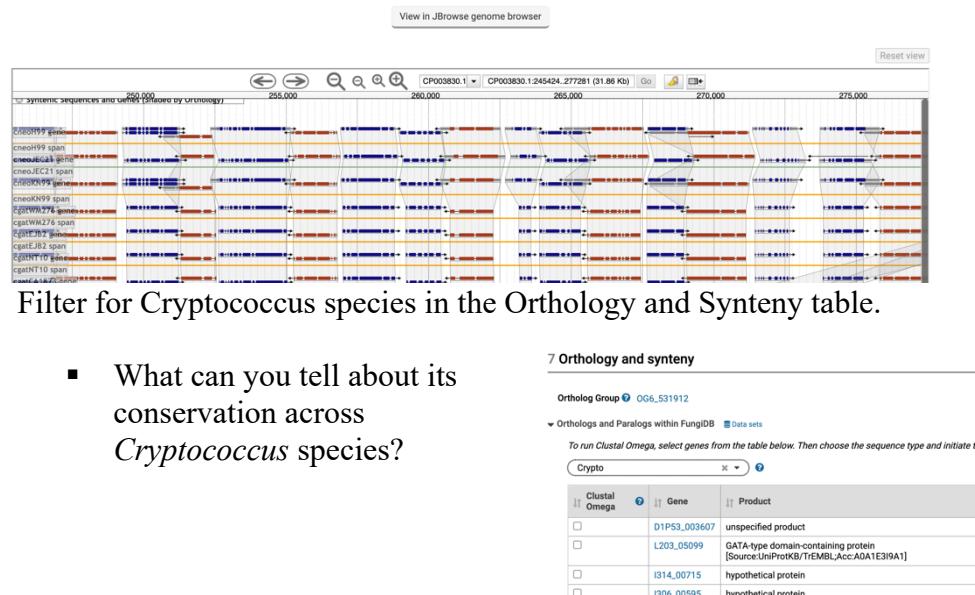


FungiDB: Synteny in JBrowse

- **Navigate to the gene record page for *Gat201* in *Cryptococcus neoformans* H99 and examine the evidence within the Orthology and Synteny section.**
 1. Use site search to locate the gene record page.
 2. Use the contents menu on the left to navigate to the Orthology and Synteny section.



- **Navigate to JBrowse and create a custom JBrowse view for this gene's synteny across *Cryptococcus*, *Malassezia*, and *Trichosporon*.**
 1. Click on the “View in JBrowse gene browser” button.
 2. When in JBrowse, left click at the end of the “Syntenic sequences and Genes (Shaded by Orthology)” tracks to bring up the pull-down menu.
 3. Click on the “Select subtracks” option.
 4. Use the main check box to clear all selections.
 5. Select tracks for *Cryptococcus*, *Malassezia*, and *Trichosporon* (*and don't forget save your choices by clicking on the “save” option at the bottom of the track*).

Gat201 is a positive regulator of titanization under specific conditions in *Cryptococcus*. Titan cell formation is a rare phenomenon in *C. neoformans/C. gattii* species complex. What can you conclude about the conservation of this gene across the selected fungal pathogens? Do the results make sense based on what you know about Gat201?

Examine neighboring genes in *Cryptococcus* species. Can you spot any genes that have undergone expansions, possible truncations or simply not present in all gene models?

Mining synteny and orthology information for hypothetical genes.

- Navigate to FOXG_17458 gene record page in FungiDB and view the Orthology and Synteny section.



Notice that this hypothetical protein in *Fusarium oxysporum* f. sp. *lycopercisi* 4287 has no syntenic orthologs. Why do you think this is?

How can you test if there are orthologs of this gene in other *Fusarium* species?

- Create a search strategy looking for orthologs of FOXG_17458 in *Fusarium* species.
 1. Use site search and export FOXG_17458 as a strategy step.
 2. Click on the Add Step button.
 3. Deploy the “Transform into related record” search and choose to transform genes into “Orthologs”
 4. Select all *Fusarium* species and click on the “Run Step” button.

