

Gramene Datasets

MARKERS: A key primary source for information about maps and markers of various types. The marker information includes, name, synonyms, source species, map positions and its as- sociations to other markers in the database. It also provides SSR prediction Toolkit.

MAPS/CMAP: A perfect online resource for viewing the standalone versions of genetic, physi- cal and sequence maps from major cereal crop plants. It also allows comparing them for inter and intraspecific genetic colinearity.

GENOMES: Hosting data integration and visualization tools for genome annotations and ge- nome comparisons. The list of available genomes is growing, and includes the Rice-Japonica (*Oryza sativa*), Rice-Indica (*Oryza sativa*), Red Rice (*Oryza rufipogon*), Arabidopsis (*Arabi- dopsis thaliana*) genomes, and the maize genome information is provided via a link to maiz- esequence.org.

BLAST: Search for DNA and peptide sequence similarities with rice and several other major cereal crops. Refine your results, or view HSP (Full form of HSP) in the genome browser.

PROTEINS: Search for protein(s) of interest, locate information on its functional characteriza- tion and get best hits to the rice gene models.

GENES: Get information about genes and alleles, their associations to important phenotypes, functions, sequences and citations.

QTL: Use this module to find qualitative trait locus (QTL) associated with traits from major cereal crops and their map positions on genetic and sequence maps.

DIVERSITY: Search for genotype and phenotype information on rice, maize, and wheat germ- plasm accessions.

PATHWAYS: It is a home for the metabolic pathway database for rice, called RiceCyc. It allows users to browse, search and compare pathways from multiple plant sources, and provides a tool to overlay and view your expression, proteomics and metabolomics data on pathways in real time.

ONTOLOGIES: Find keywords for plant structure, growth stages, traits, molecular function, biological process, cellular component, environment and taxonomy and links to the associ- ated data sets e.g. genes, QTL, maps and proteins.

LITERATURE: Find articles about curated genes, proteins, QTL, markers, and maps.

| Species | | |
|---------|-------|-------------|
| Rice | Maize | Wheat |
| Barley | Oats | Sorghum |
| Millet | Rye | Arabidopsis |



Gramene is a comparative genomics database with tools to visualize and analyze data using genetic, genomic, proteomic, and biochemical data from cereal crops and other model organisms.

Gramene uses ontologies in collaboration with the Gene Ontology and Plant Ontology Consortia to describe gene function, genes expression and phenotypic variation.

Researchers who have published data that is not currently in the Gramene database are encouraged to contact Gramene to request curation of their articles.



The Gramene project is a collaboration between Cold Spring Harbor Laboratory and Cornell University, NY, USA.

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GRAMENE



A Resource for Comparative Grass Genomics

WEB SITE:

www.gramene.org

CONTACT:

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or use “Feedback” link from the website

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A Resource for Comparative Grass Genomics

Release # 26

September 2007

News

NEW

Gramene Receives NSF Grant funding. See NSF Award announcement

NEW

Gramene uses Google Outreach Calendar

NEW

Sept 2007, V 26 release notes.

NEW

October 15-17, 2007 - 5th International Symposium of Rice Functional Genomics in Tsukuba, Japan

NEW

September/October Gramene Newsletter

Have Questions...?

Quick Search Help

Tutorials - See what you can do and how to do it.

Ask questions through Feedback or Email.

See FAQ.

Genomes-Ensembl

Maps-CMap

Markers

QTL

Diversity

Genes

Proteins

Pathways

Ontologies

Literature

Sequences-BLAST

All-GrameneMart

Quick Start

ed genomes for *Oryza Sativa indica* and *japonica*, *Oryza rufipogon*, *Zea mays* & *rice/maize* synteny; Narrow your search with GrameneMart; Search for sequence by Gene Ontology.

or ProSite or Browse by Gene Ontology using GO Slim.

the genetic or physical maps for Wild Rice (*Oryza* sp. from OMAP), Rice, Maize, Wheat, other grasses, or use the Comparative Map Viewer (CMap) to compare maps of different detail information

c markers (RFLPs, SSRs, etc.), DNA Probes (Primers, Overgos, etc.), Genomic Regions Sequences (GSSs, ESTs, etc.). Search by species such as Sorghum, by type such as and type such as Rice SSR. Use the Simple Sequence Repeat Identification Tool

TRAITS:

Search the Genes or QTL database for important phenotype-related loci such as Rice Genes, Rice QTL, Maize QTL. Don't forget to explore traits in Ontologies.

