 | Pelfr_0942 | 23.6 | 184.13 |
| **Autophagy-related genes: conidiation, appressorium formation and pathogenicity** | | | | | |
| Atg1 | MGG_06393 | Mycgr3_73716 | Pelfr_1850 | 0.83 | 16.61 |
| Atg2 | MGG_05998 | Mycgr3_83423 | Pelfr_1077 | 1.14 | 11.44 |
| Atg3 | MGG_02959 | Mycgr3_99699 | Pelfr_1591 | 13.75 | 173.12 |
| Atg4 | MGG_03580 | Mycgr3_49421 | Pelfr_1738 | 0 | 58.2 |
| Atg5 | MGG_09262 | Mycgr3_86699 | Pelfr_2519 | 0 | 1.28 |
| Atg6 | MGG_03694 | Mycgr3_72630 | Pelfr_6195 | 3.26 | 51.55 |
| Atg7 | MGG_07297 | Mycgr3_100434 | Pelfr_4877 | 43.06 | 55.44 |
| Atg8 | MGG_01062 | - | Pelfr_3311 | 190.88 | 1511.44 |
| Atg9 | MGG_09559 | Mycgr3_100550 | Pelfr_3729 | 14.7 | 75.6 |
| Atg10 | MGG_14737 | - | Pelfr_1301 | 0 | 7.06 |
| Atg12 | MGG_00598 | Mycgr3_40907 | Pelfr_3199 | 0 | 7.09 |
| Atg13 | MGG_00454 | Mycgr3_58223 | Pelfr_3154 | 2.6 | 44.51 |
| Atg15 | MGG_12828 | Mycgr3_108706 | Pelfr_6428 | 11 | 68.77 |
| Atg16 | MGG_05255 | Mycgr3_90647 | Pelfr_6215 | 0 | 156.39 |
| Atg17 | MGG_07667 | Mycgr3_70424 | Pelfr_6704 | 21.13 | 18.96 |
| Atg18 | MGG_03139 | Mycgr3_75475 | Pelfr_5073 | 9.29 | 61.54 |
| **Ros related genes: conidium germination and appressorium formation** | | | | | |
| Des1 | MGG_04163 | - | - | - | - |
| Hyr1 | MGG_07460 | Mycgr3_102589 | Pelfr_5909 | 161.59 | 535.79 |
| Nox1 | MGG_00750 | Mycgr3_65626 | Pelfr_0062 | 0 | 32.21 |
| Nox2 | MGG_06559 | - | - | - | - |
| NoxR | MGG_05280 | Mycgr3_67898 | Pelfr_6118 | 32.13 | 120.48 |
| Rac1 | MGG_02731 | Mycgr3_106564 | Pelfr_4271 | 1.51 | 164.27 |

| | | | | | |
|---|---|---|---|---|---|
| Rho3 | MGG_10323 | Mycgr3_64768 | Pelfr_4285 | 14.82 | 127.61 |

[1] Gene expression was quantified by RPKM in RNA-seq analysis; RPKM, reads per kilobase per million mapped reads.

[2] *In vivo* refers to transcripts expressed by *P. fructicola* infecting apple fruit about 1 month after inoculation; *In vitro* refers to transcripts expressed by *P. fructicola* growing on PDA at 22 °C for 15 days.

Note: Orthologous genes were aligned in the same lines.

**Supplementary Table S10. Fungi used for identification of multigene families and phylogenetic analysis in this study.**

| **Species** | **Taxonomy** | **Lifestyle** | **Gene number** |
|---|---|---|---|
| *Laccaria bicolor* | Basidiomycota | Symbiosis | 23,132 |
| *Rhizophagus irregularis* | Glomeromycota | Symbiosis | 30,282 |
| *Rhizopus oryzae* | Zygomycota | Saprotroph | 17,467 |
| *Saccharomyces cerevisiae* | Ascomycota | Saprotroph | 6,575 |
| *Neurospora crassa* | Ascomycota | Saprotroph | 10,785 |
| *Puccinia graminis* | Basidiomycota | Biotroph | 20,534 |
| *Ustilago maydis* | Basidiomycota | Biotroph | 6,522 |
| *Botrytis cinerea* | Ascomycota | Necrotroph | 16,447 |
| *Colletotrichum higginsianum* | Ascomycota | Hemibiotroph | 16,172 |
| *Magnaporthe oryzae* | Ascomycota | Hemibiotroph | 11,054 |
| *Zymoseptoria tritici* | Ascomycota | Hemibiotroph | 10,933 |
| *Peltaster fructicola* | Ascomycota | Ectophyte | 8,334 |

