Fig. S1. Representative whole-genome alignments of *F. xylarioides* robusta strains sequenced in this study with publically available *F. xylarioides* robusta strains. Each dot represents chromosomal correspondence, with absences representing absent chromosomes. Genomes were aligned using nucmer in the MUMmer3 package, with outputs processed using DotPrep.py and visualised using Dot in DNANexus. Blue indicates forward alignments, green indicates reverse alignments, orange indicates repetitive alignments.
**Fig. S2.** Representative whole-genome alignments of *F. xylarioides* strains against the 15 *F. oxysporum f. sp. lycopersici* (Fol) chromosomes. Each Fol chromosome is labelled, with the four fully mobile chromosomes annotated in red: chromosomes 3, 6, 14 and 15. The remaining 11 chromosomes are the syntenic, core chromosomes shared with sister *Fusarium* species. Each dot represents chromosomal correspondence, with absences representing absent chromosomes. Genomes were aligned using nucmer in the MUMmer3 package, with outputs processed using DotPrep.py and visualised using Dot in DNANexus. Blue indicates forward alignments, green indicates reverse alignments, orange indicates repetitive alignments.
Fig. S3. Representative whole-genome alignments of *F. xylarioides* strains against the 11 *F. verticillioides* syntenic, core chromosomes shared with sister *Fusarium* species. Each dot represents chromosomal correspondence, with absences representing absent chromosomes. Genomes were aligned using nucmer in the MUMmer3 package, with outputs processed using DotPrep.py and visualised using Dot in DNANexus. Blue indicates forward alignments, green indicates reverse alignments, orange indicates repetitive alignments.
**Fig. S4.** *F. xylarioides* scaffolds mapped to *F. oxysporum* f. sp. *lycopersici* (Fol) chromosomes using reference-guided scaffolding. 

A The type of *F. xylarioides* scaffold group which match each Fol chromosome: yellow, scaffolds which match to core chromosomes in the *F. xylarioides* assembly mapped to *F. verticillioides* (FV); green, scaffolds which match the *F. xylarioides* and *F. udum* (FXU) specific scaffolds (i.e. shared by these species and absent in *F. verticillioides*); purple, scaffolds which match the Lineage Specific (LS) scaffolds and are not shared across the *F. xylarioides* strains. 

B The total megabase pair match between *F. xylarioides* scaffolds and Fol chromosomes, with mobile chromosomes annotated with a red asterisk.
**Fig. S5.** Functional diversity of *F. xylarioides* across the core chromosomes and by scaffold group: FV, scaffolds which match to un-aligned *F. verticillioides* scaffolds; FXU LS, scaffolds which are absent in *F. verticillioides* but which are shared by *F. xylarioides* and *F. udum* (FXU) or scaffolds which are unique to each *F. xylarioides* strain and are lineage-specific (LS). A High level functional diversity across the 11 syntenic chromosomes and scaffold groups based on the number of hits to each Level 1 SEED category in SUPER-FOCUS (Silva et al 2017); B Detailed functional diversity across chromosome 11 and the FXU and LS scaffold groups for *F. xylarioides* based on the number of hits to each Level 3 SEED category in SUPER-FOCUS. Abbreviations: PPCA, Predictions based on Plant Prokaryote Comparative Analysis; CVPP, Cofactors, Vitamins, Prosthetic Groups Pigments; PPTE, Phages, Prophages Transposable Elements; FALI, Fatty Acids, Lipids and Isoprenoids.
Table S1. Genome statistics for the *F. xylarioides* strains sequenced in this study, compared with sister species. Abbreviations for *Fusarium* sister species: Fol, *F. oxysporum* f. sp. *lycopersici*; Fv, *F. verticillioides*.

