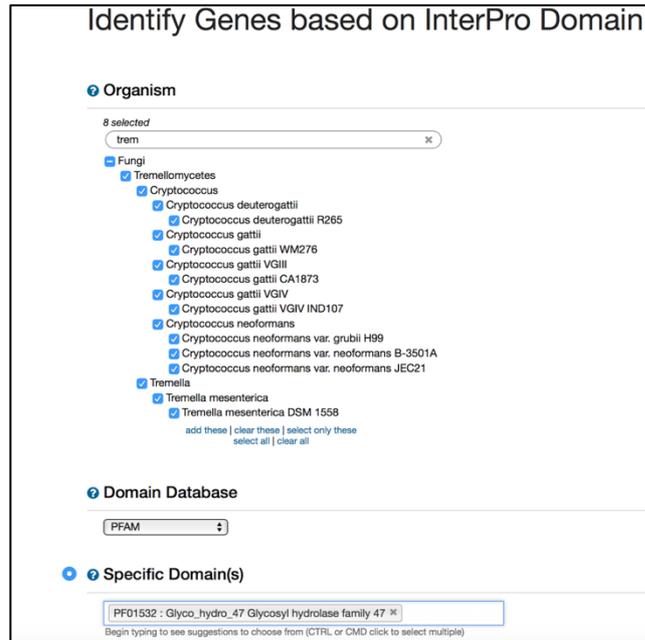


FungiDB: Synteny in GBrowse

Fungal organisms produce a wide range of extracellular enzymes to break down organic materials. Glycoside hydrolases (GH) are a large family of enzymes that facilitate degradation processes.

1. Initiate a gene search for Glycosyl hydrolase family 47 proteins in *Cryptococcus*. Use the InterPro Domain search and enter **PF01532** (the PFAM ID for Glycosyl hydrolase family 47).

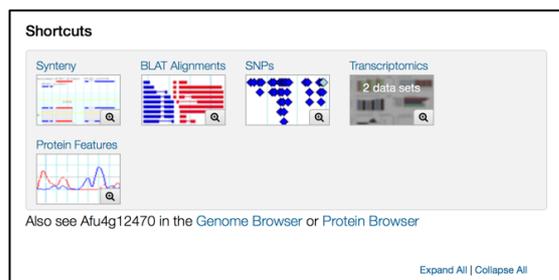


2. Navigate to the gene page of CNBG_9313. This gene belongs to the family of CAZy genes

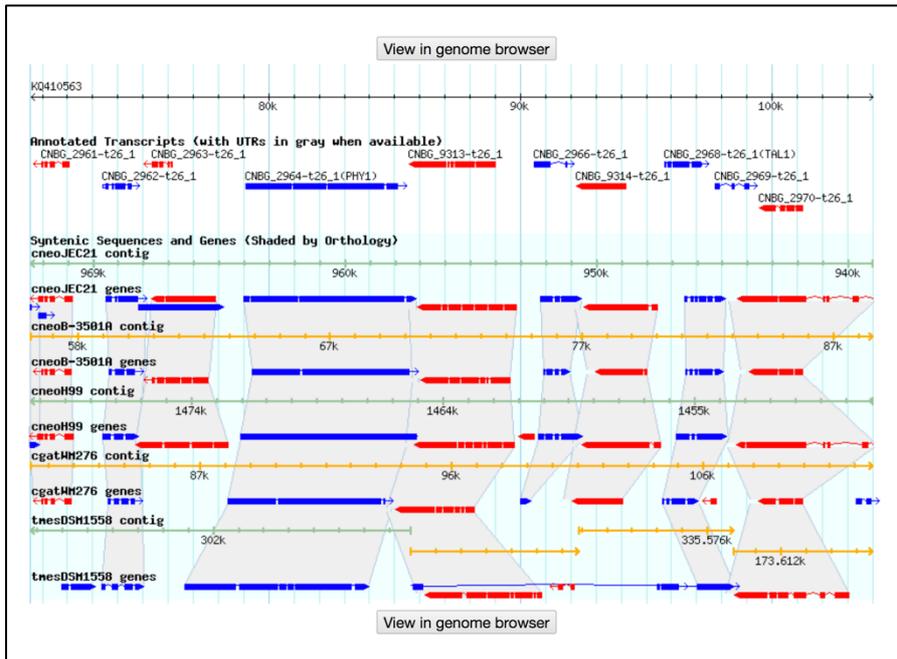
Gene ID	Transcript ID	Organism	Genomic Location (Gene)	Product Description	Score / E value
CNBG_2351	CNBG_2351-t26_1	C. deuterogattii R265	KQ410561:860,016..862,851(+)	mannosyl-oligosaccharide 1,2-alpha-mannosidase	.0E+00
CNBG_5230	CNBG_5230-t26_1	C. deuterogattii R265	KQ410571:160,190..162,783(-)	mannosyl-oligosaccharide alpha-1,2-mannosidase	.0E+00
CNBG_9313	CNBG_9313-t26_1	C. deuterogattii R265	KQ410563:85,561..89,006(-)	carbohydrate binding protein	1.6E-121
CGB_E6120W	CGB_E6120W-t26_1	C. gattii WM276	CP000290:1,169,905..1,172,487(+)	endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha-mannosidase (ER alpha-1,2-mannosidase)	.0E+00
CGB_G2080C	CGB_G2080C-t26_1	C. gattii WM276	CP000292:392,095..394,973(-)	mannosyl-oligosaccharide 1,2-alpha-mannosidase	.0E+00
CGB_K0370C	CGB_K0370C-t26_1	C. gattii WM276	CP000296:94,573..97,577(-)	carbohydrate binding protein	3.4E-99
CNAG_02081	CNAG_02081-t26_1	C. neoformans var. grubii H99	CP003825.1:1,248,606..1,251,401(+)	mannosyl-oligosaccharide alpha-1,2-mannosidase	.0E+00
CNAG_03240	CNAG_03240-t26_1	C. neoformans var. grubii H99	CP003827.1:419,423..422,891(-)	mannosyl-oligosaccharide 1,2-alpha-mannosidase	.0E+00

Note: You can further explore clusters and other data in MycoCosm CAZy Browser as was shown previously.

