

Genomes & Diversity

As of January of 2014, Gramene hosts a total of 28 complete and 10 partial genomes. In collaboration with Ensembl Genomes, for each reference genome we incorporate community annotation from primary sources and enrich this information with a series of standardized analyses. These include functional annotation by InterProScan and classification using controlled vocabularies (e.g., GO and PO). Evolutionary histories are provided by Compara phylogenetic gene trees and complemented by analyses of whole genome alignments. In recent years, Gramene has also positioned itself as a resource for genome variation data in *Arabidopsis*, rice & “African rice”, barley, maize, sorghum, wheat, grape, and *Brachypodium*.

Pathways & Networks

Gramene produces and hosts or mirrors metabolic pathways databases and visualization tools in the BioCyc collection.

We recently introduced the Plant Reactome [<http://plantreactome.gramene.org>], a new platform for the comparative analysis of plant metabolic and regulatory networks, produced in collaboration with the Human Reactome Project. The current release of Plant

Reactome includes a beta version of the rice pathways database based on RiceCyc v3.3. We plan to include *Arabidopsis* pathways later this year, and eventually projections to maize and other plant species.



Outreach & Releases

Our release cycle has moved from two to five major releases per year, ensuring timely updates to data and software. We reach our users at key scientific meetings including *Plant and Animal Genomes*, *Maize Genetics Conference*, *ICAR* and *ASPB's Plant Biology*. Gramene also participates in several Research Coordination Networks to understand community needs and to establish and promote common data exchange formats.

Web Services

- Gramene Mart for customized data dumps
- Public MySQL & DAS servers
- RESTful API

Cite Us

Monaco *et al* (2014). Gramene 2013: comparative plant genomics resources. *NAR* 42 (D1): D1193

Contact us

feedback@gramene.org

Visit our  Facebook page!

Funding

Current work is being supported by the NSF Plant Genome Research Resource grant award #1127112 and the USDA-ARS.

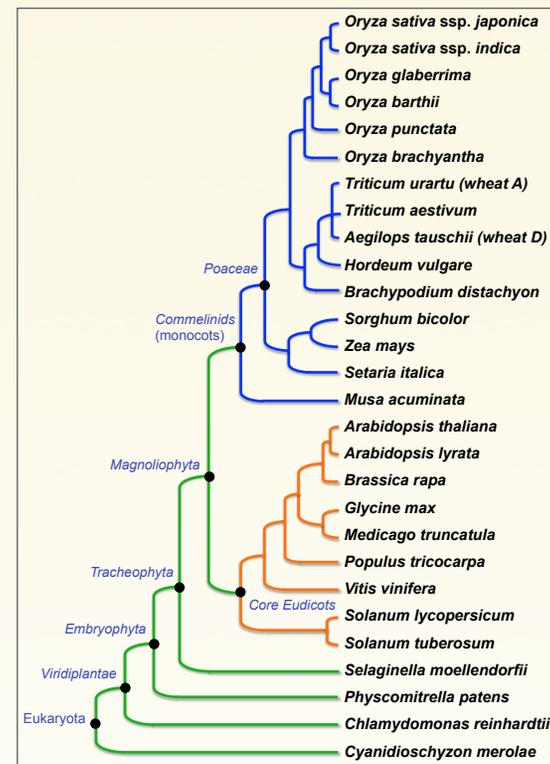
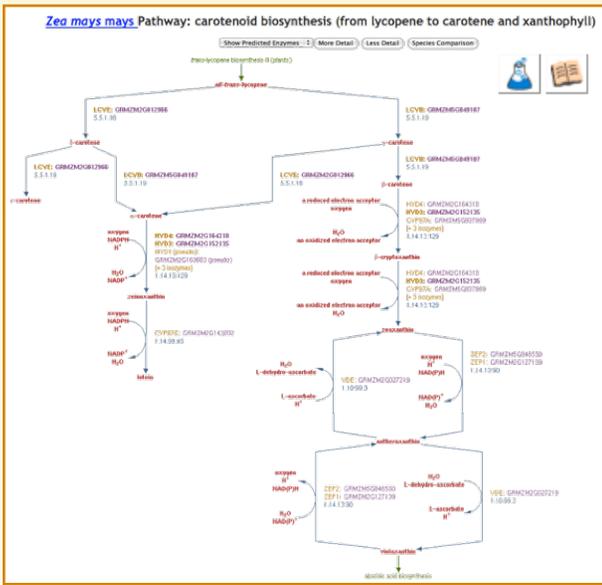


Image: Gramene 40 (Jan 2014). By J Stein

Comparative genomics across the plant kingdom

<http://www.gramene.org/>

Gramene continues to grow, now at 28 complete genomes (build 40), including crops, model organisms and lower plants. Together these serve as a reference resource for comparative analyses, for the broad scientific community, in support of basic and translational research which impact societal interests in food security, energy production, and climate change.



