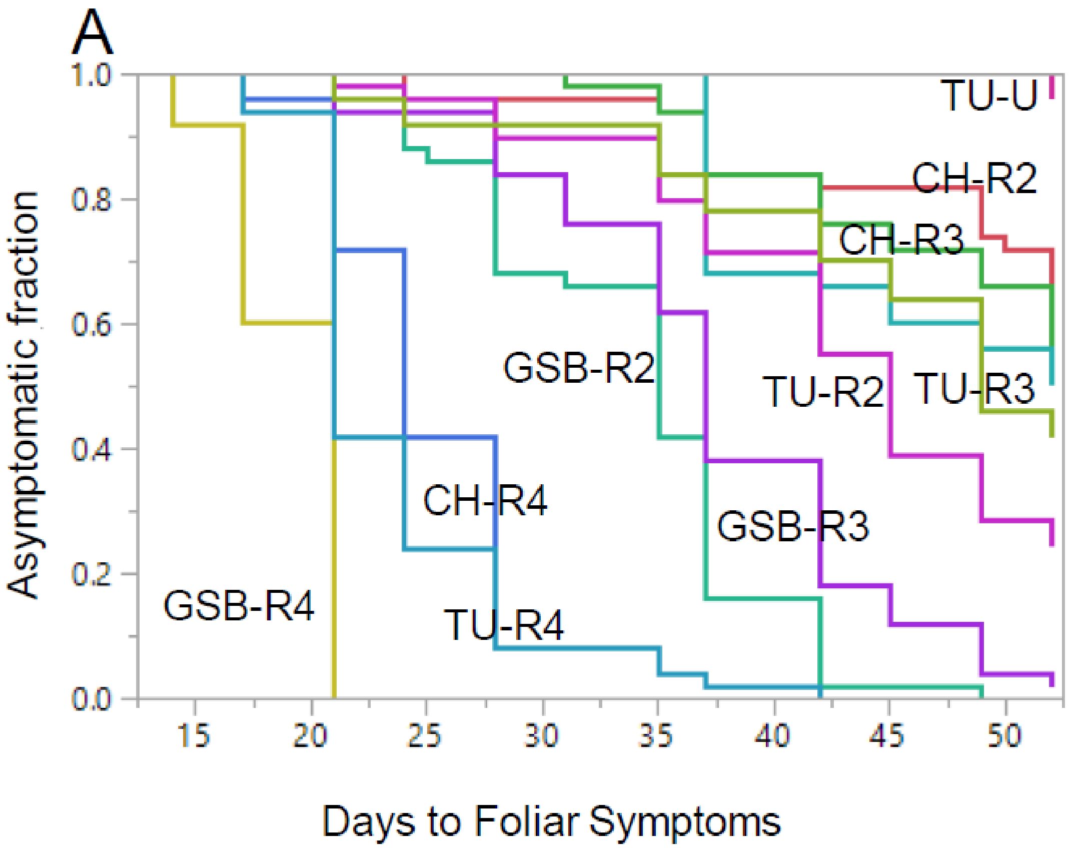
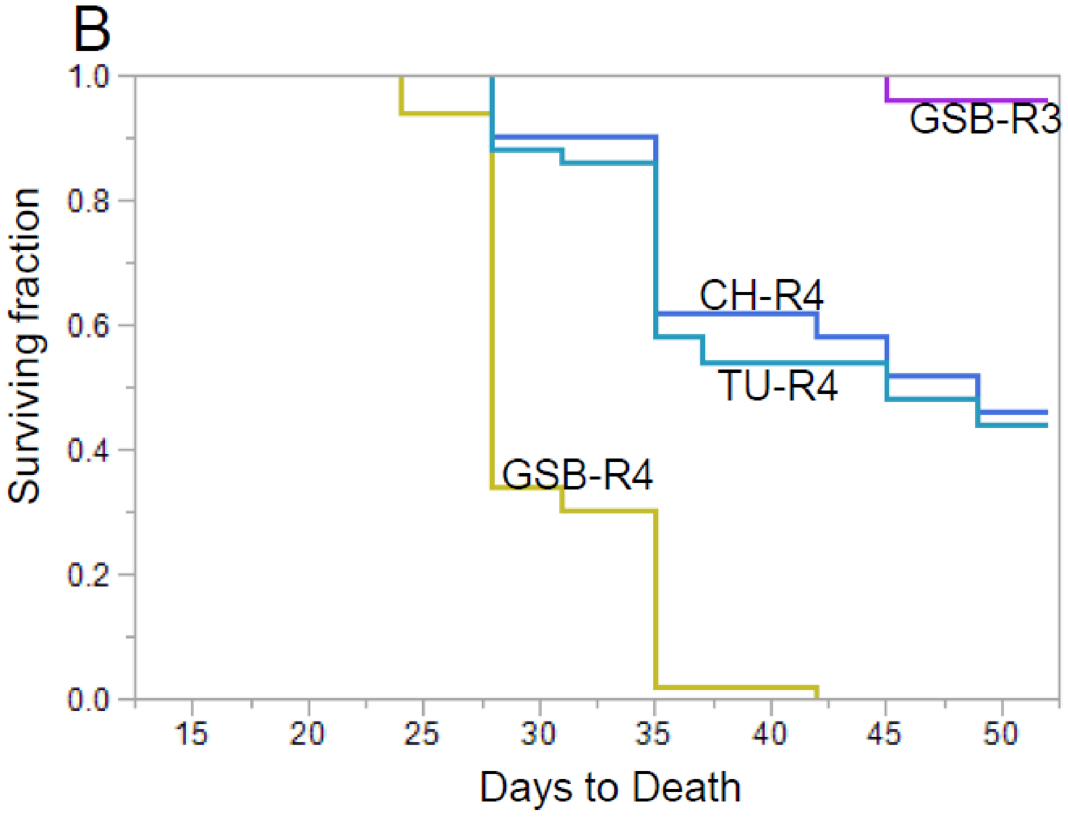
Additional file 1. Isolate collection

Isolates of *F. oxysporum* f. sp. *apii* from symptomatic celery were characterized by pathogenicity testing and two-locus sequence typing with *ef1* and *igs*; there were two isolates of *Foa* race 1, 22 isolates of *Foa* race 2, one isolate of *Foa* race 3-type from a culture collection, and 11 isolates of *Foa* race 4 [3]. Anecdotal evidence suggests that celery in "Field 0" for *Foa* race 4 were infected in ca. 2011. In 2013, we identified *Foa* race 4 in three fields in the Camarillo-Oxnard area in Ventura County in California. Between 2014 and 2019, as the pathogen spread to an increasingly larger area within Ventura County, we identified 46 *Foa* race 4 isolates from an additional 38 celery fields.

Between 2016 and 2018, we observed a syndrome in coriander and isolated *F. oxysporum* from symptomatic plants from seven fields in California; eight isolates were characterized by pathogenicity on coriander and celery, two-locus sequence typing (*ef1*/*igs*), and by PCR primers that are described later in this paper. *Foci*3-2 was selected for genome assembly (Table 1), as was *Foci*GL306, which was previously isolated in 2004 from neighboring Santa Barbara County [12].


A
Asymptomatic fraction
1.0
0.8
0.6
0.4
0.2
0.0
TU-U
CH-R2
CH-R3
GSB-R2
TU-R2
TU-R3
CH-R4
GSB-R3
GSB-R4
TU-R4
15
20
25
30
35
40
45
50
Days to Foliar Symptoms


B
Surviving fraction
1.0
0.8
0.6
0.4
0.2
0.0
GSB-R3
CH-R4
TU-R4
GSB-R4
15
20
25
30
35
40
45
50
Days to Death

C. Response of celery after 56 days

Foa race	Celery cultivar	Vascular discoloration-based rating from 0, asymptomatic to 5, dead	Aerial symptoms, %	Dead, %
Foa race 2	Golden Self Blanching	1.8 d	60 abc	0 c
	Tall Utah	2.0 d	50 bc	0 c
	Challenger	0.4 e	22 cd	0 c
Foa race 3	Golden Self Blanching	2.9 c	92 ab	2 c
	Tall Utah	1.7 d	18 cd	0 c
	Challenger	1.4 d	44 c	0 c
Foa race 4	Golden Self Blanching	5.0 a	100 a	100 a
	Tall Utah	4.1 b	90 ab	62 b
	Challenger	4.4 ab	100 a	56 b
Uninfested control	Golden Self Blanching	0.1 e	0 d	0 c
	Tall Utah	0.0 e	0 d	0 c
	Challenger	0.0 e	0 d	0 c

Additional file 2. Virulence of *F. oxysporum* f. sp. *apii* (*Foa*) races in three differential celery cultivars. In each of two trials, each with 25 replicate plants per treatment, cv. Golden Self Blanching (GSB), Tall Utah 52-70 R Improved (TU), and Challenger (CH) were transplanted in the greenhouse into either uninfested soil (U) or soil infested with *Foa* races 2 (R2), 3 (R3) or 4 (R4) and monitored weekly. A-B) Kaplan-Meier curves over 52 days. Treatments with 0% affected during the entire trial are not shown. A) The fraction of asymptomatic plants. Symptoms included yellowing (most frequently), stunting and/or wilting (least frequently). A log rank test (Chi-square=922, df=11, *P*<0.0001) and a Wicoxon (Chi-square=825, df=11, *P*<0.0001) indicate highly significant differences between cultivar-strain combinations. The combined days to symptoms was 40 with SEM=0.5. B) The fraction of survivors. A log rank test (Chi-square=664, df=11, *P*<0.0001) and a Wicoxon (Chi-square=646, df=11, *P*<0.0001) indicate highly significant differences between cultivar-strain combinations. The combined days to symptoms was 49 with SEM=0.3. C) ANOVA of symptoms at 56 days post-transplant. Within a column, for analyses with a significant F test, means followed by the same letter are not significantly different (α=0.05) by Tukey's HSD. Vascular discoloration was scored on a scale of 0, asymptomatic; 1, some discoloration in the vasculature in lateral roots; 2, some discoloration in the vasculature of the main roots; 3, some discoloration in the vasculature of the crown; 4, extensive discoloration of the crown vasculature; and 5, plant dead. Percentage data were analyzed using trials as replicates.

Additional file 3. Virulence of *F. oxysporum* f. sp. *apii* and f. sp. *coriandrii* in celery and coriander[a].

F. oxysporum strain	Celery cv. Tall Utah	Celery cv. Challenger	Coriander cv. Longstanding
	Vascular discoloration-based rating from 0=asymptomatic to 5=dead[b]		
Foa race 2	3.8 b	0.4 b	4.4 a
Foa race 3	2.2 c	0.4 b	4.6 a
Foa race 4	4.7 a	4.3 a	4.7 a
*Foci*3-2	0.1 d	0 b	5.0 a
*Foci*GL306	0.1 d	0 b	5.0 a
Uninfested	0 d	0 b	0 b

[a] The pathogenicity and virulence of *F. oxysporum* f. sp. *apium* (*Foa*) races 2, 3, and 4 and two *F. oxysporum* f. sp. *coriandrii* (*Foci*) isolates in either the celery cultivars Tall Utah 52-70 R Improved or Challenger, and in the coriander cultivar Longstanding.

[b] These data were collected 56 days after either transplanting the celery or seeding the coriander. n=20. The scoring system is 0, asymptomatic; 1, some discoloration in the vasculature in lateral roots; 2, some discoloration in the vasculature of the main roots; 3, some discoloration in the vasculature of the crown; 4, extensive discoloration of the crown vasculature; and 5, plant dead. Within a column, for analyses with a significant F test, means followed by the same letter are not significantly ($\alpha=0.05$) different by Tukey's HSD.

Additional file 4. Locations of the core genome in the *Foa* and *Foci* assemblies[a]

Fol reference chromosome no.	*Fusarium oxysporum* strain				
	Foa race 4	*Foa* race 3	*Foa* race 2	*Foci*3-2	*Foci*GL306
	Contig, Unitig (U) or Superscaffold (SS): bp_{start} – bp_{end}[b]				
1	SS12:72573-6058608	1:29926-5981626	1:65662-6035196	1:162038-6137829	1:179442- 6153615
2	SS11:396569-5061175	5:3057497-1489	4:4719646-9761	6:4664059-739	6:4657892-90
		5:3060960-3180414		6:4818032-4913602	
		5:4654206-3184969			
4	U7:5282662-61072	2:5266514-47724	2:166795-5451515	3:453038-5645653	3:5276569-67101
5	SS10:120094-5137752	3:87531-5082748	3:4899109-40504	4:131063-5127215	4:5036752-41672
7	U11:283068-421629	4:1-4282420	5:4633510-56578	5:5050022-555610	5:77842-4576828
	U11:739260-5088771	4:4729699-4602449			
8	U22:4026363-60183	7:1-3933658	6:96225-4205359	8:145491-4270898	7:127323-4095931
9	SS3:2854310-78881	8:32899-2806522	7:3466954-138153	7:3554426-469659	8:3556918-468550;
	SS12:6421088-6323837	18:530595-153433		22:514515-164628	26:89705-448060
	SS12:6427888-6586853	1:6260911-6523362			
	SS15:447349-516576				
	SS15:612952-820663				
10	U19:145997-3107921	6:3857323-890704	8:3076403-113319	2:6046770-3088076[c]	2:5956519-2988178 [d]
11	SS5:313551-2541971	9:302789-2524023	10:464068-2622175	2:279367-2715249[c]	2:288703-2616039[d]
			10:2698091-2642939		

			10:2809707-3043442		
12	U26:2613327-160962	10:2614471-305965	11:210336-2393423	10:262376-2575949	14:293931-1188452 30:361203-10502 11:1364702-333626
13	SS4:471270-2296753	11:1810057-25921	12:389064-2232701	9:465874-2327815	9:2537220-674297

[a] The core genome is conserved amongst *F. oxysporum* strains. We identified conserved colinear blocks using progressiveMauve and the *F. oxysporum* f. sp. *lycopersici* (*Fol*) 4287 reference.

[b] SS denotes a Superscaffold that was constructed with Bionano. Sequences where the bp$_{start}$ is greater than the bp$_{end}$ are in reverse orientation relative to the *Fol* 4287 reference.

[c] A subsequent analysis identified a 198 bp juncture between Chromosomes 11 and 10 in *Foci*3-2 contig 2:2399802-2399999.

[d] A subsequent analysis identified a 198 bp juncture between Chromosomes 11 and 10 in FociGL306 contig 2:2498982-2499179.

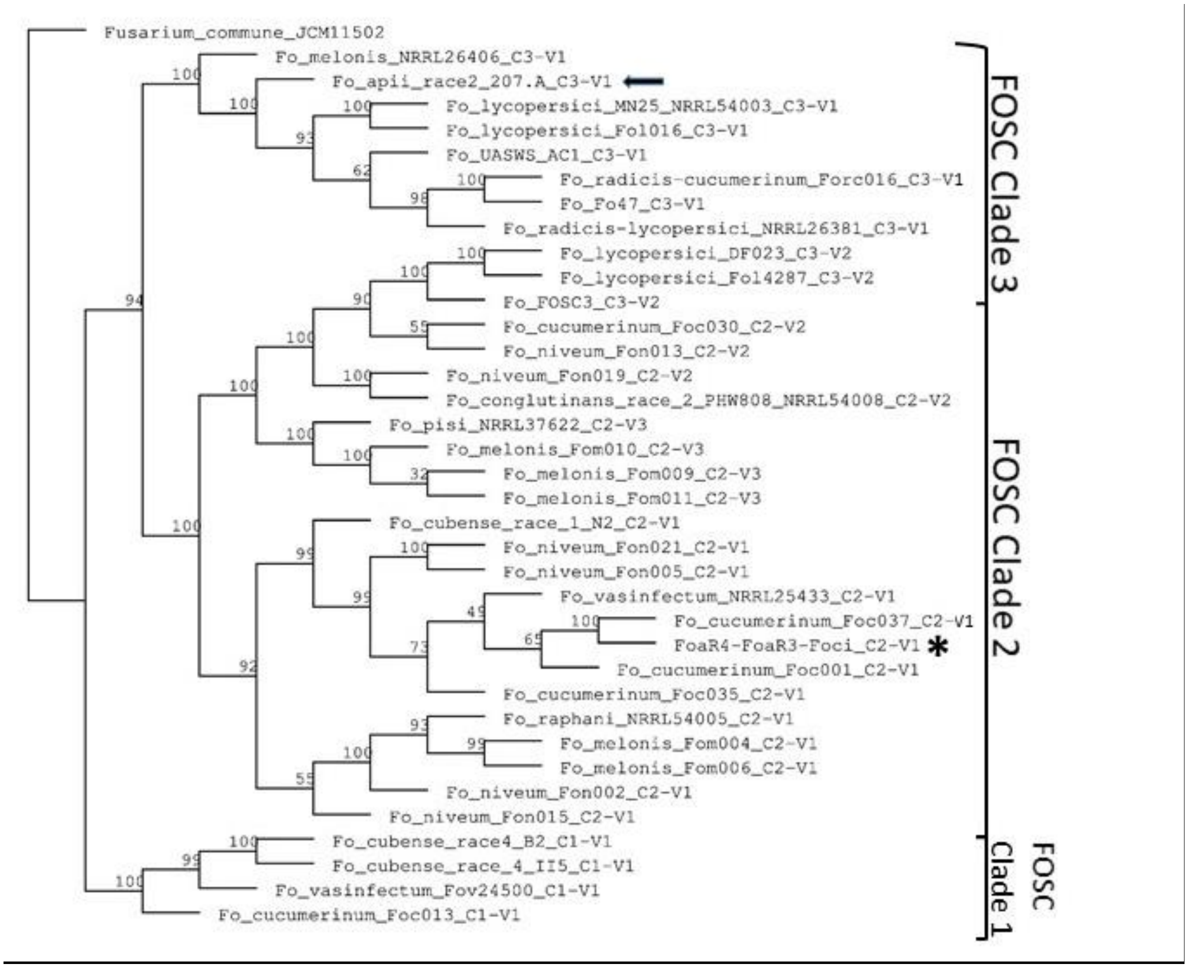
Additional file 5. Percentage of the 3,725 Benchmarking Universal Single-Copy Orthologs (BUSCO) in Sordariomycetes in the sequenced strains[a]**.**

Fusarium oxysporum strain[b]	Full-length genes present in assembly, %	Genes correctly assembled as a full-length, single copy, %	Genes complete but present as two or three homologs, %	Genes frag-mented, %	Genes missing, %
Foa race 4	98.8	98.1	0.8	0.8	0.4
Foa race 3	98.8	98.1	0.6	0.9	0.4
Foa race 2	98.7	97.6	1.1	0.9	0.4
*Foci*3-2	98.7	98.0	0.8	0.9	0.4
*Foci*GL306	98.8	97.9	0.9	0.9	0.4
*Fol*4287 reference[c]	95.6	94.8	0.9	3.2	1.2

[a] BUSCO v2.0 [14]

[b] Strains of *Fusarium oxysporum* f. sp. *apii* (*Foa*), f. sp. *coriandrii* (*Foci*) and the f. sp. *lycopersici* (*Fol*) reference are described in Table 1.