3. Click on the Synteny shortcut to examine tracks in closely related species.



- Next, let's explore synteny in Basidiomycota phylum. Click on the *View in genome browser* button to be re-directed to GBrowse session.



- Activate custom tracks by clicking on the Select Tracks tab.
- Navigate to the *Orthology and synteny* menu and click on the “showing... subtracks” link. Now you have an option to select tracks for Basidiomycetes.

Select the tracks you wish to display. Sort the tracks by clicking on the column headings, or by clicking any of the buttons below.

Select	Kingdom	Class	Phylum	Genus
All off	All	All	All	All
All on	All	All	All	All
<input checked="" type="checkbox"/>	Fungi	Tremellomycetes	Basidiomycota	Filobasidiella
<input checked="" type="checkbox"/>	Fungi	Tremellomycetes	Basidiomycota	Filobasidiella
<input checked="" type="checkbox"/>	Fungi	Tremellomycetes	Basidiomycota	Filobasidiella
<input checked="" type="checkbox"/>	Fungi	Tremellomycetes	Basidiomycota	Filobasidiella
<input checked="" type="checkbox"/>	Fungi	Tremellomycetes	Basidiomycota	Filobasidiella
<input checked="" type="checkbox"/>	Fungi	Tremellomycetes	Basidiomycota	Filobasidiella
<input checked="" type="checkbox"/>	Fungi	Tremellomycetes	Basidiomycota	Filobasidiella
<input checked="" type="checkbox"/>	Fungi	Tremellomycetes	Basidiomycota	Filobasidiella
<input checked="" type="checkbox"/>	Fungi	Agaricomycetes	Basidiomycota	Coprinopsis
<input checked="" type="checkbox"/>	Fungi	Agaricomycetes	Basidiomycota	Coprinopsis
<input checked="" type="checkbox"/>	Fungi	Agaricomycetes	Basidiomycota	Phanerochaete
<input checked="" type="checkbox"/>	Fungi	Agaricomycetes	Basidiomycota	Phanerochaete

Once you are done selecting tracks, click on the Change button at the bottom of the pop-up window.

7. Is the region containing this gene syntenic in all species you selected?



- What can you conclude about the conservation of this gene across various species?
- What is the direction of the CNBG_9313 (highlighted in red) gene relative to the chromosome?
- What genes are upstream or downstream of the CNBG_9313?
- Do you observe changes in the number of exons?
- Notice that some of the genomes have contigs that are not contiguous. Why is that?
- Mouse over the two contigs and look at the information in the popups – do these pieces belong to the same chromosome? What does this mean?
- Observe the last track on the bottom of the screen – *Ustilago maydis*. Why do you think this gene is not detected here? Hint: examine contigs.

- Examine neighboring genes in *Cryptococcus* species. Which genes have undergone expansions or possible truncations (highlighted in blue)?
8. Navigate to FOXG_17458, a hypothetical protein in *Fusarium oxysporum* f. sp. *lycopercisi* 4287

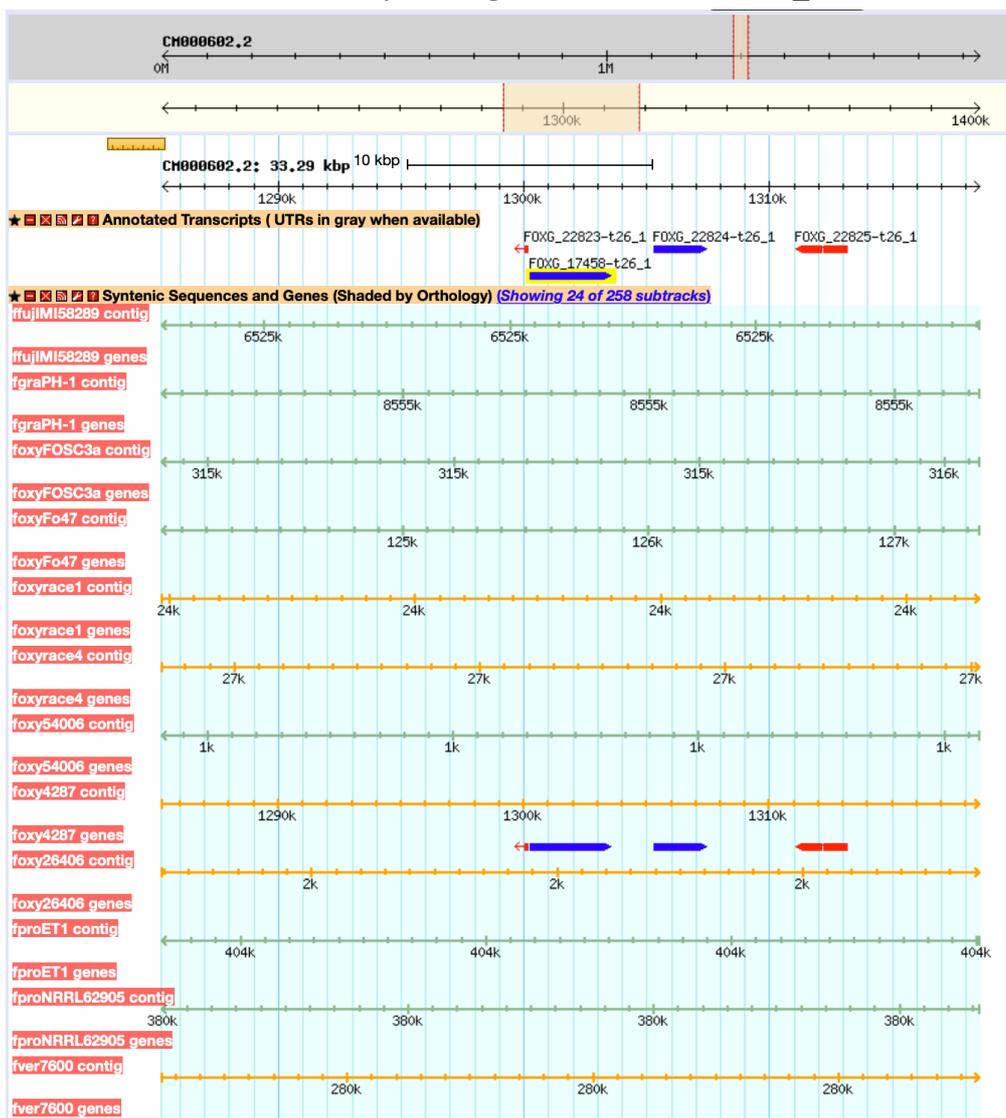
Select the tracks you wish to display. Sort the tracks by clicking on the column headings, or by clicking and dragging rows into position.