- Examine phyletic distribution by clicking on the “Ortholog Group” link within the results table.

▼ Phylogenetic Distribution of Proteins [?](#) [Download](#)

Numbers refer to the number of proteins in that organism or taxonomic group.

Hide zero counts

fusarium

		x	?
Eukaryota (EUKA)	514		
Fungi (FUNG)	514		
Ascomycota (ASCO)	465		
Fusarium circinatum NRRL 25331 (fcir)	7		
Fusarium fujikuroi IMI 58289 (ffuj)	7		
Fusarium graminearum PH-1 (fgra)	2		
Fusarium mangiferae MRC7560 (fman)	6		
Fusarium odoratissimum NRRL 54006 (foxc)	9		
Fusarium odoratissimum strain race 4 (foxt)	9		
Fusarium oxysporum Fo47 (foxf)	3		
Fusarium oxysporum NRRL 32931 (foxa)	4		
Fusarium oxysporum f. sp. conglutinans Fo5176 (focf)	10		
Fusarium oxysporum f. sp. cubense race 1 (foxr)	6		
Fusarium oxysporum f. sp. lycopersici 4287 (foxy)	14		
Fusarium oxysporum f. sp. melonis 26406 (foxm)	8		
Fusarium proliferatum ET1 (fpzo)	8		
Fusarium proliferatum strain NRRL62905 (fpzn)	6		
Fusarium vanettenii 77-13-4 (fvan)	8		
Fusarium verticillioides 7600 (fver)	4		

Is there evidence of possible expansion across different Fusarium species?

- Examine evidence for non-syntenic orthologs in MycoCosm.

1. 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

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 (Michelise 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., Miglieli,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.

2. Use the Fusox2 portal's search page to identify the proteinID of "FOGX_17458T0" (Transcript 0 of FOXG_17458). You will find that the proteinID of FOXG_17458 in Fusox2 is 23236.

FOXG_17458T0	<input type="button" value="Search"/>	
Search By:	Across: Terms:	
Keywords	Default exact - fast	
<input type="button" value="Download"/>	as CSV compressed by Gzip	
Total genes found: 1 25		
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 • DNA-binding transcription factor activity GO:0005634 • nucleus GO:0006351 • DNA-templated transcription GO:0006355 • regulation of DNA-templated transcription GO:0008270 • zinc ion binding	PF04082 • Fungal specific transcription factor domain PF00172 • Fungal Zn(2)-Cys(6) binuclear cluster domain IPR007219 • IPR001138 • IPR002409 • missing_ipr002409

3. 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**

Filter: **Fusarium-orthomcl 1.5.2900**

Rows: any all

Clusters: 76,126 Singletons: 5,743 Tracks: 5

Show Charts: Show Counters: Show Domains:

21 22 23 24 25 26 27 28 29 30 Last 100 rows per page

Domains

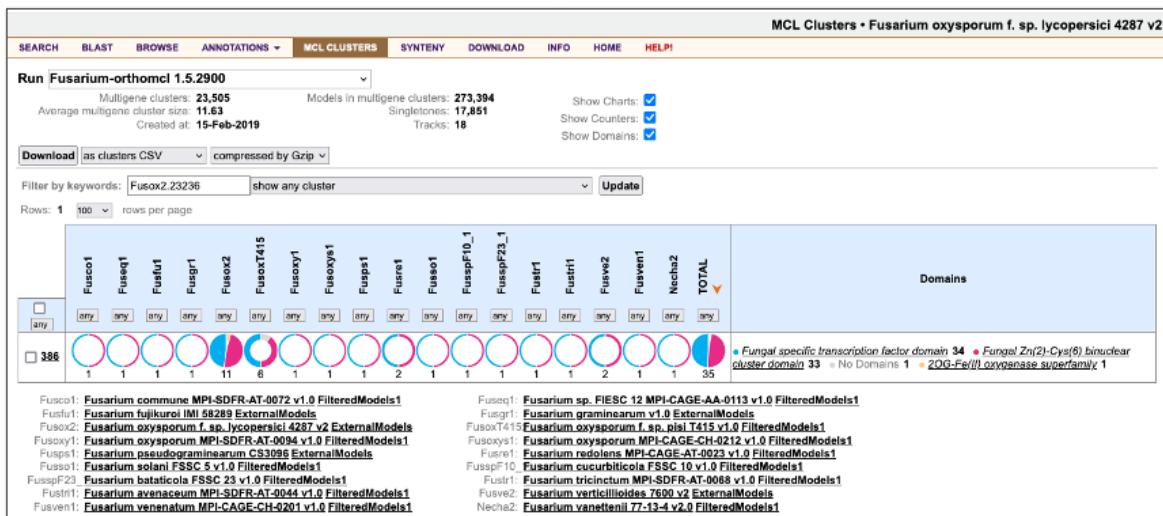
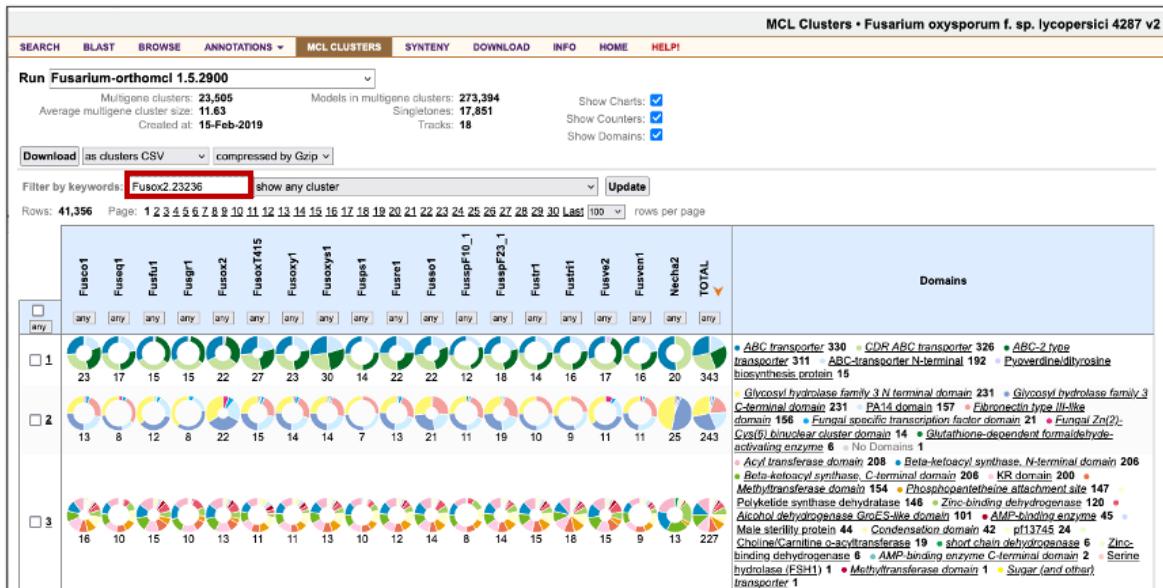
Enzyme 363 • No Domains 6 • Zinc-binding dehydrogenase 3 • Shikimate / isoleucine 1

Transporter 262 • No Domains 95 • Sugar (and other) transporter 4 • ABC transporter 1

Methyltransferase 182 • No Domains 132 • Methyltransferase domain 41 • ABC transporter 1

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

4. Enter keyword Fusox2.23236 (databaseID.proteinID) and select “Update” 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 Fusoxyl1.