[c] Genbank GCA_000149955.2 ASM14995v2



Additional file 6. A cladogram of the mitochondrial genomes of the *Foa*, *Foci*, and 34 FOSC strains. The 34 *Fusarium oxysporum* species complex (FOSC) references are from NCBI GenBank [15]. *F. commune* was used as an out-group. *F. oxysporum* f. sp. *apii* (*Foa*) races 3 and 4 and *F. oxysporum* f. sp. *coriandrii* strains *Foci* GL306 and *Foci*3-2 have an identical mitochondrial sequence and were collapsed into a single entry; they are shown with an asterisk. *Foa* race 2 is shown with an arrow. After the name of each strain, the value indicates the FOSC Clade and the V value indicates the Mitochondrial Variable Region Type. The tree was generated in Geneious (v.2020.0) with RaxML with the general time reversible evolutionary model and a search for the best-scoring maximum parsimony tree. Support for the tree is based on 1,000 bootstrap replicates.

Additional file 7. The numbers of genes and the sizes of the core and accessory genomes[a]

Strain[b]	Total no. of predicted coding nuclear genes	No. genes detected by 3’ RNA TagSeq[b]	DNA in the core genome, Mbp	DNA in the accessory genome, Mbp
Foa race 4	20,528	10,556	42.1	25.3
Foa race 3	20,165	10,250	41.8	23.5
*Foci*3-2	20,287	NA[c]	42.5	23.0
*Foci*GL306	20,208	NA	42.1	22.9
Foa race 2	20,334	10,430	42.3	22.5
Fol 4287[d]	20,925	NA[c]	43.4	18.0

[a] The core genome was selected based on homology to the *F. oxysporum* f. sp. *lycopersici* 4287 core chromosomes 1, 2, 4, 5, and 7 through 13. The specific regions on the core contigs in our strains are indicated in Additional file 4.

[b] All detected genes had a minimum of a total of 10 or more “hits” in broth, or in the case of *Foa* race 4, in either broth and/or *in planta* libraries.

[c] NA, not applicable.

[d] *F. oxysporum* f. sp. *lycopersici* 4287 reference (Genbank GCA_000149955.2 ASM14995v2)

Additional file 8. Classification of contigs in the *Foa* race 4 accessory genome as either lineage- or host-specific.

			Strain[c]					
			Fo f. sp. *apii* race			*Foci*		
			2	4	3	3-2	GL306	
Fol homolog[a]	*Foa* race 4 contig[b]	*Foa* race 4 contig length, Mb	Fraction of the *Foa* race 4 assembly with highest-quality Illumina read coverage from the indicated strain[d]					Differentiation between *Foa* races 3 and 4 vs. *Foci*?[e]
Chr1	SS12	7.0	0.89	1.00	1.00	1.00	1.00	No, a core chromosome
Chr2	SS11	5.2	0.92	1.00	1.00	0.99	0.99	No, a core chromosome
Chr4	U7	5.5	0.90	1.00	1.00	1.00	0.97	No, a core chromosome
Chr5	SS10	5.3	0.91	1.00	0.99	1.00	1.00	No, a core chromosome
Chr7	U11	5.2	0.85	1.00	1.00	1.00	1.00	No, a core chromosome
Chr8	U22	4.0	0.94	1.00	1.00	0.99	0.99	No, a core chromosome
Chr9	SS3	4.4	0.78	0.98	0.98	0.95	0.96	No, a core chromosome
Chr9	SS15	0.9	0.50	0.89	0.89	0.89	0.84	No, a core chromosome
Chr10	U19	4.0	0.82	1.00	1.00	1.00	1.00	No, a core chromosome
Chr11	SS5	5.2	0.70	1.00	0.98	0.69	0.69	Yes
Chr12	U26	2.9	0.80	1.00	1.00	1.00	1.00	No, a core chromosome
Chr13	SS4	3.4	0.66	0.96	0.96	0.95	0.94	No, a core chromosome
Acc	SS2	2.1	0.47	0.95	0.94	0.95	0.95	No, LS
Acc	SS17	1.9	0.49	0.95	0.94	0.50	0.49	Yes, HS
Acc	SS6	1.9	0.60	0.97	0.96	0.96	0.96	No, LS
Acc	SS13	1.3	0.46	0.94	0.94	0.65	0.65	Yes, HS
Acc	SS19	1.0	0.43	0.87	0.88	0.86	0.87	No, LS
Acc	U56	0.9	0.61	1.00	1.00	1.00	1.00	No, LS
Acc	SS9	0.9	0.44	0.99	0.95	0.94	0.94	No, LS
Acc	SS14[f]	0.9	0.54	0.87	0.87	0.58	0.58	Yes, HS
Acc	SS8	0.8	0.55	0.92	0.92	0.92	0.92	No, LS

[a] Homologs of *F. oxysporum* f. sp. *lycopersici* (*Fol*) chromosomes were assigned with progressiveMauve. Chr, chromosome; Acc, Classified as part of the **acc**essory genome, i.e., without a homolog in the *Foa* and *Foci* strains.

[b] Only contigs with length greater than 150k bp were evaluated. U, unitig; SS, Superscaffold, which were based on the connection of unitigs from a Bionano optical map.

[c] *F. oxysporum* f. sp. *apii* (*Foa*) race 2 is in *F. oxysporum* species complex (FOSC) Clade 3. *F. oxysporum* f. sp. *apii* races 3 and 4, and *F. oxysporum* f. sp. *coriandrii* (*Foci*) are in FOSC Clade 2.

[d] 6.5 Gbp (≈100X) of quality-filtered (Phred score >20) Illumina reads were mapped onto the reference assembly and sequences were considered to be present in the query strain if greater than 10x coverage was observed. Here, the most saturated green indicates the most similar DNA with the *Foa* race 4 reference, yellow indicates moderately similar DNA and the most saturated red indicates the most dissimilar DNA.

[e] ”No, a core chromosome” is expected. In the accessory (Acc) contigs, “No” indicates that the contig is “lineage-specific” (LS), i.e., shared between the *Foa* races 3 and 4 and the *Foci*. “Yes” indicates that *F. oxysporum* f. sp. *apii* races 3 and 4 and the *Foci* have different accessory contigs, i.e., these contigs are “host-specific” (HS).

[f] Has two *SIX1* homologs.

Additional file 9. Classification of contigs in the *Foci*3-2 accessory genome as either lineage- or host-specific.

			Strain[c]					
			Fo f. sp. *apii* race			*Foci*		
			2	4	3	3-2	GL306	
Fol homolog[a]	*Foci*3-2 contig[b]	*Foci*3-2 contig length, Mb	Fraction of the *Foci* 3-2 assembly with highest-quality Illumina read coverage from the indicated strain[d]					Differentiation between *Foci vs. Foa* races 3 and 4?[e]
Chr1	1	6.7	0.92	0.94	0.98	1.00	1.00	No, a core chromosome
Chr2	6	5.0	0.93	1.00	1.00	1.00	1.00	No, a core chromosome
Chr4	3	5.7	0.87	0.97	0.99	1.00	0.94	No, a core chromosome
Chr5	4	5.2	0.92	0.99	0.98	1.00	0.99	No, a core chromosome
Chr7	5	5.2	0.84	1.00	1.00	1.00	1.00	No, a core chromosome
Chr8	8	4.4	0.90	0.97	0.97	1.00	0.98	No, a core chromosome
Chr9	7	4.9	0.79	0.98	0.98	1.00	1.00	No, a core chromosome
Chr9	22	0.6	0.65	0.98	0.98	1.00	1.00	No, a core chromosome
Chr10&11	2	6.2	0.86	1.00	1.00	1.00	1.00	No, a core chromosome
Chr12	10	2.9	0.80	0.99	0.99	1.00	1.00	No, a core chromosome
Chr13	9	3.0	0.74	0.99	0.99	1.00	1.00	No, a core chromosome
Acc	11	2.4	0.54	0.96	0.97	1.00	0.96	No, LS
Acc	12	1.7	0.35	0.30	0.29	1.00	1.00	Yes, HS
Acc	13	1.1	0.55	1.00	1.00	1.00	1.00	No, LS
Acc	14	1.1	0.56	1.00	1.00	1.00	1.00	No, LS
Acc	15[f]	1	0.54	0.30	0.30	1.00	1.00	Yes, HS
Acc	16	1	0.47	0.23	0.23	1.00	1.00	Yes, HS
Acc	17	0.8	0.61	0.61	0.61	0.61	0.61	Unclear
Acc	19	0.8	0.22	0.18	0.18	0.99	0.99	Yes, HS
Acc	20	0.6	0.41	0.45	0.44	1.00	1.00	Yes, HS
Acc	21	0.6	0.65	0.35	0.35	1.00	1.00	Yes, HS
Acc	23	0.6	0.60	1.00	1.00	1.00	1.00	No, LS

Acc	24	0.6	0.51	0.99	0.98	0.99	0.99	No, LS
Acc	25	0.4	0.51	1.00	0.96	1.00	1.00	No, LS
Acc	26	0.4	0.61	0.95	0.95	1.00	1.00	No, LS
Acc	27	0.3	0.52	0.99	0.99	0.99	0.99	No, LS
Acc	28	0.3	0.54	0.97	0.97	0.98	0.98	No, LS
Acc	29	0.2	0.47	1.00	1.00	1.00	1.00	No, LS
Acc	30	0.2	0.52	1.00	1.00	1.00	1.00	No, LS
Acc	31	0.2	0.75	0.99	0.99	1.00	0.99	No, LS
Acc	32	0.2	0.50	0.85	0.87	0.99	0.99	Somewhat

[a] Homologs of *F. oxysporum* f. sp. *lycopersici* (*Fol*) chromosomes were assigned with progressiveMauve. Chr, chromosome; Acc, Classified as part of the **acc**essory genome, i.e., without a homolog in the *Foa* and *Foci* strains.

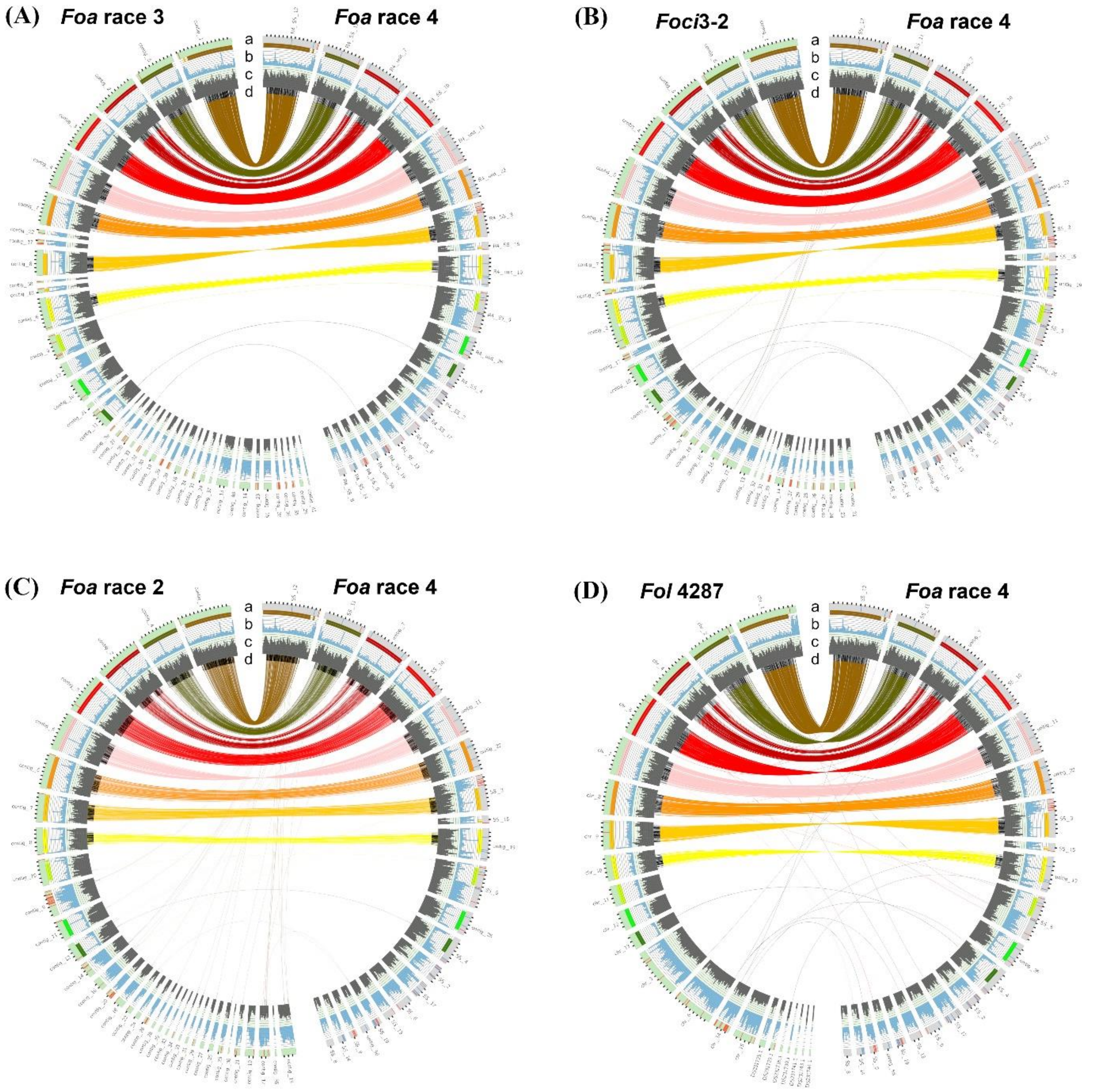
[b] Only contigs with length greater than 150k bp were evaluated.

[c] *F. oxysporum* f. sp. *apii* race 2 is in *F. oxysporum* species complex (FOSC) Clade 3. *F. oxysporum* f. sp. *apii* races 3 and 4, and *F. oxysporum* f. sp. *coriandrii* (*Foci*) are in FOSC Clade 2.

[d] 6.5 Gbp (≈100X) of quality-filtered (Phred score >20) Illumina reads were mapped onto the reference assembly and sequences were considered to be present in the query strain if greater than 10x coverage was observed. Here, the most saturated green indicates the most similar DNA with the *Foci*3-2 reference, yellow indicates moderately similar DNA and the most saturated red indicates the most dissimilar DNA.

[e] ”No, a core chromosome” is expected. In the accessory (Acc) contigs, “No” indicates that the contig is “lineage-specific” (LS), i.e., shared between the *Foci* and *Foa* races 3 and 4. “Yes” indicates that the *Foci* versus *Foa* races 3 and 4 have different accessory contigs, i.e., these contigs are “host-specific” (HS).

[f] Has the *SIX1* homolog.



Additional file 10. Conserved synteny of BUSCOs in *Foa* race 4 and other *Foa*, *Foci* and a reference. An average of 3633 ± 16 full-length Benchmarking Universal Single-Copy Orthologs [14] were analyzed per pair. *Fusarium oxysporum* f. sp. *apii (Foa)* race 4 is shown on the right side and, on the left side, the indicated strain. Contigs less than 150k bp are not shown. Tic marks on ring "a" are 500 kb apart. Within ring a, red lines indicate miniature impala transposable elements (mimps), and blue lines indicate all genes with significantly (adjusted $P<0.05$) increased expression *in planta* in celery crowns that were infected with *Foa* race 4 compared to *Foa* race 4 grown *in vitro*. In ring b, the solid colors within the upper portion denote a region with homology to one of the *Fol* core chromosomes. Blue shows the density of repetitive elements with a full scale of 120 per 100 kb increment. In ring c, dark grey shows the density of gene models with a full scale of 50 per 100 kb increment. In ring d, the grey lines show predicted BUSCO genes, and links between BUSCO genes indicate the position of the homolog in the other strain. Links connecting BUSCO homologs in core chromosomes are color coded, and BUSCO genes in accessory contigs are connected by black lines. The plots illustrate the high degree of synteny in all four pairs of strains in the core chromosomes, even across FOSC Clade 2 (*Foa* race 4) and FOSC Clade 3 (the *Fol* 4287 reference and *Foa* race 2). Note that the BUSCO genes are concentrated in orthologs of only core chromosomes 1,2,4,5, and 7-10 and not in core chromosomes 11-13.