| Name          | Coffea674 | Coffea659 | Robusta277 | Robusta254 | Arabica563 | Arabica908 | Robusta925 | Robusta394 | F. *udum* | Fol | Fv |
|---------------|-----------|-----------|------------|------------|------------|------------|------------|------------|-----------|-----|----|
| Strain number | IMI392674 | IMI127659i| IMI392277  | IMI392254  | IMI389563  | IMI375908i | IMI379925  | FRC L-0394 | F02845    | 4287| FGSC 7600 |
| Reference     | This study| This study| This study | This study | This study | This study | Olal et al. 2019 | Wingfield et al. 2019 | Srivastava et al. 2018 | Ma et al. 2010 | Ma et al. 2010 |
| Date isolated | 1951      | 1955      | 2003       | 1997       | 2002       | 1997       | 1998       | 2000       | 2010      |
| Origin        | Cote d'Ivoire | CAR | Tanzania | Uganda | Ethiopia | Ethiopia | Uganda | Uganda | India |
| Host          | Coffea | C. *excelsa* | C. *c. robusta* | C. *c. robusta* | C. *arabica* | C. *arabica* | C. *c. robusta* | C. *canephora* | Pigeonpea | Tomato | Maize |
| Size (genome assembly) Mb | 57.2 | 59.4 | 61.3 | 60.3 | 63.3 | 62.6 | 55.1 | 55.2 | 56.4 | 61.4 | 42.5 |
| Genome size (Mb, >500bp) | 54.4 | 55.1 | 56.5 | 56.3 | 58.0 | 57.8 | 55.1 | 55.2 | 56.4 | 61.4 | 42.5 |
| Total repeats (genome assembly) Mb | 13.3 | 14.9 | 15.9 | 15.3 | 18.6 | 17.8 | 12.6 | 10.8 | 1.0 |
| Total repeats % | 23 | 25 | 26 | 25 | 30 | 29 | 22 | 18 | 2 |
| Interspersed repeats Mb | 5.8 | 4.9 | 5.8 | 4.3 | 5.0 | 5.4 | 18.9 | 6.4 | 0.5 |
| Interspersed repeats % | 10 | 8 | 9 | 7 | 8 | 9 | 33 | 10.5 | 1 |
| Interspersed repeats (raw reads) Mb | 3.9 | 3.7 | 3.9 | 3.8 | 4.4 | 3.9 | 2.4 |

Total repeats includes unclassified repeats. Interspersed repeats include retroelements, DNA transposons, simple and low complexity repeats.
Table S2. Genome statistics for our strains mapped to the chromosomal assembly of *F. verticillioides* using reference-guided scaffolding. Abbreviations: FV, the contigs in each genome mapped to the syntenic chromosomes and unaligned scaffolds of *F. verticillioides*; FXU, scaffolds which are absent from *F. verticillioides* but which are present in *F. udum* and the historic Coffea659 strain (*F. xylarioides* and *-udum* specific); FXS, scaffolds which are absent from *F. verticillioides* and *F. udum* and are shared with Coffea659 (*F. xylarioides*-specific); LS, scaffolds which are not shared with Coffea659 and are unique to each *F. xylarioides* strain (lineage-specific).

| Strain Name | IMI392674 | IMI127659i | IMI392277 robusta277 | IMI392254 robusta254 | IMI389563 arabica563 | IMI375908i arabica908 |
|-------------|-----------|------------|----------------------|----------------------|----------------------|----------------------|
| Genome Size Mb | 57.2 | 59.6 | 61.3 | 60.3 | 63.4 | 62.6 |
| Total repeats incl unclassified Mb | 13.3 | 14.9 | 15.9 | 15.3 | 18.6 | 17.8 |
| Total repeats incl unclassified % | 23 | 25 | 26 | 25 | 30 | 29 |
| TEs Mb | 5.8 | 4.9 | 5.8 | 4.3 | 5.0 | 5.4 |
| TEs % | 10 | 8 | 9 | 7 | 8 | 9 |
| FV scaffolds Mb | 51 | 49 | 51.6 | 51.3 | 52.4 | 52.3 |
| FXU scaffolds Mb | 4.5 | 7.9 | 7.5 | 7.2 | 8.9 | 7.7 |
| FXS scaffolds Mb | 0.04 | - | 0.06 | 0.04 | 0.04 | 0.5 |
| LS scaffolds Mb | 1.9 | 2.2 | 2.3 | 1.8 | 2.1 | 2.1 |
| FV scaffolds % | 7 | 5 | 5 | 5 | 6 | 6 |
| FXU scaffolds % | 8 | 13 | 12 | 12 | 14 | 12 |
| FXS scaffolds % | 0.1 | - | 0.1 | 0.1 | 0.1 | 0.8 |
| LS scaffolds % | 3 | 4 | 4 | 3 | 3 | 3 |
| FV TEs Mb | 3.6 | 2.4 | 2.8 | 2.4 | 2.9 | 3.2 |
| FXU TEs Mb | 1.2 | 1.9 | 1.8 | 1.4 | 1.6 | 1.7 |
| LS TEs Mb | 1.0 | 0.6 | 0.6 | 0.4 | 0.5 | 0.4 |
| FV TEs % | 7 | 5 | 5 | 5 | 6 | 6 |
| FXU TEs (%) | 28 | 24 | 23 | 20.1 | 18 | 22 |
| LS TEs (%) | 52 | 26 | 28 | 24 | 23 | 20 |

