



Metabolic Pathway Networks for Cereal Plants in The Gramene Database

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Introduction

The Gramene database (www.gramene.org), a comprehensive comparative plant genomics platform develops and curates RiceCyc and SorghumCyc pathway databases for cereal plants. RiceCyc with 342 known and/or predicted metabolic pathways for *Oryza sativa japonica* cv. Nipponbare has undergone several rounds of data quality enhancement and manual curation whereas SorghumCyc with 328 pathways for Sorghum bicolor Strain BTX623 is in its initial computational build. The 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. This tool allows 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.

Gramene Home Page

www.gramene.org

Click here to open the Pathways module

Quick Start

Visit with us at

Although we continually work to make Gramene compatible with all browsers, if you're having difficulty viewing Gramene, try using a different browser. Please report any problems with browsers through Gramene Feedback.

Pathways Home Page

Plant Metabolic Pathways

Pathways Browse and Other Options

Click on the species specific links such as **RiceCyc** 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.

Pathways developed & curated by Gramene

3 reference pathway databases

6 species specific pathways are mirrored

Pathway Page Navigation Options

Plant Metabolic Pathways

Pathways Browse and Other Options

Click on the species specific links such as **RiceCyc** 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.

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

Connects to The pathways specific to the species

Pathway Search Options

GRAMENE

Search Database *Oryza sativa subsp. Japonica Group cultivar Nipponbare* **change**

Home Search Tools Help

Oryza sativa subsp. Japonica Group cultivar Nipponbare Pathway Search

Submit Query Clear Form

Search by pathway name

Search by pathway ontology

Search by substrate names in pathway

Submit Query Clear Form

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.

Browse by Pathway Ontologies

Oryza sativa subsp. Japonica Group cultivar Nipponbare Pathway Search

Submit Query Clear Form

Search for pathway by name

Search/Filter by ontology

Search/Filter by number of reactions

Search/Filter by substrates present

Search/Filter by evidence code

Search/Filter by publication

Submit Query Clear Form

Pathway Information

Oryza sativa subsp. Japonica Group cultivar Nipponbare Pathway: tryptophan biosynthesis

Show Predicted Enzymes More Detail Less Detail Cross-Species Comparison

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

Information on: Gene, Protein, Reaction, Compound etc.

Oryza sativa subsp. Japonica Group cultivar Nipponbare Reaction: 4.1.3.27

Cross-Species Comparison

Superclasses: Reactions-Classified-By-Conversion-Type -> Simple-Reactions -> Chemical-Reactions -> 4.1 -- Carbon-carbon lyases -> 4.1.3 -- Oxo-acyl-lyases

Reactions-Classified-By-Substrate -> Small-Molecule-Reactions

Enzymes and Genes: defense-related protein, putative, expressed: LOC_Os09g25610.1; carbanoyl-phosphate synthase small chain, putative, expressed: LOC_Os02g47850.1; defense-related protein, putative, expressed: LOC_Os02g49270.1; 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

In Pathway: tryptophan biosynthesis

chorismate

Gene summary

Gene type: Known protein coding

Prediction Method: Gene annotation by MSU through a process of automatic and manual curation

The reaction direction shown, that is, system.

Enzyme Commission Primary Name for this system.

Enzyme Commission Synonyms for this system.

Citations: [1]

Gene-Reaction Schematic: [1]

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 identified.

Select two or more organisms:

☐ Arabidopsis thaliana col ☐ Medicago truncatula ☐ Solanum lycopersicum ☐ Capsicum ☐ Oryza sativa subsp. Japonica Group cultivar Nipponbare ☐ Solanum tuberosum ☐ Coffea canephora ☐ PlantCyc ☐ Sorghum bicolor ☐ Escherichia coli K-12 substr. MG1655

Submit Clear All Select All

Select species for pathway comparison

Cellular overview and Omics Viewer

Biosynthetic pathways TCA Cycle Catabolic Orphan

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.

Ongoing Pathway Curation

O. sativa japonica Pathway: phenylpropanoid biosynthesis

Curated pathways are updated with each Gramene release

Your contribution to pathway curation is welcome

Curated pathway

More About Gramene

- Gramene is a collaboration between CSHL, Cornell University and Oregon State University supported by National Science Foundation grant No. 0703908
- Gramene is accessed by researchers in over 140 countries around the world. Online tutorials and help documents provide users with an overview of how to conduct a search within each module. Workshops are held frequently to train users in using the website.
- Gramene is a work in progress, holding a biannual release schedule with both updated data and software tools in each release.
- 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
- Please visit Gramene related posters P843 and P835

