

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

[illegible]

Pathways Home Page

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Plant Metabolic Pathways

Pathways section in the Gramene databases is home for the RiceCyc and the SorghumCyc, the pathway databases for rice and Sorghum respectively. It also provides mirrors of pathway databases from Arabidopsis, tomato, potato, pepper, coffee, Medicago, E. coli and the MetaCyc database. In addition to search and browse functions, the database allows users to find genes mapped to respective reactions and pathways and draw interactive comparison between the pathways.

Pathways Browse and Other Options

Click on the species specific links such as **browse** to go through the list of pathways; **summary** to get a summarized overview. Click on the **more info** link to learn more details on the respective pathway database.

RiceCyc ver 2.0.3 <i>Oryza sativa</i> , japonica Strain: Nipponbare Browse Summary More info	ArabCyc ver 2.0.0 <i>Arabidopsis thaliana</i> Strain: Columbia Browse Summary More info	EcoCyc ver 13.0 <i>Escherichia coli</i> Strain: K-12 MG1655 Browse Summary More info
SorghumCyc ver 1.0 <i>Sorghum bicolor</i> Strain: BTx623 Browse Summary More info	SorghumCyc ver 1.0.0.1.1 <i>Medicago truncatula</i> , Baudouin Strain: n/a Browse Summary More info	MetaCyc ver 13.0 Reference Pathway Database Strain: not applicable Browse Summary More info
TomatoCyc ver 1.0.1.1 <i>Solanum lycopersicon</i> , Tomato Strain: n/a Browse Summary More info	PotatoCyc ver 1.0.1.1 <i>Solanum tuberosum</i> , Potato Strain: n/a Browse Summary More info	PlantCyc ver 2.0 Plant Metabolic Pathway Database Strain: not applicable Browse Summary More info
PepperCyc ver 1.0.1.1 <i>Capiscum annuum</i> , Pepper Strain: n/a Browse Summary More info	CoffeeCyc ver 1.0.1.1 <i>Coffea canephora</i> , Coffee Strain: n/a Browse Summary More info	


Pathways developed & curated by Gramene

3 reference pathway databases

6 species specific pathways are

* Mirror database. Not curated by the Gramene database. Click on **more info** links for details.

Pathway Page Navigation Options



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




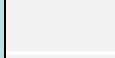

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Plant Metabolic Pathways

Pathways section in the Gramene databases is home for the RiceCyc and the SorghumCyc, the pathway databases for rice and Sorghum respectively. Arabidopsis, tomato, potato, pepper, coffee, Medicago, E. coli and the MetaCyc reference database. In addition to search and browse functions, reactions and pathways are drawn in a stepwise comparison between the pathways.

Pathways Browse and Other Options

Click on the species specific links such as **browse** to go through the list of pathways; **summary** to get a summarized overview. Click on the **more info** link to get more details.

RiceCyc ver 2.0.3 <i>Oryza sativa</i> japonica Download Nucleotides Browse Summary More info	 AraCyc ver 5.0 <i>Arabidopsis thaliana</i> Strain: Columbia Browse Summary More info	 EcoCyc ver 13.0 <i>Escherichia coli</i> Strain: K-12 MG1655 Browse Summary More info
SorghumCyc ver 1.0 <i>Sorghum bicolor</i> Strain: BTx623 Browse Summary More info	 SorghumCyc ver 1.0.1.1 <i>Medicago truncatula</i> , Bancelor Strain: n/a Browse Summary More info	 MetaCyc ver 13.0 Reference Pathway Database Strain: not applicable Browse Summary More info
PlantCyc ver 2.0 Plant Metabolic Pathway Database Strain: not applicable Browse Summary More info	 LycoCyc ver 1.0.1.1 <i>Solanum lycopersicon</i> , Tomato Strain: n/a Browse Summary More info	 CapCyc ver 1.0.1.1 <i>Capsicum annuum</i> , Pepper Strain: n/a Browse Summary More info
 PotatoCyc ver 1.0.1.1 <i>Solanum tuberosum</i> , Potato Strain: n/a Browse Summary More info	 CoffeaCyc ver 1.0.1.1 <i>Coffea canephora</i> , Coffee Strain: n/a Browse Summary More info	

