Gramene Database: Pathway Networks for Cereals and their applications

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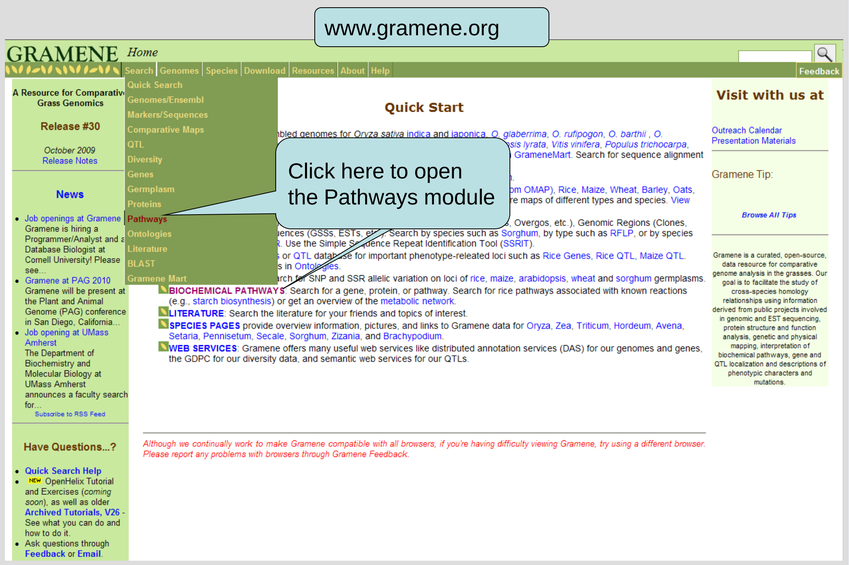
Introduction

The Gramene database (www.gramene.org), develops and curates RiceCyc and SorghumCyc pathway databases for cereal plants.In the near future we will be incorporating pathways for maize and *Brachypodium* as well as signaling pathways for rice. In addition plant metabolic pathways module within Gramene mirrors several other species specific pathways such as *Arabidopsis*, *Medicago*, Tomato, Potato and Coffee as well as MetaCyc reference database allowing the user to extract interspecific comparison between pathways and associated genes. The user is also able to download lists of genes associated with each pathway. The database comes with the Omics Viewer data visualization tool allowing users to overlay microarray, transcriptomic, proteomic, and metabolomic datasets with expressed values on pathway maps. The overlaid views allow to visualize the pathways and reactions that are up/down regulated in an experiment or a set of experiments. We have also built an Omics Validator tool to validate user provided expression data files by mapping probe IDs from various microarray platforms to their respective gene IDs. An example of the utility of the RiceCyc pathway database in the analysis and interpretation of a transcriptomic dataset is depicted here.