Syntenic Sequences and Genes (Shaded by Orthology) Subtracks

Select	Kingdom	Class	Phylum	Genus	Species	Organism
All off	(All)	(All)	(All)	(Fusarium)	(All)	(All)
All on	(All)	(All)	(All)	(Fusarium)	(All)	(All)
<input checked="" type="checkbox"/>	Fungi	Sordariomycetes	Ascomycota	Fusarium	Fusarium fujikuroi	Fusarium fujikuroi IMI 58289
<input checked="" type="checkbox"/>	Fungi	Sordariomycetes	Ascomycota	Fusarium	Fusarium fujikuroi	Fusarium fujikuroi IMI 58289
<input checked="" type="checkbox"/>	Fungi	Sordariomycetes	Ascomycota	Fusarium	Fusarium graminearum	Fusarium graminearum PH-1
<input checked="" type="checkbox"/>	Fungi	Sordariomycetes	Ascomycota	Fusarium	Fusarium graminearum	Fusarium graminearum PH-1
<input checked="" type="checkbox"/>	Fungi	Sordariomycetes	Ascomycota	Fusarium	Fusarium oxysporum	Fusarium oxysporum FOSC 3-a
<input checked="" type="checkbox"/>	Fungi	Sordariomycetes	Ascomycota	Fusarium	Fusarium oxysporum	Fusarium oxysporum FOSC 3-a
<input checked="" type="checkbox"/>	Fungi	Sordariomycetes	Ascomycota	Fusarium	Fusarium oxysporum	Fusarium oxysporum Fo47
<input checked="" type="checkbox"/>	Fungi	Sordariomycetes	Ascomycota	Fusarium	Fusarium oxysporum	Fusarium oxysporum Fo47
<input checked="" type="checkbox"/>	Fungi	Sordariomycetes	Ascomycota	Fusarium	Fusarium oxysporum	Fusarium oxysporum f. sp. cubense race 1
<input checked="" type="checkbox"/>	Fungi	Sordariomycetes	Ascomycota	Fusarium	Fusarium oxysporum	Fusarium oxysporum f. sp. cubense race 1
<input checked="" type="checkbox"/>	Fungi	Sordariomycetes	Ascomycota	Fusarium	Fusarium oxysporum	Fusarium oxysporum f. sp. cubense race 4
<input checked="" type="checkbox"/>	Fungi	Sordariomycetes	Ascomycota	Fusarium	Fusarium oxysporum	Fusarium oxysporum f. sp. cubense race 4
<input checked="" type="checkbox"/>	Fungi	Sordariomycetes	Ascomycota	Fusarium	Fusarium oxysporum	Fusarium oxysporum f. sp. cubense tropical race 4
<input checked="" type="checkbox"/>	Fungi	Sordariomycetes	Ascomycota	Fusarium	Fusarium oxysporum	Fusarium oxysporum f. sp. cubense tropical race 4
<input checked="" type="checkbox"/>	Fungi	Sordariomycetes	Ascomycota	Fusarium	Fusarium oxysporum	Fusarium oxysporum f. sp. lycopersici 4287
<input checked="" type="checkbox"/>	Fungi	Sordariomycetes	Ascomycota	Fusarium	Fusarium oxysporum	Fusarium oxysporum f. sp. lycopersici 4287
<input checked="" type="checkbox"/>	Fungi	Sordariomycetes	Ascomycota	Fusarium	Fusarium oxysporum	Fusarium oxysporum f. sp. melonis 26406
<input checked="" type="checkbox"/>	Fungi	Sordariomycetes	Ascomycota	Fusarium	Fusarium oxysporum	Fusarium oxysporum f. sp. melonis 26406
<input checked="" type="checkbox"/>	Fungi	Sordariomycetes	Ascomycota	Fusarium	Fusarium proliferatum	Fusarium proliferatum ET1
<input checked="" type="checkbox"/>	Fungi	Sordariomycetes	Ascomycota	Fusarium	Fusarium proliferatum	Fusarium proliferatum ET1
<input checked="" type="checkbox"/>	Fungi	Sordariomycetes	Ascomycota	Fusarium	Fusarium proliferatum	Fusarium proliferatum strain NRRL62905
<input checked="" type="checkbox"/>	Fungi	Sordariomycetes	Ascomycota	Fusarium	Fusarium proliferatum	Fusarium proliferatum strain NRRL62905
<input checked="" type="checkbox"/>	Fungi	Sordariomycetes	Ascomycota	Fusarium	Fusarium verticillioides	Fusarium verticillioides 7600
<input checked="" type="checkbox"/>	Fungi	Sordariomycetes	Ascomycota	Fusarium	Fusarium verticillioides	Fusarium verticillioides 7600