Table S3. Published genomes used for comparison

| Genome          | Accession number               |
|-----------------|-------------------------------|
| *F. udum*       | GCA_002194535.1               |
| *F. oxysporum f.sp. lycopersici* | GCA_000149955.2 |
| *F. oxysporum f.sp. cubense*     | GCA_005930515.1               |
| *F. verticillioides* | GCA_003316975.2 |
| *F. fujikuroi*     | GCA_900079805.1               |
| *F. mangiferae*    | GCA_900044065.1               |
| *F. solani*        | GCA_002215905.1               |
| *Verticillium dahliae* | GCA_000150675.2 |
| *V. albo-atrum*    | GCA_002285175.1               |
| *F. graminearum*   | GCA_002240135.3               |
| *F. proliferatum*  | GCF_900067095.1               |
| *F. xylarioides IMI379925* | GCA_004329255.1 |
| *F. xylarioides FRC L-0394*    | GCA_013183765.1               |
**Fig. S6.** Fol chromosome 14 aligned with all known SIX effectors and the nine effectors described in this study which match regions of chromosome 14 (prefixed with a *). Five SIX chromosomal mini-clusters (described by [?] ) are marked on the genome plot. Eight effectors all reside close to four of these clusters: FOXG_14254 and Orx1 are 1.8 kb and 24 kb from six11 (which is clustered with six6 and five genes (including orx1 in Fol) and a transcription factor); OG001377, OG0014741 and OG0014743 are 30 kb, 12.5 kb and 33 kb respectively from six8 (which resides in a solo block with class two transposons and a gene encoding an unknown protein); six7 (from 659_00950) shares a locus with Fol six7 and its cluster with six10 and six12. The orthogroups OG0014741 and OG0014743 are both also <40 kb from this six10, six12, six7 minicluster. Finally, catalase-peroxidase is 45 kb from the six3, six5 minicluster. OG0013765 is 95 kb from the six1, six2, six14 minicluster. Sequences aligned with MAFFT and drawn in Geneious 9.1.

**Table S4.** Predefined effector protein genes analysed in this study. Genes marked with an * show predicted roles and locations only

| Name               | Role                                      | Query Accession | Query species | Length | Reference |
|--------------------|-------------------------------------------|-----------------|---------------|--------|-----------|
| FOXG_02706.2       | Glucosyltransferase*                      | KNJ98333.1      | Fol           | 1493   | [1]       |
| FOXG_10732.2       | Cytoskeletal*                             | KNB10567.1      | Fol           | 449    | [1]       |
| FOXG_04660.2       | Chloroplast/ vacuole*                     | KNB01401.1      | Fol           | 797    | [1]       |
| Nep1               | Microbial elicitors of plant necrosis     | ARJ36580.1      | Foe*          | 2617   | [2]       |
| Fmk1               | MAP kinase                                | KC257048.1      | F. oxysporum  | 603    | [3]       |
| Fow1               | Mitochondrial carrier protein             | KC134256.1      | F. oxysporum  | 725    | [4]       |
| Pda1               | Pisatin demethylase                       | KR85581.1       | F. oxysporum  | 455    | [5]       |
| PelA               | Pectate lyase                             | MK918256.1      | Fol           | 539    | [6]       |
| PelD               | Pectate lyase                             | KC294608.1      | F. proliferatum | 552    | [6]       |
| Pep1               | Pea pathogenicity protein                 | EU436568.1      | Fusarium sp.  | 216    | [7]       |
| Rho1               | Rho GTP-ase activating protein            | KC17411.1       | F. oxysporum  | 665    | [8]       |
| Sge1               | SIX (secreted in xylem) gene expression 1 | LC369105.1      | For*          | 565    | [9]       |
| Snf1               | Protein kinase sucrose non-fermenting     | KU048959.1      | F. commune    | 625    | [10]      |
| FOXG_14254         | Conserved secreted protein                | KNY1932.1       | Fol           | 1592   | [11]      |
| Orx1               | In-planta secreted oxidoreductase enzyme  | KNY1937.1       | Fol           | 1860   | [11]      |
| Catalase-peroxidase| Secreted enzyme                           | KNY19974.1      | Fol           | 2385   | [11]      |
| SIX10              | Secreted in xylem 10                     | KNY2046.1       | Fol           | 736    | [11]      |

