

Gramene datasets

Markers: A key database at Gramene. Contains all map sets, maps, & mappings, and should be considered to be the primary source for information about maps and markers of various types. The exact information displayed depends on the marker type, but all will display the name, synonyms, source species, and a listing of map positions. Markers also links to several SSR Marker resources, and several other documents and resources.

Maps/CMap: Visualizations in the CMap views (map sets, maps, features, and correspondences) are generated from the Markers Module. Search, view, and compare mapped genes, markers, QTL and clones using various types of maps (including genetic, physical, sequence and QTL) to view correlations and genetic colinearity between and within species. All features (and only those features) that have correspondences to other maps have been assembled on the Gramene Annotated Nipponbare Sequence for use as the main reference map in map comparisons.

Genomes: Use Genome Browser to browse assembled genomes and their associated gene models. Feature mappings are taken from the Marker and Protein DBs. Further Cross-genome analyses provide data on syntenic blocks and gene paralogs/orthologs. The list of genomes is growing, and includes the Rice-Japonica (*Oryza sativa*), *Oryza rufipogon*, Maize (*Zea mays*) and Arabidopsis (*Arabidopsis thaliana*) genomes and organelles.

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

Proteins: Find a protein and it's sequence; Determine it's cellular location and function (each associated reference is supported with an evidence code, suggesting the type of experiment/assertions used in inferring the association). Explore protein families.

Genes: Get information about genes and alleles associated with important phenotypes and functions. Rice genes have been curated in-house from publications, and maize genes have been imported from MaizeGDB.

QTL: Use this module to find qualitative trait locus (QTL) associated with traits from major cereal crops. QTL for rice, sorghum, pearl millet, foxtail millet and wild rice have been curated in-house from research publications. Other QTL (roughly 1/6 of the QTL) have been imported from MaizeGDB and GrainGenes.

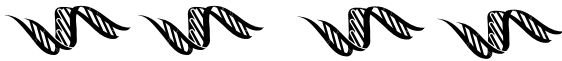
Ontologies: The use of ontologies provides a strong framework for integrating the data between the Gramene modules. Find keywords for plant structure, growth stages, traits, function, process, cellular component, environment and taxonomy and link to associated data in genes, QTL, maps and proteins.

Diversity- Repository for allelic variation data of SSR, SNP and RFLP loci in rice, maize, and wheat germplasm accessions. The module also contains passport descriptions. Data can be viewed by searching using germplasm accession identifiers or marker names. Useful for germplasm management, marker assisted selection and DNA-based variety identification. The Diversity module links to advanced software search tools.

Pathways- The RiceCyc database integrates the latest genomic data with functional descriptions of metabolic pathways. This allows the user to visualise predicted rice metabolic pathways and aids them in the analyses of gene and protein expression. Through the use of the RiceCyc Omics viewer the user is able to paint their own microarray and proteomics research data onto the metabolic network of the organism; this allows for visualisation of metabolic pathway across multiple datasets. The RiceCyc database is manually curated and incorporates new rice information as it comes to fruition.

Literature: Gramene's in-house curation relies on collecting data from published articles. These articles, as well as several other of interest, are in the literature module. Find articles about genes, proteins, QTL, markers, or ontologies and link to that information in the database. Gramene can't provide the full article, but when available there is a link to the online-resource, which may be available to you depending upon the permissions of your institution.

Species		
Rice	Wild Rice	Maize
Wheat	Oats	Sorghum
Barley	Foxtail & Pearl Millet	Other Grasses



Gramene has developed a database and tools to store, visualize and analyze data on the genetics, genomics, proteomics and biochemistry of grass plants.

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 article.



