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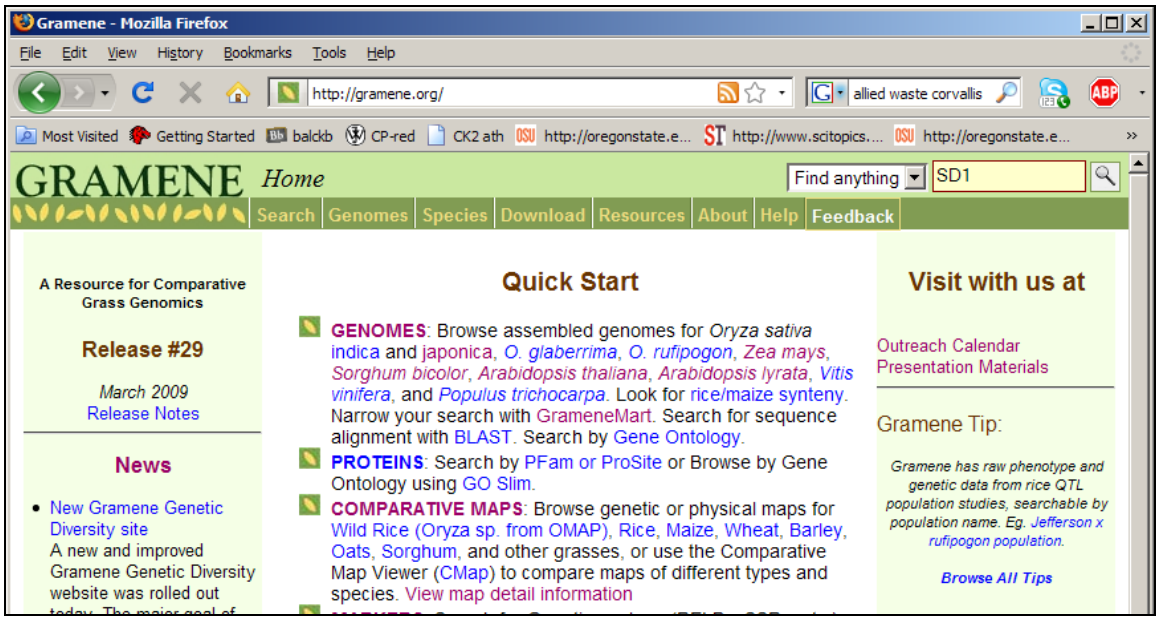
Date: 06/18/2009
MCB, Bioinformatics Symposium at OSU, Corvallis, OR
Workshop-III
Reference: Gramene database build #29

Fill in the blanks as part of the hands on training

Go to the Gramene database (www.gramene.org)

Search for SD1 using the Gramene search box on the right top corner of the page.
Type SD1 and select *'find anything'*



You will get a page with _____ results found.

Open the toggle button [+] next to each section and see the results.

In the genes section of the search results, click on the gene SD1 (GR:0060842): semidwarf-1. This is the gene page with lots of detailed information.
Tell us about:

Q1 What kind of revolution was associated with this gene (clue look for synonyms).

Q2 Name the enzyme and the EC (Enzyme commission) numbers associated with the gene. What is the function of this enzyme*? (Clue: click on the EC number with full ID x.x.x.x)*

Q3 **name the reaction and the pathway with which the gene is associated with?** (*clue: click on the pathway reaction link and then find the reaction name and the associated pathway from subsequent webpages that open*)

Q4 **How many alleles and germplasms are associated with the gene.**
Alleles_#_____; germplasms __#_____

Q5 **Identify the Rice Ensembl Gene locus ID**

Q6 **Gene is mapped on how many genetic and sequence maps.**

Q7 **Name the Trait ontology term name associated with the genes that have something to do with the 'length'.** *(For curiosity, look at other ontologies as well)*

Q8 **Are there any QTLs associated to this gene. If yes, how many? What's their trait symbol and what does it stand for** (*clue : click on the QTL accession and get the details on trait name*).

Q9 **Can you build a comparative map view of JRGP RFLP map and Rye Ds2 x RxL10 1993 map.** (*Clue: click on the 'view comparative map' link. It opens a CMap view with the gene highlighted. Scroll down the page and you will find a 'map option'. Open the toggle [+] and select a map called genetic Rye Rye Ds2 x RxL10 1993*). Use the same procedure for building any other comparison. You can add as many maps on either side of your reference map.

(a) Tell names of three markers that are shared between the two maps.

(b) Name the nearby genes (green text) and tell us about the phenotype of the gene PLA2.

(c) Do you think you can use comparative maps like these to use RFLP markers from one species to populate /enrich maps from another species? Same applies to maps from same species. If so name the markers present between W170A and B183 that you can use to enrich the Rye map.