Semi-transparent overlap | Cancel | Change

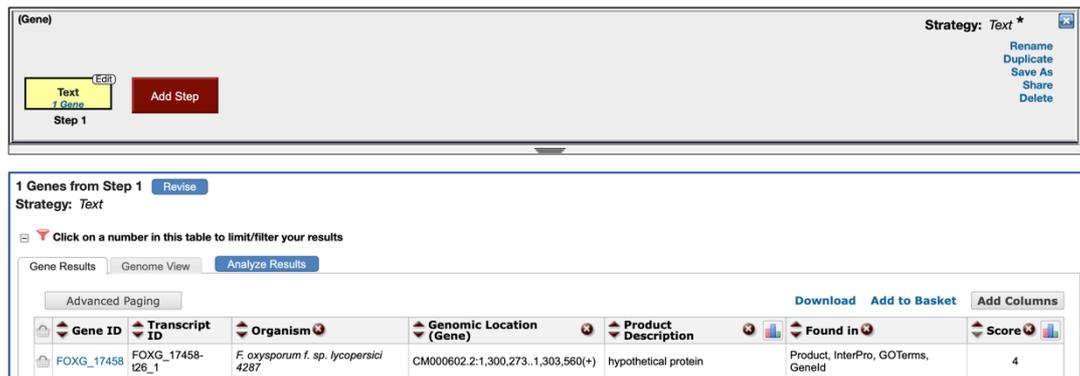
- a. Generate GBrowse view of syntenic genes in *Fusarium* species only:
Notice that there are no syntenic genes shown for FOXG_17458:



Why do you think this is?

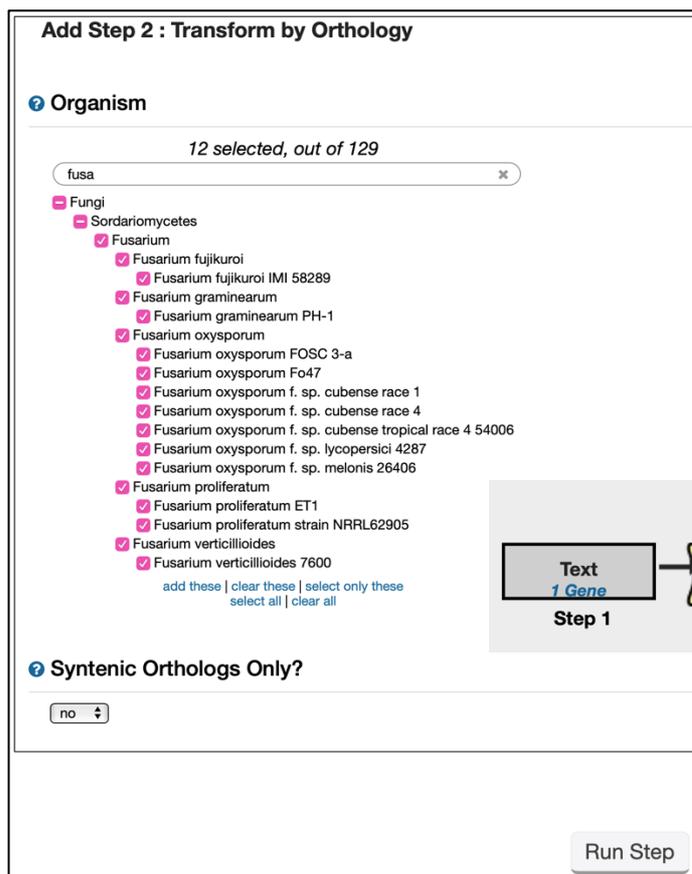
Investigate this further by looking into non-syntenic *Fusarium* orthologs in FungiDB and examine Fusarium resources offered at MycoCosm.

- b. Create a search for FOXG_17458. To generate a search query with a single gene, use the text search box at the top of FungiDB page:



Gene ID	Transcript ID	Organism	Genomic Location (Gene)	Product Description	Found In	Score
FOXG_17458	FOXG_17458-t26_1	<i>F. oxysporum f. sp. lycopersici</i> 4287	CM000602.2:1,300,273..1,303,560(+)	hypothetical protein	Product, InterPro, GOTerms, GeneID	4

- c. Next, look for non-syntenic orthologs in *Fusarium* species:



Add Step 2 : Transform by Orthology

Organism

12 selected, out of 129

fusa

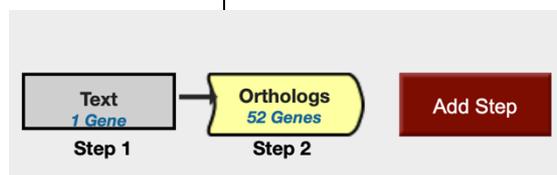
- Fungi
 - Sordariomycetes
 - Fusarium
 - Fusarium fujikuroi
 - Fusarium fujikuroi IMI 58289
 - Fusarium graminearum
 - Fusarium graminearum PH-1
 - Fusarium oxysporum
 - Fusarium oxysporum FO3C 3-a
 - Fusarium oxysporum Fo47
 - Fusarium oxysporum f. sp. cubense race 1
 - Fusarium oxysporum f. sp. cubense race 4
 - Fusarium oxysporum f. sp. cubense tropical race 4 54006
 - Fusarium oxysporum f. sp. lycopersici 4287
 - Fusarium oxysporum f. sp. melonis 26406
 - Fusarium proliferatum
 - Fusarium proliferatum ET1
 - Fusarium proliferatum strain NRRL62905
 - Fusarium verticillioides
 - Fusarium verticillioides 7600

add these | clear these | select only these | select all | clear all

Syntenic Orthologs Only?

no

Run Step



What can you conclude about conservation and function of this gene?