Gramene Home Page

www.gramene.org



Click here to open the Pathways module

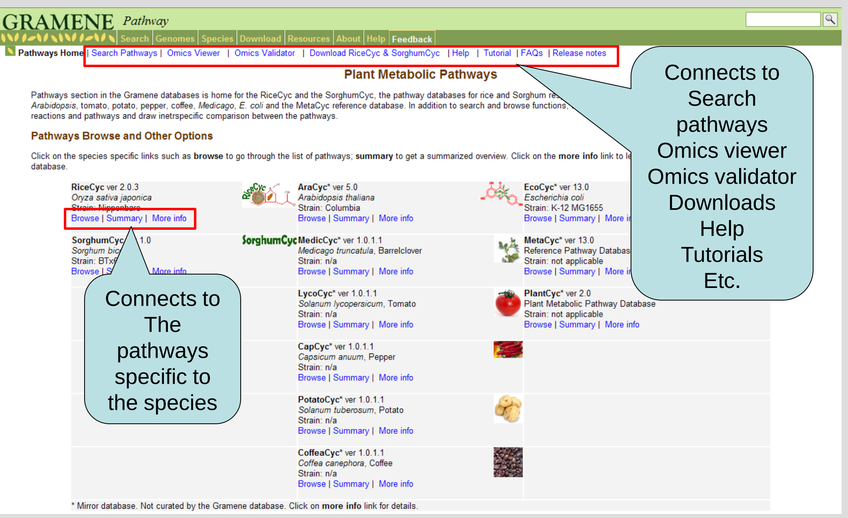
Pathways Home Page

Pathways developed & curated by Gramene

3 reference pathway databases

6 species specific pathways are mirrored

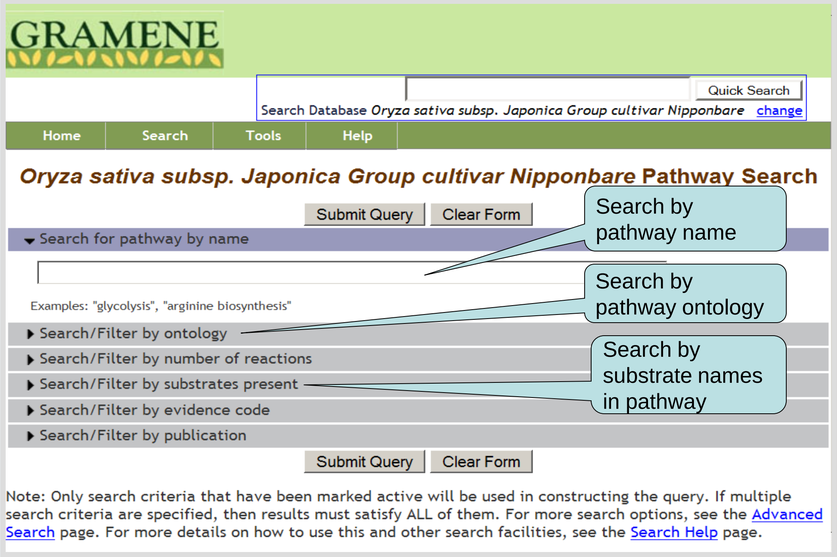
Pathway Page Navigation Options



Connects to Search pathways Omics viewer Omics validator Downloads Help Tutorials Etc.

