FungiDB: Synteny in JBrowse

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

1. Using Synteny tracks in FungiDB

- Initiate a gene search for Glycosyl hydrolase family 47 proteins in *Cryptococcus gatii R265. Use the InterPro Domain search and enter* **PF01532**.

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

- Click on the *Synteny* shortcut to examine tracks in closely related species.
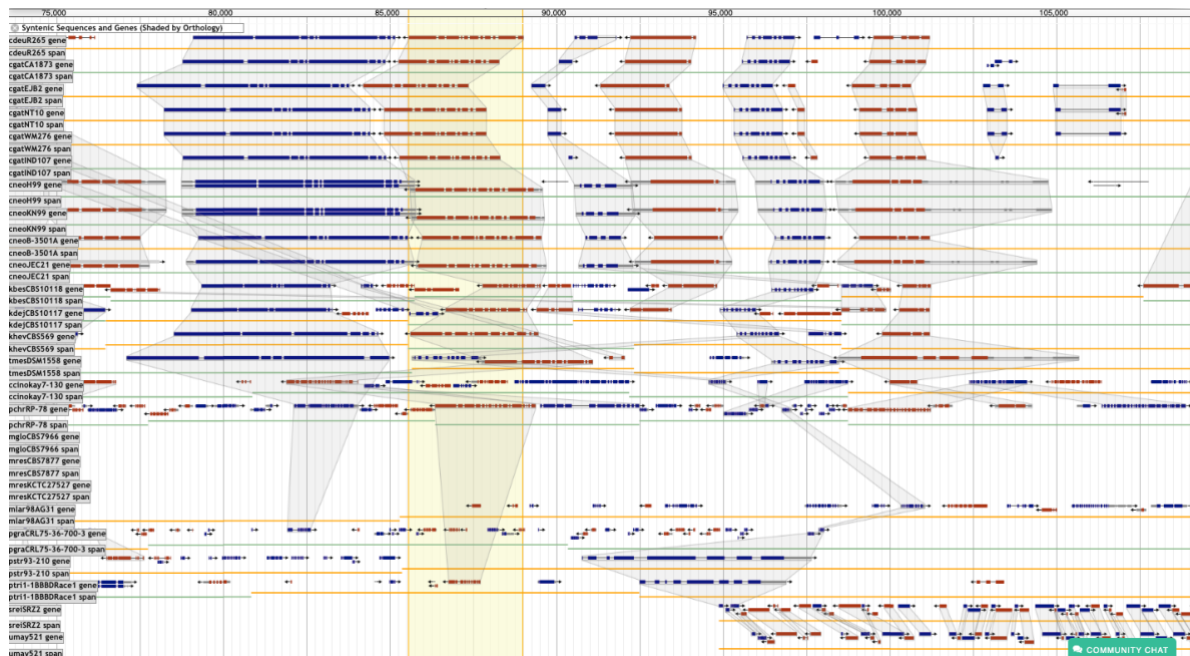
Let's explore synteny in Basiodiomycota. Click on the *View in genome browser* button to be re-directed to a JBrowse session and the activate custom tracks by clicking on the Select subtracks tab.
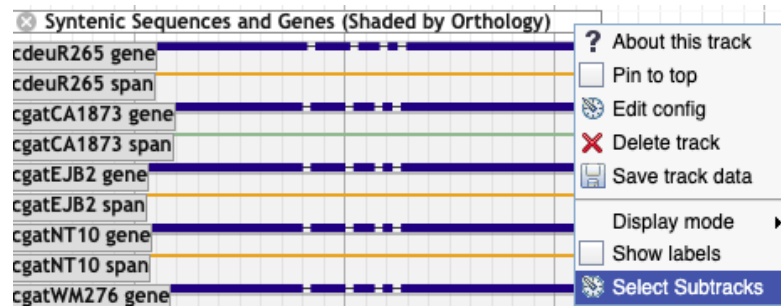
Is the region containing this gene syntenic in all species you selected?

- What can you conclude about the conservation of this gene across various species?

- What is the direction of the CNBG_9313 (highlighted in yellow) gene relative to the chromosome?

- Do you observe changes in the number of exons in different species?

- 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?

Mining synteny and orthology information for hypothetical genes.

1. Navigate to FOXG_17458, a hypothetical protein in *Fusarium oxysporum* f. sp. *lycopercisi* 4287

- View of syntenic genes in *Fusarium* species only:

Notice that there are no syntenic genes shown for FOXG_17458:
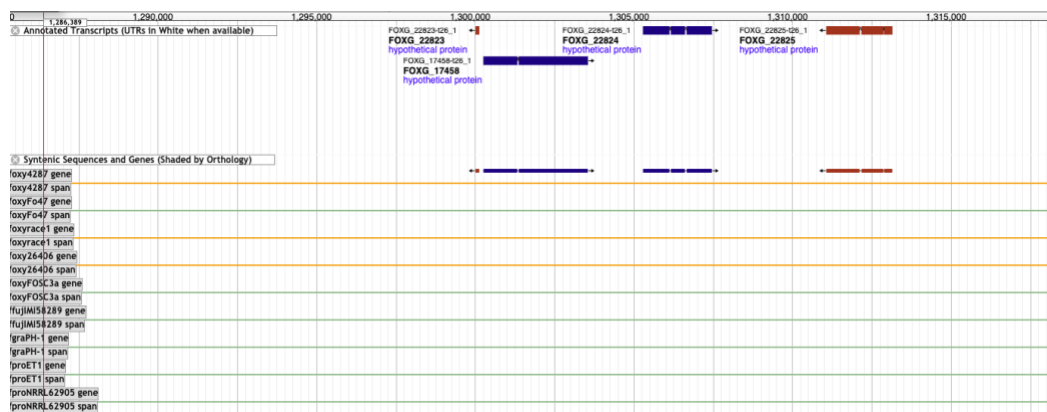
- Why do you think this is?