Additional file 11: The number of homologs and their synteny in the accessory genomes[a]

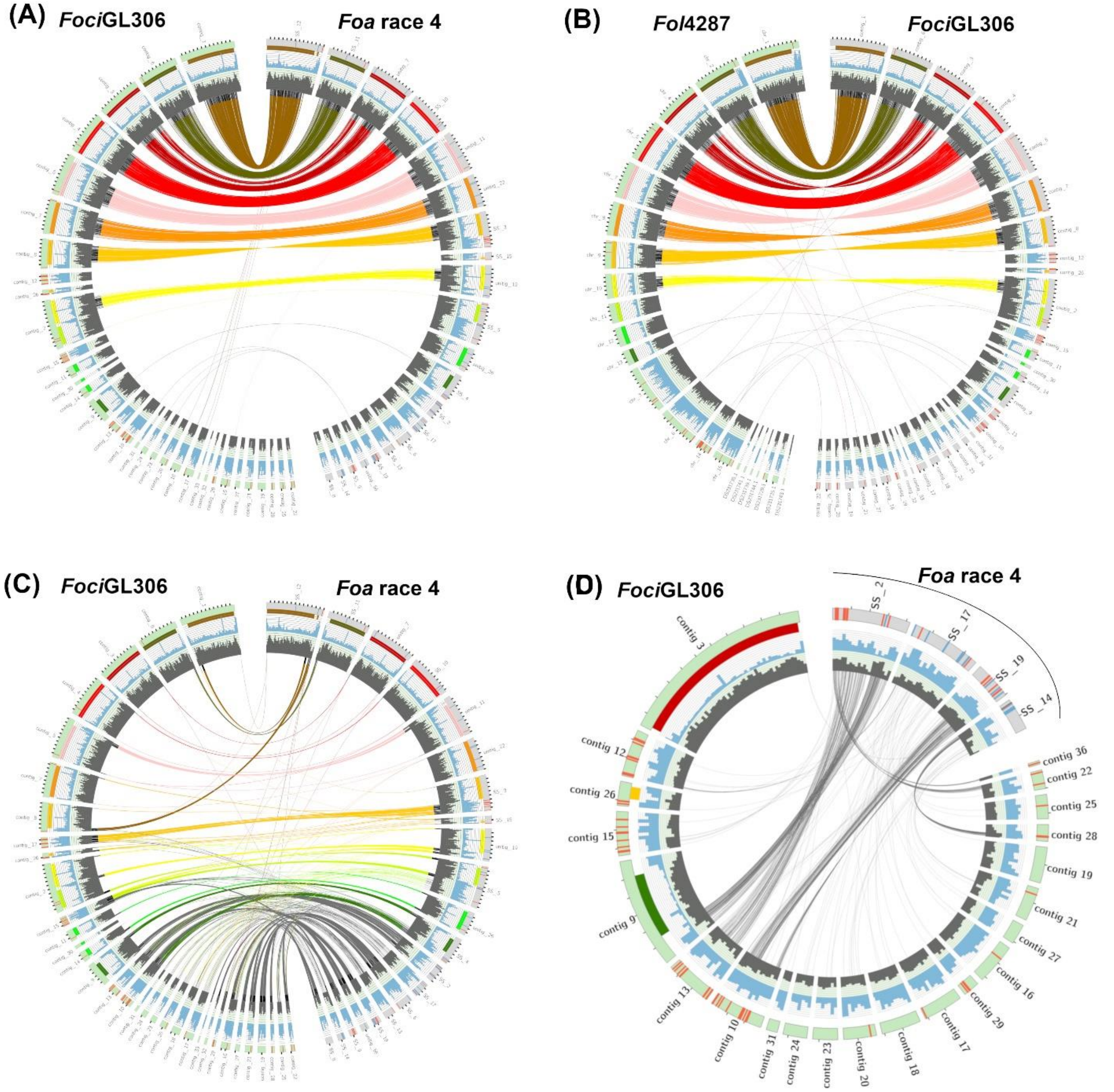
Reference strain	Target Strain	Homologous gene models in the accessory genome, % of the total in the reference genome[b]	No. homologous genes in the accessory genomes[b]	No. syntenic genes in the accessory genome of the target strain[c]	Syntenic genes in the common accessory genome, %
Foa race 4	*Foa* race 3	64	3949	3546	90
Foa race 4	*Foci*3-2	50	3011	2523	84
Foa race 4	*Foci*Gl306	46	2854	2342	82
Foa race 4	*Foa* race 2	15	943	390	41
Foa race 4	*Fol*4287[d]	14	853	302	35
*Foci*GL306	*Foci*3-2	75	4317	4079	94
*Foci*GL306	*Fol*4287	15	853	274	32

[a] The accessory genomes include all gene models that are not in the *F. oxysporum* core genome (Additional file 4) and are on contigs larger than 150 kbp.

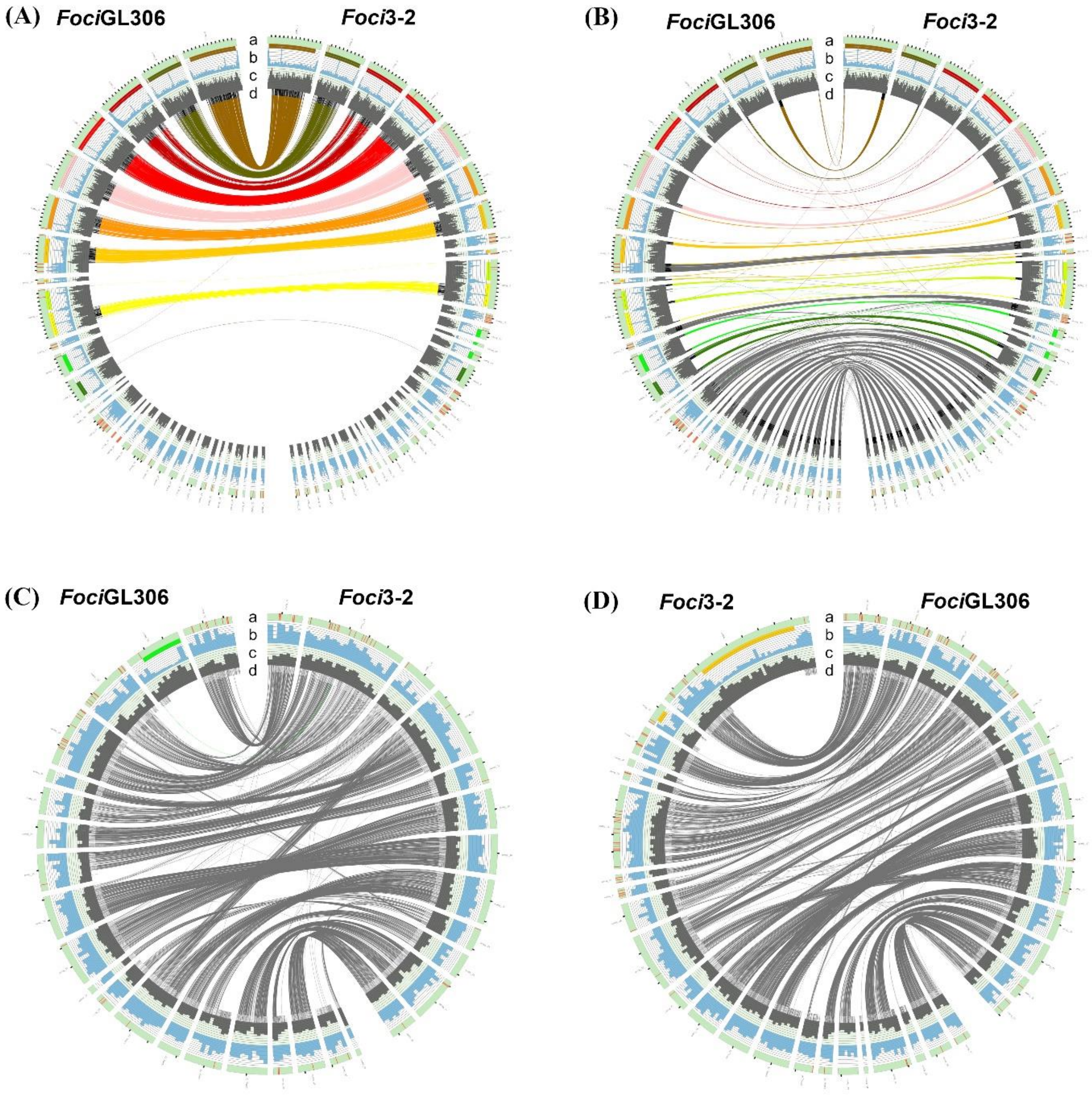
[b] Homologous pairs of gene models have $\geq$ 80% identity over $\geq$ 80% of the predicted nucleotide sequence. When a single gene model could have multiple partners, only the "reciprocal best BLAST" (RBBH) is selected. The lines in the centers of Fig. 4, and Additional files 12 and 13B-D connect the homologous pairs.

[c] After the genes in each reference contig were sorted by locus, a gene in the target strain of a homologous pair was considered syntenic if belonged to an ascending or a decending run of at least three target genes within a single target contig.

[d] *F. oxysporum* f. sp. *lycopersici* 4287 reference (Genbank GCA_000149955.2 ASM14995v2).



Additional file 12. Synteny between *Foci*GL306 and *Foa* race 4 in the conserved and accessory genomes. A, C, and D) *Foa* race 4 contigs are on the right and *F. oxysporum* f. sp. *coriandrii Foci*GL306 contigs are on the left. B) *Foci*GL306 contigs are on the right and contigs of the *Fol*4287 reference are on the left. A, B) “reciprocal best BLAST hits” (RBBH) of full-length, single copy BUSCO Sordariomycete genes. C) RBBH of genes in the non-core/accessory regions of the *F. oxysporum* genome, and D) Best BLAST hits (BBH) of genes in the four accessory contigs of *Foa* race 4 that have the most up-expressed genes *in planta* compared to *in vitro*. Within ring a, red lines indicate miniature impala inverted-repeat transposable elements (mimps). In ring b, the solid colors within the upper portion of ring b denote a region with homology to one of the *Fol* core chromosomes. Blue shows the density of repetitive elements with a full scale of 120 per 100 kb increment. In ring c, dark grey shows the density of gene models with a full scale of 50 per 100 kb increment. In ring d, the grey lines show genes that have a BBH with $\geq$ 80% identity over $\geq$ 80% of the predicted nucleotide sequence. In the center, lines connect the BBH; genes connected by black lines are in accessory contigs and genes connected with other colors denote the particular core chromosome. Genes that have a grey line in ring d but no connecting line have a BBH in a contig that is not shown in that figure. The plots indicate that the synteny of *Foci*GL306 to both *Foa* race 4 and *Fol*4287 are similar to those observed with *Foci*3-2.



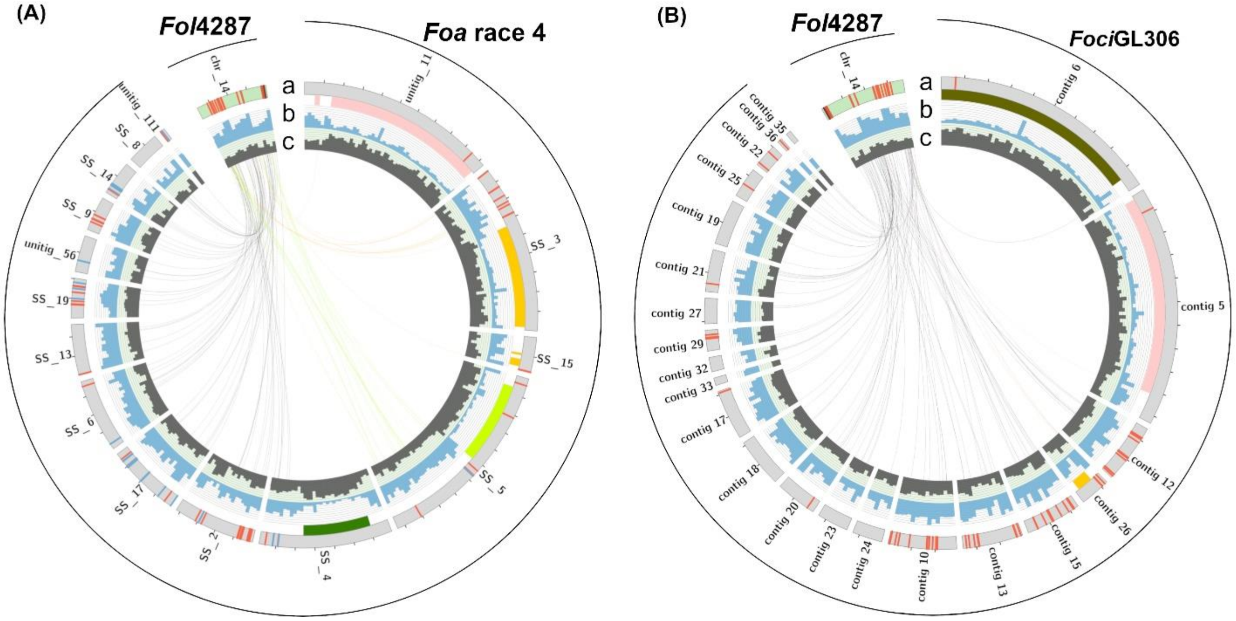
Additional file 13. Synteny between the two *Foci* strains in the conserved and accessory genomes. Circos plot comparisons of homologs of A-C) *F. oxysporum* f. sp. *coriandrii* (*Foci*3-2) on the right side and, on the left side to *Foci*GL306. A-B) Contigs less than 150 kb are not shown. A*)* 3,650 and 3,645 single copy, full-length, single-copy BUSCO Sordariomycete genes in *Foci*3-2 and *Foci*GL306, respectively, B) "Reciprocal best BLAST hits" (RBBH) with ≥ 80% identity over ≥ 80% of the nucleotide sequence in non-core regions of the *F. oxysporum* genome. C-D) Contigs less than 100k bp are not shown. C) RBBH of genes in the 12 accessory contigs of *Foci*3-2. D) RBBH of genes in the 14 accessory contigs of *Foci*GL306 are shown on the right with *Foc*3-2 on the left. Within ring a, red lines indicate miniature impala transposable elements (mimps). In ring b, the solid colors within the upper portion of ring b denote a region with homology to one of the *Fol* core chromosomes. Blue shows the density of repetitive elements with a full scale of 120 per 100 kb increment. In ring c, dark grey shows the density of gene models with a full scale of 50 per 100 kb increment. In ring d, the grey lines indicate genes that have a RBBH. In the center, lines connect the RBBH; black lines connect genes in accessory contigs and lines in other colors denote the particular core chromosome. Genes that have a grey line in ring d but no connecting line have a RBBH in a contig that is not shown in that figure. The plots show that *Foci*3-2 and *Foci*GL306 are highly syntenic in both the conserved and accessory contigs. Nevertheless, there are some rearrangements between the genomes, most notably in the accessory contigs, as shown in C and D.

Additional file 14. *Foa* race 4 putative accessory chromosomes: percentage of genes that have homologs in other strains

	Selected *Foa* race 4 accessory superscaffolds (SS)[a]			
	SS2	SS17	SS19	SS14
Strain	Percent of predicted genes with a reciprocal Best Blast Hit[b]			
Foa race 3	63	59	73	61
*Foci*3-2	70	8	58	25
*Foci*GL306	56	9	41	25
Foa race2	20	7	6	12
*Fol*4287 reference	17	7	5	11

[a] The four superscaffolds that were selected for the Circos plots in Fig. 5 are part of the accessory genome and have a minimum length of 800 kbp. SS2 (2.1 Mbp) and SS19 (1.0 Mbp) are lineage-specific contigs (see Additional File 8). SS17 (1.9 Mbp) and SS14 (0.9 Mbp) are host-specific contigs. Of the 23 highly-expressed putative effectors in Table 4, SS17 has eight, SS14 has five and SS19 has two.

[b] To be considered a reciprocal Best Blast Hit, gene X must have a BLAST hit with gene Y that has the lowest E-value and $\geq$ 80% identity over $\geq$ 80% of the predicted nucleotide sequence, and gene Y must also have a BLAST hit with gene X that has the lowest E-value and >80% identity over 80% of the sequence.



Additional file 15. Homologs of gene models from *Fol*4287 chromosome 14 in *Foa* race 4 and *Foci*GL306. A Circos plot of homologs of genes in the pathogenicity chromosome 14, which is in the accessory genome of *F. oxysporum* f. sp. *lycopersici* (*Fol*) 4287, in contigs > 150 kbp of A) *Fusarium oxysporum* f. sp. *apii* (*Foa*) race 4 and B) *Foci*GL306. Tic marks on ring a are 500 kb. Within ring a, red lines indicate miniature impala transposable elements (mimps), and blue lines indicate all genes with significantly ($P<0.05$) increased expression *in planta* in celery crowns that are infected with *Foa* race 4 than in *Foa* race 4 grown *in vitro*. Within ring b, the solid colors on the upper portion denote a region with homology to one of the *Fol* core chromosomes (shown in Additional files 10D and 12B); the blue represents the density of repetitive elements with a full scale of 120 per 100 kb increment. In ring c, dark grey shows the density of gene models with a full scale of 50 per 100 kb increment. In ring d, the grey lines show genes that have a "best BLAST hit" (BBH) with a $\geq$ 80% identity over $\geq$ 80% of the predicted nucleotide sequence. In the center, lines connect the BBHs. Black lines connect BBH genes in both accessory genomes; colored lines denote a color-coded core chromosome. *Fol*4287 chromosome 14 has 414 genes; based on the BBH criterion, *Foa* race 4 and *Foci*GL306 have homologs of 28 and 23% of these genes, respectively.