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:

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

e! EnsemblFungi ▾ HMMER | BLAST | BioMart | Tools | Downloads | Documentation | Website help

Fusarium oxysporum (FO2) ▾

Location: 14:1,108,371-1,111,923 Gene: FOXG_17458 Transcript: FOXG_17458T0 Jobs ▾

Gene-based displays

- Summary
- Splice variants
- Transcript comparison
- Gene alleles
- Sequence
- Secondary Structure
- Gene families
- Literature
- Fungal Compara
- Genomic alignments
- Gene tree**
- Gene gain/loss tree
- Orthologues
- Paralogues
- Pan-taxonomic Compara
- Gene Tree
- Orthologues
- Ontologies
- GO: Biological process
- GO: Molecular function
- GO: Cellular component
- PHI: Phibase identifier
- Phenotypes
- Genetic Variation
- Variant table
- Variant image
- Structural variants
- Gene expression
- Pathway
- Regulation
- External references

Gene: FOXG_17458

Description: conserved hypothetical protein [Source:BROAD_F_oxysporum;Acc:FOGX_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

Name	Transcript ID	bp	Protein	Biotype	UniProt	Flags
Novel	FOGX_17458T0	2832	943aa	Protein coding	J9NQH9	rf

Gene tree ?

GeneTree ENSGT0093000001158

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

Legend:

- Branch Length: $\times 1$ branch length, $\times 10$ branch length, $\times 100$ branch length
- Nodes:
 - Gene node (blue square)
 - speciation node (black square)
 - duplication node (red square)
 - ambiguous node (green square)
 - gene split event (purple square)
- Collapsed Nodes:
 - collapsed sub-tree (grey triangle)
 - collapsed (paralog) (blue triangle)
 - collapsed (gene of interest) (red triangle)
- Collapsed Alignments:
 - 0 - 33% aligned AA (light green)
 - 33 - 66% aligned AA (medium green)
 - 66 - 100% aligned AA (dark green)

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:

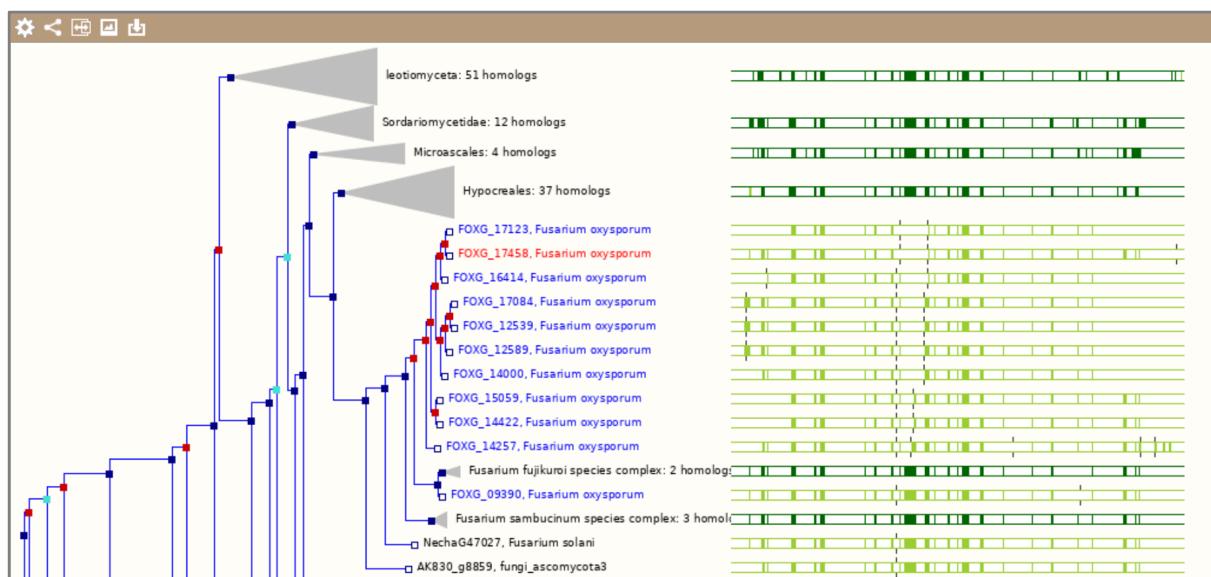
Expanded Alignments
gap
aligned AA
Add/remove tracks | Share | Resize image | Export image | Export

View options:

- View current gene only (Default)
- View paralogues of current gene
- View all duplication nodes
- View fully expanded tree
- Collapse all the nodes at the taxonomic rank -- Select a rank --

Use the 'configure page' link in the left panel to set the default. Further options are available from menus on individual tree nodes.