Connects to The pathways specific to the species

Pathway Search Options

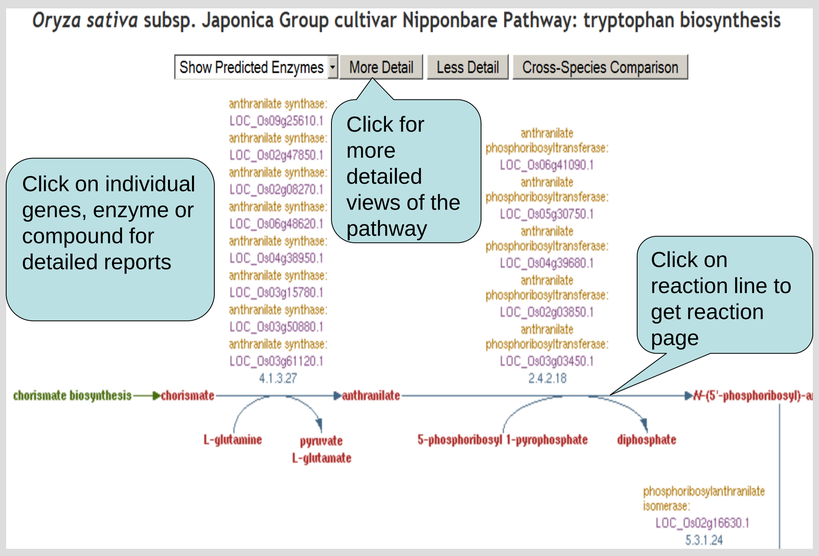


Search by pathway name

Search by pathway ontology

Search by substrate names in pathway

Pathway Information

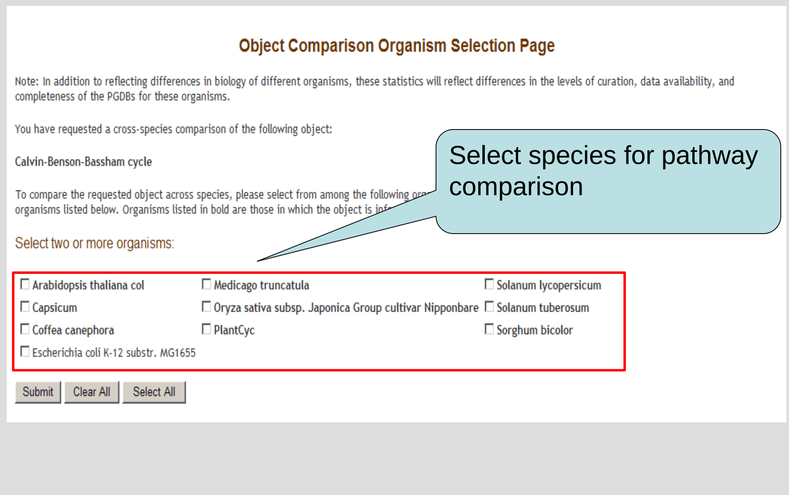


Click on individual genes, enzyme or compound for detailed reports

Click for more detailed views of the pathway

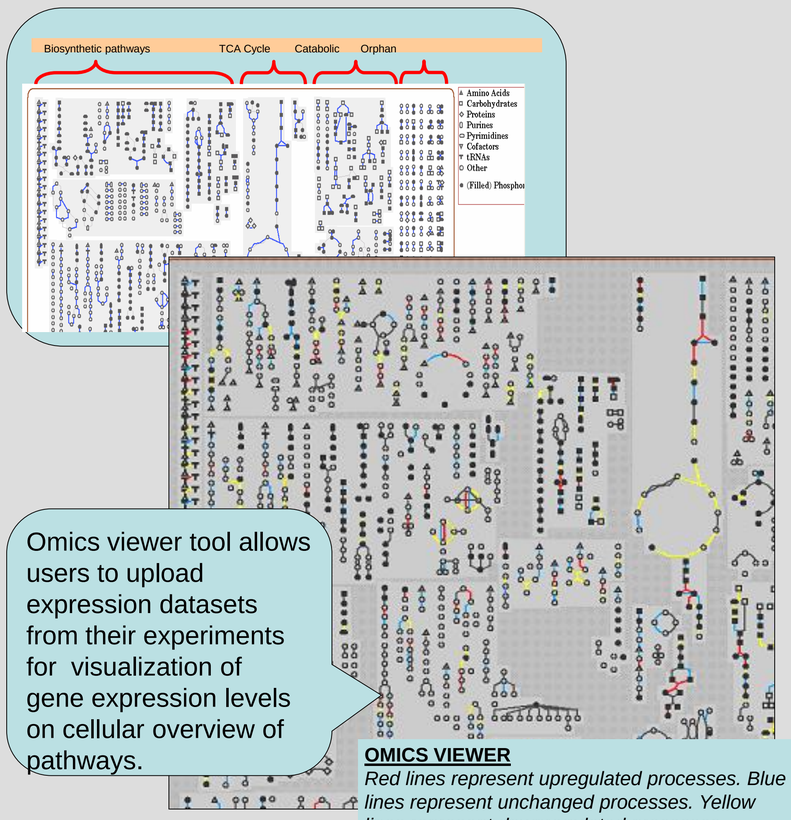
Click on reaction line to get reaction page

Comparative Analysis



Select species for pathway comparison

Cellular overview and Omics Viewer



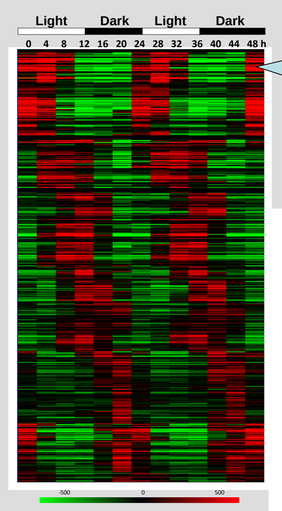
Omics viewer tool allows users to upload expression datasets from their experiments for visualization of gene expression levels on cellular overview of pathways.

OMICS VIEWER

Red lines represent upregulated processes. Blue lines represent unchanged processes. Yellow lines represent downregulated processes.