Additional file 16. Up-expressed *in planta* RNA TagSeq-predicted effectors in *Foa* race 4: sequences, distribution, and mimp associations[a]

Gene	Predicted amino acid sequence	DNA identity in *Foa &Foci* strains[b]	Distance of mimp(s) from ORF start, bp[c]
NS.09678	MVKHIQLPGLSLAATAMLAARGADSKVVCVNPNKEVVADTKCENVKAPGNFYMVRSMSDSLAPGSLVSADADMNDAFYPIDRANALFPPDMTSGGFGKRDCGGSGANGGNGSGGRGGTVIVGGGYHGG	100% in all FOSC Clade 2; 95% identity in *Foa* race 2; 2nd copy in *Foa* races 3 & 4	480
NS.05815	MAPYSMVLLGTLSILGFSAYAQEAAVPEPQVFFNLTYAEHLEKVAASSGSVPDNSDLPWEDTIPWNGTDDGVQTETGSSLSRRGRIFNLGKREPVGGETRNDAVTNDMLQALHEMCVERFGTGHRATNGRCRGRHKQVECGHPDVAGRVGQVGKSCAEGQECTTFQAVNFRNRRATFPVCGPRIEVKERHDIGRHTEWEGTWYPESPKSPGTYDSFAQMAGSLNGYFDFNGVYSSGEGMSSRGSGHSWSCIACPGGKLTITSTLRATWAIGYTSP	100% in *Foa* races 3 and 4; 100% within the *Foci;* two copies (one is NS.05829) in all *Foa*	NA[d]
PGN.06282	MHVKNAIVLLFAASAISMPLESVHNSGHGAIGLERRDISHSETTEEKRELIG	Assembly indicates that this sequence is only present as two copies in *Foa* race 4, but PCR and	979[e]

		raw reads indicate that there it is present in *Foa* race 3; absent in *Foa* race 2 and *Foci*	
NS.06742	MIARTSTVLSLALTALSLGAYAAPGPAPNNDVSQALRSPLEARASLCCAVATNNRYIQTVCQYMYESCRGWNKCLKGLPNDSDWCHYCVVVHPEDKACLTKTWPPVGHAPISKRGIDDATILPPEDSAKDNAETAAPVSRRSLDMAPGSDDSSNAAPDLEDFRDTTSKHLDKRAWSDQNIHTRNLHNEAQSYRRAIGLVTIRIIISASNVMTWSVQNSGATDVAFHVIDRVSGWKVERTIHAGQTDGGAPGSQVLAQGGDTFTVGIQR	100% in all FOSC Clade 2; three copies in *Foa* race 2	NA
NS.06525	MVKHIQLPGLSLAATAILAARGADSKVVCVNPNKEVVADTKCEDVKAPGNFYMVRSMSDNLALGSLVSADAEMNDAFYPIDRANALFPPDMTSGGFGKRDCGGSGGNGGNGSGGRGGTVVIVGGGYGG	100% in *Foa* races 3 and 4; 100% within the *Foci;* two copies in *Foa* races 3 and 4; one copy in *Foci* and *Foa* race 2	764 and 1100
PGN.05952	MLLNTIWKVVAFSPAAFAAIRARESHGWCFCARKGIEGNDGLDWGLTSVVCGDFPVSVSFDQKDHKCYTTSGESRIDGDTWEAHCKSYASDGYEFEGVKYKWNARDIKGKCS	100% in *Foa* races 3 and 4; one copy in *Foa* race 2; absent in *Foci*	NA
PGN.20363	MRAYVSLTVFSLFLRVSAWNKCYCTGSDQAVADTTANTCCTDGDGVSFPHTKGDVKGRWDSSNKICVFSGQVLSQNSENDATAAFAACCRPTGGSTIWGGACS	100% in all FOSC Clade 2; absent in *Foa* race 2	NA

PGN.05922	MRFATFGLLVVLPTFSLAKDCGIFYDWSGTSHLDVWRDLKAVSMCSDIGGDIPNDELALKNGNGVHRCAVCRNARGGTKDYTRTITQQNDKIIYSVRCGWFGKGKCSA	100% in all FOSC Clade 2 with a 2nd copy in *Foa* race 3; absent in *Foa* race 2	NA
PGN.15680	MHPFTALSATFVAIMSPALINAQSAVSTAVAPAPTGMGCICMAPTSSGKDEAMYDRTWRCCRQEQGHMRSTNDFWGRGSFYCNFEKGINPAEWDGNCCRRVFGDGTYGFCNKAV	100% in each of 3 copies of *Foa* races 3 and 4; one copy in *Foa* race 2; absent in *Foci*	NA
PGN.06635	MSASMRISTFGIFAVLPILGLAKDCAVYYDYVGDVVKVGSSMGFAETDPDLNEKRRATASKICTHDIGGHINSPGGWAPEAGITNGHNPVNRCTICRGARGGTRDYDKAADGITYSIRCGYFGPYLCSAK	100% in *Foa* races 3 and 4; 100% in the *Foci* and a 2nd copy in *Foa* races 3 and 4. Absent in *Foa* race 2.	383
NS.06362	MKFITLTLLFGTGILGVKGDWDLYRDVQCNYKKSSVPLWHNCFVNGKEPYTDNDCGLACARAGMNEGNKFVHGSNYNGGQSCGLICYFK	100% in *Foa* races 3 and 4; one copy in *Foci*;. two copies with 79.5 and 79.9% identity over 99% in Foa race 2	183
PGN.09917	MKFSSLLLGVPFLVRIHAAECPRASVSGNAITGFRYFNDCTTWTWRSRDKGTTVTLSPDCILRQAWPNPQNVWAVCIRLEGGEYQCFQTGANGAECSVPSPWCSTTAKIANMWGW	100% in *Foa* races 3 and 4; 100% in the *Foci*; *Foa* races 3 and 4 have an identical 2nd copy, and *Foa* race 3 has a 3rd copy. Foa race 2 has one copy	NA
NS.05829	MAPYSMVLLGALSILGSAAYAQEAAVQEPQIFFNLTYTEYLDKVAAASGRSPPENSDLPWDDTMSSLPLNETDDDVQPEIASSLSRRGRIFNLGKREPVGGETRNDAVTNDMLQALH	100% in *Foa* races 3 and 4; these strains have an identical 2nd copy;	NA

	DLCVERHGTGWRATGGRCDGRTRRINCGNPGIGQSIRRVSSACPQNQECTTFEAINFRRSRTNFPVCGPRIEVAEKHDIGSHTEWEGTWYPESPKSPGTYDSFAQMAGSLNGYFDFNGVYSNGNGMSSRGSGHSWSCIACPGGKLTITSTYRSTWAVGYTSPH	*Foa* race 2 has two copies. *Foci* have one copy with 79.5% identity.	
PGN.07042	MSASMRISTFGIFAVLPILGLAKDCAVYYDFVGDVVKVGSSMGFAETDPGLNEKRRATASKICTHDIGGHVNSPGGWAPEAGITNGNNPVNRCTICRGARGGTRDYDKAADGITYSIRCGYFGPYLCSAK	100% in all FOSC Clade 2; *Foa* races 3 and 4 have an identical 2nd copy; absent in *Foa* race 2	NA
PGN.06691	MKFSSLLLGAPFLVRIHAAECPRASVSGNAITGFKYFNYCTTWTWRSRDKGTTVTLSPDCILRQAWPNPQNVGAVCVRLEGGGDQCFQTGANGAECSVPSPWCSTTAKIANMWGW	100% in *Foa* races 3 and 4; All FOSC Clade 2 have a 2nd, identical copy; *Foa* race 3 has a 3rd copy; *Foa* race 2 has one copy	270 and 605
NS.01422	MFGSISTYFVTLLAAASTVANAAATSKNPVYTGLGTRYGDSDGCTEEDCWQKGACSFVDYKLPAGIDGTTCVSEDIWKDGANCGGCIQVSYKGKSLKIMVTNKTGGDKNHLDMTPATWSKLTSGMTGGGVDGIKWKWIACPLKSPLQVHMHGGASKYWFAATIENITHRVKAVEVSSDSGKTWKATTLKDPNMWILKGTLPNDTAWVRVTSVNNKKVIVKNVALKSGVVTKGTSNF	100% in all FOSC Clade 2; Foa race 2 has one copy	NA
NS.09643	MLYPRFQSATVAVIAAVLTPLVLGAATPTPQPSIQWETTTKDILLSEIGPFDLESQLTSSGSTGTSSTMNKRSSYSAGVCFA	100% in all FOSC Clade 2; Foa races 3 and 4 have an identical 2nd	NA

	IPFKPQTGGAWGFKQAWCDRTGTDVNTFRVDCFGGRNYIETLPNRKGACGKGQWCVDYHGRNSKGDAADDVLCVNRKDIHTWVANTQTRPVEDKVTCSSGWRNDYKQSAKATFEVDVMDSAGINRIAPENVYYILNQKRIGVSRSNDAEVGSGYITIPPGGAIQACVTAKVAQNQILNMLGAITSFKLL	copy; the *Foci* have an identical 2nd & 3rd copy; *Foa* race 2 has 17 copies	
NS.16793	MKLLTLISAFATATLVSADQRAQLSAPDGSVHHLSARDGTCPRPMCKTPASQGPNDPPACGDSYAACKFDQFPCDEHFSPKVTDTHHCYCILANKKAMDAYCQERGFKSGTNPWKYYYAVECHGAVSNQVCNKDCHDQGRGNGRIDKAHPNGACACDKPNPPYDTCKA	100% in all FOSC Clade 2; *Foa* race 2 has two copies	NA
NS.06528	MEHLGIATNSSTPNSLYGQQILRFRCDTRQHRLLYKMHITKFVVAVALPLLAAANEHVGCKCNTGDATCLEVACNSYSAAGVFFNKPKGHENSVFSQTQDGKCYAVYNNGQEYLTFKGLGGKEWLQQCEAHCGGGSTC	100% in *Foa* races 3 and 4; all FOSC Clade 2 have three other copies except *Foci*GL306, which has four; *Foa* race 2 has two copies	NA
PGN.06376	MHPFTALSATFVAIMSPALINAQSAVSTAVAPAPTGMGCICMAPTSSGKDEAMYDRTSRCCRQEQGHMRSTNDFWGRGSFYCNFEKGINPAEWDGNCCRRVFGDGTYGFCNKAV	100% in *Foa* races 3 and 4; 100% in two other copies in *Foa* races 3 and 4; *Foa* race 2 has one copy; absent in *Foci*	215
NS.15045	MKLSAVTLLTLATGILAAPVAEANYDVSYSSYEAPKAPKPHYEKPKPKPHHEKPKHEYPAPHHEKPKPKPHPKPHYEKPKKPEYQAPKPHYEKPKPKPHPKPAYEAPKPAPKPHKPEYTKPKAPKPHKPEYTAPKPVKPKYTKPEAPKPHKPEYTKP	100% in all FOSC Clade 2; one copy in *Foa* race 2	NA

	KAPKPHPKPAYEAPKPAPKPHKPEYTKPKAPKPHKPEYT APKPHHEKPKPHPKPTYQAPKPAPKPHKPEYTKPKTEKP KPAPKPEYKAPTYQAPHY		
PGN.05959	MKITSIAILAFLSATATAQTGSKYLSYCKGTSQDLGQSLCK KKGGTWGPRTDAPAEYRSRSGYYCLGAGWWGTDPCPA EYGKGFQVVNFNT	100% in *Foa* races 3 and 4; absent in *Foa* race 2 and *Foci*	NA
PGN.06650	MHPFTALSATFVAIMSPALINAQSAVSTAVPPAPTGMGCIC MAPTSSGKDEAMYDRTSRCCRQEQGHMRSTNDFWGRG GFYCNFEKGINPAEWDGNCCRRVFGDGTYGFCNKAV	100% in *Foa* races 3 and 4; 100% in two other copies in *Foa* races 3 and 4; one copy in *Foa* race 2; absent in *Foci*	NA

[a] Based on 3’RNA QuantSeq read mapping, all genes 1) had significantly (adjusted $P<0.05$) higher expression *in planta* in celery crowns than *in vitro* and 2) accounted for more than 0.1% of the total fungal reads *in planta*, i.e., were relatively highly expressed *in planta*. Based on DNA sequence analysis, all predicted proteins were 1) secreted into the plant, 2) had a predicted mol wt of ≤ 35 kDa, and 3) were neither “house-keeping” nor nutrition-associated genes.

[b] The DNA sequence of predicted effector genes of *Foa* race 4 were used as a reference for the other strains: *Foa* races 2 and 3, *Foci*3-2, and *Foci*GL306. Identical sequences are indicated as 100%. Sequences with DNA identities ≥80<100% over the full length are called copies, unless specifically identified as ≥ 70% identity. Absence is defined as an e>0.1. *Foa* races 3 and 4 and the two *Foci* are in FOSC Clade 2.

[c] Miniature impala (*mimp*) transposable elements were identified with TIRmite (version 1.1.3). Using the sequence "..CAGTGGG..GCAA[TA]AA," hidden Markov models were used to identify terminal inverted repeats using a four-time reiterative process (https://github.com/SamuelBrinker/Repertoire_v6). *Foa* race 4 has 117 *mimps*.

[d] NA, no mimps are within 2.5 kb upstream of the start of the predicted ORF.

Additional file 17. The percentage identity of the *Secreted In Xylem 1* (*SIX1*) orthologs in the *Foa*, *Foci*, and reference strain[a].

	SIX1 ortholog by strain_location for those with two orthologs							
	melonis[c]	*Foa*R2_ C9	*Foa*R3_ C35+	*Foa*R4_ SS14+	*Foa*R3_ C35-	*Foa*R4_ SS14-	*Foa*R2_ C26	*Foci*
Strain_Location[b]	Identity, %							
*Foa*R2_C9	82							
*Foa*R3_C35:182653+	84	87						
*Foa*R4_SS14:278932+[d]	84	87	100					
*Foa*R3_C35:135680-	82	85	86	86				
*Foa*R4_SS14:228927-[d]	82	85	86	86	100			
*Foa*R2_C26	82	86	85	85	85	85		
*Foci*3-2_C15	79	80	82	82	79	79	79	
*Foci*GL306_C17	79	80	82	82	79	79	79	100

[a] *Foa* race 2 (*Foa*R2), *Foa* race 3 (*Foa*R3), and *Foa* race 4 (*Foa*R4) have a *SIX1* in two locations. There are two *Foci* strains (*Foci*3-2 and *Foci*GL306), each with an identical, single ortholog.

[b] Locations of the contig (C) or superscaffold (SS) are shown. Both *Foa* race 3 and 4 orthologs are on the same contig but are on different strands ~500 kbp apart. This is noted with a "+" and "-" for positive and negative strands respectively.

[c] Ref, Reference *F. oxysporum* f. sp. *melonis SIX1* (GenBank KR811364.1)

[d] Based on RNA TagSeq, both of the *Foa* race 4 *SIX1* orthologs were highly expressed *in planta*, but not *in vitro*. The two *Foa* race 4 copies are on a single host-specific accessory contig. The *Foci*3-2 *SIX1* ortholog is also on a host-specific accessory contig.

Additional file 18 Test of PCR primers for *Foa* races 2 and 4 and *Foci* on a diversity of *Fusarium* spp.[a]

			Previously published primers [Epstein et al. 2017]		New primers			
			N4851 for *Foa* race 2	N3875 for *Foa* race 4	FOA R2-76k for *Foa* race 2	FOA R4-447 for *Foa* race 4	FOCI 2-21 for *Foci*	FOCI-g_c31 for *Foci*
Fusarium taxon[b]	Isolate ID(s)[c]	Host [d]	Amplicon produced?[e]					
F. commune, non-pathogenic on celery (two isolates)[f]	250-10A, 250-12A	Celery	**yes** (faint)	no	no	no	no	no
F. commune, non-pathogenic on celery (two isolates) [f]	252, 271-4	Celery	no	no	no	no	no	no
F. commune, non-pathogenic on celery	270-C	Celery	no	no	no	no	no	no
F. commune, non-pathogenic on celery	271-5	Celery	**yes**	no	no	no	no	no
F. foetens	NRRL 31852 (=CBS 110286)	Begonia	no	no	no	no	no	NT

F. foetens	NRRL 38302	Pine seedling	no	no	no	no	no	NT
F. oxysporum[j]	NRRL 54002, (=Fo47)	Soil (Biocontrol strain)	no	no	no	no	no	NT[i]
F. oxysporum[j]	NRRL 32931	Human	no	no	no	no	no	NT[i]
F. oxysporum, non-pathogenic on celery	295	Celery	no	no	no	no	no	no
F. oxysporum, non-pathogenic on celery	274-3A	Celery	no	no	no	no	no	no
F. oxysporum, non-pathogenic on celery	273-2B	Celery	no	**yes**	no	no	no	no
F. oxysporum, non-pathogenic on celery	273-1B	Celery	no	**yes**	no	no	no	no
F. oxysporum, non-pathogenic on celery	270-B	Celery	no	no	no	no	no	no
F. oxysporum, non-pathogenic on celery	258-1A	Celery	no	no	no	no	no	no
F. oxysporum, non-pathogenic on celery	251-2	Celery	no	no	no	no	no	no
F. oxysporum, non-pathogenic on celery	249-1A	Celery	yes	no	no	no	no	no

F. oxysporum, non-pathogenic on celery	223-3B	Celery	no	no	no	no	no	no
F. oxysporum, non-pathogenic on celery	222-1B	Celery	no	no	no	no	no	no
F. oxysporum, non-pathogenic on celery	220-C	Celery	no	no	no	no	no	no
F. oxysporum, non-pathogenic on celery	210-A	Celery	no	no	no	no	no	no
F. oxysporum, non-pathogenic on celery	017	Celery	yes	no	no	no	no	no
F. oxysporum, non-pathogenic on celery	221-B	Celery	no	no	no	no	no	no
F. oxysporum, non-pathogenic on celery	261-1A	Celery	no	no	no	no	no	no
F. oxysporum, non-pathogenic on celery	223-1A	Celery	no	no	no	no	no	no
F. oxysporum, non-pathogenic on celery	226-1A	Celery	no	no	no	no	no	no
F. oxysporum, non-pathogenic on celery	226-1B	Celery	no	no	no	no	no	no