- d. Navigate to MycoCosm main page and select a *Fusarium oxysporum* f. sp. *lycopersici* strain 4287 genome. [genome.jgi.doe.gov/Fusox2]

Home • **Fusarium oxysporum f. sp. lycopersici 4287 v2**

SEARCH BLAST BROWSE ANNOTATIONS ▾ MCL CLUSTERS SYNTENY DOWNLOAD INFO HOME **HELP!**



The genome of *Fusarium oxysporum* f. sp. *lycopersici* strain 4287 (race 2, VCG 0030) was sequenced by the [Broad Institute](#) and the text below is copied from there. In order to allow comparative analyses with other fungi, a copy of this genome was imported into MycoCosm.

Fungi of the *Fusarium oxysporum* species complex (FOSC) are ubiquitous soil and plant inhabiting microbes. As plant pathogens, FOSC strains can cause wilt and root rot diseases on over 120 plant species (Michielse and Rep, 2009). Many FOSC strains can infect plant roots without apparent effect or can even protect plants from subsequent infection (Alabouvette et al., 2009). FOSC isolates also have been identified as human pathogens causing localized or disseminated infections that may become life-threatening in neutropenic individuals (O'Donnell et al., 2004).

The first genome made available in 2007 was from a tomato wilt strain FOL 4287 (NRRL 34936) which was used for comparative analysis with the genomes of *F. graminearum* and *F. verticillioides*. Results of this comparison led to the discovery of mobile supernumerary chromosomes in this strain of *F. oxysporum* f. sp. *lycopersici* (race 2 - VCG 0030) containing genes required for host specific infection and disease (Ma et al., 2010).

References :

- Alabouvette, C., Olivain, C., Migheli, Q., and Steinberg, C. (2009) Microbiological control of soil-borne phytopathogenic fungi with special emphasis on wilt-inducing *Fusarium oxysporum*. *New Phytologist* 184: 529-544.
- Ma, L.J., van der Does, H.C., Borkovich, K.A., Coleman, J.J., Daboussi, M.J., Di Pietro, A. et al. (2010) Comparative genomics reveals mobile pathogenicity chromosomes in *Fusarium*. *Nature* 464: 367-373.
- O'Donnell, K., Sutton, D.A., Rinaldi, M.G., Magnon, K.C., Cox, P.A., Revankar, S.G. et al. (2004) Genetic diversity of human pathogenic members of the *Fusarium oxysporum* complex inferred from multilocus DNA sequence data and amplified fragment length polymorphism analyses: Evidence for the recent dispersion of a geographically widespread clonal lineage and nosocomial origin. *Journal of Clinical Microbiology* 42: 5109-5120.

Fusarium wilt of tomato caused by *Fusarium oxysporum* f. sp. *lycopersici*.
Image Credit: David B. Langston, University of Georgia, [Bugwood.org](#)

- e. Use the Fusox2 portal's search page to identify the proteinID of "FOXG_17458T0" (Transcript 0 of FOXG_17458). You will find that the proteinID of FOXG_17458 in Fusox2 is 23236.

FOXG_17458T0

Search By: Across: Terms:

Download

Total genes found: 1

Gene	Gene Ontology	Annotations
Portal: Fusox2 Portal Name: Fusarium oxysporum f. sp. lycopersici 4287 v2 Protein Id: 23236 Transcript Id: 23236 Location: Scaffold_51:76759-80046 Model Name: FOXG_17458T0 Track: ExternalModels	GO:0003677 • DNA binding GO:0003700 • transcription factor activity, sequence-specific DNA binding GO:0005634 • nucleus GO:0006351 • transcription, DNA-templated GO:0006355 • regulation of transcription, DNA-templated GO:0008270 • zinc ion binding	PF04082 • Fungal specific transcription factor domain PF00172 • Fungal Zn(2)-Cys(6) binuclear cluster domain IPR007219 • Transcription_factor_dom_fun IPR001138 • Zn2-C6_fun-type_DNA-bd IPR002409 • missing_ipr002409

- f. Click on MCL clusters tab and then use the pull down menu to select clustering run "Fusarium-orthomcl 1.5.2900".

MCL Clusters • *Fusarium oxysporum* f. sp. *lycopersici* 4287 v2

SEARCH BLAST BROWSE ANNOTATIONS MCL CLUSTERS SYNTENY DOWNLOAD INFO HOME HELP!

Run **Fusox2 comparative clustering.829**

Multigene clusters: 76,126
Average multigene cluster size: 5,743
Singletons: 5,743
Tracks: 5

Show Charts:
Show Counters:
Show Domains:

Filter by keywords: Update

Rows: 19 20 21 22 23 24 25 26 27 28 29 30 Last 100 rows per page

Domains

oxigenase 363 • No Domains 6 • Zinc-binding dehydrogenase 3 • Shikimate / anase 1

uperfamily 262 • No Domains 95 • Sugar (and other) transporter 4

<https://genome.jgi.doe.gov/clm/run/Fusarium-orthomcl.2900?organism=Fusox2>

- g. Enter keyword Fusox2.23236 (databaseID.proteinID) to find clusters with that protein in it. Remember, for FOXG_17458 (FOXG_17458T0 protein ID in MycoCosm is 23236 and genome ID is Fusox2)

JGI MycoCosm THE FUNGAL GENOMICS RESOURCE

JGI HOME GENOME PORTAL MYCOCOSM LOGIN

MCL Clusters • *Fusarium oxysporum* f. sp. *lycopersici* 4287 v2

SEARCH BLAST BROWSE ANNOTATIONS MCL CLUSTERS SYNTENY DOWNLOAD INFO HOME HELP!

