

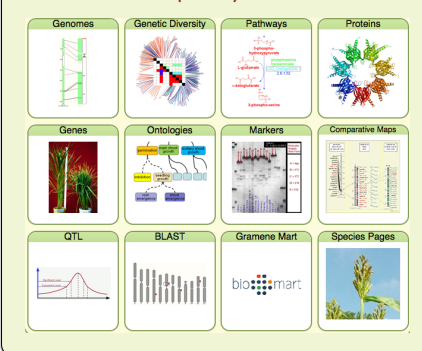
# Gramene: A Database Platform For Comparative Genomics in Plants

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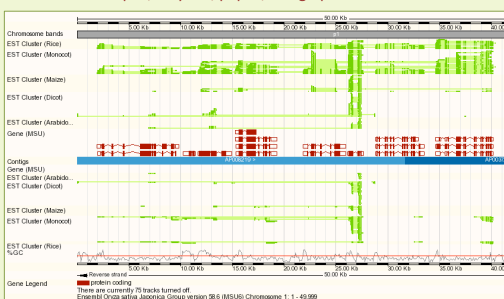
*Gramene is used by plant biologists to conduct basic and applied research in genomics. Its power comes from the integration of functional, genetic & comparative information*

## Gramene Provides Multiple Entry Points into Genomic Data



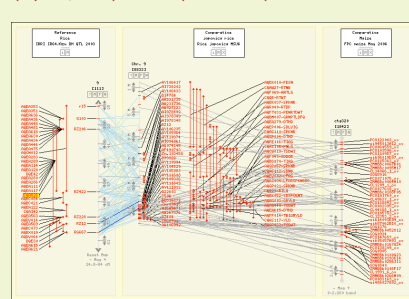
## Genome Browsers for 15 Species

Grasses rice, maize, sorghum, Brachypodium and wild rices. Eudicots Arabidopsis, A. lyrata, poplar, and grape



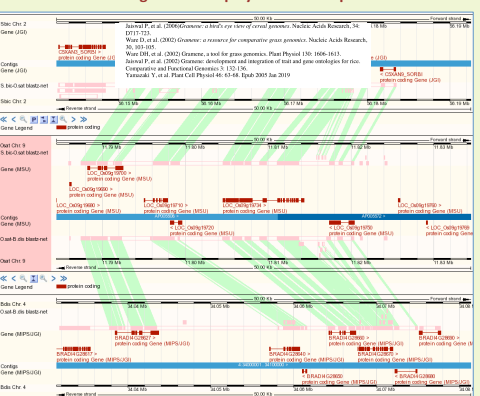
## Comparative Map Viewer (CMAP)

View correspondences between over 200 genetic, QTL, physical, & sequence maps from 30 species



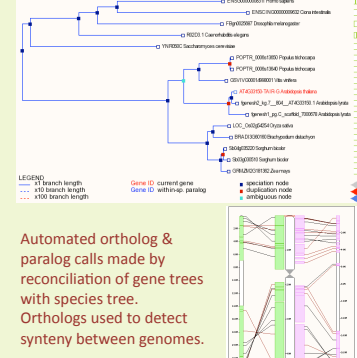
**ABSTRACT:** Gramene (<http://www.gramene.org>) is a curated resource for comparative functional genomics in plants. The database integrates genomic sequence and annotation with ontologies, metabolic pathways, maps and markers, QTL, germplasm, and genetic and phenotypic diversity data. Gramene additionally provides comparative information in the form of phylogenetic trees, ortholog and paralog designation, molecular marker alignment, and whole genome alignments. Navigation and visualization tools promote interspecies browsing and the simultaneous display of multiple species over conserved locations. The site currently hosts complete genomes of nine crop and model plant species. Online tutorials and help documents provide users with an overview of how to conduct a wide variety of operations on the database. All data in Gramene is publicly-available and all code is open source. The database is updated semi-annually for its data content and website interface with the 31st build released in spring 2010. Gramene is supported by NSF grant #0703908 and represents a collaborative effort between Cold Spring Harbor Lab, Oregon State University, Cornell University and various national and international projects dedicated to plant genomics and genetics research.

## Whole Genome Alignments Displayed in Multi-species View



## Phylogenomics

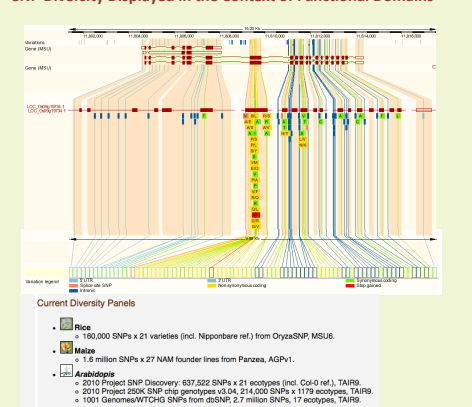
### Ensembl Compara GeneTrees



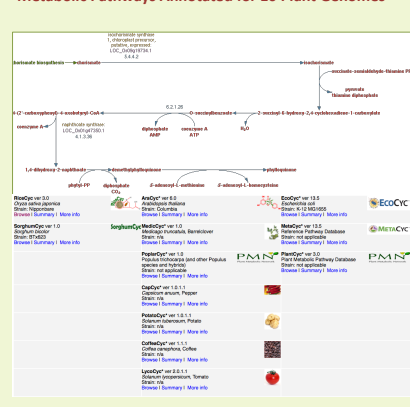
Automated ortholog & paralog calls made by reconciliation of gene trees with species tree. Orthologs used to detect synteny between genomes.

Vilella AJ et al. Genome Res. 2009 9:327-35.

## SNP Diversity Displayed in the Context of Functional Domains



## Metabolic Pathways Annotated for 10 Plant Genomes



## Publications

Jaiswal P, et al. (2006) Gramene: a bird's eye view of cereal genomes. *Nucleic Acids Research*, 34: D717-D723.  
Ware D, et al. (2002) Gramene: a resource for comparative grass genomics. *Nucleic Acids Research*, 30: 103-105.  
Ware DH, et al. (2002) Gramene, a tool for grass genomics. *Plant Physiology* 130: 1606-1613.  
Jaiswal P, et al. (2002) Gramene: development and integration of trait and gene ontologies for rice. *Comparative and Functional Genomics* 3: 132-136.  
Yamazaki Y, et al. *Plant Cell Physiol* 46: 63-68. Epub 2005 Jan 19

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