Q10 **From the original views of SD1 gene page (see instructions before Q1).click on the Rice Ensembl gene ID and tell us the number of alternative transcript forms that are mapped to the same gene locus.** (*clue: now you have left the curated gene page and have entered in the section of genome browser*)

Q11 **Find the total number of SNPs mapped to this gene and how many are non-synonymous.** (*clue when you are in the ensemble genome browser view click on the 'variation table/image link in the left side navigation section)*

Q12 **How many orthologous genes do you find in this database with reference to the rice SD1 gene. Provide their IDs/Name them by species** (Clue: *click on the 'Orthologue link in the left side navigation section under 'comparative genomics').*

Q13 **Rice SD1 is orthologous to how many grape and poplar genes. What's the genomic position of the Poplar gene(s). Provide Chromosome # and bp position.**
(Clue: Click on Poplar gene IDs to get information from subsequent views).

Q14 **How can one use pathway database to upload their microarray datasets and see the real-time expression profile matches to the pathways.**

See instructions:

- -Download/save the file available from http://pathway.gramene.org/expr-examples/sample.dat
- -Go to Pathway page (http://www.gramene.org/pathway/) and click on the 'Omics Viewer' Link on top navigation bar or go directly to http://pathway.gramene.org/expression.html
- -Select the species of choice (in this case. sativa japonica Nipponbare)
- -Upload your file that you just saved by clicking on the browse button and selecting the file.
- Select 'relative' values
- Followed by selection for 'the ratio of two data column'
- -select 0-centred scale
- -select the gene names/ids option from dropdown
- -based on your experiment provide data information. Which column of the file has data column. [*Remember the column with gene_IDs in the sample file/or rather any of the files you upload is considered as ZERO numbered column. For example the data in sample file is in columns 1/2/3*].

- -in the Data column (numerator in ratios) enter the column # of the column if you want to analyze results from any one given column of your choice. Alternatively if it's a time series/multiple experiment data and you want to use data from multiple columns, enter the column # (One column # per row in the section 'Data column (numerator in ratios)').
- Choose a color scheme to your liking. e.g. use the default
- Paint data on cellular overview chart (default)
- -Click on the 'submit button'

Wait for the screen to refresh. It may take 1-several minutes depending on the data points

After you have the view with expression values painted on the cellular overview of the pathways, users can click on the pathway of interest to get details, by hovering your computer mouse on the pathways and when a widget/popup shows up click on the pathway name.

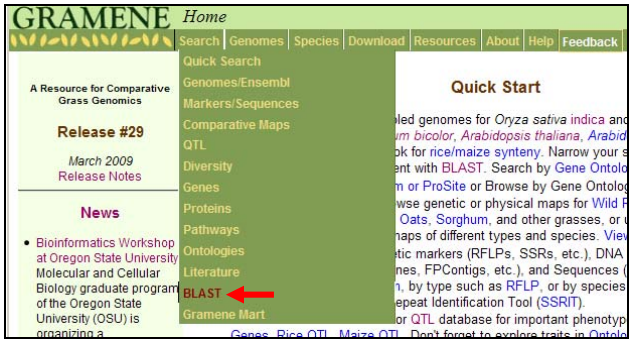
For more information about the Omics Viewer, including sample data files and displays, please visit http://pathway.gramene.org/ov-expr.shtml

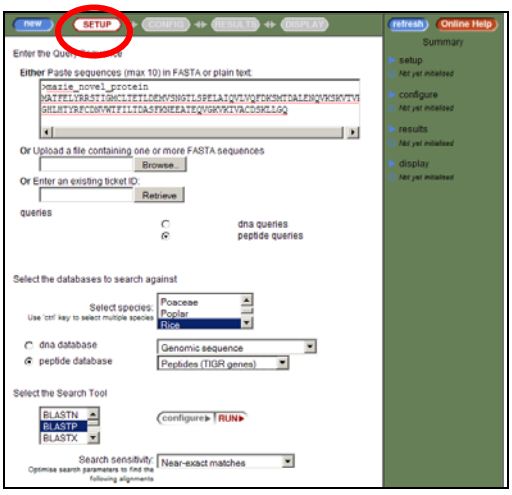
Q15 Find the function of the novel maize gene encoding for the following protein sequence. (*Clue: perform BLAST on Gramene database by copying the following sequence in the query section and run against the Arabidopsis or rice peptide sequenced from TAIR and TIGR database sources respectively*)

```
>maize_novel_protein
MATFELYRRSTIGMCLTETLDEMVSNGTLSPELAIQVLVQFDKSMTDALENQVKSKVTVK
GHLHTYRFCDNVWTFILTDASFKNEEATEQVGKVKIVACDSKLLGQ
```

The protein function is "Putative…….