*Abbreviations for *Fusarium* *oxysporum* formae speciales sister species: Fol, *F. oxysporum* f. sp. lycopersici; Foe, *F. oxysporum* f. sp. erythoxyli; For, *F. oxysporum* f. sp. ricini
**Fig. S7.** Putative effectors’ characteristics and presence or absence across *F. xylarioides* strain and *F. udum*. The four effector classes are shown in: yellow for pre-defined effectors; purple for small and cysteine-rich secreted effectors; blue for carbohydrate-active enzymes; and red for transposon-adjacent effectors. The symbols highlight: the presence of transposons is represented by names in bold with its distance from the genes promoter described if less than 1500bp (if not, the transposon is over 1500bp away); genes under positive selection by an asterisk; genes in an AT-rich region by a tilde; genes with evidence of horizontal transfer from *F. oxysporum* are a darker shade; genes which are absent from more closely-related *Fusarium* species (namely *F. graminearum*, the Asian clade GFC species and *F. verticillioides* - *F. solani* and *F. udum* were excluded here because *F. solani* also infects coffee ([7 ] and thus could be a source of pathogenicity and *F. udum* is also a vascular wilt-inducer) and *F. oxysporum* is the closest match with a percent identity (%) >=90 are represented by a quotation mark; and closest species is shown for each protein with its percent identity (%), where a BLASTp hit was returned.
Fig. S8. Representative alignments of *F. xylarioides* robusta254 scaffolds which contain the putative 15 effectors under horizontal gene transfer against the genome of *F. oxysporum f. sp. lycopersici* (Fol). Line colour indicates the alignment percentage identity, and y axes have been adjusted to display regions which match. Scaffolds were aligned using nuclmer in the MUMmer3 package, with outputs processed in RStudio. An annotated blue line indicates a gene, an annotated and labelled blue line indicates a putative effector gene, yellow boxes indicate *mimps* and purple boxes indicate class 1 and class 2 transposable elements. A Scaffold 529 (35kb long) with three putative HGT effectors: OG15458, OG13785 and OG973; a Hop3 DNA transposon and a *mimp*; B Scaffold 168 (79 kb) with 20 genes including one putative HGT effector OG16247, a hAT DNA transposon and two *Copia* retrotransposons; C Scaffold 159 (80 kb) with 18 genes including the putative HGT effector Nep1 and two *TeMar-Te1* DNA transposons; D Scaffold 105 (96 kb) with three genes, four DNA transposons (*PiggyBac*, *TeMar-Te1*, MGR583-like, *Fot6*).

Table S5. Enriched CAZyme gene families across Fusarium species (*F. xylarioides*, *F. udum*, Fol, *F. verticillioides*, *F. fujikuroi*, *F. graminearum*) genomes, compared with three different ascomycete fungi (*Trichoderma reesei*, *Aspergillus niger* and *Magnaporthe grisea*)

| Species                      | AA* | CBM* | CE* | GH* | GT* | PL* |
|------------------------------|-----|------|-----|-----|-----|-----|
| *Fol*                        | 165 | 330  | 70  | 746 | 396 | 35  |
| *F. xylarioides* (*Coffeea 674*) | 111 | 232  | 62  | 488 | 248 | 28  |
| *F. udum*                    | 119 | 228  | 63  | 503 | 257 | 30  |
| *F. verticillioides*          | 130 | 265  | 66  | 597 | 336 | 28  |
| *F. fujikuroi*               | 105 | 220  | 61  | 476 | 274 | 29  |
| *F. graminearum*             | 92  | 191  | 52  | 394 | 241 | 27  |
| *Trichoderma reesei*         | 57  | 127  | 25  | 304 | 196 | 8   |
| *Aspergillus niger*          | 94  | 151  | 55  | 434 | 321 | 10  |
| *Magnaporthe grisea*         | 118 | 207  | 60  | 378 | 258 | 9   |

*Abbreviations: AA, Auxiliary Activities; CBM, Carbohydrate-Binding Modules; CE, Carbohydrate Esterase; GH, Glycoside Hydrolases; GT, Glycosyltransferases; PL, Pectate Lyases*
Fig. S9. Representative alignments of *F. xylarioides* arabica908 scaffolds which contain four of the effectors, unique to arabica and one, both or neither of the *Coffeea* strains, under horizontal gene transfer, plotted against the genome of *F. oxysporum* f. sp. *lycopersici* (Fol). Line colour indicates the alignment percentage id match, x and y axes have been adjusted to display regions which match. Scaffolds were aligned using nucmer in the MUMmer3 package, with outputs processed in RStudio. An annotated blue line indicates a gene, an annotated and labelled blue line indicates a putative effector gene, yellow boxes indicate *mimps* and purple boxes indicate class 1 and class 2 transposable elements. A Scaffold 861 (20kb long) with the Six10 putative HGT effector, two *TeMar-Te1* class II DNA transposons, one *Copia* retrotransposon and four *mimps*. B Scaffold 64 (93 kb long) with three putative HGT effectors: OG14180, OG14179, OG409 and a *Yaret2* class II DNA transposon.
Fig. S10. Gene copy number for CAZyme-encoding orthologous groups shared across the vascular wilt-inducing *Fusarium* and *Verticillium*. Groups which also included one non-vascular wilt inducer were additionally included, and those which are also a putative effector are shaded the same colour as in figure 5. Where a species has a gene in the orthologous group which is not recognised as a CAZyme is represented with an asterisk.
### Table S6. Accession numbers and source details for each impala, miniature impala (mimp) and newly described class II transposable elements

