Genomes & Diversity

As of March of 2013, Gramene hosts a total of 23 complete and 13 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 positioned itself as a resource for genome variation data, with focus on *Arabidopsis*, rice, and maize. The current release includes maize HapMap2, a collection of 55 million SNPs and InDels from over 100 germplasm accessions, and also includes new variation data for sorghum, wheat, and *Brachypodium*.

Pathways & Networks

Gramene also produces and hosts or mirrors metabolic pathways databases and visualization tools. The current release includes the latest update to MaizeCyc 2.0.2 (Monaco et al, 2013). We are also pleased to introduce Plant Reactome, 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 [http://plantreactome.oicr.on.ca].

Outreach & Releases

Our release cycle consists of two major and two interim releases per year, ensuring timely updates to both, data and software. We reach our users at key scientific meetings including the *Plant and Animal Genomes*, *Maize Genetics Conference*, *International Conference on Arabidopsis Research*, and *Plant Biology*. Gramene 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
- DAS for sequence alignments
- Public MySQL server
- Entry points for TASSEL, Flapjack and PICARA
- RESTful API

Cite Us

Youens-Clark et al (2010). Gramene database in 2010: updates and extensions. *NAR* 39:D1085-94

Monaco et al (2013). Maize Metabolic Network Construction and Transcriptome Analysis. *The Plant Genome*. In Press
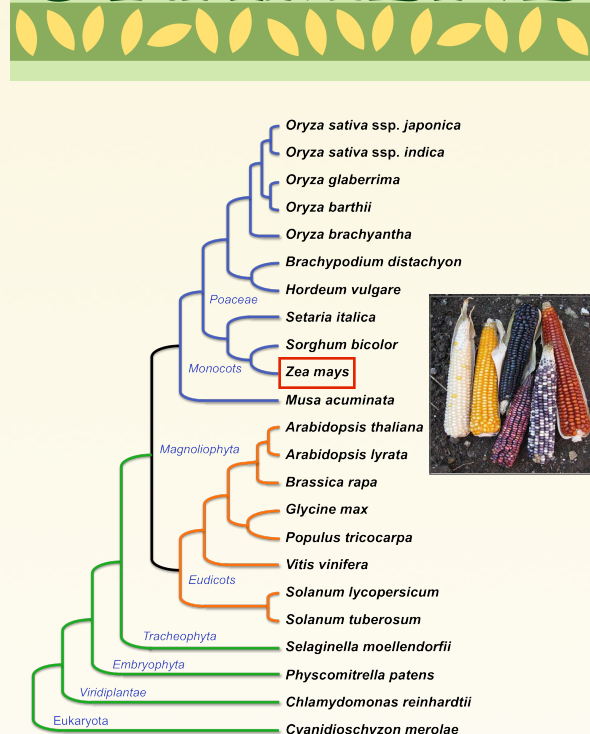
Contact us

gramene@gramene.org

Funding

GRAMENE

Oryza sativa ssp. *japonica*
Oryza sativa ssp. *indica*
Oryza glaberrima
Oryza barthii
Oryza brachyantha
Brachypodium distachyon
Hordeum vulgare
Setaria italica
Sorghum bicolor
Zea mays
Musa acuminata
Arabidopsis thaliana
Arabidopsis lyrata
Brassica rapa
Glycine max
Populus tricocarpa
Vitis vinifera
Solanum lycopersicum
Solanum tuberosum
Selaginella moellendorfii
Physcomitrella patens
Chlamydomonas reinhardtii
Cyanidioschyzon merolae

Poaceae / *Monocots* / *Magnoliophyta* / *Eudicots* / *Tracheophyta* / *Embryophyta* / *Viridiplantae* / *Eukaryota*

Comparative genomics in maize and across the plant kingdom

http://www.gramene.org/

Gramene continues to grow, now at 23 complete genomes, including crops, model organisms and lower plants. Together these serve as a reference resource for compartive 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.