**Supplementary Table S11. Summary of CAZyme families involved in plant cell wall degradation.**

| Substrate | | Enzyme activity | Abbreviation | EC number | CAZyme family(ies) |
|---|---|---|---|---|---|
| Cutin | Backbone chain | Cutinase | - | 3.1.1.74 | CE5 |
| Cellulose | Backbone chain | β-1,4-Endoglucanase | EG | 3.2.1.4 | GH3, -5, -6, -7, -9, -12, -45 |
| | Backbone chain | Cellobiohydrolase (reducing end) | CBHI | 3.2.1.176 | GH7 |
| | Backbone chain | Cellobiohydrolase (nonreducing end) | CBHII | 3.2.1.91 | GH6 |
| | Backbone chain | β-1,4-Glucosidase | BGL | 3.2.1.21 | GH1, -3 |
| Pectin | Backbone chain | Endopolygalacturonase | PGA | 3.2.1.15 | GH28 |
| | Backbone chain | Exopolygalacturonase | PGX | 3.2.1.67 | GH28 |
| | Backbone chain | Endo-xylogalacturonan hydrolase | XGH | 3.2.1.- | GH28 |
| | Backbone chain | Rhamnogalacturonase | RHG | 3.2.1.171 | GH28 |
| | Backbone chain | Rhamnogalacturonan α-1,2-galacturonohydrolase | RHX | 3.2.1.173 | GH28 |
| | Backbone chain | Rhamnogalacturonan α-L-rhamnopyranohydrolase | RGXB | 3.2.1.174 | GH28 |
| | Backbone/side chain | α-L-rhamnosidase | RHA | 3.2.1.40 | GH78 |
| | Backbone chain | Pectin lyase | PEL | 4.2.2.10 | PL1 |
| | Backbone chain | Pectate lyase | PLY | 4.2.2.2 | PL1, -2, -3, -9, -10 |
| | Backbone chain | Rhamnogalacturonan lyase | RGL | 4.2.2.23 | PL4, -11 |
| | Backbone chain | Unsaturated rhamnogalacturonan hydrolase | URH (*Bacillus subtilis*) | 3.2.1.172 | GH105 |
| | Backbone chain | Unsaturated glucuronyl hydrolase | UGH (*Bacillus sp.*) | 3.2.1.179 | GH88, -105 |
| | Side chain | Endoarabinanase | ABN | 3.2.1.99 | GH43 |
| | Side chain | Exoarabinanase | ABX | 3.2.1.- | GH93 |
| | Side chain | β-1,4-Endogalactanase | GAL | 3.2.1.89 | GH53 |
| | Side chain | α-Arabinofuranosidase | ABF | 3.2.1.55 | GH51, -54, -62 |
| | Side chain | β-1,4-Xylosidase | BXL | 3.2.1.37 | GH3, -43 |
| | Side chain | β-1,4-Galactosidase | LAC | 3.2.1.23 | GH2, -35 |
| | Side chain | Pectin methyl esterase | PME | 3.1.1.11 | CE8 |
| Xylan/Heteroxylan | Backbone chain | β-1,4-Endoxylanase | XLN | 3.2.1.8 | GH10, -11 |
| | Backbone chain | β-1,4-Xylosidase | BXL | 3.2.1.37 | GH3, -43 |
| | Side chain | α-Arabinofuranosidase | ABF | 3.2.1.55 | GH51, -54, -62 |
| | Side chain | α-Glucuronidase | AGU | 3.2.1.139 | GH67, -115 |
| Galactomannan | Backbone chain | β-1,4-Endomannanase | MAN | 3.2.1.78 | GH5, -26 |
| | Backbone chain | β-1,4-Mannosidase | MND | 3.2.1.25 | GH2 |
| | Side chain | α-1,4-Galactosidase | AGL | 3.2.1.22 | GH27, -36 |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| Xyloglucan | Backbone chain | Xyloglucan β-1,4-endoglucanase | XEG | 3.2.1.151 | GH12, -74 |
|  | Backbone chain | β-1,4-Endoglucanase | EG | 3.2.1.4 | GH3, -5, -6, -7, -9, -12, -45 |
|  | Backbone chain | Cellobiohydrolase (reducing end) | CBHI | 3.2.1.176 | GH7 |
|  | Backbone chain | Cellobiohydrolase (nonreducing end) | CBHII | 3.2.1.91 | GH6 |
|  | Backbone chain | β-1,4-Glucosidase | BGL | 3.2.1.21 | GH1, -3 |
|  | Side chain | α-Xylosidase | AXL | 3.2.1.177 | GH31 |
|  | Side chain | α-Fucosidase | AFC | 3.2.1.51 | GH29, -95 |
|  | Side chain | β-1,4-Galactosidase | LAC | 3.2.1.23 | GH2, -35 |