Ensembl Fungi release 56 - Feb 2023 © EMBL-EBI



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

Download data from this image

Ascomycetes: 5 homologs

leotiomyceta: 51 homologs

File name: FOXG_17458_gene_tree

File format: FASTA

Preview Download Download Compressed

Guide to file formats

CLUSTALW	FASTA	Mega	MSF	Newick
<pre>CLUSTAL W(1.81) multiple sequence homo_sapiens 1-465588 CCTCAGAAC pan_trichodites 1-465588 CCCAGAAC *****</pre>	<pre>>homo_sapiens 1-464300 CCTCAGAACCGACGGAAACCAACAGAA CCCAGTCCTTGCAGTCGCTCTGGGCC TGGGACAGAGAGAACCCAGCTGCGCT AGGGGCCCTGTGGGGGGTTAGATCAAAC CCGAGCTGGATCTGTATTGGCACCTC CCAGGCTCTGTGCAAAAAGGTTGCTGTG/ AGGAAGACCCGTGGTGCCTCTGCTGTT AAAGATGGGGGGTGGTGTGGATTCTCTT GGGAGAGGGAGAAGAAAGGGGCCCTGGG CACCCCTGGGGCTCTAGCCCCACTGGGC</pre>	<pre>#mega !Title: ProjectedMultiAlign; !Format datatype=dna identical=.</pre>	<pre>ProjectedMultiAlign MSF: 2 Type:- Name: homo_sapiens 1-465588 Le Name: pan_trichodites 1-465588 Le //</pre>	<pre>(((((EBESTRUP00000015630_Trib: 0.07 ENSTT190000002435_7nig: 0.103149):0, ENSGCP00000015199_Gacu: 0.161942):0, (ENSPFVQ000000001957_Pfor: 0.042925, ENSOPIP000000000993_Xmc: 0.050011):0, ENSOIIP00000000064997_Cat: 0.058211):0, ENSOILP00000004773_Olat: 0.050213):0, ENSGMP00000010385_Gmer: 0.360616):0.1 ((ENSGAP00000015990_Mgal: 0.043749):0, ENSAFLP00000007411_Apia: 0.122877):0,</pre>
Nexus	NX	OrthoXML	Pfam	Phylip
<pre>#NEXUS [TITLE: ProjectedMultiAlign] begin date; dimensions ntax=2 nchar=465588; format interleave datatype=dna gap=. matrix homo_sapiens CCTCAGAAC pan_trichodites CCCAGAAC homo_sapiens GGGCAACAC pan_trichodites GGGCAACAC</pre>	<pre>((((0.046083 64NHX:D=N:T=48 :0.065551 64NHX:D=N:t=8083) Root :0.359035 64NHX:D=N:t=8128) oval ((0.077336 64NHX:D=N:t=31033), 0.099898 64NHX:D=N:t=99883)) tet (0.102771 64NHX:D=N:t=8491) canc :0.27365 64NHX:D=N:t=8491) ancant :0.780276 64NHX:D=N:t=8090) Acant :0.41377 64NHX:D=N:t=7994), :0.582768 64NHX:D=N:t=7955) otop :0.225188 64NHX:D=N:T=7918) Neop ((((0.031221 64NHX:D=N:T=90</pre>	<pre><?xml version="1.0" encoding="UTF-8"?> <xsi: schemaLocation="http://www.w3.org/2001/XMLSchema.xsd" xmlns:xsi="http://www.w3.org/2001/XMLSchema.xsd"> <orthoxML xsi:schemaLocat xmlns:xsi="http://www.w3.org/2001/XMLSchema.xsd"> <species NCBI TaxID="925 <database name="Unkn <genes> <gene id="6053741 <gene id="5945247 </genes> </species> </orthoxML> </xsi: schemaLocat xmlns:xsi="http://www.w3.org/2001/XMLSchema.xsd"></pre>	<pre>homo_sapiens 1-465588 CCTCAGAAC pan_trichodites 1-465588 CCCAGAAC GGGCAACAC ACTGTGTGGC TTCAAGCTA ACTGTGTGGC TTCAAGCTA GCTCAGGGGA CCTCTGGAT GCTCAGGGGA CCTCTGGAT</pre>	<pre>2 465588 homo_sapien CCTCAGAAC GACGGCAA pan_trichodite CCCAGAAC GACGGCAA GGGCAACAC CCACTGGC ACTGTGTGGC TTCAAGCTA ACTGTGTGGC TTCAAGCTA GCTCAGGGGA CCTCTGGAT GCTCAGGGGA CCTCTGGAT</pre>
PhyloXML	PSI	Stockholm	Text	
<pre><xm <?xml version="1.0" encoding="UTF-8"?> <phyloxml xsi:schemaLocation="http://w <phylogeny rooted="true" type="gene t</pre>	<pre>homo_sapiens CCTCAGAACCGACGGAA pan_trichodites CCCAGAACCGACGGAA</pre>	<pre># STOCKHOLM 1.0</pre>	<pre>(B=0 T=Euteleostomi 1035 --- (B=67 T=Neopterygii 1 ---- (B=2 T=Clunioencom)</pre>	