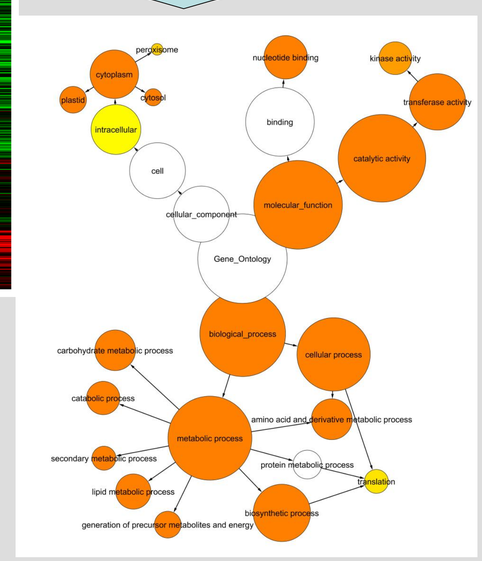
Application example: Analysis of Circadian regulated genes in rice

Data source: Filichkin and Mockler (http://mocklerlab.cgrb.oregonstate.edu/)

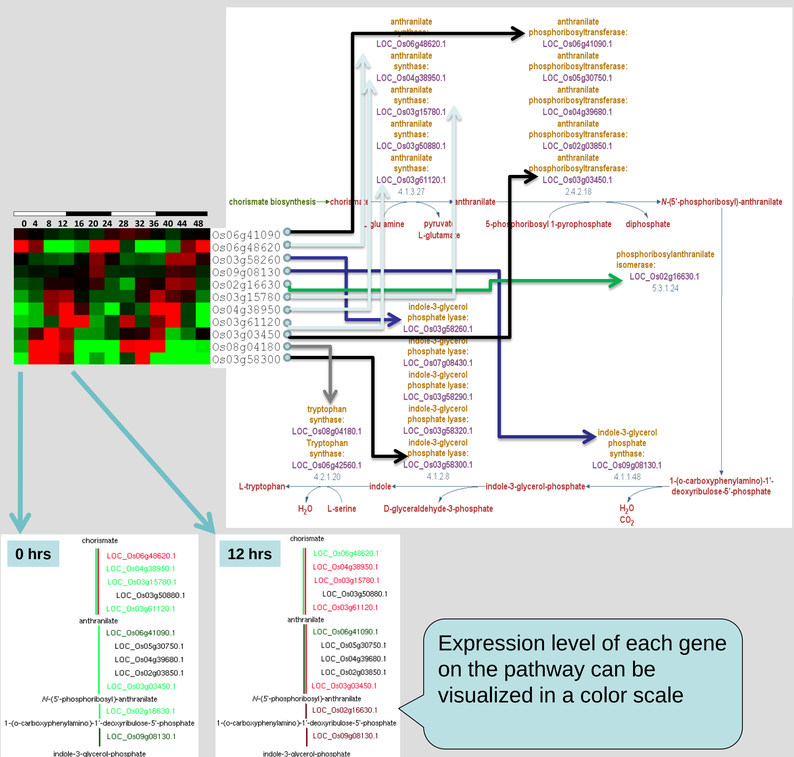


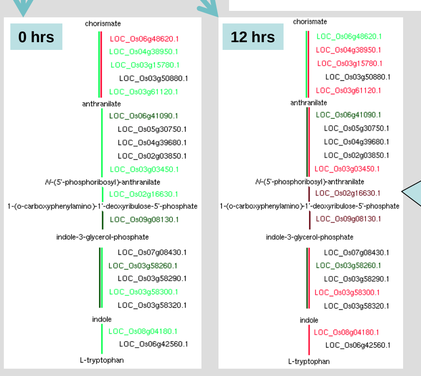
Clustering of cycling genes mapping to RiceCyc metabolic pathways

Over-represented gene ontology categories of cycling genes mapping to pathways



Visualizing diurnal variation of Trp biosynthetic gene expression





Expression level of each gene on the pathway can be visualized in a color scale

More About Gramene Pathways

- Gramene is a collaboration between CSHL, Cornell University and Oregon State University supported by National Science Foundation (Grant No. 0703908)
- The data content and web interface of the database is updated semi-annually.
- Gramene will be adding pathway databases for Maize and *Brachipodium* in the near future
- For up to date information, please visit Gramene website **www.gramene.org**) or send feedback to gramene@gramene.org

SPECIES