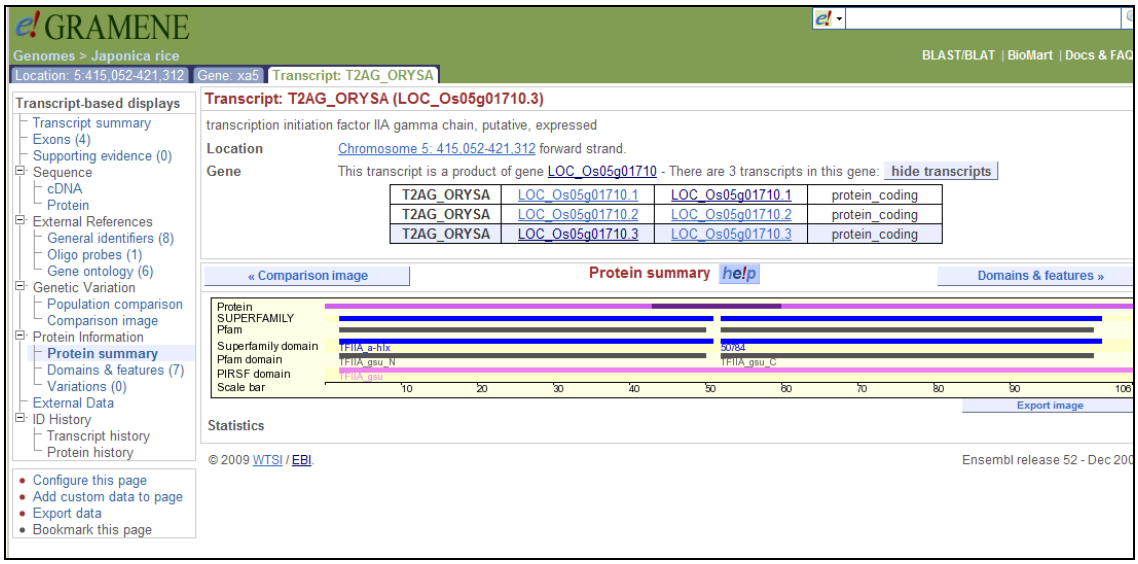
_____"





After you get the results from the BLAST click on the Gene_ID to find gene details

OR
In the left side column of the BLAST results table click on [A] to get alignment, [S] for sequence, [G] for the genomic sequence and [C] for the genome browser view where your BLAST hit is found. [*The results table view is configurable. The BLAST search parameters can be configured by clicking on the 'setup' button on BLAST menu*].



By clicking on the gene/transcript ID in the BLAST results it takes you to the page as above. See several **tabs (on top called: location/gene/transcript).**

-Location tab

-takes user to the genome browser/contig view of the gene placed in reference to the genome sequence

-Transcript tab

-details about alternative transcript forms (if any)
-Several information type options available from left side options in a tree format
-Looks for gene Ontology link for assigned functional terms (in the process of being updated to display term names)

-Gene tab

-alternate transcript structures
- orthologs and paralogs
- mappings to curated genes via 'external references'
e.g. Gramene Curated Gene: ***Xa5****
-Looks for polymorphism and genetic variation data on mapped SNPs

Click on the Xa5 link to Gramene curated gene, to find details about the rice gene, its functions and phenotypes (see ontology section and description).

Use this information to provide function to your query sequence from maize.

OPTIONAL SECTION

Use GRAMENE MART for bulk download and complex queries.

#1 Find all the homologous (ortholog and paralog) gene pairs of the gene of interest.

-Go to http://www.gramene.org/biomart/martview/
-"CHOOSE DATABASE" = "Gramene XX Ensembl Genes" (where XX= database release #)
-"CHOOSE DATASET" = "Oryza sativa japonica genes"
-then click on 'attributes' link in the grey colored column and select homologs.
- select species and mark geneID to get orthologs from desired species
-Click on the results section will give you options to download.

 # 2 Find all the genes mapped in the given chromosomal region for example of rice.

-Go to http://www.gramene.org/biomart/martview/
-"CHOOSE DATABASE" = "Gramene XX Ensembl Genes" (where XX= release #)
-"CHOOSE DATASET" = "Oryza sativa japonica genes"
-click on the 'Filters' and open the 'region' section by clicking on the [+] icon.
-Select the chromosome and the region start-stop positions
-Select the "Attributes" on the left, select the options on features-open the 'gene' section by clicking on the [+] icon a check the box for gene ID
-after selecting all these hit the 'result' button in the navigation bar in black color
-it will give you a results table.-select your export format to get the complete results.

 # 3 Find functional annotations (Gene Ontology and Interpro domain assignments) of the genes and does genome also have other genes with similar functional annotations.

-Start the same way as in #1 or #2 and in the attribute sections
-select for Features and open 'external' section and check mark GO ID and GO description
-Follow the steps to retrieve your results as described above.

Useful links:

Help documents	http://www.gramene.org/db/help?state=display_topic_in_context&topic_name=Help+Documents&sticky=0
FAQs	http://www.gramene.org/db/help?state=display_topic_in_context&topic_name=FAQ&sticky=0
Tutorials (may be old)	http://www.gramene.org/tutorials/
Contact	Email: Gramene@gramene.org
Feedback	Click on the feedback button (Top Navigation Menu option after 'help') from any page you are visiting, to report suggestions, inaccuracies, updates, etc.

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