F. oxysporum, non-pathogenic on celery	241-1A	Celery	no	no	no	no	no	no
F. oxysporum f. sp. *apii* (race 1 presumed)	NRRL 22534 (=CBS 175.35)	Celery	no	no	no	no	no	NT
F. oxysporum f. sp. *apii* (race 1 presumed) (2 isolates)[f]	NRRL 36287 (=CBS 176.35), NRRL 36316 (=CBS 184.38)	Celery	no	no	no	no	no	NT
F. oxysporum f. sp. *apii* (race 1 presumed)	NRRL 36312 (=CBS 183.38)	Celery	no	no	no	no	no	NT
F. oxysporum f. sp. *apii* race 1	268-2	Celery	no	no	no	no	no	no
F. oxysporum f. sp. *apii* race 1	250-7	Celery	no	no	no	no	no	no
F. oxysporum f. sp. *apii* race 1-like haplotype (same as isolate 250-7), but non-pathogenic on celery	270-A	Celery	no	no	no	no	no	no
F. oxysporum f. sp. *apii* race 2 (22 isolates)[f]	003, 004, 013, 018, 032, 051, 062, 067, 073, 202, 207-A, 225-2A, 226-2A, 240-B, 243-1A,	Celery	yes	no	yes	no	no	no

	247-1A, 249-2A, 250-9, 251-1, 258-1B, 269, 272-5A							
F. oxysporum f. sp. apii race 2-like haplotype, but non-pathogenic on celery (18 isolates)[f]	005, 071, 074, 205-C, 222-2A, 232, 239-B, 235-A, 241-2C, 244-1A, 244-2B, 246-C, 251-4, 256-1, 262-1, 265-1A, 260-1, 272-2B	Celery	yes	no	yes	no	no	no
F. oxysporum f. sp. *apii* race 3	NRRL 38295	Celery	no	no	no	no	no	no
F. oxysporum f. sp. *apii* race 4 (11 isolates)[f]	274.AC, 273-1A, 273-1C, 283-1.2, 283-4.1, 284-1, 284-5.1, 291, 292-B, 294-B, 296	Celery	no	yes	no	yes	no	no
F. oxysporum f. sp. *apii* race 4, DNA variant[g]	FoaR4V-313-2.2	Celery	no	yes	no	yes	no	no
F. oxysporum f. sp. *apii* race 4, DNA variant[g]	FoaR4V-7.5B	Coriander	no	yes	no	yes	no	no
F. oxysporum f. sp. *coriandrii* (six isolates)[f]	*Foci*3-2, *Foci*GL306, *Foci*8.1a, *Foci*10E, *Foci*11, *Foci*12A	Coriander	no	**yes**	no	no	yes	yes
F. oxysporum f. sp. *coriandrii* (one isolate)	*Foci*10T	Coriander	no	**yes**	no	**yes**[h]	**no**[h]	**no**[h]

F. oxysporum f. sp. *canariensis*	NRRL 26035	Date palm	no	no	no	no	no	NT
F. oxysporum f. sp. *conglutinans* race 2[j]	NRRL 54008 (=PHW808)	Cabbage	no	no	no	no	no	NT[i]
F. oxysporum f. sp. *cubense*	NRRL 36114 (=CBS 102025)	Banana	no	no	no	no	no	NT
F. oxysporum f. sp. *cubense* tropical race 4[j]	NRRL 54006 (=IL5)	Banana	no	no	no	no	no	NT[i]
F. oxysporum f. sp. *fragariae*[j]	GL-1080	Strawberry	no	no	no	no	no	NT[i]
F. oxysporum f. sp. *lycopersici* race 2[j]	NRRL 34936 (=4287)	Tomato	no	no	no	no	no	NT[i]
F. oxysporum f. sp. *lycopersici* race 3[j]	NRRL 54003 (=MN25)	Tomato	no	no	no	no	no	NT[i]
F. oxysporum f. sp. *lycopersici*	NRRL 26380	Tomato	no	no	no	no	no	NT
F. oxysporum f. sp. *lycopersici*	NRRL 36379 (=CBS 249.52, =ETH 5414)	Tomato	no	no	no	no	no	NT
F. oxysporum f. sp. *lycopersici*	NRRL 36423 (= CBS 305.91)	Tomato	no	no	no	no	no	NT
F. oxysporum f. sp. *lycopersici*	NRRL 36425 (= CBS 307.91)	Tomato	no	no	no	no	no	NT

F. oxysporum f. sp. *melonis*[j]	NRRL 26406	Melon	no	no	no	no	no	NT[i]
F. oxysporum f. sp. *pisi*[j]	NRRL 54007 (=HDV247)	Pea	no	no	no	no	no	NT[i]
F. oxysporum f. sp. *radicis-lycopersici*[j]	NRRL 26381, (=CL57)	Tomato	no	no	no	no	no	NT[i]
F. oxysporum f. sp. *radicis-lycopersici*[j]	NRRL 26379	Tomato	no	no	no	no	no	NT
F. oxysporum f. sp. *raphani*[j]	NRRL 54005 (=PHW815)	Radish	no	no	no	**yes**[h]	no	NT[i]
F. oxysporum f. sp. *vasinfectum*[j]	NRRL 25433	Cotton	no	no	no	**yes**[h]	no	NT[i]

[a] *Foa*, *F. oxysporum* f. sp. *apii*; *Foci, F. oxysporum* f. sp. *coriandrii*. Primers are described in Table 5. *Foa* are defined as as pathogenic on celery and, to a lesser extent, on coriander. *Foci* are defined as pathogenic on coriander and not on celery.

[b] Except for the five isolates from celery that were in the NRRL collection (which were all collected before 1981), all isolates from celery were from plants that had symptoms of Fusarium yellows. From each symptomatic plant, we typically isolated one isolate that was pathogenic, i.e., that could be classified as a *Foa* race and one from a diversity of *Fusarium oxysporum* species complex Clades 3 and 2 that were non-pathogenic on the celery cultivars that were used for race testing [3].

[c] Isolates with a NRRL number were from the USDA ARS collection. GL-1080 and FociGL306 were obtained from T. Gordon, UC Davis. All other isolates were collected by the authors. Details about the isolates in the authors' collection from celery are in Epstein et al. [3].

[d] Except for the five isolates from celery that were in the NRRL collection, all isolates from celery were ef1- and igs-sequenced and bioassayed for *Foa* race. All isolates from coriander were ef1- and igs-sequenced and bioassayed for pathogenicity on coriander and celery.

[e] Tests for all isolates included a positive control with either ITS1F-ITS4 or EF1-EF2 and a no-template negative control.

[f] Rows that have multiple isolates in the multiple isolate column had an identical ef1 and igs haplotype, and were tested by PCR individually. The ef1 and igs GenBank accession numbers of all isolates are either in O'Donnell et al. [2], Epstein et al. [3], or in this manuscript.

[g] The "*F. oxysporum* f. sp. *apii* race 4, DNA variant" was isolated from one symptomatic celery and one symptomatic coriander. These isolates are pathogenic on celery cv. Challenger and on coriander cv. Longstanding, and have an indentical ef1 and igs haplotype. That haplotype has one SNP in the ef1; all the other *Foa* races 3 and 4, and six of the seven *Foci* have an identical ef1-igs haplotype without the SNP.

[h] Undesired positives are indicated in bold. However, an isolate from symptomatic celery can be identified as a true positive for *Foa* race 4 based on a positive result with both the FOA R4-447 and the N3875 primers. Identification of the *Foci* from symptomatic coriander is more complex; the majority of isolates from symptomatic coriander were positive with both the *Foci* primers. Amongst the *Foci*, which are defined as pathogenic on coriander and not on celery, isolate 10T was negative for both *Foci* primers and positive for both *Foa* race 4 primers. One isolate from coriander, was a *bona fide Foa* race 4, i.e., was pathogenic on celery and on coriander. Differentiation of a *Foci*10T-type from a *Foa* race 4 isolate requires a pathogenicity test.

[i] NT, not tested empirically. For those indicated as NT[i], there are whole-genome sequences at NCBI; an *in silico* analysis indicated that none would produce this amplicon.

[j] *F. oxysporum* strains that were tested empirically with DNA for the indicated primers and *in silico* from whole genome sequences included the following (GenBank Assemblies in Bold): Fo47, NRRL 54002, GCA_000260175.2; NRRL 32931, GCA_000271745.2; f. sp. *conglutinans* race 2, NRRL 54008 (=PHW808), GCA_000260215.2; f. sp. *cubense* tropical race 4, NRRL 54006 (=IL5), GCA_000260195.2; f. sp. *fragariae* GL-1080, WIMO00000000 version 2; *f. sp. lycopersici* race 2, NRRL 34936 (=4287), GCA_003315725.1; *f. sp. lycopersici* race 3, NRRL 54003 (=MN25), GCA_000259975.2; f. sp. *melonis*, NRRL 26406, GCA_002318975.1; f. sp. *pisi*, NRRL 54007 (=HDV247), GCA_000260075.2; f. sp. *radicis-lycopersici*, NRRL 26381, (=CL57), GCA_000260155.3; f. sp. *raphani*, NRRL 54005 (=PHW815), GCA_000260235.2; and f. sp. *vasinfectum*, NRRL 25433, GCA_000260175.2

Additional file 19: Whole genome-sequenced *Fusarium* spp. included in analyses in GenBank wgs

Fusarium species	Strain	Assembly ID	No. contigs	Total length, Mbp
F. acuminatum	F829	JABEEU01	4438	46.9
F. acuminatum CS5907	CS5907	CBMG01	3907	44.0
F. acutatum	NRRL 13308	JAADJF01	982	43.3
F. agapanthi	NRRL 54464	LTDI01	1842	42.0
F. agapanthi	NRRL 31653	LUFC02	2350	41.3
F. albidum	NRRL_22152	JABFEP01	5413	36.9
F. albosuccineum	NRRL 20459	JAADYS01	4197	50.9
F. algeriense	NRRL 66648	PVPY01	3323	50.0
F. algeriense	NRRL 66647	PVPZ01	3535	48.9
F. ambrosium	NRRL 20438	NIZV01	1366	49.0
F. anguioides	NRRL 25385	JAALXK01	743	38.9
F. anthophilum	NRRL 25214	JABEVY01	1118	45.8
F. armeniacum	NRRL 25141	JABFER01	429	37.1
F. asiaticum	NRRL6101	LHTY01	265	36.5
F. asiaticum	NRRL28720	LHTZ01	353	36.4
F. asiaticum	NRRL 26156	JABFEQ01	490	36.5
F. austroafricanum	NRRL 53441	JAADJG01	1963	45.7
F. austroamericanum	28FRS	VSSU01	534	37.5
F. austroamericanum	3FSP	VSSV01	619	37.3
F. austroamericanum	NRRL 2903	JAAMOD01	899	36.9
F. avenaceum	Fa05001	JPYM01	83	41.6
F. avenaceum	FaLH03	JQGD01	105	42.7
F. avenaceum	FaLH27	JQGE01	78	43.2
F. avenaceum	KA13	JABCRA01	34	41.7
F. avenaceum	NRRL 13321	JABSSY01	778	41.7
F. aywerte	NRRL 25410	JABCQV01	911	36.0
F. azukicola	NRRL 54364	MAEG01	32428	51.3
F. babinda	NRRL 25533	JAALXL01	1090	43.8
F. babinda	NRRL 25539	JABCKA01	2053	42.9
F. bactridioides	NRRL 66639	JACCKW01	1826	42.9
F. begoniae	NRRL 25300	JAAOAG01	1002	43.9
F. beomiforme	NRRL 25174	PVQB02	1868	46.5
F. brasilicum	NRRL 31281	JABCJS01	627	36.8
F. brasiliense	NRRL 31757	MAEC01	22229	49.4
F. brevicatenulatum	NRRL 25447	JABEEJ01	1763	42.5
F. bulbicola	NRRL 22947	JAAOAH01	3116	42.3
F. bulbicola	NRRL 25176	JAAOAI01	1719	43.6
F. burgessii	NRRL 66654	PVQA01	3437	49.3
F. caatingaense	NRRL 66470	JABKKP01	1238	37.8
F. camptoceras	NRRL 13381	QGED01	467	36.8

F. cerealis	isolate Fcer1134NY13	JAAVVS01	3537	37.2
F. circinatum	GL1327	JRVE01	909	42.5
F. circinatum	FSP 34	AYJV02	585	43.9
F. circinatum	isolate KS17	LQBB01	6033	46.3
F. circinatum	isolate V	JABACP01	426	46.3
F. circinatum	isolate S	JABACQ01	481	46.1
F. circinatum	isolate LB	JABAYB01	207	45.3
F. circinatum	NRRL 25331	JAAQPE01	1223	42.6
F. citri	NRRL 66334 (ITEM 10392)	QHHH01	445	37.9
F. clavum	CS3069	CBMI01	5111	38.1
F. clavum	NRRL 66337 (ITEM 11348)	QGEC01	854	38.6
F. coffeatum	FIESC_28	QKXC01	550	37.8
F. coffeatum	NRRL 66322 (ITEM 1616)	QGDX01	654	37.0
F. coicis	NRRL 66233	JAAOAJ01	1267	42.7
F. commune	JCM 11502	BCHB01	19	46.2
F. commune	NRRL 28387	JABFES01	1931	48.1
F. compactum	NRRL 13829	JABFET01	516	37.9
F. concolor	NRRL 13459	JABCJY01	3171	49.6
F. continuum	NRRL 66286	JABCKB01	2038	38.1
F. cortaderiae	1FP	VSSW01	573	37.3
F. cortaderiae	NRRL 29297	JABCJT01	639	36.7
F. culmorum		FJUU01	2	5.0
F. culmorum	PV	PVEM01	36	38.1
F. culmorum	NRRL 25475	JABFEU01	799	36.6
F. culmorum CS7071	CS7071	CBMH01	2274	37.7
F. cuneirostrum	NRRL 31157	MAEA01	18692	49.0
F. decemcellulare	NRRL 13412	JAAGWO01	3482	53.7
F. denticulatum	NRRL 25311	JAAOAK01	909	43.2
F. dimerum	NRRL 20691	JABGLY01	2223	37.6
F. dlaminii	NRRL 13164	JAAOAL01	484	44.1
F. domesticum	NRRL 29976	JABFEV01	3048	32.6
F. equiseti	CS5819	MTPY01	267	39.6
F. equiseti	isolate D25-1	QOHM01	16	40.8
F. equiseti	D25-1	QJGT01	205	40.6
F. equiseti	NRRL 66338 (ITEM 11363)	QGEB01	643	40.0
F. euwallaceae	HFEW-16-IV-019	NHTE02	287	48.3
F. euwallaceae	UCR1854	MIKF01	1773	50.6
F. falciforme	NRRL 43529	JABEEK01	3427	48.2
F. flagelliforme	NRRL 13405	PXXK01	1073	39.6
F. flagelliforme	NRRL 66336 (ITEM 11294)	QHHI01	1363	40.4
F. foetens	NRRL 38302	JABFMM01	3842	46.3
F. fracticaudum	CBS 137234	PDNT01	50	46.3
F. fractiflexum	NRRL 43689	JABSTE01	1442	44.4
F. fujikuroi	FGSC 8932	JRVF01	835	43.1
F. fujikuroi	KSU X-10626	JRVG01	187	43.1
F. fujikuroi	KSU 3368	JRVH01	2959	43.5

F. fujikuroi	B14	FMSL01	66	44.0
F. fujikuroi	FSU48	FMSM01	182	46.1
F. fujikuroi		FMJS01	318	44.3
F. fujikuroi	E282	FMJT01	227	46.1
F. fujikuroi	C1995	FMJU01	86	45.8
F. fujikuroi	m567	FMJV01	241	44.0
F. fujikuroi	MRC2276	FMJW01	28	45.0
F. fujikuroi	NCIM1100	FMJX01	240	45.3
F. fujikuroi	FUS01	NCQQ02	881	49.1
F. fujikuroi	isolate F250	MBPO01	3872	42.5
F. fujikuroi	ke1	VJME01	502	48.7
F. fujikuroi	NRRL 66331	JABSTJ01	1506	42.5
F. fujikuroi B14	B14	ANFV01	455	43.8
F. gaditjirri	NRRL 45417	JABFAI01	834	41.9
F. globosum	NRRL 26131	JAAQPF01	1696	44.6
F. graminearum	CS3005	JATU01	424	36.6
F. graminearum	233423	LAJZ01	869	36.5
F. graminearum	241165	LAKA01	486	36.6
F. graminearum	DAOM180378	LHUC01	520	36.4
F. graminearum	NRRL28336	LHUD01	303	36.7
F. graminearum	ITEM 124	NQOC01	67	36.9
F. graminearum	FN009	UCPH01	715	36.8
F. graminearum	MDC_Fg1	UIHA01	96	36.8
F. graminearum	MDC_Fg13	CABDWO01	283	36.8
F. graminearum	FG078	VIGE01	335	36.8
F. graminearum	TaB10	JABCRB01	54	36.8
F. graminearum PH-1	PH-1; NRRL 31084	AACM02	435	36.3
F. guttiforme	NRRL 22945	JAAQRL01	1384	43.3
F. hainanense	NRRL 66475	JABFEW01	667	36.6
F. heterosporum	NRRL 20692	JAAGWP01	977	35.0
F. heterosporum	NRRL 20693	JAAGWQ01	793	35.7
F. hostae	Hy14	NJCQ01	3725	54.4
F. hostae	Hy9	NJCR01	3686	54.6
F. hostae	NRRL 29888	JABCJX01	3090	46.0
F. humuli	NRRL 66335 (ITEM 10395)	QHHG01	602	39.0
F. humuli	NRRL 66339 (ITEM 11401)	QHKN01	735	39.2
F. humuli	NRRL 66681	JABSTA01	1121	39.5
F. illudens	NRRL 22090	JABFEX01	3457	40.3
F. incarnatum	MOD1-FUNGI18	RBBZ01	340	38.3
F. incarnatum	MOD1-FUNGI17	RBJE01	325	38.3
F. incarnatum	NRRL 66325 (ITEM 7155)	QGDZ01	381	37.5
F. irregulare	NRRL 31160	QGEA01	627	37.4
F. kuroshium	isolate UCR3666	NKUJ01	1403	46.6
F. kyushuense	NRRL 25348	JABCJU01	325	36.0
F. langsethiae	Fl201059	JXCE01	1586	37.5
F. longipes	NRRL 20695	PXOG01	544	35.3

