RiceCyc: A metabolic pathway database for rice

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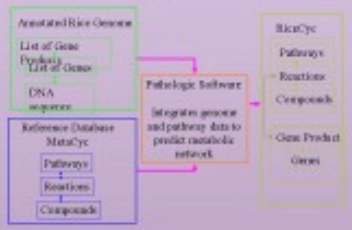
Introduction

- RiceCyc is a database of metabolic pathways in rice (Oryza) developed as part of Gramene (http://www.gramene.org/).
- The goal of RiceCyc is to provide a user-friendly web interface for rice metabolism.
- The database is based on the Pathway Tools software (http://bioinformatics.ai.sri.com/ptools/) developed at SRI International.
- Rice gene models used in the analyses are based on the TIGR assembly of oryza sativa japonica cv. nipponbare genome sequenced by IRGSP.

RiceCyc Creation



RiceCyc homepage
http://www.gramene.org/pathway/

In addition to providing a link to the RiceCyc module, the Gramene pathways page provides a short summary of the models, links to major pathways and links to other pathway databases.

Search or Browse the Pathway Database

Pathway information can be found by using the search or browse functions. Summary information is also available from this page.

RiceCyc Overview Diagram

All of the rice biochemical pathways and reactions have been created for RiceCyc are shown in the interactive Metabolic Map Overview page.

Different classes of metabolic compounds are represented by different shapes, the key is given on the right hand side of the metabolic map overview.

Pathway Example: *aspartate superpathway* (a)

The user is able to browse the pathways using a multi-level interface, this allows visualization of the pathways, compounds and enzymatic reactions. By clicking the 'More Detail' button, the user is able to zoom in to details of the view as seen in the following figure.

Pathway Example: *aspartate superpathway* (b)

By zooming into the pathway, the schematics of individual compounds can be seen as well as information on the enzymes involved in the pathways. A link is provided to the gene page of Gramene, where detailed information on the specific gene is available.

Ensembl Gene in Gramene Genome Browser

Genes used in pathways are linked to the Gramene genome browser, reciprocal links are provided from each of the views.

Omics Viewer Display

The Omics viewer makes use of the Metabolic Overview to globally display the results of high throughput experiments. Users are able to upload their own microarray data, for genes or proteins, which is then mapped onto the reactions shown on the Metabolic Overview. The chart is color coded so that pathways with differential changes in expression can easily be identified.

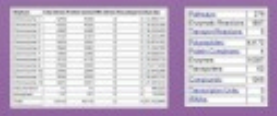
Comparative Analysis

A feature of RiceCyc within Gramene, is that it allows comparisons to be made between Rice and Arabidopsis datasets. Analysis can be performed on several sets including: Reactions; Pathways; Compounds; Proteins and Transcription Units.

Pathway tutorial and FAQ

Pathways tutorial and FAQ will tell the user more about RiceCyc in Gramene.

Summary of RiceCyc version 1.2



Since version 1.1, we have added 7 new curated pathways and deleted 46 computational predicted pathways.

The manual curation of ricecyc pathways is an ongoing process at Gramene. We welcome feedback from the research community.