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A Bird's Eye View of Grass Genomes



A Resource for Comparative Grass Genomics

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www.gramene.org

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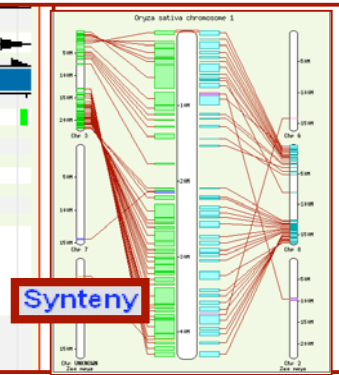
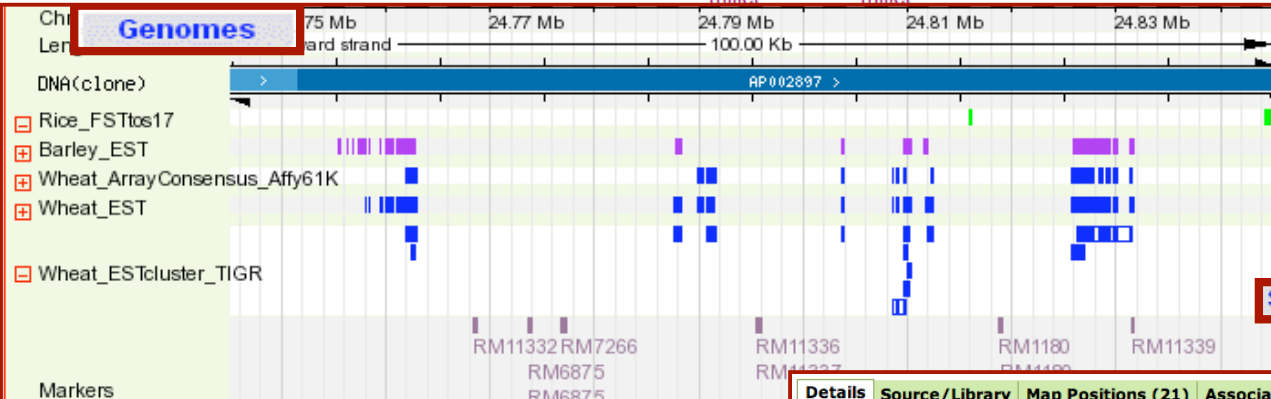
Search database

Download Gramene software and
data installation information.

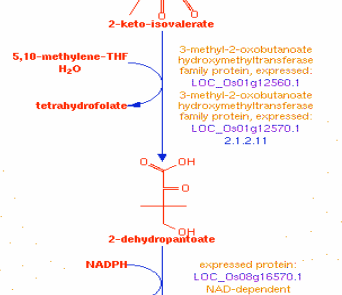
Use the "Feedback" button for
questions or suggestions. We
would like to hear from you.

Genomes-Ensembl
Maps-CMap
Markers
QTL
Diversity
Genes
Proteins
Pathways
Ontologies
Literature
Sequences-BLAST
All-GrameneMart

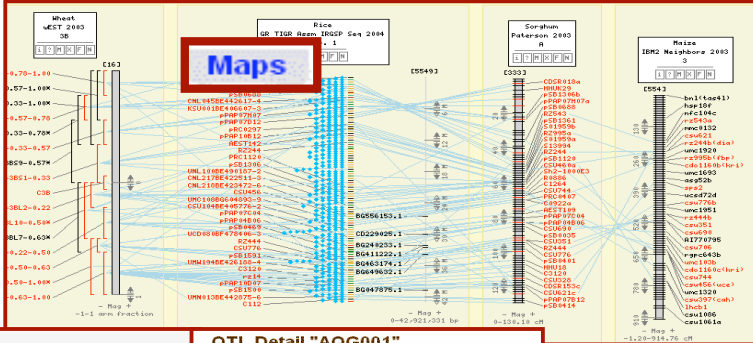
Cereal Species Pages:



Pathways



Maps



Details Source/Library Map Positions (21) Associations (4) Images (0)

Markers

16402333	RM1
GA12	RM1 (K)
GENBANK ACCESSION	AF344003
SSR	Oryza sativa (Rice)
UNKNOWN	
(AG)26	
55	
Product Size	113

General Information	
Accession	GR:000042
Gene Symbol	
Gene Name	Genes
Gene Synonym(s)	green revolution gene
Species	Rice
Chromosome No.	1
Gene Type	CDS (Protein coding)
Has Phenotype	yes
Description	
1. Semidwarfism of an isogenic line (sd1) in the 'Shiokan' background. Dwarfism is intensified in this 'early' background compared to CG10G. The background is a near-isogenic line of Sasanishiki with a chromosomal deletion.	
2. Stature of normal-type and semidwarf rice at ripening. Right: normal-type (Sasanishiki japonica cultivar). Left: semidwarf-type (sd1) background.	
Phenotypic Image	