F. longipes	NRRL 13317	JABFEY01	285	35.3
F. longipes	NRRL 13368	JABFEZ01	492	35.5
F. longipes	NRRL 13374	JACCKV01	393	35.3
F. luffae	NRRL 66473	JABCJV01	1049	37.4
F. mangiferae	MRC7560	FCQH01	254	46.3
F. mangiferae	NRRL 25226	JABSTF01	2060	48.6
F. meridionale	NRRL28721	LHUA01	676	36.5
F. meridionale	NRRL28723	LHUB01	287	36.4
F. meridionale	38FSP	VSSX01	694	36.9
F. metavorans	FSSC_6	LWBZ01	103	46.9
F. mexicanum	NRRL 53147	JAAOAM01	958	44.0
F. mundagurra	NRRL 66235	JAAOAN01	1616	49.1
F. musae	NRRL 25059	JACCKU01	1114	42.5
F. nanum	NRRL 66324 (ITEM 6748)	QGDY01	530	37.2
F. napiforme	NRRL 25196	JAAOAO01	1411	42.1
F. nematophilum	NRRL 54600	JABFFA01	5027	52.5
F. neocosmosporiellum	NRRL 22166	SSHR01	5494	54.0
F. newnesense	NRRL 66241	JABCJW01	5456	48.8
F. nisikadoi	NRRL 25179	JABFFB01	1085	40.9
F. nurragi	NRRL 36452	JAALXI01	854	35.5
F. nygamai	MRC8546	LBNR01	409	51.6
F. nygamai	CS10214	MTQA01	991	50.2
F. nygamai	NRRL 66327	JAAOAP01	2753	48.5
F. odoratissimum	race 4	AMGQ01	3834	48.8
F. odoratissimum NRRL 54006	54006	AGND01	716	46.4
F. oxysporum	UASWS AC1	JNNQ01	1166	50.6
F. oxysporum	FoMN14	MALU01	1978	49.0
F. oxysporum	IMV 00293	MSJJ02	876	51.3
F. oxysporum	Tu58	NJBT01	1277	50.4
F. oxysporum	KOD888	NJBU01	11382	59.4
F. oxysporum	KOD887	NJBV01	1275	50.4
F. oxysporum	KOD886	NJBW01	488	47.2
F. oxysporum	V64-1	FMJY01	49	49.1
F. oxysporum	CS5870	MTPZ01	1295	51.4
F. oxysporum	VEG-01C2	PXUN01	3653	48.5
F. oxysporum	VEG-01C1	PXUO01	2969	48.8
F. oxysporum	Fo_A13	MRCX01	3121	54.8
F. oxysporum	Fo_A28	MRCY01	2373	53.0
F. oxysporum	Fo_CB3	MRCZ01	1719	50.5
F. oxysporum	Fo_PG	MRDA01	920	50.3
F. oxysporum	MOD1-FUNGI16	RBCA01	944	44.4
F. oxysporum	MOD1-FUNGI11	RBCF01	1377	46.3
F. oxysporum	MOD1-FUNGI9	RBCG01	2370	47.5
F. oxysporum	MOD1-FUNGI10	RBJF01	1950	46.3
F. oxysporum	ISS-F3	QUWZ01	2964	53.1
F. oxysporum	ISS-F4	QUXA01	3405	53.3

F. oxysporum	RBG5689	WGOF01	4075	50.5
F. oxysporum	RBG5714	WGOG01	7964	55.7
F. oxysporum	RBG5783	WGOH01	8531	51.1
F. oxysporum	RBG5831	WGOI01	4723	51.9
F. oxysporum	RBG5833	WGOJ01	11714	57.2
F. oxysporum	RBG5836	WGOK01	7253	53.0
F. oxysporum	RBG5844	WGOL01	5223	52.4
F. oxysporum	RBG5862	WGOM01	4352	50.8
F. oxysporum	RBG6301	WGON01	5001	52.4
F. oxysporum	RBG6309	WGOO01	4303	48.7
F. oxysporum	RBG6313	WGOP01	3298	45.8
F. oxysporum	RBG6324	WGOQ01	12866	51.7
F. oxysporum	RBG6358	WGOR01	2995	50.9
F. oxysporum	RBG6396	WGOS01	5820	49.2
F. oxysporum	RBG6397	WGOT01	6674	51.8
F. oxysporum	RBG6398	WGOU01	2261	47.8
F. oxysporum	RBG6400	WGOV01	6304	49.8
F. oxysporum	RBG6406	WGOW01	23217	63.1
F. oxysporum	RBG6416	WGOX01	5786	50.4
F. oxysporum	RBG6417	WGOY01	5340	51.8
F. oxysporum	RBG6418	WGOZ01	5516	52.8
F. oxysporum	RBG6419	WGPA01	3403	49.1
F. oxysporum	RBG6420	WGPB01	3580	48.4
F. oxysporum	RBG6421	WGPC01	7415	50.4
F. oxysporum	RBG6422	WGPD01	5462	49.5
F. oxysporum	RBG6423	WGPE01	9155	60.7
F. oxysporum	RBG6425	WGPF01	4601	50.4
F. oxysporum	RBG6429	WGPG01	7453	49.5
F. oxysporum	RBG6431	WGPH01	2707	48.2
F. oxysporum	RBG6433	WGPI01	6441	53.7
F. oxysporum	RBG6442	WGPJ01	8036	52.3
F. oxysporum	RBG6444	WGPK01	9085	54.4
F. oxysporum	RBG6448	WGPL01	3571	48.0
F. oxysporum	RBG6450	WGPM01	5755	48.6
F. oxysporum	RBG6454	WGPN01	12368	53.0
F. oxysporum	RBG6462	WGPO01	4614	50.3
F. oxysporum	RBG6464	WGPP01	11735	56.2
F. oxysporum	RBG6466	WGPQ01	4619	49.3
F. oxysporum	RBG6475	WGPR01	7651	59.1
F. oxysporum	RBG6477	WGPS01	7838	49.4
F. oxysporum	RBG6480	WGPT01	7934	55.8
F. oxysporum	RBG6494	WGPU01	7564	50.6
F. oxysporum	RBG6499	WGPV01	8772	52.3
F. oxysporum	RBG6503	WGPW01	5720	52.0
F. oxysporum	RBG6505	WGPX01	12642	54.5
F. oxysporum	RBG7064	WGPY01	9049	51.2

F. oxysporum	RBG7070	WGPZ01	11791	54.1
F. oxysporum	VPRI10351	WGQA01	2962	47.7
F. oxysporum	VPRI10358	WGQB01	5509	53.8
F. oxysporum	VPRI10403	WGQC01	1488	48.0
F. oxysporum	VPRI10405	WGQD01	4639	52.1
F. oxysporum	VPRI10408	WGQE01	3187	49.1
F. oxysporum	VPRI10605	WGQF01	3019	51.4
F. oxysporum	VPRI11235	WGQG01	4901	50.4
F. oxysporum	VPRI11409	WGQH01	7718	53.4
F. oxysporum	VPRI11681	WGQI01	10624	50.2
F. oxysporum	VPRI11762	WGQJ01	892	47.5
F. oxysporum	VPRI12300	WGQK01	4286	54.1
F. oxysporum	VPRI13039	WGQL01	4932	51.3
F. oxysporum	VPRI16234	WGQM01	5786	54.5
F. oxysporum	VPRI16235	WGQN01	7972	55.4
F. oxysporum	VPRI16963	WGQO01	3454	49.6
F. oxysporum	VPRI17577	WGQP01	1626	48.3
F. oxysporum	VPRI17796	WGQQ01	2778	50.0
F. oxysporum	VPRI19293	WGQR01	3353	52.5
F. oxysporum	VPRI31638	WGQS01	4144	53.6
F. oxysporum	VPRI32264	WGQT01	6149	54.6
F. oxysporum	VPRI32287	WGQU01	2446	45.4
F. oxysporum	VPRI32288	WGQV01	1495	46.9
F. oxysporum	VPRI32289	WGQW01	24336	57.9
F. oxysporum	VPRI32441	WGQX01	3584	46.3
F. oxysporum	VPRI32442	WGQY01	6771	54.9
F. oxysporum	VPRI41207	WGQZ01	2808	46.9
F. oxysporum	VPRI41208	WGRA01	1929	46.1
F. oxysporum	VPRI41778	WGRB01	6155	54.0
F. oxysporum	VPRI41836	WGRC01	6179	54.5
F. oxysporum	VPRI41884	WGRD01	4931	52.7
F. oxysporum	VPRI41920	WGRE01	4233	49.9
F. oxysporum	VPRI42109	WGRF01	2063	48.0
F. oxysporum	VPRI42117	WGRG01	3897	49.2
F. oxysporum	VPRI42118	WGRH01	4826	54.2
F. oxysporum	VPRI42119	WGRI01	5714	55.5
F. oxysporum	VPRI42176	WGRJ01	4898	48.0
F. oxysporum	VPRI42180	WGRK01	6639	52.4
F. oxysporum	VPRI42181	WGRL01	1976	45.8
F. oxysporum	VPRI42190	WGRM01	2110	50.1
F. oxysporum	VPRI42198	WGRN01	3244	50.4
F. oxysporum	VPRI42252	WGRO01	4801	51.7
F. oxysporum	VPRI42253	WGRP01	1101	48.7
F. oxysporum	VPRI42327	WGRQ01	7345	55.5
F. oxysporum	VPRI42339	WGRR01	3249	56.7
F. oxysporum	VPRI42420	WGRS01	5371	53.2

F. oxysporum	VPRI42760	WGRT01	2073	51.2
F. oxysporum	VPRI42882	WGRU01	3786	51.1
F. oxysporum	VPRI42888	WGRV01	5155	52.3
F. oxysporum	VPRI42889	WGRW01	2962	49.8
F. oxysporum	VPRI43193	WGRX01	6063	51.1
F. oxysporum	VPRI43194	WGRY01	3931	50.3
F. oxysporum	VPRI43195	WGRZ01	2843	49.9
F. oxysporum	MRL8996	VLJC01	252	50.1
F. oxysporum	EtdFoc-1	WESF01	4639	59.0
F. oxysporum	EtdFoc-10	WESG01	2289	54.5
F. oxysporum	EtdFoc-102	WESH01	14465	54.6
F. oxysporum	EtdFoc-109	WESI01	5364	53.4
F. oxysporum	EtdFoc-113	WESJ01	24914	61.1
F. oxysporum	EtdFoc-13	WESK01	3196	53.3
F. oxysporum	EtdFoc-136	WESL01	6480	54.3
F. oxysporum	EtdFoc-139	WESM01	34591	50.2
F. oxysporum	EtdFoc-155	WESN01	1944	55.0
F. oxysporum	EtdFoc-158	WESO01	3013	52.1
F. oxysporum	EtdFoc-16	WESP01	5985	58.3
F. oxysporum	EtdFoc-160	WESQ01	5118	54.3
F. oxysporum	EtdFoc-167	WESR01	1378	56.7
F. oxysporum	EtdFoc-17	WESS01	27789	63.1
F. oxysporum	EtdFoc-174	WEST01	25995	52.7
F. oxysporum	EtdFoc-178	WESU01	7839	59.6
F. oxysporum	EtdFoc-18	WESV01	29403	45.3
F. oxysporum	EtdFoc-183	WESW01	6667	56.2
F. oxysporum	EtdFoc-184	WESX01	2161	59.3
F. oxysporum	EtdFoc-185	WESY01	4759	59.1
F. oxysporum	EtdFoc-186	WESZ01	1515	59.3
F. oxysporum	EtdFoc-19	WETA01	2428	59.2
F. oxysporum	EtdFoc-190	WETB01	6304	62.7
F. oxysporum	EtdFoc-193	WETC01	7090	60.8
F. oxysporum	EtdFoc-195	WETD01	2768	59.4
F. oxysporum	EtdFoc-198	WETE01	10886	63.5
F. oxysporum	EtdFoc-2	WETF01	12359	52.8
F. oxysporum	EtdFoc-203	WETG01	2697	55.4
F. oxysporum	EtdFoc-204	WETH01	3888	60.5
F. oxysporum	EtdFoc-208	WETI01	2429	57.0
F. oxysporum	EtdFoc-209	WETJ01	8039	56.5
F. oxysporum	EtdFoc-213	WETK01	9839	52.5
F. oxysporum	EtdFoc-216	WETL01	1797	52.5
F. oxysporum	EtdFoc-218	WETM01	1864	53.0
F. oxysporum	EtdFoc-219	WETN01	1690	52.4
F. oxysporum	EtdFoc-22	WETO01	1060	50.7
F. oxysporum	EtdFoc-221	WETP01	2944	53.6
F. oxysporum	EtdFoc-222	WETQ01	3761	59.4

F. oxysporum	EtdFoc-223	WETR01	1903	53.6
F. oxysporum	EtdFoc-228	WETS01	18787	54.5
F. oxysporum	EtdFoc-229	WETT01	2792	52.6
F. oxysporum	EtdFoc-23	WETU01	1933	53.4
F. oxysporum	EtdFoc-233	WETV01	5514	56.8
F. oxysporum	EtdFoc-234	WETW01	1561	52.2
F. oxysporum	EtdFoc-236	WETX01	1906	53.9
F. oxysporum	EtdFoc-237	WETY01	23533	50.5
F. oxysporum	EtdFoc-240	WETZ01	272	40.2
F. oxysporum	EtdFoc-243	WEUA01	6542	57.9
F. oxysporum	EtdFoc-245	WEUB01	3400	53.8
F. oxysporum	EtdFoc-247	WEUC01	7745	62.3
F. oxysporum	EtdFoc-248	WEUD01	2494	50.5
F. oxysporum	EtdFoc-25	WEUE01	30013	46.0
F. oxysporum	EtdFoc-250	WEUF01	11764	62.8
F. oxysporum	EtdFoc-253	WEUG01	15576	50.2
F. oxysporum	EtdFoc-256	WEUH01	2941	53.7
F. oxysporum	EtdFoc-258	WEUI01	1685	51.4
F. oxysporum	EtdFoc-259	WEUJ01	2294	53.1
F. oxysporum	EtdFoc-29	WEUK01	11694	55.8
F. oxysporum	EtdFoc-30	WEUL01	1766	52.2
F. oxysporum	EtdFoc-34	WEUM01	18766	51.9
F. oxysporum	EtdFoc-35	WEUN01	18965	52.7
F. oxysporum	EtdFoc-38	WEUO01	2323	59.1
F. oxysporum	EtdFoc-39	WEUP01	1287	51.7
F. oxysporum	EtdFoc-4	WEUQ01	15289	52.3
F. oxysporum	EtdFoc-46	WEUR01	2393	53.1
F. oxysporum	EtdFoc-47	WEUS01	3804	52.1
F. oxysporum	EtdFoc-48	WEUT01	2806	54.5
F. oxysporum	EtdFoc-49	WEUU01	3907	52.4
F. oxysporum	EtdFoc-5	WEUV01	2295	52.2
F. oxysporum	EtdFoc-52	WEUW01	8137	53.5
F. oxysporum	EtdFoc-55	WEUX01	3236	54.8
F. oxysporum	EtdFoc-58	WEUY01	3653	61.4
F. oxysporum	EtdFoc-6	WEUZ01	4160	57.5
F. oxysporum	EtdFoc-61	WEVA01	3836	52.5
F. oxysporum	EtdFoc-63	WEVB01	5198	61.1
F. oxysporum	EtdFoc-68	WEVC01	3070	59.9
F. oxysporum	EtdFoc-69	WEVD01	23250	51.1
F. oxysporum	EtdFoc-7	WEVE01	3798	52.8
F. oxysporum	EtdFoc-72	WEVF01	5193	53.9
F. oxysporum	EtdFoc-75	WEVG01	34308	54.0
F. oxysporum	EtdFoc-79	WEVH01	2717	53.2
F. oxysporum	EtdFoc-8	WEVI01	1900	52.6
F. oxysporum	EtdFoc-86	WEVJ01	6322	53.7
F. oxysporum	EtdFoc-87	WEVK01	2186	52.9