GENETIC DIVERSITY:

Search for SNP and SSR allelic variation on loci of rice, maize, and wheat germplasm.

BIOCHEMICAL PATHWAYS:

Search for a gene, protein, or pathway. Search for rice pathways associated reactions (exempli gratia starch biosynthesis) or get an overview of the metabolic network.

LITERATURE:

Search the literature for your friends and topics of interest.

SPECIES PAGES

provide overview information, pictures, and links to Gramene data for Oryza, Zea, Triticum, Hordeum, Avena, Setaria, Pennisetum, Secale, Sorghum, Zizania and Brachypodium.

SUBMISSION:

Submit a Rice Gene or Ontology Term to Gramene, or ask a question.

Visit with us at

Jan 12-16, 2008 PAG XVII Attend the Gramene Computer Demonstration and the Ontologies Workshop and computer demo. See our Posters!

Outreach Calendar

Presentation Materials

Gramene Tip:

You can limit your BLAST search in Gramene to a specific plant species.

Browse All Tips

Gramene is a curated, open-source, data resource for comparative genome analysis in the grasses. Our goal is to facilitate the study of cross-species homology relationships using information derived from public

Note! Although we continually work to make Gramene compatible with all browsers, if you're having difficulty viewing Gramene, try using a different browser. Please report any problems through Gramene Feedback.

SPECIES

USDA

DARS

NSF

CSH

Cornell University

www.gramene.org

Markers

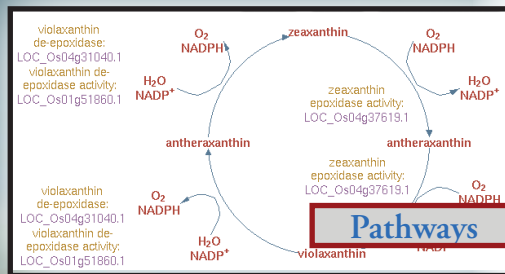
| Avena sativa RFLP "CDO17" | |
|-------------------------------|--------------|
| ID | 3354 |
| Name | CDO17 (GR) |
| Synonyms (6) | CDO0017 |
| | CDO17B |
| | Xcdo17 |
| MAIZEGDB PROBE | p-cdo17 |
| Type | RFLP |
| Species | Avena sativa |
| Germplasm | Brooks Class |
| Analysis | UNKNOWN |
| Description | |
| Source/Library | |
| Details | |
| Database Cross-References (1) | |
| Sequences (2) | |
| Map Positions (20) | |
| Associations (22) | |
| Images (2) | |

| Oryza sativa gene "d1" (GR) | |
|--------------------------------|--|
| Genes | |
| Gene Symbol | |
| Gene Name | |
| Synonyms (7) | |
| E.C. Numbers (0) | |
| Chromosome No. | |
| Gene Type | |
| Has Phenotype | |
| Description | |
| Curator Comment | |
| Alleles (12) | |
| Germplasm (27) | |
| Sequences (12) | |
| Gene-To-Gene Interactions (0) | |
| Gene Interactions (0) | |
| Map Positions (3) | |
| Gene Map Positions (3) | |
| Associated Ontologies (46) | |
| Associated QTL (0) | |
| Database Cross-References (32) | |
| Images (3) | |

Data details include species, symbols, names, synonym, germplasm, marker type, source, literature abstracts and authors, accession numbers, and curator comments. Primary data is integrated so that users may move fluidly from one module to another by associated data including map positions, associated markers, sequences, associated ontologies, database cross references, associations, images and germplasm, among others.