Run **Fusarium-orthomcl 1.5.2900**

Multigene clusters: 23,505
Average multigene cluster size: 11.63
Created at: 15-Feb-2019

Models in multigene clusters: 273,394
Singletons: 17,851
Tracks: 18

Show Charts:
Show Counters:
Show Domains:

Download (as clusters CSV) (compressed by Gzip)

Filter by keywords: **Fusox2.23236** show any cluster Update

Rows: 41,356 Page: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 Last 100 rows per page

Domains

ABC transporter 330 • CDR ABC transporter 326 • ABC-2 type transporter 311 • ABC-transporter N-terminal 192
Pyoverdine/diacyltosine biosynthesis protein 15

Glycosyl hydrolase family 3 N-terminal domain 231 • Glycosyl hydrolase family 3 C-terminal domain 231
PA14 domain 157
Fibronectin type III-like domain 156 • Fungal specific transcription factor domain 21 • Fungal Zn(2)-Cys(6) binuclear cluster domain 14 • Glutathione-dependent formaldehyde-activating enzyme 6 • No Domains 1

Acyl transferase domain 208 • Beta-ketoacyl synthase, N-terminal domain 206 • Beta-ketoacyl synthase, C-terminal domain 206
KR domain 200 • Methyltransferase domain 154 • Phosphopantetheine attachment site 147
Polyketide synthase dehydratase 146 • Zinc-binding dehydrogenase 120 • Alcohol dehydrogenase GroCS-like domain 101 • AMP-binding oxzyme 45
Male sterility protein 44 • Condensation domain 42 • p13745 24
Choline/Carnitine o-acyltransferase 19 • short chain dehydrogenase 6 • Zinc-binding dehydrogenase 6 • AMP-binding enzyme C-terminal domain 2 • Serine hydrolase (FSH1) 1 • Methyltransferase domain 1 • Sugar (and other) transporter 1

JGI MycoCosm THE FUNGAL GENOMICS RESOURCE

JGI HOME GENOME PORTAL MYCOCOSM LOGIN

MCL Clusters • *Fusarium oxysporum* f. sp. *lycopersici* 4287 v2

SEARCH BLAST BROWSE ANNOTATIONS MCL CLUSTERS SYNTENY DOWNLOAD INFO HOME HELP!

Run **Fusarium-orthomcl 1.5.2900**

Multigene clusters: 23,505
Average multigene cluster size: 11.63
Created at: 15-Feb-2019

Models in multigene clusters: 273,394
Singletons: 17,851
Tracks: 18

Show Charts:
Show Counters:
Show Domains:

Download (as clusters CSV) (compressed by Gzip)

Filter by keywords: **Fusox2.23236** show any cluster Update

Rows: 1 100 rows per page

Domains

Fungal specific transcription factor domain 34 • Fungal Zn(2)-Cys(6) binuclear cluster domain 33 • No Domains 1 • 2OG-Fe(II) oxygenase superfamily 1

Fusco1: *Fusarium commune* MPI-SDFR-AT-0072 v1.0 FilteredModels1
Fusuf1: *Fusarium fujikuroi* IMI 58289 ExternalModels
Fusox2: *Fusarium oxysporum* f. sp. *lycopersici* 4287 v2 ExternalModels
Fusox2: *Fusarium oxysporum* MPI-SDFR-AT-0094 v1.0 FilteredModels1
Fusox1: *Fusarium oxysporum* MPI-SDFR-AT-0094 v1.0 FilteredModels1
Fusps1: *Fusarium pseudograminearum* CS3096 ExternalModels
Fusso1: *Fusarium solani* MPI-SDFR-AT-0091 v1.0 FilteredModels1
FusppF23: *Fusarium* sp. FSSC 23 v1.0 FilteredModels1
Fusm1: *Fusarium tricinatum* MPI-SDFR-AT-0044 v1.0 FilteredModels1
Fusven1: *Fusarium venenatum* MPI-CAGE-CH-0201 v1.0 FilteredModels1

Fuseq1: *Fusarium equiseti* MPI-CAGE-AA-0113 v1.0 FilteredModels1
Fusgr1: *Fusarium graminearum* v1.0 ExternalModels
FusoxT415: *Fusarium oxysporum* f. sp. *pisii* T415 v1.0 FilteredModels1
Fusoxys1: *Fusarium oxysporum* MPI-CAGE-CH-0212 v1.0 FilteredModels1
Fusar1: *Fusarium redolens* MPI-CAGE-AT-0023 v1.0 FilteredModels1
FusppF10: *Fusarium* sp. FSSC 10 v1.0 FilteredModels1
Fustr1: *Fusarium tricinatum* MPI-SDFR-AT-0068 v1.0 FilteredModels1
Fusve2: *Fusarium verticillioides* 7600 v2 ExternalModels
Necha2: *Nectria haematococca* v2.0 FilteredModels1

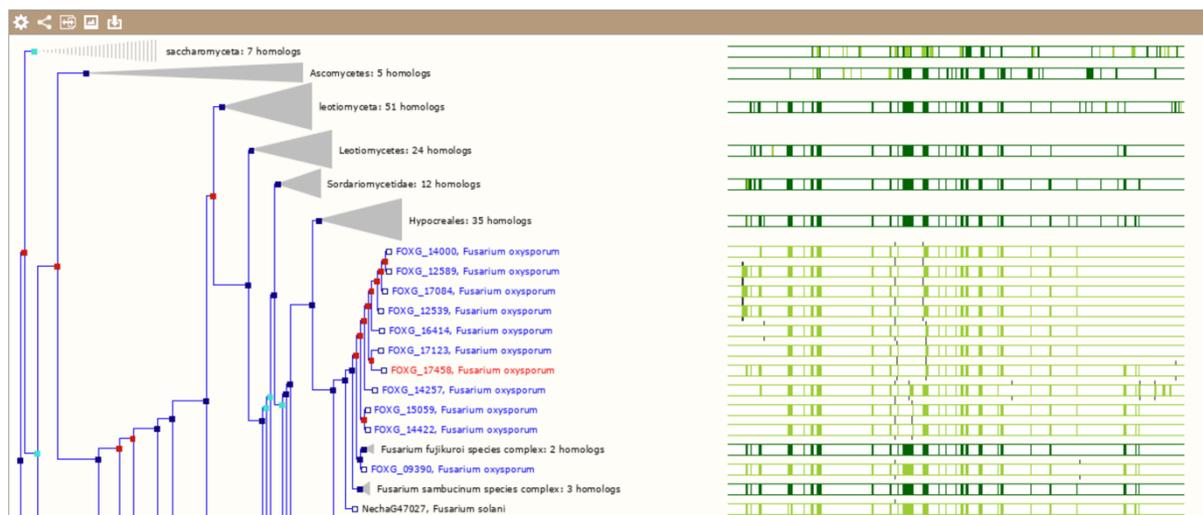
This will bring up cluster #386. Notice that this family is expanded only in the two known pathogens of the *Fusarium oxysporum* species complex with dispensable chromosomes (Fusox2 and FusoxT415), but not in other *Fusarium* species including endophytic *Fusarium oxysporum* like Fusoxys1 and Fusoxyl.