## Supplementary Notes

### Gene prediction and annotation.

The draft genome of *P. fructicola* was closed by GapFiller[1] with the dataset of paired reads, then masked using RepeatMasker[2] with both the latest RepBase fungal library[3] and *ab initio* library generated by RepeatModeler[2]. The modified assembly containing only scaffolds larger than 200 bp was used as input for gene model prediction and other downstream analyses. Gene calling was conducted using an annotation pipeline and genome-database management tool MAKER2[4], which combines three different *ab initio* predictors: GeneMark-ES[5], Augustus[6], and SNAP[7]. In addition, proteomes of several fungi within the same order as *P. fructicola* were downloaded from JGI Fungal Genome Portal MycoCosm[8] and served as experimental evidence for quality control of the result of the above computational methods. A set of 248 CEGs identified by Parra *et al.*[9] were used to evaluate the completeness of the gene space in the genome of *P. fructicola*.

All predicted gene models were functionally annotated using an all-in-one bioinformatics software suite, Blast2GO, based on the Gene Ontology vocabulary[10]. This high-throughput functional annotation pipeline integrates various annotation strategies and tools, including BLASTp alignment against GenBank with non-redundant set[11], GO (Gene Ontology) terms mapping[12], InterProScan[13], Enzyme Commission (EC) numbers assigning[14], and Kyoto Encyclopedia of Genes and Genomes (KEGG)[15]. In addition, they were subjected to Conserved Domains Database (CDD)[16], Pfam[17], and Clusters of Orthologous Group (COG) analysis[18]. The rRNA-coding region (rDNA) was designated using RNAmmer[19], but the copy number of rDNA (tandem repeat and low polymorphism)[20] in the assembly could be estimated only by calculating its average sequencing depth (divided by the global depth).

### Multigene families and phylogenetic analysis.

Eleven representative fungi (Supplementary Table S10) that collectively span diverse lifestyles (symbiotic, saprophytic, biotrophic, hemibiotrophic and necrotrophic) and phyla (Ascomycota, Basidiomycota, Zygomycota and Glomeromycota) were selected to predict multigene families along with *P. fructicola*. Gene clusters containing both orthologs and paralogs were built among a total of 178,237 proteins (retrieved from JGI Fungal Genome Portal MycoCosm except *P. fructicola*) using OrthoMCL[21] based on the Markov cluster algorithm (MCL)[22].

To construct a genome-based phylogenetic tree of the above 12 species, single-copy orthologous families (having exactly one gene for each organism) were collected from the MCL clustering result. Multiple alignments of the protein sequences belonging to the same families were parallelly performed in batch mode using MAFFT[23]. Conservative positions in the alignment result were extracted through GBlocks[24] and then used to estimate the best protein evolution model with ProtTest 3.4[25]. Maximum-likelihood phylogenetic analysis of the concatenated well-aligned regions was carried out using RAxML[26] with a bootstrap value of 1000 replications. The RAxML tree obtained was visualized in FigTree v1.4.2 (http://tree.bio.ed.ac.uk/software/). The divergence times between species were estimated with the method provided by MEGA 6[27], using the previously published calibration points as a reference: Ascomycota-Basidiomycota split 500 Myr, and Pezizomycotina-Saccharomycotina split 350 Myr[28].