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

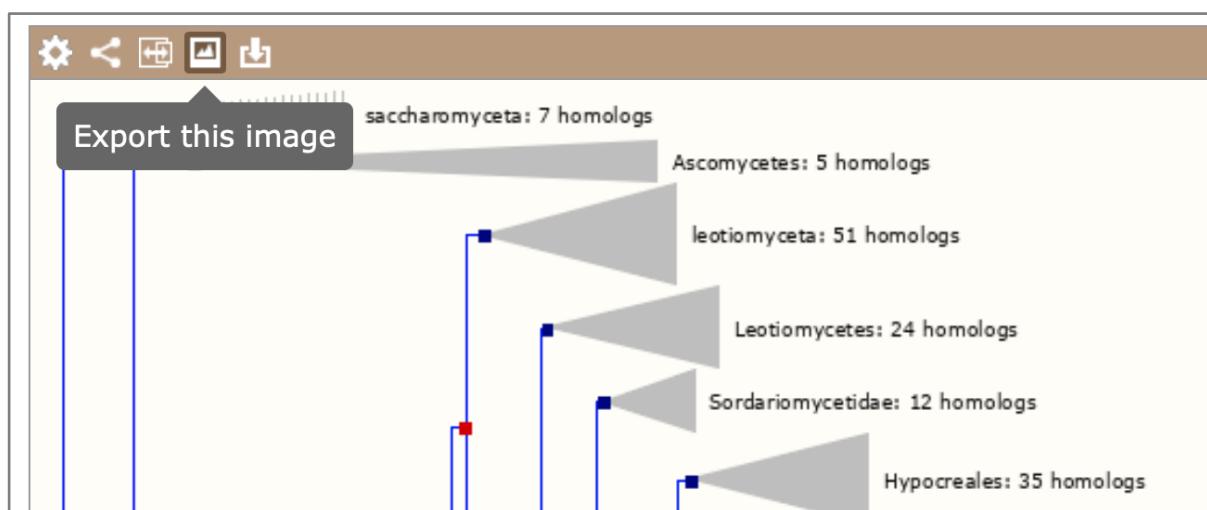


Image download

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.
- Custom image** - Select from a range of formats and sizes

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