Photo: Maize diversity in a Oaxacan market. Courtesy of Lila Downs
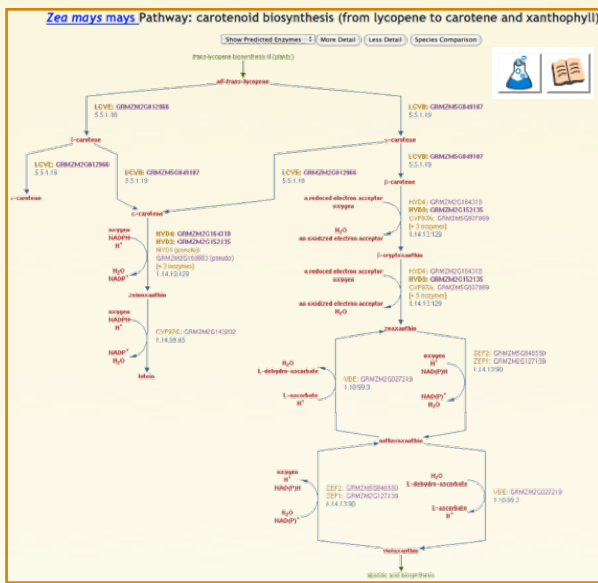
Gramene has biological pathways for various plant species, including *Zea mays* (MaizeCyc) and a reference plant pathway database (PlantCyc)
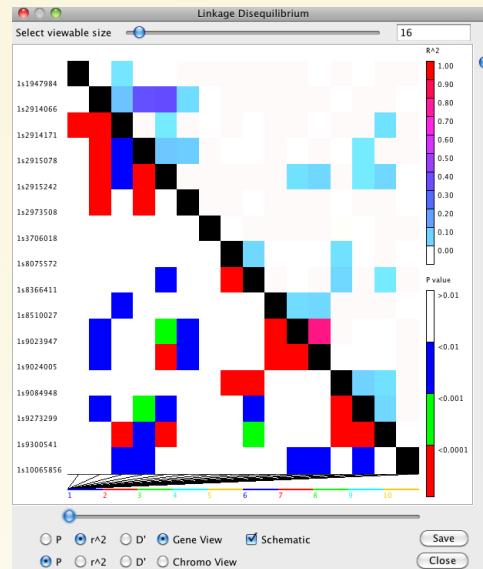

The Tassel program can be used to analyze Gramene's diversity data, generate LD plots, run MLM/GLM analyses, and more

The multi-species view shows alignments in the context of gene annotations across multiple species
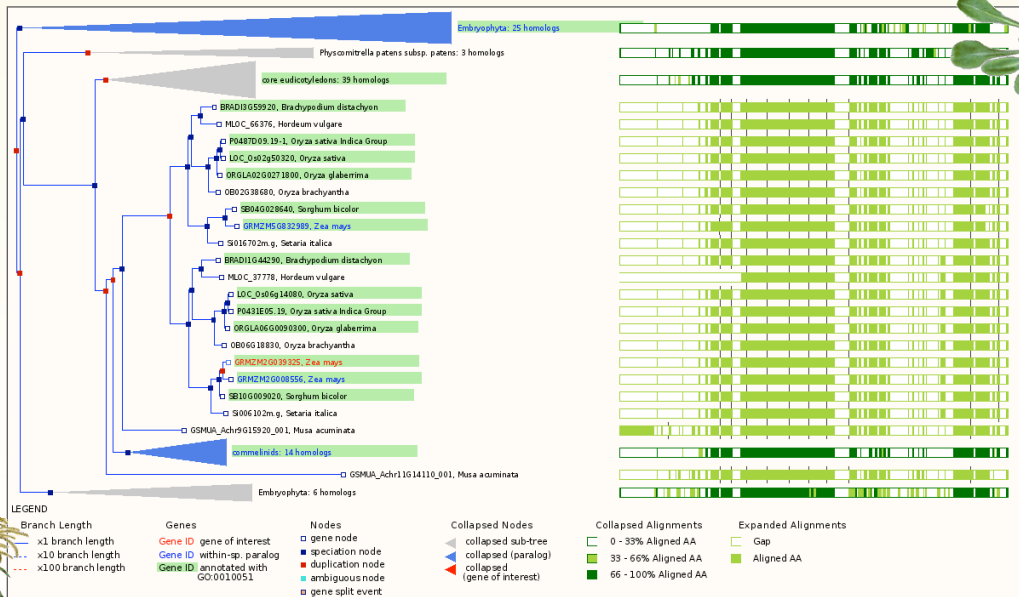
Phylogenetic tree for a *Zea mays* gene encoding a hypothetical protein associated with xylem and phloem pattern formation (GO:0010051), showing conservation throughout the eukaryotic lineage
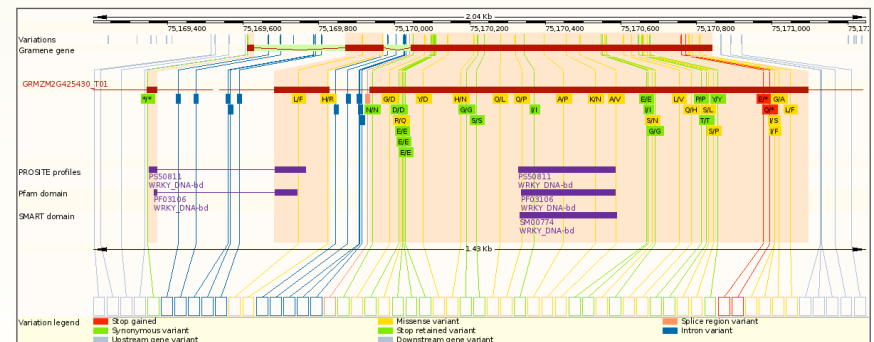
SNP diversity displayed in the context of functional protein domains. Population genotypes also available in graphical & tabular form