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

Connects to The pathways specific to the species

Pathway Search Options

The screenshot shows the GRAMENE database search page. At the top is the GRAMENE logo. Below it is a search bar with the text "Search Database *Oryza sativa* subsp. *Japanica* Group cultivar *Nipponbare*" and a "Quick Search" button. The main heading is "Oryza sativa subsp. Japanica Group cultivar Nipponbare Pathway Search". Below this is a table with four columns: Home, Search, Tools, and Help. The "Search" column is highlighted. Under "Search" is a section "Search for pathway by name" with a text input field and a "Submit Query" button. To the right of this section are three callout boxes: "Search by pathway name", "Search by pathway ontology", and "Search by substrate names in pathway". Below the "Search for pathway by name" section is a list of search criteria: "Search/Filter by ontology", "Search/Filter by number of reactions", "Search/Filter by substrates present", "Search/Filter by evidence code", and "Search/Filter by publication". Each criterion has a "Submit Query" button next to it. At the bottom, a note states: "Note: Only search criteria that have been marked active will be used in constructing the query. If multiple search criteria are specified, then results must satisfy ALL of them. For more search options, see the [Advanced Search](#) page. For more details on how to use this and other search facilities, see the [Search Help](#) page."

GRAMENE

Search Database *Oryza sativa* subsp. *Japanica* Group cultivar *Nipponbare* [Quick Search](#)

Oryza sativa subsp. Japanica Group cultivar Nipponbare Pathway Search

Home	Search	Tools	Help
<div> <div>▼ Search for pathway by name</div> <div> <input type="text"/> <div> <div>Submit Query</div> <div>Clear Form</div> </div> </div> <div> <div>Examples: "glycolysis", "arginine biosynthesis"</div> <div> <div>▶ Search/Filter by ontology</div> <div>▶ Search/Filter by number of reactions</div> <div>▶ Search/Filter by substrates present</div> <div>▶ Search/Filter by evidence code</div> <div>▶ Search/Filter by publication</div> </div> <div> <div>Submit Query</div> <div>Clear Form</div> </div> </div> </div>			

Note: Only search criteria that have been marked active will be used in constructing the query. If multiple search criteria are specified, then results must satisfy ALL of them. For more search options, see the [Advanced Search](#) page. For more details on how to use this and other search facilities, see the [Search Help](#) page.

Pathway Information

Oryza sativa subsp. Japonica Group **metabolic pathway** Nipponbare Pathway: tryptophan biosynthesis

Show Predicted Enzymes More Detail Less Detail Cross-Species Comparison

anthranilate synthase:
LOC_Os09g25610.1
anthranilate synthase:
LOC_Os02g47850.1
anthranilate synthase:
LOC_Os02g36270.1
anthranilate synthase:
LOC_Os06g48620.1
anthranilate synthase:
LOC_Os04g38950.1
anthranilate synthase:
LOC_Os03g15780.1
anthranilate synthase:
LOC_Os03g50880.1
anthranilate synthase:
LOC_Os03g61120.1
4.1.3.27

Click for more detailed views of the pathway

anthranilate phosphoribosyltransferase:
LOC_Os06g41090.1
anthranilate phosphoribosyltransferase:
LOC_Os05g30750.1
anthranilate phosphoribosyltransferase:
LOC_Os04g36680.1
anthranilate phosphoribosyltransferase:
LOC_Os02g03850.1
anthranilate phosphoribosyltransferase:
LOC_Os03g03450.1
2.4.2.18

Click on reaction line to get reaction page

chorismate biosynthesis → chorismate → anthranilate → L-glutamine → pyruvate → L-glutamate → 5-phosphoribosyl 1-pyrophosphate → diphosphate → L-tryptophan

anthranilate phosphoribosyltransferase:
LOC_Os02g16630.1
5.3.1.24

Comparative Analysis

Object Comparison Organism Selection Page

Note: in addition to reflecting differences in biology of different organisms, these statistics will reflect differences in the levels of curation, data availability, and completeness of the PGDBs for these organisms.

You have requested a cross-species comparison of the following object:

Calvin-Benson-Bassham cycle

To compare the requested object across species, please select from among the following organisms listed below. Organisms listed in bold are those in which the object is implemented.