| Oryza sativa QTL "AQD" | |
|----------------------------|--------------|
| QTL Accession ID | AQD001 |
| Species | Oryza sativa |
| Trait Symbol | LOI |
| Trait Name | lodg |
| Pub. QTL Symbol | |
| Trait Synonym(s) | lod, lodg |
| Trait Category | Abiotic |
| Chromosome | 12 |
| Comments | |
| Map Positions (2) | |
| QTL DB Map Position (1) | |
| Associated Markers (40) | |
| Associated Genes (0) | |
| Associated Ontologies (10) | |
| Database Cross-References | |

www.gramene.org



Gene/Protein annotations are mapped to various biochemical pathways

Primary Data

Grounded in Literature
Annotated and integrated
by Ontologies

Protein
Gene
Chr. (eg rice)
Clone (BAC)
Marker
Chr. (eg maize)
Locus
Allele
Gene/QTL
Trait
Phenotype

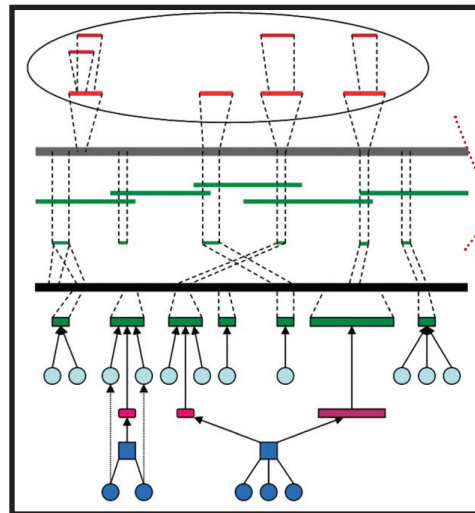
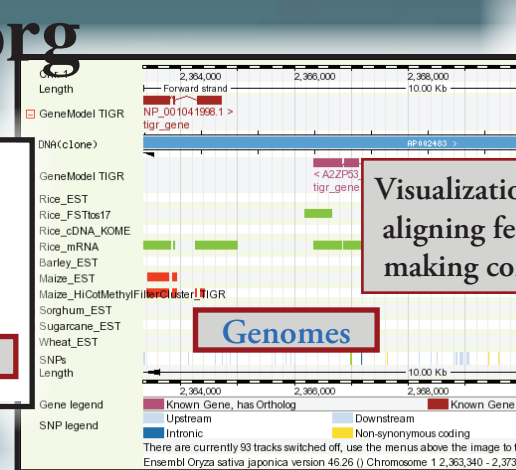
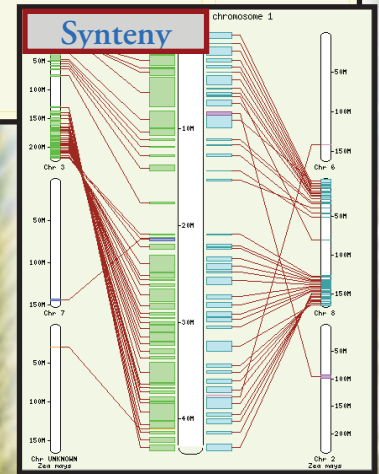
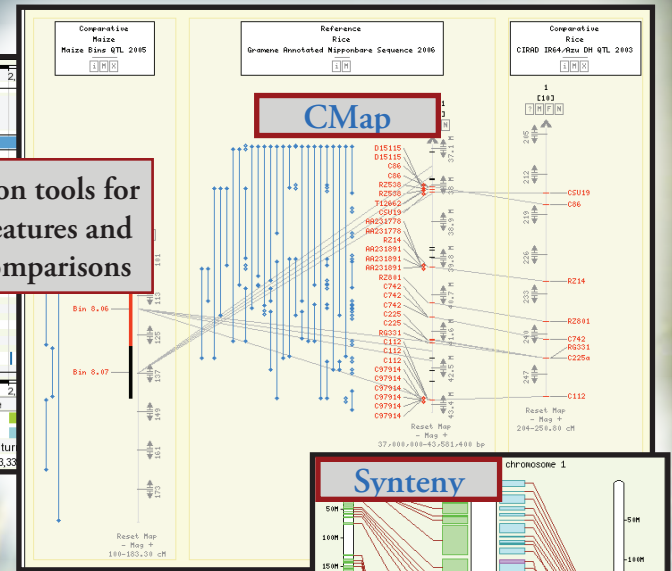


Image from Liang et al. NAR, doi:10.1093/nar/gkm968



Visualization tools for aligning features and making comparisons



Complex & Evolutionary data

Get information on protein families,
Link to external datasources.