| Accession      | Transposon                                      | Sequence           |
|----------------|------------------------------------------------|--------------------|
| AF076624.1     | F. o. repetitive element mimp1                  |                    |
| AF076625.1     | F. o. repetitive element mimp2                  |                    |
| EU833100.1     | F. o. f. sp. melonis MITE mimp3 complete sequence |                    |
| EU833101.1     | F. o. f. sp. lycopersici MITE mimp4 complete sequence |                    |
| AF282722.1     | F. o. f. sp. melonis transposon impala transposase gene complete cds |                    |
| AF363407.1     | F. o. f. sp. melonis transposon impala M24-impE partial sequence |                    |
| AF363412.1     | F. o. f. sp. lini transposon impala Ln3-1 partial sequence |                    |
| AF363413.1     | F. o. f. sp. lini transposon impala Ln88-23 partial sequence |                    |
| AF363414.1     | F. o. f. sp. cubense transposon impala Cu-12 partial sequence |                    |
| AF363416.1     | F. o. f. sp. phaseoli transposon impala Ph-5 partial sequence |                    |
| AF363417.1     | F. o. f. sp. phaseoli transposon impala Ph-9 partial sequence |                    |
| AF363418.1     | F. o. f. sp. albedinis transposon impala A-33 partial sequence |                    |
| AF363419.1     | F. o. f. sp. soil transposon impala S47-35 partial sequence |                    |
| AF363420.1     | F. o. f. sp. raphani transposon impala R-8 partial sequence |                    |
| AF363425.1     | F. o. f. sp. melonis transposon impala M24-impD partial sequence |                    |
| AF363426.1     | F. o. f. sp. melonis transposon impala MK14 partial sequence |                    |
| AF363427.1     | F. o. f. sp. lini transposon impala Ln88-8 partial sequence |                    |
| AF363428.1     | F. o. f. sp. radicis-lycopersici transposon impala RL28delta22 partial sequence |                    |
| AF363429.1     | F. o. f. sp. melonis transposon impala MKdelta208 partial sequence |                    |
| AF363430.1     | F. o. f. sp. lycopersici transposon impala L15delta5 partial sequence |                    |
| AF363432.1     | F. o. f. sp. lycopersici transposon impala L15-15 partial sequence |                    |
| AF363433.1     | F. o. f. sp. radicis-lycopersici transposon impala RL28-17 partial sequence |                    |
| AF363434.1     | F. o. f. sp. lini transposon impala Ln86-10 partial sequence |                    |
| AF363435.1     | F. o. f. sp. ciceris transposon impala Ci-36 partial sequence |                    |
| AF363436.1     | F. o. f. sp. ciceris transposon impala Ci-16 partial sequence |                    |
| AF363437.1     | F. o. f. sp. melonis transposon impala MK28 partial sequence |                    |
| AF363438.1     | F. o. f. sp. lycopersici transposon impala L15-16 partial sequence |                    |
| AJ608703.3     | F. o. f. sp. lycopersici shh1 gene |                    |
| AJ608703.3     | F. o. f. sp. lycopersici fot5 gene |                    |
| JX204302.1     | F. o. f. sp. fragariae transposon Impala1 complete sequence |                    |
| Schmidt et al 13 | FoCrypton |                    |
| Schmidt et al 13 | FoHelitron |                    |
| Schmidt et al 13 | Fot6 |                    |
| Schmidt et al 13 | Fot8 |                    |
| Schmidt et al 13 | Hop3 |                    |
| Schmidt et al 13 | Hop6 |                    |
| Schmidt et al 13 | MGR583-like |                    |
| Schmidt et al 13 | Nht2-like |                    |
| Schmidt et al 13 | YahAT4 |                    |
| Schmidt et al 13 | YahAT6 |                    |
| Schmidt et al 13 | Yaret1 |                    |
| Schmidt et al 13 | Yaret2 |                    |
Table S7. The median overlap distance to transposable elements and Large RIP Affected Areas (LRAR) for our putative effectors and the same number of random genes (randomisation trials, repeated 1000 times, * = p < 0.05) for each *F. xylarioides* strain.