Select two or more organisms:

<input type="checkbox"/> Arabidopsis thaliana col	<input type="checkbox"/> Medicago truncatula	<input type="checkbox"/> Solanum lycopersicum
<input type="checkbox"/> Capsicum	<input type="checkbox"/> Oryza sativa subsp. Japonica Group cultivar Nipponbare	<input type="checkbox"/> Solanum tuberosum
<input type="checkbox"/> Coffea canephora	<input type="checkbox"/> PlantCyc	<input type="checkbox"/> Sorghum bicolor
<input type="checkbox"/> Escherichia coli K-12 substr. MG1655		

Cellular overview and Omics Viewer

Biosynthetic pathways TCA Cycle Catabolic Orphan

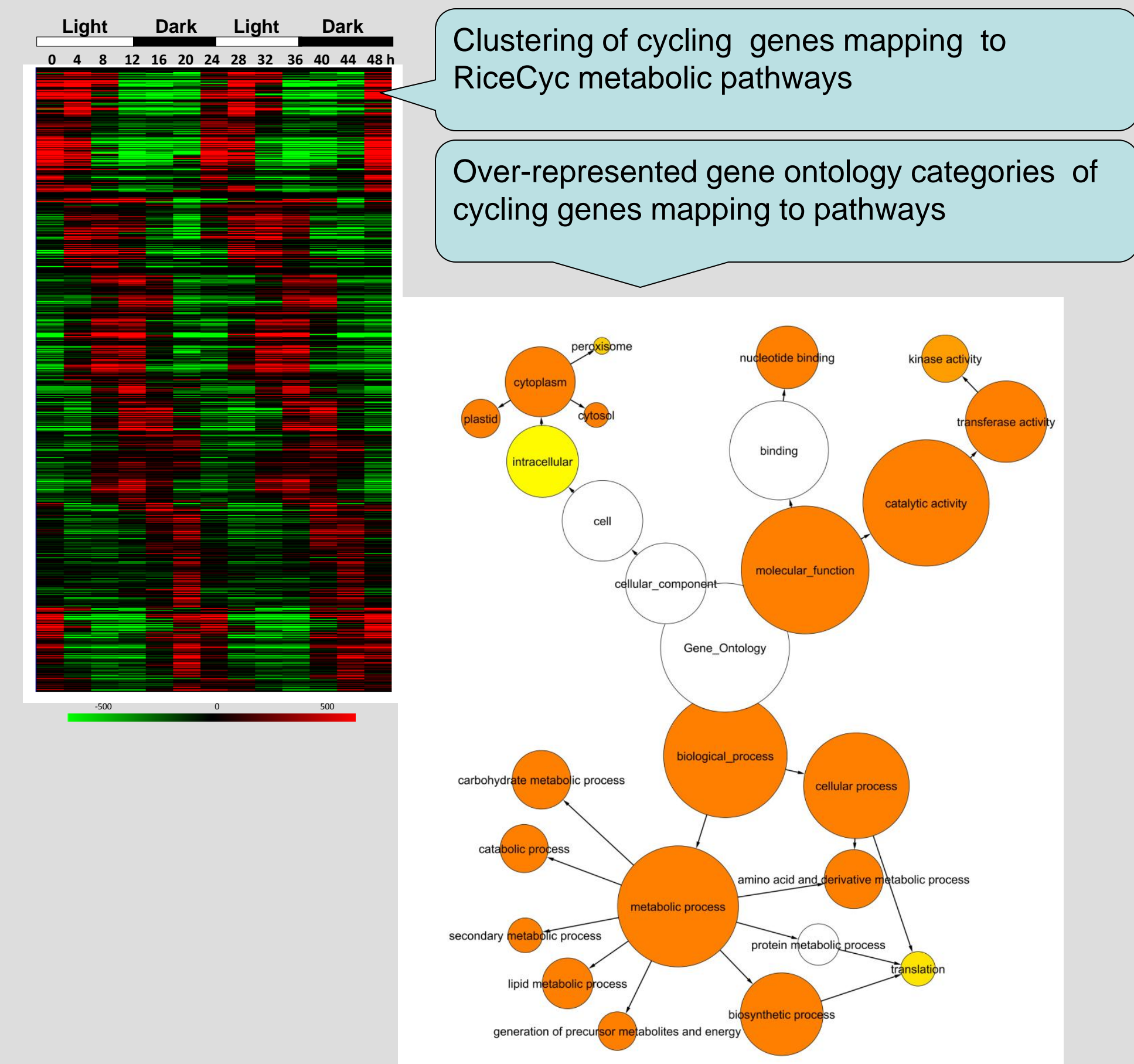
- Amino Acids
- Carbohydrates
- Proteins
- Purines
- Pyrimidines
- Cofactors
- tRNAs
- Other
- (Filled) Phosphate