Now having this information at hand, you can either return to FungiDB and examine underlying transcriptomics, proteomics, *etc.* data or use other databases to enrich your analysis. For example:

- Navigate to Ensembl Fungi, search for FOXG_17458 and visualize the gene-tree:

The screenshot shows the Ensembl Fungi interface for the gene FOXG_17458. The main content area includes the following information:

- Gene: FOXG_17458**
- Description:** conserved hypothetical protein [Source:BROAD_F_oxysporum;Acc:FOXG_17458]
- Location:** Chromosome 14: 1,108,371-1,111,923 forward strand. FO2:CM000602.1
- About this gene:** This gene has 1 transcript (splice variant), 318 orthologues, 15 paralogues and is a member of 2 Ensembl protein families.
- Transcripts:** Hide transcript table
- Table:** A table with columns: Name, Transcript ID, bp, Protein, Biotype, UniProt, and Flags. The entry for FOXG_17458T0 is highlighted.
- Gene tree:** A section titled "Gene tree" with a link to the GeneTree ENSGT0093000001158. Below it, statistics are provided:
 - Number of genes: 345
 - Number of speciation nodes: 270
 - Number of duplication nodes: 47
 - Number of ambiguous nodes: 26
 - Number of gene split events: 1
- Highlight annotations:** Hide annotations table

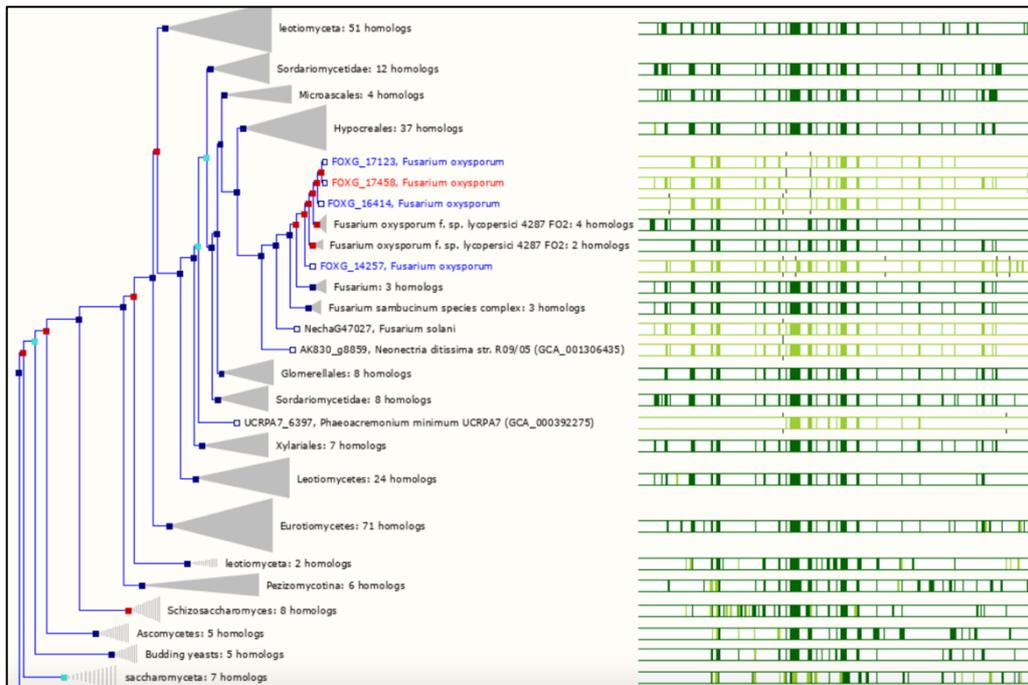


Take a look at the between species paralogues. Is your data consistent with observations in MycoCosm? (Hint: look for duplication nodes).

- Click on the link at the bottom of the gene tree image to view all paralogues on the tree:

View options:

- [View current gene only](#) (Default)
- [View paralogs of current gene](#)
- [View all duplication nodes](#)
- [View fully expanded tree](#)



- To export this data you can click on the *Download data for this image* button and choose form multiple formats:



File name:

File format:

[Preview](#) [Download](#) [Download Compressed](#)

Guide to file formats

CLUSTALW

```
CLUSTAL W(1.81) multiple sequence
homo_sapiens/1-465388 CCTCAGGACC
pan_troglydotes/1-465588 CCCAGGACC
**
homo_sapiens/1-465388 CCTCAGGACC
pan_troglydotes/1-465588 CCCAGGACC
*****
```