| Random genes | Transposons (kb) | LRAR (kb) | Transposons (kb) | LRAR (kb) | P-value |
|--------------|-----------------|-----------|-----------------|-----------|---------|
| Robusta254   | 6.43            | 22.39     | 4.00            | 15.16     | p > 0.05 |
| Robusta277   | 5.79            | 22.45     | 2.48            | 16.69     | *       | p > 0.05|
| Coffea659    | 6.17            | 24.94     | 3.00            | 14.07     | p > 0.05| p > 0.05|
| Coffea674    | 7.41            | 26.99     | 2.97            | 22.50     | *       | p > 0.05|
| Arabica563   | 5.26            | 18.54     | 2.16            | 7.51      | *       | *       |
| Arabica908   | 4.59            | 18.14     | 3.66            | 6.46      | p > 0.05| *       |
| Effector   | Effector present in FFC | Fx nested with FFC | BSV | Fx nested in Fo by phylogeny | BSV | Fx nested in Fo by distance | Pairwise id % | Class |
|-----------|------------------------|--------------------|-----|-------------------------------|-----|----------------------------|--------------|-------|
| fow1      | Y                      | Y                  | N   |                               |     |                           |              | 1     |
| pelD      | Y                      | Y                  | N   |                               |     |                           |              | 1     |
| fmk1      | Y                      | Y                  | N   |                               |     |                           |              | 1     |
| sge1      | Y                      | Y                  | N   |                               |     |                           |              | 1     |
| snf1      | Y                      | Y                  | N   |                               |     |                           |              | 1     |
| pep1      | N                      | N                  | Y   |                               | 91  | 94                         |              | 3a    |
| chlo_vacu | Y                      | Y                  | N   |                               |     |                           |              | 1     |
| rho1.1    | Y                      | Y                  | N   |                               |     |                           |              | 1     |
| rho1.2    | Y                      | Y                  | N   |                               |     |                           |              | 1     |
| pelA      | Y                      | Y                  | N   |                               |     |                           |              | 1     |
| FOXG_14254| Y                      | Y                  | N   |                               |     |                           |              | 1     |
| orx1      | Y                      | Y                  | N   |                               |     |                           |              | 1     |
| catalase-peroxidase | Y | Y | N |                               |     |                           |              | 1     |
| nep1      | Y                      | N                  | Y   |                               | 99  | 92                         |              | 2     |
| gluco     | Y                      | Y                  | N   |                               |     |                           |              | 1     |
| pda1      | Y                      | Y                  | N   |                               |     |                           |              | 1     |
| six10     | N                      | N                  | N   |                               | 100 | Y                         | 84           | 3b    |
| six7      | N                      | N                  | N   |                               |     |                           | 91           | 4     |
| cytoskeletal | Y*                 | Y                  |     |                               |     |                           |              | 1     |
| OG13899   | Y                      | Y*                 | 100 | N                             |     |                           |              | 1     |
| OG13871   | Y                      | Y                  | N   |                               |     |                           |              | 1     |
| OG13861   | Y                      | Y                  | N   |                               |     |                           |              | 1     |
| OG13877   | Y                      | Y*                 | N   |                               |     |                           |              | 1     |
| OG14828   | Y                      | Y                  | N   |                               |     |                           |              | 1     |
| OG14864   | Y                      | Y                  | N   |                               |     |                           |              | 1     |
| OG13645   | N                      | no blast match     | N   |                               |     |                           |              | 5     |
| OG13792   | Y                      | Y                  | N   |                               |     |                           |              | 1     |
| OG13763   | N                      | no blast match     | N   |                               |     |                           |              | 5     |
| OG13738   | Y                      | Y                  | N   |                               |     |                           |              | 1     |
| OG14398   | N                      | N                  | Y   |                               |     |                           | 84.4         | 4     |
| OG14238   | N                      | N                  | N   |                               |     |                           | 88.9         | 4     |
| OG14165   | Y                      | Y*                 | N   |                               |     |                           |              | 1     |
| OG15453   | N                      | no blast match     | N   |                               |     |                           |              | 5     |
| OG14836   | Y                      | Y*                 | Y   |                               | 100 | 65.8                       |              | 1     |