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

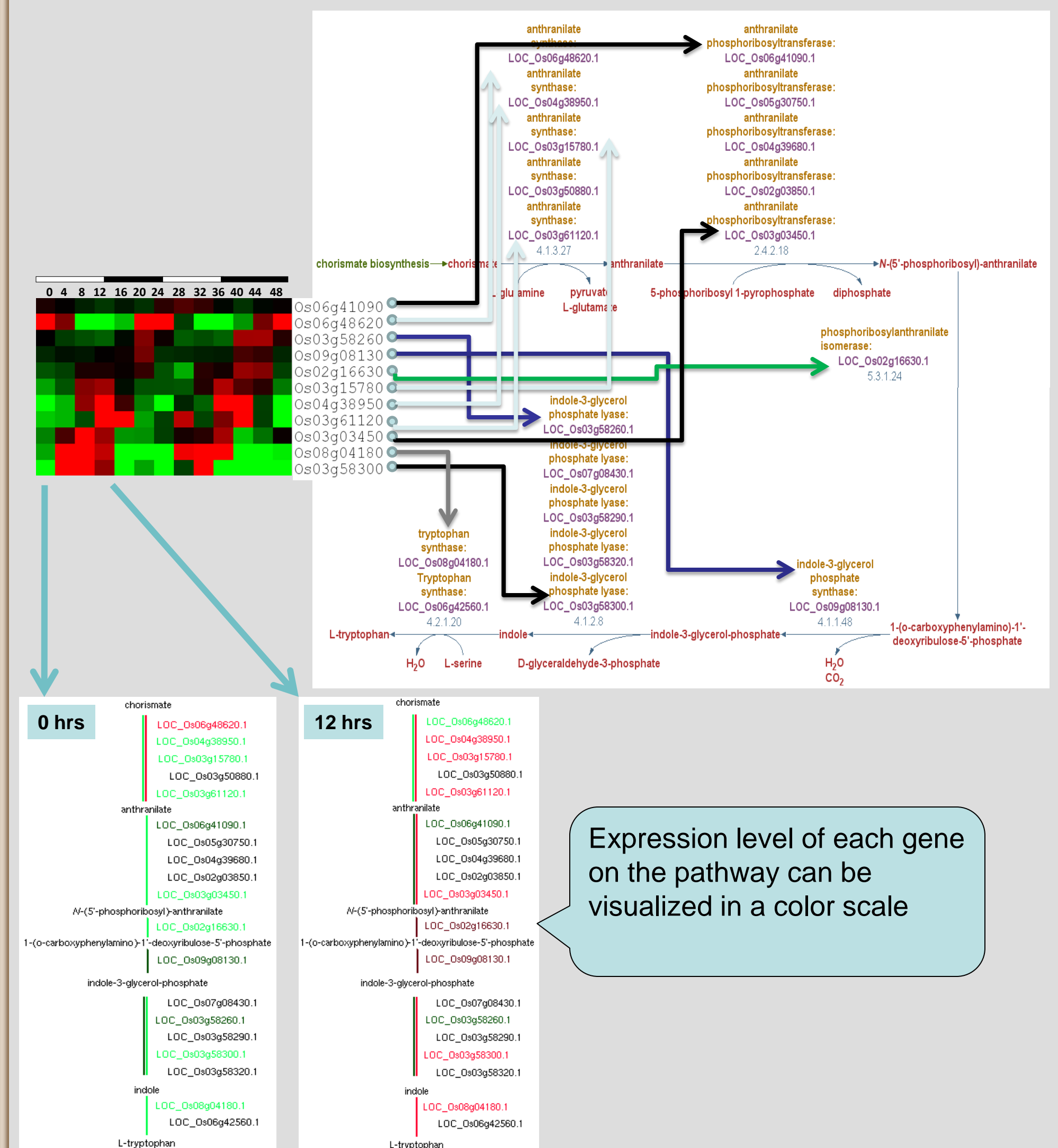
OMICS VIEWER
 Red lines represent upregulated processes. Blue lines represent unchanged processes. Yellow lines represent downregulated processes.

Application example: Analysis of Circadian regulated genes in rice

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



Visualizing diurnal variation of Trp biosynthetic gene expression



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