F. oxysporum	EtdFoc-88	WEVL01	1790	52.8
F. oxysporum	EtdFoc-92	WEVM01	12352	59.3
F. oxysporum	EtdFoc-94	WEVN01	10092	53.1
F. oxysporum	EtdFoc-99	WEVO01	17061	52.2
F. oxysporum	EthFoc-10	WEVP01	14538	53.1
F. oxysporum	EthFoc-100	WEVQ01	23909	46.8
F. oxysporum	EthFoc-101	WEVR01	2006	52.8
F. oxysporum	EthFoc-102	WEVS01	3240	53.4
F. oxysporum	EthFoc-106	WEVT01	2217	51.8
F. oxysporum	EthFoc-11	WEVU01	1648	52.5
F. oxysporum	EthFoc-111	WEVV01	1785	52.7
F. oxysporum	EthFoc-113	WEVW01	1727	51.8
F. oxysporum	EthFoc-116	WEVX01	8532	60.0
F. oxysporum	EthFoc-118	WEVY01	2031	53.4
F. oxysporum	EthFoc-119	WEVZ01	906	49.2
F. oxysporum	EthFoc-12	WEWA01	2584	52.8
F. oxysporum	EthFoc-120	WEWB01	1842	52.4
F. oxysporum	EthFoc-122	WEWC01	9926	57.4
F. oxysporum	EthFoc-124	WEWD01	1779	52.0
F. oxysporum	EthFoc-125	WEWE01	2239	52.8
F. oxysporum	EthFoc-126	WEWF01	1635	52.2
F. oxysporum	EthFoc-127	WEWG01	1819	52.2
F. oxysporum	EthFoc-129	WEWH01	2050	52.3
F. oxysporum	EthFoc-13	WEWI01	2151	53.2
F. oxysporum	EthFoc-130	WEWJ01	1523	51.3
F. oxysporum	EthFoc-131	WEWK01	1696	51.1
F. oxysporum	EthFoc-133	WEWL01	360	42.7
F. oxysporum	EthFoc-135	WEWM01	2778	51.9
F. oxysporum	EthFoc-136	WEWN01	1654	52.6
F. oxysporum	EthFoc-138	WEWO01	31481	40.3
F. oxysporum	EthFoc-139	WEWP01	27775	46.1
F. oxysporum	EthFoc-144	WEWQ01	13369	58.6
F. oxysporum	EthFoc-146	WEWR01	19291	49.6
F. oxysporum	EthFoc-148	WEWS01	5198	55.0
F. oxysporum	EthFoc-158	WEWT01	31261	51.1
F. oxysporum	EthFoc-159	WEWU01	34674	41.5
F. oxysporum	EthFoc-16	WEWV01	2209	52.5
F. oxysporum	EthFoc-164	WEWW01	26531	41.4
F. oxysporum	EthFoc-165	WEWX01	36743	40.4
F. oxysporum	EthFoc-167	WEWY01	22139	49.8
F. oxysporum	EthFoc-18	WEWZ01	21751	54.0
F. oxysporum	EthFoc-2	WEXA01	1348	52.2
F. oxysporum	EthFoc-20	WEXB01	20233	50.5
F. oxysporum	EthFoc-21	WEXC01	1840	53.1
F. oxysporum	EthFoc-22	WEXD01	2133	53.4
F. oxysporum	EthFoc-23	WEXE01	2310	54.2

F. oxysporum	EthFoc-25	WEXF01	2529	53.6
F. oxysporum	EthFoc-26	WEXG01	20993	49.2
F. oxysporum	EthFoc-27	WEXH01	5931	54.4
F. oxysporum	EthFoc-28	WEXI01	18218	51.9
F. oxysporum	EthFoc-29	WEXJ01	17492	53.0
F. oxysporum	EthFoc-3	WEXK01	2410	52.7
F. oxysporum	EthFoc-30	WEXL01	7643	58.2
F. oxysporum	EthFoc-34	WEXM01	2105	54.4
F. oxysporum	EthFoc-36	WEXN01	1380	51.9
F. oxysporum	EthFoc-36a	WEXO01	33971	45.0
F. oxysporum	EthFoc-38	WEXP01	3317	56.3
F. oxysporum	EthFoc-4	WEXQ01	2152	53.2
F. oxysporum	EthFoc-40	WEXR01	1508	51.6
F. oxysporum	EthFoc-41	WEXS01	1853	52.2
F. oxysporum	EthFoc-42	WEXT01	2498	53.6
F. oxysporum	EthFoc-43	WEXU01	3406	53.2
F. oxysporum	EthFoc-44	WEXV01	1573	52.3
F. oxysporum	EthFoc-45	WEXW01	31527	46.3
F. oxysporum	EthFoc-48	WEXX01	2674	53.1
F. oxysporum	EthFoc-49	WEXY01	9150	53.6
F. oxysporum	EthFoc-52	WEXZ01	1720	52.3
F. oxysporum	EthFoc-55	WEYA01	12910	58.3
F. oxysporum	EthFoc-56	WEYB01	2088	52.1
F. oxysporum	EthFoc-57	WEYC01	38587	40.0
F. oxysporum	EthFoc-61	WEYD01	2107	52.5
F. oxysporum	EthFoc-62	WEYE01	1316	43.0
F. oxysporum	EthFoc-7	WEYF01	2205	55.4
F. oxysporum	EthFoc-75	WEYG01	2057	53.6
F. oxysporum	EthFoc-77	WEYH01	2138	58.7
F. oxysporum	EthFoc-78	WEYI01	1889	51.6
F. oxysporum	EthFoc-8	WEYJ01	2097	55.6
F. oxysporum	EthFoc-81	WEYK01	3090	55.5
F. oxysporum	EthFoc-83	WEYL01	1937	53.0
F. oxysporum	EthFoc-84	WEYM01	2091	53.1
F. oxysporum	EthFoc-86	WEYN01	3099	59.4
F. oxysporum	EthFoc-88	WEYO01	8064	52.6
F. oxysporum	EthFoc-90	WEYP01	2235	54.3
F. oxysporum	EthFoc-93	WEYQ01	10282	52.4
F. oxysporum	EthFoc-95	WEYR01	2075	51.8
F. oxysporum	EthFoc-98	WEYS01	20735	49.9
F. oxysporum	EthFoc-99	WEYT01	3200	53.3
F. oxysporum	EthFoc-DSP1	WEYU01	22007	44.7
F. oxysporum	EthFoc-DSP12	WEYV01	8308	52.9
F. oxysporum	EthFoc-DSP2	WEYW01	23318	51.8
F. oxysporum	EthFoc-DSP9	WEYX01	27833	49.0
F. oxysporum	EthFoc-35	WEYY01	2273	54.6

F. oxysporum	EthFoc-173	WEYZ01	33788	40.1
F. oxysporum	EthFoc-DSP6	WEZA01	35863	38.2
F. oxysporum	EthFoc-168	WEZB01	34434	38.9
F. oxysporum	EthFoc-152	WEZC01	35107	38.1
F. oxysporum	EthFoc-142	WEZD01	36102	38.4
F. oxysporum	EtdFoc-81	WEZE01	6341	64.4
F. oxysporum	EtdFoc-89	WIKT01	30490	56.7
F. oxysporum	EtdFoc-85	WIKU01	5081	59.5
F. oxysporum	EtdFoc-3	WIKV01	1596	58.1
F. oxysporum	EtdFoc-220	WIKW01	5717	58.0
F. oxysporum	EtdFoc-214	WIKX01	860	58.1
F. oxysporum	EtdFoc-206	WIKY01	5774	60.6
F. oxysporum	EtdFoc-20	WIKZ01	25892	52.1
F. oxysporum	EtdFoc-192	WILA01	1870	58.3
F. oxysporum	EtdFoc-191	WILB01	1576	58.1
F. oxysporum	EtdFoc-189	WILC01	3207	58.6
F. oxysporum	EtdFoc-182	WILD01	28859	52.9
F. oxysporum	EtdFoc-181	WILE01	8664	55.3
F. oxysporum	EtdFoc-176	WILF01	24937	55.2
F. oxysporum	EtdFoc-143	WILG01	28349	52.1
F. oxysporum	Fus259	JAALGK01	821	49.3
F. oxysporum	Fus250	JAALGL01	1139	50.1
F. oxysporum	Fus191	JAALGM01	387	47.6
F. oxysporum	Fus187	JAALGN01	998	49.2
F. oxysporum	Fus017	JAALGS01	1518	51.4
F. oxysporum	NRRL 39464	JAAFOW01	5286	47.0
F. oxysporum	isolate Fo74	JAAMUY01	1912	52.5
F. oxysporum	isolate Fo68	JAAMUZ01	1371	51.5
F. oxysporum	isolate Fo59	JAAMVA01	680	48.8
F. oxysporum	isolate Fo14	JAAMVB01	2740	53.6
F. oxysporum	isolate Fo9	JAAMVC01	530	47.8
F. oxysporum	isolate Fo7	JAAMVD01	1809	53.4
F. oxysporum	isolate Fo5	JAAMVE01	2423	53.6
F. oxysporum	isolate Fo47	WXUE01	60	50.2
F. oxysporum	isolate Fo75	WXUF01	721	49.8
F. oxysporum	isolate Fo69	WXUG01	1419	53.3
F. oxysporum	isolate Fo65	WXUH01	2173	53.6
F. oxysporum	isolate Fo63	WXUI01	1510	52.3
F. oxysporum	isolate Fo58	WXUJ01	672	49.8
F. oxysporum	isolate Fo57	WXUK01	779	49.9
F. oxysporum	isolate Fo54	WXUL01	1094	50.8
F. oxysporum	isolate Fo53	WXUM01	1307	50.4
F. oxysporum	isolate Fo52	WXUN01	1523	51.2
F. oxysporum	isolate Fo49	WXUO01	1272	51.5
F. oxysporum	isolate Fo48	WXUP01	1272	51.5
F. oxysporum	isolate Fo46	WXUQ01	948	50.7

F. oxysporum	isolate Fo45	WXUR01	1443	50.5
F. oxysporum	isolate Fo44	WXUS01	856	49.3
F. oxysporum	isolate Fo41	WXUT01	1576	51.3
F. oxysporum	isolate Fo39	WXUU01	1175	50.1
F. oxysporum	isolate Fo35	WXUV01	616	48.1
F. oxysporum	isolate Fo29	WXUW01	1176	50.7
F. oxysporum	isolate Fo28	WXUX01	1834	52.1
F. oxysporum	isolate Fo26	WXUY01	1677	52.3
F. oxysporum	isolate Fo25	WXUZ01	1492	50.5
F. oxysporum	isolate Fo24	WXVA01	2026	52.6
F. oxysporum	isolate Fo20	WXVB01	1346	52.1
F. oxysporum	isolate Fo18	WXVC01	2144	54.9
F. oxysporum	isolate Fo17	WXVD01	1190	51.8
F. oxysporum	isolate Fo16	WXVE01	1476	51.7
F. oxysporum	isolate Fo15	WXVF01	1047	48.7
F. oxysporum	isolate Fo13	WXVG01	1253	50.8
F. oxysporum	isolate Fo12	WXVH01	1218	50.2
F. oxysporum	isolate Fo11	WXVI01	1086	49.9
F. oxysporum	isolate Fo10	WXVJ01	1683	52.7
F. oxysporum	isolate Fo8	WXVK01	1464	50.5
F. oxysporum	isolate Fo6	WXVL01	2072	52.6
F. oxysporum	isolate Fo4	WXVM01	1911	53.7
F. oxysporum	isolate Fo3	WXVN01	2910	56.7
F. oxysporum	isolate Fo2	WXVO01	616	47.5
F. oxysporum	isolate Fo1	WXVP01	723	49.1
F. oxysporum f. sp. albedinis	Foa 133	JAAVJG01	3325	56.2
F. oxysporum f. sp. capsici	14003	JACYOB01	739	47.5
F. oxysporum f. sp. cepae	FoC_Fus2	MRCU01	34	53.4
F. oxysporum f. sp. cepae	FoC_125	MRCV01	2119	51.4
F. oxysporum f. sp. cepae	FoC_A23	MRCW01	1997	51.0
F. oxysporum f. sp. ciceris	38-1	MEHF01	1482	54.8
F. oxysporum f. sp. conglutinans	1	LPZQ01	13202	52.5
F. oxysporum f. sp. conglutinans	58385	NRHZ01	5119	55.9
F. oxysporum f. sp. conglutinans	FGL03-6	NRIA02	1079	61.1
F. oxysporum f. sp. conglutinans	Fo5176	JACDXP01	19	68.0
F. oxysporum f. sp. conglutinans	race 1	JABTBS01	64	71.1
F. oxysporum f. sp. conglutinans race 2 54008	54008	AGNF01	3350	53.2
F. oxysporum f. sp. cubense	C1HIR_9889	MBFV01	1370	46.7
F. oxysporum f. sp. cubense	160527	SRMI01	12	51.1
F. oxysporum f. sp. cubense	isolate UK0001, TR4	VMNF01	15	48.6
F. oxysporum f. sp. cubense	TC1-1	VLOF01	2635	48.6
F. oxysporum f. sp. cubense	BC2-4	VYQK01	4022	47.0
F. oxysporum f. sp. cubense race 1	race 1	AMGP01	2185	46.9
F. oxysporum f. sp. cucumerinum	Foc013	MABJ01	1129	48.9
F. oxysporum f. sp. cucumerinum	Foc015	MABK01	1743	52.0
F. oxysporum f. sp. cucumerinum	Foc021	MABL01	3634	56.9

F. oxysporum f. sp. cucumerinum	Foc018	MABM01	3866	57.4
F. oxysporum f. sp. cucumerinum	Foc030	MABN01	3557	56.8
F. oxysporum f. sp. cucumerinum	Foc035	MABO01	1501	51.6
F. oxysporum f. sp. cucumerinum	Foc037	MABP01	1314	48.4
F. oxysporum f. sp. cucumerinum	Foc011	MABT01	1133	48.7
F. oxysporum f. sp. cucumerinum	Foc001	MAKZ01	1325	51.4
F. oxysporum f. sp. gladioli	G76	NJCK01	3146	56.1
F. oxysporum f. sp. gladioli	G2	NJCL01	2454	53.2
F. oxysporum f. sp. gladioli	G14	NJCM01	2859	56.3
F. oxysporum f. sp. lagenariae	Lag1-1	NJCG01	2079	54.6
F. oxysporum f. sp. lagenariae	Lag3-1	NJCH01	764	47.9
F. oxysporum f. sp. lagenariae	03-05118	NJCI01	2650	56.1
F. oxysporum f. sp. lagenariae	01-03008	NJCJ01	1728	53.9
F. oxysporum f. sp. lilii	Fol39	NJCF01	1677	53.4
F. oxysporum f. sp. lini	39	WHMS01	35	59.2
F. oxysporum f. sp. lini	39	JABJUA01	26	69.5
F. oxysporum f. sp. lini	F282	JABJUB01	185	48.0
F. oxysporum f. sp. lini	F287	JABJUC01	180	47.6
F. oxysporum f. sp. lini	F324	JABJUD01	35	47.5
F. oxysporum f. sp. lini	F329	JABJUE01	197	46.9
F. oxysporum f. sp. luffae	Fol-167	NJCD01	590	48.3
F. oxysporum f. sp. luffae	Fol-114	NJCE01	589	48.2
F. oxysporum f. sp. lycopersici	Fol004	MALH01	3433	51.9
F. oxysporum f. sp. lycopersici	Fol007	MALI01	1999	51.3
F. oxysporum f. sp. lycopersici	Fol014	MALJ01	2589	50.1
F. oxysporum f. sp. lycopersici	Fol026	MALK01	3302	51.8
F. oxysporum f. sp. lycopersici	Fol018	MALL01	2140	49.0
F. oxysporum f. sp. lycopersici	Fol016	MALM01	2336	49.6
F. oxysporum f. sp. lycopersici	Fol029	MALN01	2270	50.0
F. oxysporum f. sp. lycopersici	Fol038	MALO01	3188	51.3
F. oxysporum f. sp. lycopersici	Fol069	MALP01	1888	49.1
F. oxysporum f. sp. lycopersici	Fol072	MALQ01	1859	50.1
F. oxysporum f. sp. lycopersici	Fol073	MALR01	3317	51.8
F. oxysporum f. sp. lycopersici	Fol074	MALS01	3410	51.5
F. oxysporum f. sp. lycopersici	Fol075	MALT01	2009	50.6
F. oxysporum f. sp. lycopersici	Fol002	MAMG01	3451	51.7
F. oxysporum f. sp. lycopersici	isolate D11, race 3	RBXW01	39	57.3
F. oxysporum f. sp. lycopersici 4287	4287	AAXH01	1371	60.0
F. oxysporum f. sp. lycopersici 4287	4287	MALV01	4285	51.1
F. oxysporum f. sp. lycopersici 4287	4287	MALW01	1955	51.0
F. oxysporum f. sp. lycopersici 4287	4287	QESU01	499	53.9
F. oxysporum f. sp. lycopersici MN25	MN25	AGBH01	801	48.5
F. oxysporum f. sp. matthiolae	PHW726	WJXY01	583	57.3
F. oxysporum f. sp. medicaginis	isolate Fom-5190a	LSNI01	5373	49.2
F. oxysporum f. sp. melongenae	14004	MPIL01	1631	54.0
F. oxysporum f. sp. melongenae	J-71	NJCC01	1726	52.3