We also constructed the phylogenetic profiles for all gene families to reflect the absence or presence of a particular gene family in a given species. These profiles were combined with the above species tree using the DOLLOP program from the PHYLIP package[29] to reconstruct the parsimonious series of gene gain and loss events for these fungal genomes. To define the minimum gene set for each ancestral node, the DOLLOP program was used, which follows the Dollo parsimony principle assuming that every gene appears exactly once on the tree and can be lost independently in different evolutionary lineages.

**CAZymes and plant cell wall degrading enzymes.**

Proteomes were screened for carbohydrate-active modules using a web server for automated carbohydrate-active enzyme (CAZyme) annotation, dbCAN[30]. CAZyme module annotation by this program uses E-value, alignment length and coverage, with an E-value of <1e-5 for alignments of >80 amino acids and an E-value of <1e-3 for alignments of <80 amino acids. To eliminate those selected by dbCAN but not really CAZymes, proteins with CAZyme motifs with a dbCAN E-value >e-10 were individually examined using two online tools, Pfam[17] and BLASTp of non-redundant protein sequences in NCBI (http://www.ncbi.nlm.nih.gov).

Cellulases, hemicellulases, pectinases and cutinases collectively constituted the plant cell wall-degrading enzymes (PCWDEs) that we considered in this study. According to previous research[31-33], the above four types of PCWDEs are distributed in a range of different CAZyme families (despite including some non-PCWDEs) (Supplementary Table S11) belonging to three functional classes, i.e., glycoside hydrolases (GHs), polysaccharide lyases (PLs), and carbohydrate esterases (CEs). We could therefore pick out these PCWDE-involved families from the predicted CAZymes and considered them as putative PCWDEs. Additionally, to identify the function of each putative PCWDE more accurately and discard the false positives, the BLASTp program and two online databases, mycoCLAP[34] and Fungal PCWDE Database[35] were jointly applied.

**Secretomes, secreted peptidases and small secreted proteins.**

In the current study, secretomes were identified using a custom pipeline including SignalP version 4.1[36], TMHMM Server version 2.0[37], TargetP 1.1 Server[38], GPIsom[39] and WoLF PSORT[40]. Initially, all proteins of one organism with a SignalP SP = 'YES' or a TargetP Loc = S were selected and combined[41]. These proteins were then scanned for transmembrane (TM) domains using TMHMM and those with 0 TM or 1 TM, if located in or very close to the predicted N-terminal signal peptide (this often corresponds to the secretion signal), were kept. Of the retained set, proteins containing a potential GPI-anchor signal as predicted by the GPIsom web service were discarded. Eventually, WoLF PSORT was used to estimate the located sites and only those proteins that were credibly positioned in the extracellular space (i.e., extracellular score >15) were included into in the final secretome. The secreted proteins were submitted to the Merops database (e-value = 1e-04) (Release 9.12; http://merops.sanger.ac.uk/) for predicting peptidases[42], and false positives were eliminated by parsing hits obtained following a BLASTp search (e-value = 1e-04) on the NCBI nr protein database. Small secreted proteins (SSPs) were defined here as the secreted proteins that are smaller than 200 aa, and an SSP was labeled as "cysteine-rich" when the percentage of cysteine residues in the protein was at least twice as high as the average percentage of cysteine residues in all predicted proteins of that species[43].

**Secondary metabolism genes.**

Nonribosomal peptide synthase (NRPS), polyketide synthase (PKS), hybrid NRPS-PKS, dimethylallyl tryptophan synthase (DMATS), and terpene cyclase (TC) genes were identified in all 12 genomes by using the web-based software packages SMURF[44] and antiSMASH 2.0[45] in combination. Employing these two functionally similar methods simultaneously allowed us to detect small conflicts generated between their results, which were further checked and corrected. Another reason for using the packages in tandem is that although SMURF and antiSMASH alone are unable to predict TC and DMATS genes, they can complement each other for this purpose.

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