FASTA

```
>homo_sapiens/1-464388
CCTCAGGACCAGCCAGCAACCAACAGAT
CCGAGCGCCTTGAGCTGCCCTCTGGGCC
TGGACAGAGAGAGAACACAGCTGGCT
AGGGCCCTGGTTGGGGGTTAGATCAAG
CCAGCTGGATCCTGATATTGGCAACTC
CCAGGCTCTGTGCAAAAGTTGCTGTGT
AGGAAGACCTGGTGCCTCTGCCCTGTGT
AAAGATGGGGTGGTGTGATTCCTCT
GGGAGGGGAGAGAGAGGGCCCTGGG
AGCGTGGGCTCTAGCCAGTGGG
```

Mega

```
#mega
!Title: ProjectedMultiAlign;
!Format datatype=dna Identical=
#homo_sap CCTCAGGACC GACGGCAAC
#pan_trog -.C-.
#homo_sap CCCAGTGCCCT TCGACTGCCT
#pan_trog
#homo_sap TGGGACAGAG AGAGAACAC
```

MSF

```
ProjectedMultiAlign MSF: 2 Type:
Name: homo_sapiens/1-465388 Len
Name: pan_troglydotes/1-465588 Len
//
homo_sapiens/1-465388 CCTCAGGACC G
pan_troglydotes/1-465588 CCCAGGACC
homo_sapiens/1-465388 GGGTCAACAC C
```

Newick

```
((((((((BMSRPP0000015030_Tsub_10_07
BMSRTP10000002435_Tsub_10_103149))0;
BMSRPP0000015199_Gene_10_143462))0;
((BMSRPP0000015170_PDoc_10_042925;
BMSRPP0000016983_Anc_10_044847))0;
BMSRTP0000006940_On1_10_29611))0;0
BMSRCP0000004773_Ola_10_050113))0;
BMSRPP0000010385_Gene_10_380661))0;1
((BMSRPP0000013445_Anc_10_474771;
BMSRPP0000009974_Diver_10_048998))0;0
BMSRCP0000009962_Locu_10_219888))0;
((((((BMSRPP0000027524_Gene_10_03
BMSRPP0000015990_Mga_10_045749))0;
BMSRPP0000007411_Ap1a_10_122877))0;
```

Nexus

```
#NEXUS
[!Title: ProjectedMultiAlign]
begin data;
dimensions nst=0 nchar=465388;
format interleavedata=penda gap=
matrix
homo_sapiens CCTCAGGACC
pan_troglydotes CCCAGGACC
homo_sapiens GGGTCAACAC
pan_troglydotes GGGCCACAC
```

NHX

```
((((((((0.046093|&NHX:D=N:T=48
|0.06551|&NHX:D=N:T=8093))Poec
|0.359033|&NHX:D=N:T=8128))Oval
|((10.077336|&NHX:D=N:T=31033))
|0.099898|&NHX:D=N:T=99883))Tet
|0.160116|&NHX:D=N:T=69293))Pee
|0.37365|&NHX:D=N:T=8049))Acant
|0.780276|&NHX:D=N:T=8090))Acan
|(0.44137|&NHX:D=N:T=7994))
|0.582748|&NHX:D=N:T=7955))Otop
|0.225188|&NHX:D=N:T=7918))Neop
|(((0.031222|&NHX:D=N:T=90
```

OrthoXML

```
<?xml version="1.0" encod
<orthoXML xsi:schemaLocat
xmlns:xsi="http://www.w3.
<species NCB|TaxID="925
<database name="Unkno
<genes>
<gene id="6053741
<gene id="5945247
</genes>
```

Pfam

```
homo_sapiens/1-465388 CCTCAGGA
pan_troglydotes/1-465588 CCCAGGA
```

Phylip

```
2 465388
homo_sap1e CCTCAGGACC GACGGCAA
pan_trog1o CCCAGGACC GACGGCAA
GGGTCAACAC CCCAGTCC
GGGCCACAC CCCAGTCC
ACTGTGTGGC TTCAGCTTA
ACTGTGTGGC TTCAGCTTA
GCTCAGGACC CCTCTGGAT
GCTCGGGCA CCTCTGGAT
```

PhyloXML

```
<?xml version="1.0" encoding="UTF-8"?>
<phyloxml xsi:schemaLocation="http://www
<phyloxml root="tree" type="gene-1
```

PSI

```
homo_sapiens CCTCAGGACCAGCCAA
pan_troglydotes CCCAGGACCAGCCAA
```

Stockholm

```
# STOCKHOLM 1.0
```

Text

```
(B=0 T=Euteleostomi 10335f
---(B=67 T=Neopterygii 1:
----(B=2 T=Clupeomor
```

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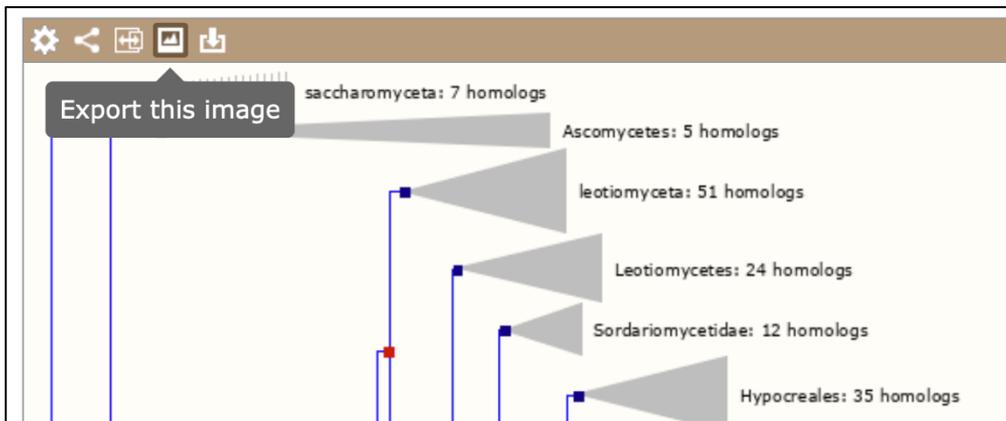


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