- Look into non-syntenic *Fusarium* orthologs in FungiDB and examine Fusarium resources offered at MycoCosm.

2. Using FungiDB site search, search for FOXG_17458 and export your results into the search strategy and look for non-syntenic orthologs in *Fusarium* species:
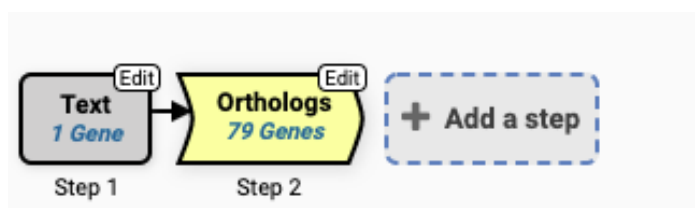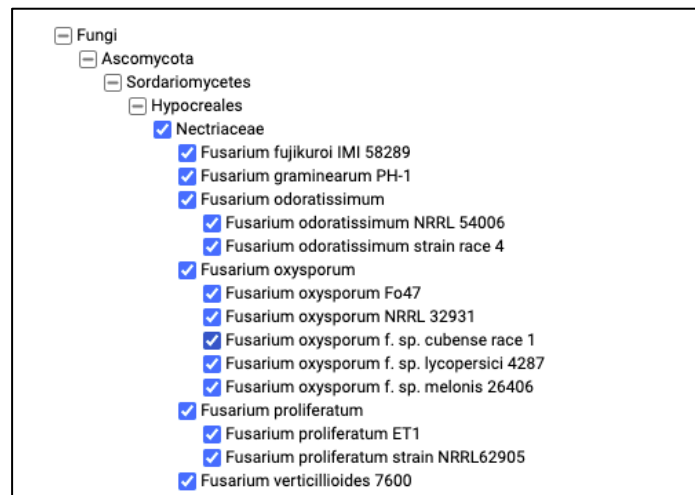
- Examine your results. What can you conclude about conservation and function of this gene?

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

Home • Fusarium oxysporum f. sp. lycopersici 4287 v2

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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).

Fusarium wilt of tomato caused by Fusarium oxysporum f.sp. lycopersici.
Image Credit: David B. Langston, University of Georgia, Bugwood.org

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 dispersal of a geographically widespread clonal lineage and nosocomial origin. Journal of Clinical Microbiology 42: 5109-5120.

- 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.

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

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

- 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)

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 Fusoxy1.

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:

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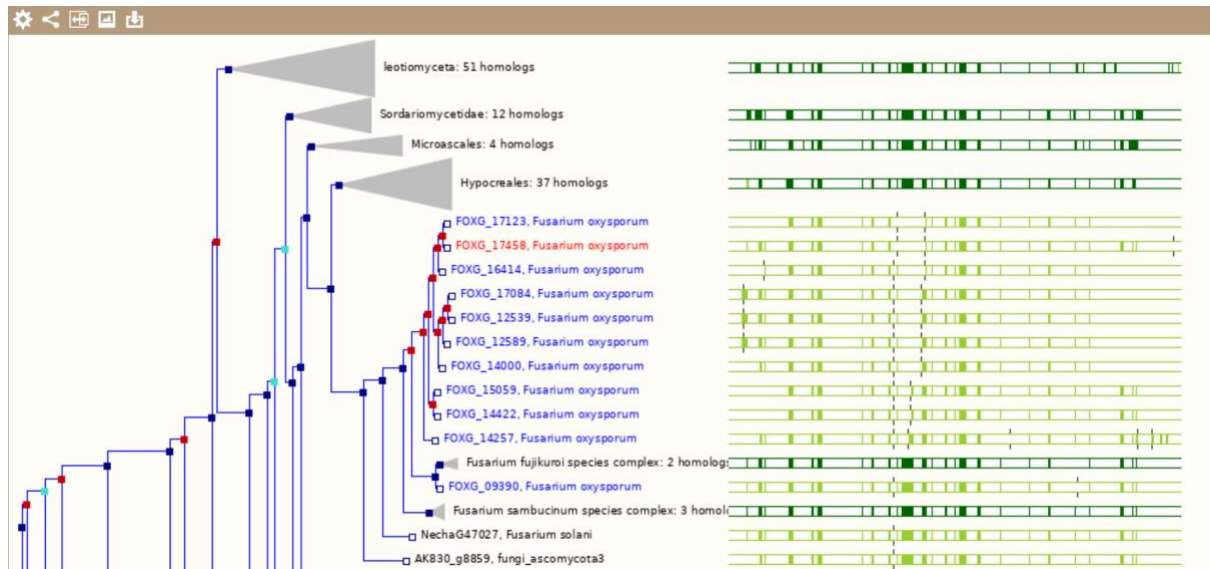
- To export this data you can click on the *Download data for this image* button and choose form multiple formats:

Or you can choose to download the image as shown by clicking on the Export this image button:

Image download

File name:

Fusarium oxysporum_FOXG_17458.pc

Select Format

- ● **PDF file** - Standard image as PDF file
- ○ **Presentation** - Saturated image, better suited to projectors
- ○ **Poster** - Very high resolution, suitable for posters and other large print uses
- ○ **Journal/report** - High resolution, suitable for printing at A4/letter size
- ○ **Web** - Standard image, suitable for web pages, blog posts, etc.
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