F. oxysporum f. sp. melonis	Fom004	MALX01	1300	57.7
F. oxysporum f. sp. melonis	Fom005	MALY01	2472	54.5
F. oxysporum f. sp. melonis	Fom006	MALZ01	2225	52.8
F. oxysporum f. sp. melonis	Fom009	MAMA01	1727	57.7
F. oxysporum f. sp. melonis	Fom010	MAMB01	3384	53.7
F. oxysporum f. sp. melonis	Fom011	MAMC01	2590	52.9
F. oxysporum f. sp. melonis	Fom012	MAMD01	2283	52.6
F. oxysporum f. sp. melonis	Fom013	MAME01	2256	51.9
F. oxysporum f. sp. melonis	Fom016	MAMF01	2257	52.9
F. oxysporum f. sp. melonis 26406	26406	AGNE01	1825	53.8
F. oxysporum f. sp. melonis 26406	26406	NJCY01	96	60.7
F. oxysporum f. sp. momordicae	90NF2-1	NJCA01	1089	51.0
F. oxysporum f. sp. momordicae	NRRL26413	NJCB01	1317	51.5
F. oxysporum f. sp. narcissi	Na5	NJCV01	3497	55.5
F. oxysporum f. sp. narcissi	N139	MQTW01	4349	57.5
F. oxysporum f. sp. nicotianae	Ft-Rob	NJBX01	1196	49.8
F. oxysporum f. sp. nicotianae	10913	NJBY01	638	50.0
F. oxysporum f. sp. nicotianae	FON-1	NJBZ01	682	50.2
F. oxysporum f. sp. nicotianae	Ft-1512	NJCU01	989	51.0
F. oxysporum f. sp. niveum	Fon005	MAKY01	3511	54.7
F. oxysporum f. sp. niveum	Fon002	MALA01	2191	52.0
F. oxysporum f. sp. niveum	Fon010	MALB01	3377	55.5
F. oxysporum f. sp. niveum	Fon013	MALC01	3008	54.2
F. oxysporum f. sp. niveum	Fon015	MALD01	2383	52.1
F. oxysporum f. sp. niveum	Fon020	MALE01	3604	55.1
F. oxysporum f. sp. niveum	Fon037	MALF01	1737	51.3
F. oxysporum f. sp. niveum	Fon021	MALG01	3081	54.8
F. oxysporum f. sp. niveum	Fon019	MAMH01	1758	49.7
F. oxysporum f. sp. niveum	R3	JACRUX01	7170	55.2
F. oxysporum f. sp. niveum	R1	JACRUY01	8668	61.2
F. oxysporum f. sp. niveum	R2	JACRUZ01	6119	54.1
F. oxysporum f. sp. pisi HDV247	HDV247	AGBI01	1744	54.5
F. oxysporum f. sp. radicis-cucumerinum	Forc024	MABR01	824	49.3
F. oxysporum f. sp. radicis-cucumerinum	Forc031	MABS01	879	49.3
F. oxysporum f. sp. radicis-cucumerinum	Forc016	MABQ02	33	52.9
F. oxysporum f. sp. radicis-lycopersici 26381	26381	AGNB01	725	49.3
F. oxysporum f. sp. raphani 54005	54005	AGNG01	2323	52.9
F. oxysporum f. sp. spinaciae	Fus254	JAALGI01	279	56.3
F. oxysporum f. sp. spinaciae	Fus322	JAALGJ01	4003	56.1
F. oxysporum f. sp. spinaciae	Fus173	JAALGO01	3021	56.2
F. oxysporum f. sp. spinaciae	Fus167	JAALGP01	3748	56.7
F. oxysporum f. sp. spinaciae	Fus059	JAALGQ01	4007	56.1
F. oxysporum f. sp. spinaciae	Fus057	JAALGR01	4042	56.2
F. oxysporum f. sp. spinaciae	Fus001	JAALGT01	3098	56.2
F. oxysporum f. sp. tulipae	Tu67	NJBS01	2263	54.3
F. oxysporum f. sp. vasinfectum	isolate TF1	VINL01	17	50.0

F. oxysporum f. sp. vasinfectum	isolate LA3B	VINM01	17	50.4
F. oxysporum f. sp. vasinfectum	isolate LA1E	VINN01	26	53.5
F. oxysporum f. sp. vasinfectum	isolate 14-004	VINO01	18	51.7
F. oxysporum f. sp. vasinfectum	isolate 89-1A	VINP01	94	63.3
F. oxysporum f. sp. vasinfectum	NRRL 25420	JAANYJ01	581	52.0
F. oxysporum f. sp. vasinfectum	NRRL 25434	JAANYK01	861	67.8
F. oxysporum f. sp. vasinfectum	NRRL 25432	JAANYL01	634	68.7
F. oxysporum f. sp. vasinfectum	NRRL 31665	JAANYM01	433	54.9
F. oxysporum f. sp. vasinfectum 25433	25433	AGNC01	1947	52.5
F. oxysporum Fo47	Fo47	AFMM01	419	49.4
F. oxysporum Fo5176	Fo5176	AFQF01	7858	54.8
F. oxysporum NRRL 32931	NRRL 32931	AFML01	545	47.2
F. penzigii	NRRL 20711	JABFFC01	1247	36.3
F. phaseoli	NRRL 31156	MAEB01	16072	50.5
F. phaseoli	NRRL 22396	JABEEL01	1483	46.1
F. phyllophilum	NRRL 13617	JAAOAQ01	1628	43.4
F. pininemorale	CMW 25243	NFZR01	153	47.8
F. poae	2516	LYXU01	181	46.5
F. poae	NRRL 26941	JABFFD01	2426	37.8
F. praegraminearum	NRRL 39664	LXHY01	481	35.3
F. proliferatum	CF-295141	MBPS01	237	44.2
F. proliferatum	NRRL62905	FCQG01	155	43.2
F. proliferatum	Fol3	NJCT01	10475	64.2
F. proliferatum	COH1152	QBDQ01	2117	47.7
F. proliferatum	ITEM 2341	PKMI01	104	45.5
F. proliferatum	Fp_A8	MRDB01	581	45.7
F. proliferatum	MOD1-FUNGI19	RBBY01	449	43.1
F. proliferatum	MOD1-FUNGI15	RBCB01	578	43.3
F. proliferatum	MOD1-FUNGI14	RBCC01	563	43.1
F. proliferatum	MOD1-FUNGI13	RBCD01	1006	43.1
F. proliferatum	MOD1-FUNGI12	RBCE01	562	43.1
F. proliferatum	MOD1-FUNGI8	RBJG01	1159	43.2
F. proliferatum	NRRL 66682	JABSTG01	1501	45.7
F. proliferatum	NRRL 43689	JABSTK01	1442	44.4
F. proliferatum ET1	ET1	FJOF01	32	45.2
F. protoensiforme	NRRL 22178	JAANQP01	1682	45.5
F. pseudoanthophilum	NRRL 25211	JAAOAR01	1816	42.8
F. pseudocircinatum	NRRL 36939	JAAOAS01	1040	43.3
F. pseudograminearum	CS3270	JTGB02	89	37.1
F. pseudograminearum	RBG5266	JTGC01	735	36.3
F. pseudograminearum CS3096	CS3096	AFNW01	685	36.9
F. pseudograminearum CS3220	CS3220	CBMC01	1479	37.3
F. pseudograminearum CS3427	CS3427	CBMD01	1715	37.2
F. pseudograminearum CS3487	CS3487	CBME01	2589	37.1
F. pseudograminearum CS5834	CS5834	CBMF01	1396	37.6
F. pseudonygamai	NRRL 13592	JAAQRH01	2619	42.2

F. ramigenum	NRRL 25208	JAAOAT01	1577	46.5
F. sacchari	NRRL 66326	JABSTH01	515	42.8
F. sambucinum	F-4	LSRD01	961	37.8
F. sarcochroum	NRRL 20472	JABEXW01	1849	46.4
F. scirpi	NRRL 66328	QHHJ01	587	39.6
F. secorum	NRRL 62593	JABEEM01	6851	51.2
F. setosum	NRRL 36526	JABFFE01	3402	46.2
F. solani	JS-169	NGZQ01	17	45.8
F. solani	isolate S2_018_000R2	SCGO01	2622	44.9
F. solani	isolate S2_009_000R2b	SCGU01	4372	31.1
F. solani	LQ1	WXYL01	1305	51.9
F. solani	IISc-1	JABJVU01	117	48.8
F. sp. AF-3	NRRL62606	NKCL01	1719	47.4
F. sp. AF-4	NRRL62579	NKCK01	1171	48.7
F. sp. AF-6	NRRL62590	NKCJ01	1182	43.1
F. sp. AF-8	NRRL62584	NKCI01	1006	47.5
F. sp. BWC	BWC	SWCQ01	435	42.1
F. sp. DS 682	DS 682	JACYFE01	11597	56.1
F. sp. JS1030	JS1030	JWIW01	107	53.7
F. sp. JS626	JS626	JWIV01	63	42.9
F. sp. KOD 1611	KOD 1611	JABKKQ01	5049	38.9
F. sp. Na10	Na10	NJCS01	971	46.6
F. sp. NRRL 22101	NRRL 22101	JABELF01	4875	65.6
F. sp. NRRL 25184	NRRL 25184	JABSSZ01	2609	48.4
F. sp. NRRL 25303	NRRL 25303	JAAOAY01	941	43.7
F. sp. NRRL 29148	NRRL 29148	JABSTL01	2621	40.7
F. sp. NRRL 47473	NRRL 47473	JABSTM01	1043	43.4
F. sp. NRRL 52700	NRRL 52700	JAAQRM01	528	43.0
F. sp. NRRL 53293	NRRL 53293	JABSTN01	859	44.0
F. sp. NRRL 53497	NRRL 53497	JABCJZ01	882	44.2
F. sp. NRRL 6227	NRRL 6227	JABFEC01	599	37.3
F. sp. NRRL 62610	NRRL 62610	JABCKE02	12062	46.1
F. sp. NRRL 62941	NRRL 62941	JAALXN01	4472	48.1
F. sp. NRRL 62944	NRRL 62944	JABCKC01	8878	48.0
F. sp. NRRL 62957	NRRL 62957	JAALXM01	18524	43.8
F. sp. NRRL 66088	NRRL 66088	JABCKD01	4445	48.7
F. sp. NRRL 66182	NRRL 66182	JABFAK01	16970	48.0
F. sp. QHM	QHM	SWCP01	435	42.1
F. sporotrichioides	NRRL 3299	PXOF01	446	37.4
F. sterilihyphosum	NRRL 25623	JAAOAU01	2178	46.9
F. subglutinans	RC 528	JAAIFQ01	1355	44.1
F. subglutinans	RC 298	JAAIFR01	3933	51.7
F. subglutinans	NRRL 66333	JAAOAV01	905	44.2
F. sublunatum	NRRL 13384	JABFFF01	986	35.7
F. subtropicale	NRRL 66764	QRAA01	1080	35.4
F. succisae	NRRL 13298	JAAOAW01	538	45.4

F. tanahbumbuense	NRRL 66471	JAALXH01	1049	37.8
F. temperatum	CMWF389	LJGR01	43	45.5
F. temperatum	RC 2914	JAAIFN01	667	43.4
F. temperatum	KFI 615	JACOPY01	20	45.2
F. temperatum	KFI 660	JACOPZ01	18	45.0
F. thapsinum	NRRL 22049	JAAOAX01	384	40.9
F. tjaetaba	NRRL 66243	JAAQRI01	867	43.1
F. torulosum	NRRL 22747	JABFMN01	1339	41.3
F. transvaalense	NRRL 31008	JABFFG01	1088	37.9
F. tricinctum	T6	PTXX01	617	42.7
F. tricinctum	INRA104	QFZF01	23	42.8
F. tricinctum		OVTS02	23	42.8
F. tricinctum	NRRL 25481	JAALXJ01	1032	41.0
F. tuaranense	NRRL 46518	JABEEN01	3977	48.9
F. tucumaniae	NRRL 31096	MAED01	15093	48.4
F. tucumaniae	NRRL 31781	MAEE01	22979	49.7
F. tucumaniae	NRRL 34546	MAEF01	54001	49.9
F. tupiense	NRRL 53984	JABEEO01	1664	45.5
F. udum	F-02845	NIFK01	712	56.4
F. udum	NRRL 25194	JAAQPG01	2353	44.6
F. vanettenii 77-13-4	isolate 77-13-4	ACJF01	233	51.2
F. venenatum	NRRL 66329	JABFFH01	616	38.0
F. verrucosum	NRRL 22566	JABFFJ01	767	34.2
F. verticillioides	BRIP14953	QFXM01	1060	42.5
F. verticillioides	BRIP53263	QJUS01	931	42.3
F. verticillioides	BRIP53590	QKXB01	1009	42.2
F. verticillioides	NRRL 20984	JABSTI01	857	41.9
F. verticillioides 7600	7600	AAIM02	213	41.8
F. virguliforme	Clinton-1B	MADX01	25997	50.9
F. virguliforme	LL0009	MADY01	25286	50.2
F. virguliforme	NRRL 34551	MADZ01	20982	49.4
F. virguliforme	NRRL 31041	JABEEP01	3852	45.4
F. virguliforme Mont-1	Mont-1	AEYB01	3098	50.4
F. xylarioides	K1	RXHO01	1132	55.1
F. xylarioides	KSU18978	SRZU01	424	55.2
F. xylarioides	NRRL 25486	JABFFK01	2987	44.0
F. xyrophilum	NRRL 66890	VYWY01	5402	38.1
F. xyrophilum	NRRL 62721	VYWZ01	5229	39.6
F. xyrophilum	NRRL 62710	VYXA01	5060	38.9
F. zanthoxyli	NRRL 66285	JABFFL01	2368	40.9
F. zealandicum	NRRL 22465	JABEYC01	1836	33.5

[a] Downloaded from GenBank on 30 September 2020.

Additional file 20. Diagnostic PCR primers for *Foa* race 2 haplogroup, *Foa* race 4, and *Foci*[a].

Target strain	Primer name	Forward primer (5'3') sequence	Reverse primer (5'3') sequence	Amplicon size, bp	Annealing temp, C	*F. oxysporum* strains that produce an undesired positive or an undersired negative based on either a NCBI GenBank wgs BLAST (D) or empirical testing (E)[b]	Location of amplicon:bp start-end in either core genome, host-specific (HS) accessory or lineage-specific (LS) accessory genome
Foa race 2	FOA R2-76k[c,d]	TGTTGAGTTGTCGGAGTTCTGC	TCCTTGTGTTTCTCGGTTCCTC	226	63	None detected	Contig_9:76612-76837 (Accessory)
Foa race 4	FOAR4-447[d]	AACCCAAGGTCTCGACGATCTG	ACCTTCCGTGCAGTCCTCATTC	196	63	Undesired Positives: *Foci*10T (E); f. sp. *vasinfectum* NRRL 25433 (D,E) and race 4, 89-1A (D), f. sp. *raphanini* NRRL 54005 (D,E), f. sp. *gladioli* G76 (D); *Fo* strains VPRI31638, VPRI16235 VPRI10405 and Fo9 (D), and *F. secorum* NRRL 62593 (D)	In *Foa* race 4, in Superscaffold_5: 4476883-4477078 (Core, Chromosome 11)[f]
Foa race 4	N3875-2[e]	AGGACTTGAATCACGGCTCG	CCTGCCACTCGCTTTTTGAG	189	60	Undesired Positives: *Foci*GL306 and *Foci*3-2 (D,E), *Foci*8.1A, *Foci*10E, *Foci*11, *Foci*12A and *Foci*10T (E); *F. oxysporum* non-pathogens from symptomatic celery (273-1B and 273-2B) (E); highly similar to f. sp. *pisi* RBG6397 and RBG6454, and *F. oxysporum* VPRI42180 (D)	In *Foa* race 4, two copies in Superscaffold_2:482422-482253 and 464741-464929 (LS Accessory); In single copies in *Foci*3-2_Contig 111586365-1586553 (LS Accessory) and in *Foci*GL306_ Contig 13:1059996-1060184 (Accessory)

Foci	FOCI2-21[d,f]	GTAGTAT CGTGGGA TTGGCGT TTG	GGCCTCTT CTGAATTG TCGCATAC	374	63	Undesired Positives: *Fo* strains VPRI11409 and f. sp. *albedinis* 133, similar to *Fo* strains Fo65 and Fo45, *F. mundagurra* NRRL 66235, *F. autroafricanum* NRRL 53441, and *Fo* strains from soil: EtdFoc-209, EtdFoc-208, RBG5714, RBG6313, Fo3, Fo4, and Fo5 (D) Undesired Negatives: *Foci*10T (E)	*Foci*3-2_Contig_21:490260-490633 (HS Accessory); *Foci*GL306_Contig_20:790595-790968 (HS Accessory)
Foci	FOCI-g_c31	TGGTTCA TCTATCC CTCAAGG AGTATC	AGCCTTTA TTCTCGTC CATCATAA GTTC	402	60	Undesired Positives: *Fo* strains from soil: Fo3 and Fo5 (D). Undesired Negatives: *Foci*10T (E)	*Foci*3-2_Contig 12:962890-962489 (HS Accessory) *Foci*GL306_Contig 31: 120557-120156 (HS Accessory)

[a] *Foa*, *F. oxysporum* f. sp. *apii*; *Foci*, *F. oxysporum* f. sp. *coriandrii*.

[b] For *in silico* testing, the amplicons were BLASTed with the GenBank database on 30 September 2020 with 1) the nr/nt database, and had no significant results, and 2) on the *Fusarium* wgs databases with 437 *F. oxysporum* isolates and 329 other *Fusarium spp*; significant hits are noted. A list of the 772 *Fusarium spp*. in the wgs database is shown in Additional file 19. For empirical testing, we included those in our *F. oxysporum* collection (including non-pathogens and pathogens from celery [3] and isolates from coriander (Additional file 18).

[c] Primer pair FOA_R2-76 is suitable for cultures. For analyses with plant debris, we include a fluorescently labeled probe, 5'56-FAM/TCTGCTTCT/ZEN/AGGCTGTGCTCGAAAGCT/3IAbkFQ/-3' (IDT, San Jose, CA); the probe eliminates cross reaction with celery tissue.

[d] These primer pairs can be reacted in a multiplex with SYBR Green.

[e] The primer sequences and the undesired positives with two non-pathogenic *F. oxysporum* strains from California celery were previously published in Epstein et al.[3].

[f] As shown in Fig. 3D, the homolog of *F. oxysporum* f. sp. *lycopersici* 4287 core chromosome 11 in *Foa* race 4 (SS5) has regions that are not conserved.

Additional file 21. Percentage of the genome with transposons and repeats in *Foa, Foci,* and the *Fol* reference[a]

	Type of transposable element					Total interspersed repeats
	DNA elements	LTR elements	LINES	SINES	Unclassified	
	Percentage of genome					
Foa race 4	6.24	4.94	2.13	0.00	6.25	19.56
Foa race 3	5.68	4.22	2.11	0.01	8.06	20.07
*Foci*3-2	6.21	3.50	1.86	0.00	6.64	18.22
*Foci*GL306	7.26	3.66	2.00	0.01	5.67	18.60
Foa race 2	7.59	3.64	1.79	0.01	5.67	18.70
*Fol*4287	7.04	1.98	2.00	0.01	5.76	16.79

[a] All elements were identified with RepeatMasker 4.0.