Gramene: A Resource for Comparative Grass Genomics

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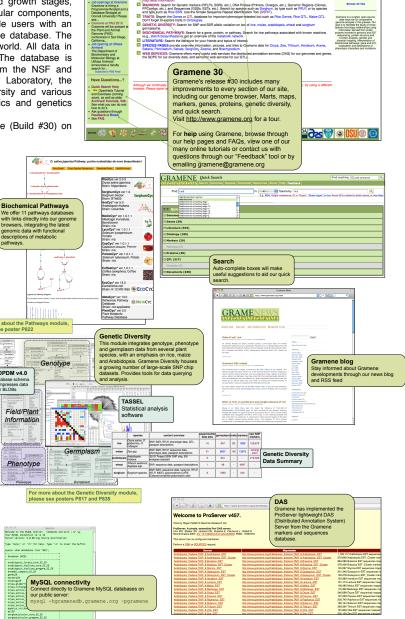
Check out the other Gramene PAG posters: P817, P822, P835, P859

Gramene (**www.gramene.org**) is a curated data resource for comparative genome analysis in grasses and other plants. The database integrates information about genomic sequence, genes, proteins, biochemical pathways, maps and markers, QTL, germplasm, and genetic and phenotypic diversity. To index and associate these different data types, Gramene makes extensive use of ontologies (controlled vocabularies); these include ontologies for plant structures and growth stages, traits and phenotypes, gene function, biological processes, cellular components, and environments. Online tutorials and help documents provide users with an overview of how to conduct a wide variety of operations on the database. The website averages more than 650 visits/day from all over the world. All data in Gramene is publicly-available and all code is open source. The database is updated semi-annually. Gramene is supported by a grant from the NSF and represents a collaborative effort between Cold Spring Harbor Laboratory, the Department of Plant Breeding and Genetics at Cornell University and various national and international projects dedicated to cereal genomics and genetics research.

The database is updated 2 times a year, with the latest release (Build #30) on October 2009.

Gramene 30
Gramene's release #30 includes many improvements to every section of our site, including our genome browser, Marts, maps, markers, genes, proteins, genetic diversity, and quick search.
Visit http://www.gramene.org for a tour.

For **help** using Gramene, browse through our help pages and FAQs, view one of our many online tutorials or contact us with questions through our "Feedback" tool or by emailing gramene@gramene.org

Comparative Map Viewer (CMAP)
Search, view, and compare mapped genes, markers, QTL, and clones on various types of maps (including genetic, physical, sequence, and QTL). View correlations and genetic colinearity within and between species.
For more about the CMap, please see poster P859

Biochemical Pathways
We offer 11 pathways databases with links directly into our genome browsers, integrating the latest genomic data with functional descriptions of metabolic pathways.
For more about the Pathways module, please see poster P822

Search
Auto-complete boxes will make useful suggestions to aid our quick search.

Gramene blog
Stay informed about Gramene developments through our news blog and RSS feed

Genetic Diversity
This module integrates genotype, phenotype and germplasm data from several plant species, with an emphasis on rice, maize and Arabidopsis. Gramene Diversity houses a growing number of large-scale SNP chip datasets. Provides tools for data querying and analysis.

GDPDM v4.0
Database schema. Compresses data with BLOBs

TASSEL
Statistical analysis software

Genomes/PlantEnsembl
Browse assembled genomes and their associated gene models with Ensembl (v. 55). We now host eight genomes: *A. thaliana, A. lyrata, Brachypodium distachyon, Oryza sativa, Oryza sativa indica group, Populus trichocarpa, Sorghum bicolor, Vitis vinifera.*

Genetic Diversity Data Summary

For more about the Genetic Diversity module, please see posters P817 and P835

Gramene Mart
New BioMarts for QTLs, markers, mappings and ontologies; improved BioMarts for genes, SNPs

MySQL connectivity
Connect directly to Gramene MySQL databases on our public server:
`mysql –hgramenedb.gramene.org –pgramene`

DAS
Gramene has implemented the ProServer lightweight DAS (Distributed Annotation System) Server from the Gramene markers and sequences database.