Proteins

General Information about P93436	
Accession	P93436
Name	Alcohol dehydrogenase class 3
Symbol	ADH3L
Synonym(s)	FALDH, FDH, GSH-FDH, Glutathione-dependent formaldehyde dehydrogenase
E.C. Number(s)	1.1.1.1, 1.2.1.1
Gene Name(s)	Adh3l
Organelle	
Best hits to TIGR rice genome	
Accession Numbers	
Organism(s)	
Term Type	
Molecular Function	

Literature

Reference ID	11383
Title	Fine mapping of the rice sd1 locus on chromosome 1
Source	Theor Appl Genet, 2006, 113, pp.885-894
Authors	Xie-X, Song-M-H, Jin-F, Ahn-S-N, Suh-J-P, Hwang-H-G, M
Abstract	A quantitative trait locus (QTL) for grain weight (GW) was identified in a near-isogenic line (NIL) derived from a cross between the Korean japonica cultivar Hwasongbyeo and Oryza rufipogon (IRGC 10549). The QTL was mapped to a 6.1 cM region in the interval between RM42 and RM210 (P = 0.0001) on chromosome 1. The NILs were developed by repeated backcrossing (BC3F3) of near-isogenic lines (NILs). gw8.1 was validated and mapped to a 6.1 cM region in the interval between RM42 and RM210 (P = 0.0001).
Cross-reference	

Ontologies

Term Name	plant height
Synonym	Ht, PHT, shoot height.
Aspect	Trait
Definition	actual measurement of plant height from soil surface to the highest point in plant as identified in the study
External References	IRRI:SES ICIS:1006
Derivation	
[i] all (all) #512041	
[i] trait ontology (TO:0000387) #13161	
[i] anatomy and morphology related trait (TO:0000017) #49771	
[i] shoot anatomy and morphology trait (TO:0000077) #3970	
[i] plant height (TO:0000207) #1548	
[i] seedling height (TO:0000019) #1	
[i] stem length (TO:0000570) #215	
[i] plant height uniformity (TO:0001000) #5	
[i] stature or vigor trait (TO:0000130) #1769	
[i] height related trait (TO:0000171) #1548	
[i] plant height (TO:0000207) #1548	
[i] seedling height (TO:0000019) #1	
[i] stem length (TO:0000570) #215	
[i] plant height uniformity (TO:0001000) #5	

QTL

QTL Accession ID	AQG001
Species	Rice
Published Symbol	qPHT-1
Trait Symbol	PHT
Trait Name	Plant height
Trait Ontology Accession	TO:0000207
Trait Synonym(s)	PHT, Seedling height
Trait Category	Vigor
Linkage Group	1
Map Position	Rice-Cornell IR64/Azu DH QTL 2
Comments	NA
DBXRef	Gramene Literature 7772

Experiments

There is allele data for germplasm "IRGC 55441" from 4 experiments.	
Title	234 rice accessions from wide geographical regions of the world
Design	SSR
Polymorphism Type	PCR products were size separated by capillary electrophoresis using ABI 3730 DNA analyzer; SSRs were analysed with GenScan 3.1.2 software and scored with Genotyper 2.5 software.
Allele Scoring Protocol	
PI(a)	McCouch, S., and Tai, T. H.
Comments	Prediction of population structure was model-based (STRUCTURE) and based on data from 169 genomic SSRs. For more information, see the paper by Garbis et al., 2005.
Data	Show Allele Data

Diversity

Accession name	Aedal	Collector	
Institute(s) holding accession	IRGC/IRRI	Collection number	
Accession number	IRGC 55441	Collection source	
Synonym(s)		Collection code	
Stock source	McCouch Lab	Collection/release date	
Stock number	RA4969	Locality	
Germplasm type	N/A	City	
Genus	Oryza	Elevation	
Species	sativa	Latitude	NA
Subspecies	japonica	Longitude	NA
Subtaxa	temperate japonica	State/province	
Taxonomy xref	GR_tax:013684	Country	Korea