Synteny - Use comparative genomics to identify functional elements and sequence variants that may have phenotypic consequences

Diversity Data - compare genotypes and phenotypes for loci from various germplasm.

| Oryza sativa Germplasm "Tondok" | | Collector | |
|---|-------------------------------|--|--|
| Accession Name | Tondok | Collection Number | CI 2584 |
| Institute(s) Holding Accession | NSGIC, IRGC/IRRI | Collection Source | |
| Accession Number | CI 2584 | Collection Code | |
| Synonym(s) | | 0000-00-00 00:00:00 | |
| IRGC 3576 (Search at IRIS/IRRI) CI 2584 (Search at GRIN) CI 2584 (Search at GRIN) IRGC 3576 (Search at IRIS/IRRI) IRGC 3575 (Search at IRIS/IRRI) | | Locality | Bantam, Lebak, Sadira |
| | | City | |
| | | Elevation | |
| | | Latitude | 6° 2' S |
| | | Longitude | 106° 9' E |
| Stock Source | CI 2584 | State/Province | Java |
| Stock Number | Traditional cultivar/landrace | Country | Indonesia |
| Germplasm Type | Oryza | Experiments (2) | |
| Genus | Oryza | Title | Design |
| Subspecies | japonica | Polymorphism Type | Allele Scoring Protocol |
| Subtaxa | | SSR | PCR products were size separated by capillary electrophoresis using ABI 3700 DNA analyzer. SSRs were analysed with GenScan 3.1.2 software and scored with Genotype 2.5 software. |
| Taxonomy Cross-Reference | GR_tax:013684 | Marker-Based approach to assessing the genetic Base of rice in the USA | 236 rice accessions were genotyped at 113 RFLP and 60 SSR loci. |
| Genotypes | | PI(s) | Comments |
| All Genotypes On "Tondok" | | McCouch, S. and Tal, T. H. | Prediction of population structure was model-based (STRUCTURE) and based on data from 169 genomic SSRs. For more information, see the paper by Garria et al., 2005. |
| All Genotypes On "Rathuete" | | McCouch, S. | For more info, please read Xu et al., 2004. |
| All Genotypes On "Kotobuki Mochi" | | | |
| All Genotypes On "Bico Branco" | | | |
| All Genotypes On "Pelita Janggut" | | | |
| All Genotypes On "O-Luen-Cheung" | | | |
| All Genotypes On "Minti" | | | |

| Germplasm Accession Name | Subsp. & subtaxa | Country of Origin | Accession Number | Stock Number | Locus Name | Genotype | View All Genotypes on Germplasm |
|--------------------------|-----------------------------|-------------------|------------------|--------------|------------|--------------|-----------------------------------|
| JC73-4 | aromatic | India | IRGC 9115 | RA4918 | RM1 | NOT DETECTED | All Genotypes On "JC73-4" |
| Rathuete | indica, indica | Sri Lanka | IRGC 8952 | RA4911 | RM1 | 102 | All Genotypes On "Rathuete" |
| Chinese | japonica | China | PI 431222 | RA5295 | RM1 | 84 | All Genotypes On "Chinese" |
| Kotobuki Mochi | japonica, tropical japonica | Japan | IRGC 2545 | RA4882 | RM1 | 98 | All Genotypes On "Kotobuki Mochi" |
| Bico Branco | aromatic | Brazil | IRGC 38994 | RA4950 | RM1 | 86 | All Genotypes On "Bico Branco" |
| Pelita Janggut | indica, indica | Indonesia | IRGC 43640 | RA4986 | RM1 | 108 | All Genotypes On "Pelita Janggut" |
| O-Luen-Cheung | indica, indica | Taiwan | IRGC 8179 | RA5018 | RM1 | 102 | All Genotypes On "O-Luen-Cheung" |
| Minti | japonica, tropical japonica | Bangladesh | IRGC 25901 | RA4970 | RM1 | 88 | All Genotypes On "Minti" |