Table S8. Investigating the support for horizontal acquisition for each putative effector gene in *F. xylarioides* (*Fx*) with *F. oxysporum* (*Fo*) as the source of pathogenicity. Following the decision tree in figure (*), this table reports the outcome for each stage of the decision tree. The stages are: is the effector present in other FFC species (Y / N); if Y, does Fx nest with the FFC gene copies (Y / N); if N, does Fx nest with Fo thus disrupting the Fo phylogeny (Y / N); branch support values (BSV) for Fx with Fo (n); if N, does Fx nest with Fo by distance i.e. less distance from Fx to Fo than greatest distance from Fo to Fo; pairwise id % for whole branch with support value for Fx nested with Fo; the HGT class that we assign, classes 2 and 3 display evidence of HGT. FFC = *F. fujikuroi* complex that *F. xylarioides* belongs to.
|     |     | Blast Match |     |     |     | \%
|-----|-----|-------------|-----|-----|-----|----
| OG16234 | N | no blast match | N |     |     | 5 |
| OG13787 | Y | Y* | 80 | N |     | 1 |
| OG16323 | N | no blast match | N |     |     | 5 |
| OG14797 | Y | Y* | 99 | N |     | 1 |
| OG14367 | N | no blast match | N |     |     | 5 |
| OG13912 | Y | Y |     | N |     | 1 |
| OG08649 | Y | Y* | Y | 100 | 88.7 | 1 |
| OG14891 | Y | Y |     | N |     | 1 |
| OG16261 | N | Weak Fo blast hit | N |     |     | 5 |
| OG16232 | Y | Y |     | N |     | 1 |
| OG16241 | Y | N | Y | 100 | 89.1 | 2 |
| OG16247 | N | N | N | Y | 80.4 | 3b |
| OG7097  | Y | Y |     | N |     | 1 |
| OG14811 | Y | Y |     | N |     | 1 |
| OG15465 | Y | N | Y | 100 | 88 | 2 |
| OG14741 | N | N | Y | 100 | Y | 90.1 | 3a |
| OG14743 | N | N | N | Y | 97.9 | 3b |
| OG16212 | Y | Y |     | N |     | 1 |
| OG006324 | Y | Y |     | N |     | 1 |
| OG11333 | Y | Y |     | N |     | 1 |
| OG14180 | N | N | N | Y | 95.6 | 3b |
| OG14392 | Y | Y* | 46 | N |     | 1 |
| OG13478 | N | N | N | 100 | Y | 98.8 | 3b |
| OG09441 | Y | Y/N |     | N |     | 2 |
| OG00973 | Y | N | Y | 100 | 83.6 | 2 |
| OG13765 | N | N | Y | 100 | 86.5 | 3b |
| OG15458 | N | N | N |     |     | 4 |
| OG00409 | Y | Y |     |     |     | 1 |
| OG14179 | N | N | Y | 99 | 82 | 3a |
| Name    | Species        | Strain  | BioProject | BioSample   | Locus tag | Reads   | Bases     | Genome size | Coverage | Run accessions |
|---------|----------------|---------|------------|-------------|-----------|---------|-----------|-------------|----------|----------------|
| Coffea674 | Fusarium xylarioides | IMI 392674 | PRJNA659227 | SAMN15901422 | H9Q69    | 2,649,496 | 763,216,608 | 57,075,484 | 13.4     | SRR12534416 |
| Coffea659 | Fusarium xylarioides | IMI 127659i | PRJNA659227 | SAMN15901423 | H9Q72    | 2,207,606 | 634,942,231 | 59,379,521 | 10.7     | SRR12534415 |
| Robusta277 | Fusarium xylarioides | IMI 392277 | PRJNA659227 | SAMN15901435 | H9Q70    | 3,330,016 | 959,882,147 | 61,161,285 | 15.7     | SRR12534414 |
| Robusta254 | Fusarium xylarioides | IMI 392254 | PRJNA659227 | SAMN15901436 | H9Q73    | 2,614,366 | 753,518,666 | 60,101,568 | 12.5     | SRR12534413 |
| Arabica563 | Fusarium xylarioides | IMI 389563 | PRJNA659227 | SAMN15901606 | H9Q71    | 2,633,060 | 759,347,660 | 63,111,562 | 12       | SRR12534412 |
| Arabica908 | Fusarium xylarioides | IMI 375908i | PRJNA659227 | SAMN15901615 | H9Q74    | 2,374,418 | 684,973,154 | 62,330,925 | 11       | SRR12534411 |
REFERENCES