Plant REACTOME beta

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Search examples: LOC_Os01g45760.1, YUC4, cytokinins, glucose

Advanced search: Browse Pathways, Retrieve SBML

Explore... a sampling of metabolic and regulatory pathways in *Oryza sativa*:

- Proline biosynthesis I
- Lysine biosynthesis I
- Jasmonic acid biosynthesis
- Cytosolic glycolysis
- COP1 Mediated Vesicle Transport
- Gibberellin biosynthesis II
- Translation elongation

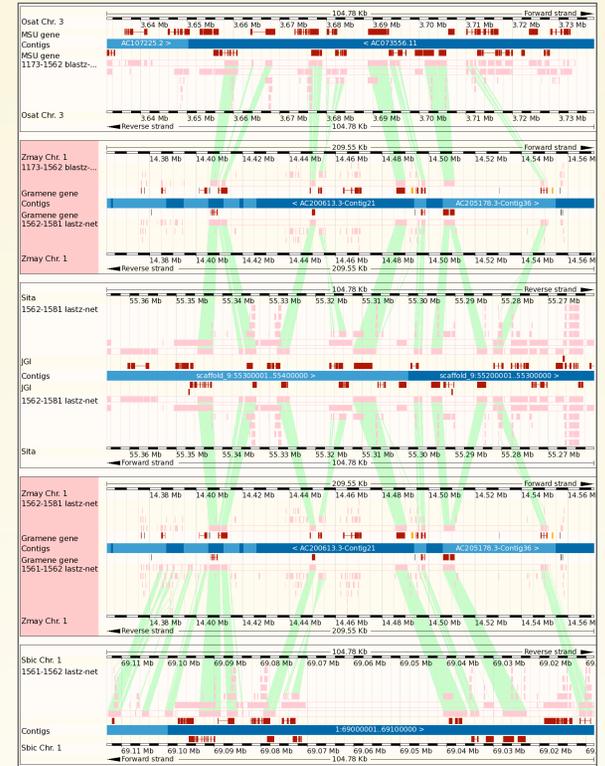
21 new rice pathways: Plant Reactome has released a new batch of rice pathways focusing on the areas of carbohydrate biosynthesis, cofactor biosynthesis, and secondary metabolite biosynthesis. Examples include: GDP-mannose metabolism, gamma-glutamyl cycle and salicylate biosynthesis.

Gramine database build 37b released: The Gramine team is happy to announce its 37th database release. [More info]

Introductory Video Tutorial: We have created a new video presentation describing the main features of the Plant Reactome. Check it out here.

Plant Reactome presented at the twenty-first Plant and Animal Genome Meeting: The Plant Reactome team presented its pathway database work at the PAG-XXI meeting in San Diego, CA (USA) on Jan 15, 2013. [view]

Useful Links: Gramene Plant Pathway Database [view], KEGG Pathway database [view], WikiPathways: Plants Portal [view], MetaCyc [view], Plant Metabolic Network [view], Reactome [view]

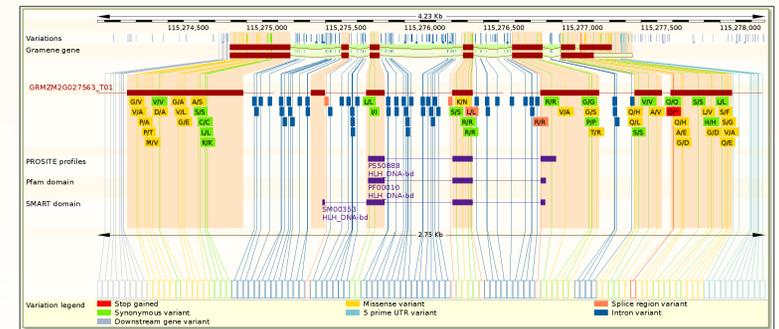
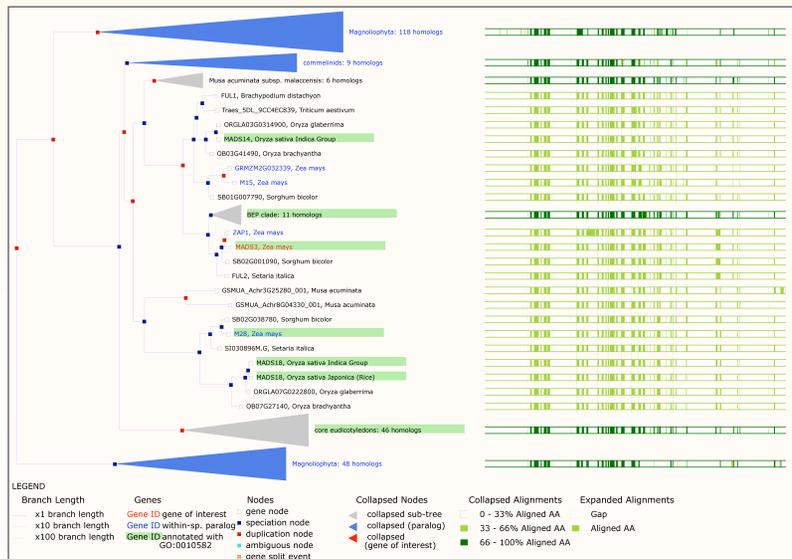


Gramene has biological pathways for various plant species, including *Zea mays* (MaizeCyc), *Oryza sativa* (RiceCyc), and a reference plant pathway database (PlantCyc)

The beta version of the Plant Reactome includes 129 curated rice pathways (Source: RiceCyc v 3.3)



The multi-species view shows alignments in the context of gene annotations across multiple species



SNP diversity displayed in the context of functional protein domains. Population genotypes also available in graphical & tabular form



Phylogenetic tree for *Zea mays* gene *mads3*, a MADS-box protein, showing conservation throughout the eukaryotic lineage. Genes associated with floral meristem determinacy (GO:0010582) are highlighted.