1. S. J. Klosterman, K. V. Subbarao, S. Kang, P. Veronese, S. E. Gold, B. P. Thomma, Z. Chen, B. Henriissat, Y. H. Lee, J. Park, M. D. Garcia-Pedrajas, D. J. Barb, A. Anchieta, R. de Jonge, P. Santhanam, K. Maruthachalam, Z. Atallah, S. G. Amyotte, Z. Paz, P. Inderbitzin, R. J. Hayes, D. I. Heiman, S. Young, Q. Zeng, R. Engels, J. Galagan, C. A. Cuomo, K. F. Dobinson, and L. J. Ma, “Comparative genomics yields insights into niche adaptation of plant vascular wilt pathogens,” PLoS Pathog. 7 (2011).

2. C. L. Pemberton and G. P. Salmond, “The Nep1-like proteins - A growing family of microbial elicitors of plant necrosis,” Mol. Plant Pathol. 5, 353–359 (2004).

3. A. Di Pietro, F. I. García-Maceira, E. Méglec, and M. I. G. Roncero, “A MAP kinase of the vascular wilt fungus Fusarium oxysporum is essential for root penetration and pathogenesis,” Mol. Microbiol. 39, 1140–1152 (2004).

4. L. Inoue, F. Namiki, and T. Tsuge, “Plant Colonization by the Vascular Wilt Fungus Fusarium oxysporum Requires FOW1, a Gene Encoding a Mitochondrial Protein,” The Plant Cell 14, 1869–1883 (2002).

5. C. Wasmann and H. VanEtten, “Transformation-mediated chromosome loss and disruption of a gene for pisatin demethylase decrease the virulence of Nectria haematococca on pea,” Mol. Plant-Microbe Interactions (USA) (1996).

6. L. M. Rogers, Y.-K. Kim, W. Guo, L. González-Candelas, D. Li, P. E. Kolattukudy, and C. A. Ryan, “Requirement for either a host- or pectin-induced pectate lyase for infection of Pism sativum by Nectria haematococca,” Natl. Acad Sci. 97 (2000).

7. Y. Han, X. Liu, U. Benny, H. Corby Kistler, and H. D. VanEtten, “Genes determining pathogenicity to pea are clustered on a supernumerary chromosome in the fungal plant pathogen Nectria haematococca,” Plant J. 25, 305–314 (2001).

8. A. L. Martínez-Rocha, M. I. G. Ronceró, A. López-Ramírez, M. Mariné, J. Guarro, G. Martinez-Cadena, and A. Di Pietro, “Rho1 has distinct functions in morphogenesis, cell wall biosynthesis and virulence of Fusarium oxysporum,” Cell. Microbiol. 10, 1339–1351 (2008).

9. C. B. Michielse and M. Rep, “Pathogen profile update: Fusarium oxysporum,” Mol. Plant Pathol. 10, 311–324 (2009).

10. M. D. Ospina-Giraldo, E. Mullins, and S. Kang, “Loss of function of the Fusarium oxysporum SNF1 gene reduces virulence on cabbage and Arabidopsis,” Curr. Genet. 44, 49–57 (2003).

11. L. J. Ma, H. C. Van Der Does, K. A. Borkovich, J. J. Coleman, M. J. Daboussi, A. Di Pietro, M. Dufresne, M. Freitag, M. Grabherr, B. Henriissat, P. M. Houterman, S. Kang, W. B. Shim, C. Woloshuk, X. Xie, J. R. Xu, J. Antoniw, S. E. Baker, B. H. Bluhm, A. Breakspear, D. W. Brown, R. A. Butchko, S. Chapman, R. Coulson, P. M. Coutinho, E. G. Danchin, A. Diener, L. R. Gale, D. M. Gardiner, S. Goff, K. E. Hammond-Kosack, K. Hilburn, A. Hua-Van, W. Jonkers, K. Kazan, C. D. Kodira, M. Koehrsen, L. Kumar, Y. H. Lee, L. Li, J. M. Manners, D. Miranda-Saavedra, M. Mukherjee, G. Park, J. Park, S. Y. Park, R. H. Proctor, A. Regev, M. C. Ruiz-Roldan, D. Sain, S. Saktikumar, S. Sykes, D. C. Schwartz, B. G. Turgeon, I. Wapinski, O. Yoder, S. Young, Q. Zeng, S. Zhou, J. Galagan, C. A. Cuomo, H. C. Kistler, and M. Rep, “Comparative genomics reveals mobile pathogenicity chromosomes in Fusarium,” Nature 464, 367–373 (2010).