Gramene Objectives

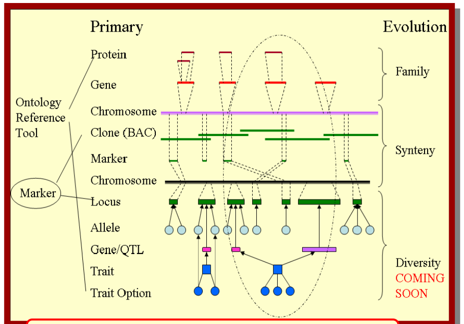
Develop a database and tools to store, visualize and analyze data on genetics, genomics, proteomics, and biochemistry of grass plants.

Provide a bird's eye view of the grass genomes and their organization.

Work with the research community to provide basic information on maps, markers, sequences, genes, gene products, mutants, QTL and literature of the major crop grasses.

Develop controlled vocabularies (ontologies) in collaboration with the Gene Ontology and Plant Ontology consortia to describe gene function, gene expression and phenotypic variation .

Develop bioinformatic community resources for gene discovery in plants.



Overview of concepts in Gramene

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

Useful Gramene Links

How to use Gramene: Tutorials, FAQs
www.gramene.org/workshop_tutorial.html

Site map: Guide to website and databases
www.gramene.org/sitemap.html

Mailing List: Join our mailing list
www.gramene.org/mailarch/

A Resource for Comparative Grass Genomics

Gramene datasets

Genomes: Browse and search genes, markers, expressed sequences, etc. on the Rice-Japonica, Maize and Arabidopsis genomes, as well as sequences from, sorghum, barley and wheat and other cereals mapped on rice; Link to maps and ontologies databases.

BLAST: Search for sequence similarity matches; select the best target sequence database and alignment parameters for your search.

Maps: Search and view mapped genes, markers, QTL and clones using various types of maps (including genetic, physical and sequence); Compare maps; Examine genetic co-linearity between species.

Markers: Find a marker based upon name, type or species; View it's detail; Link to the maps, literature and ontologies databases.

Proteins: Find a protein and it's sequence; Determine it's cellular location and function; Explore protein families; Link to ontologies and literature databases.

Genes: Learn about genes and alleles associated with important phenotypes and functions; Link to literature, ontologies, maps and genomes databases.

QTL: Find qualitative trait locus (QTL) from major cereal crops associated with traits; Link to maps.

Ontologies: Find keywords for plant structure, growth stages, traits, function, process, cellular component, environment and taxonomy; Link to genes, QTL, maps and proteins.

Literature: Find articles about genes, proteins, QTL, markers, or ontologies; Link to publication sources and Gramene's maps, genes, QTL, proteins and markers databases.

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

It is funded by a PGI grant from the National Science Foundation, an IFAFS grant from the USDA Cooperative State Research and Education Service (CSREES), and was previously supported by a Cooperative Agreement through the USDA Agricultural Research Service.

GRAMENE

A Bird's Eye View of Grass Genomes

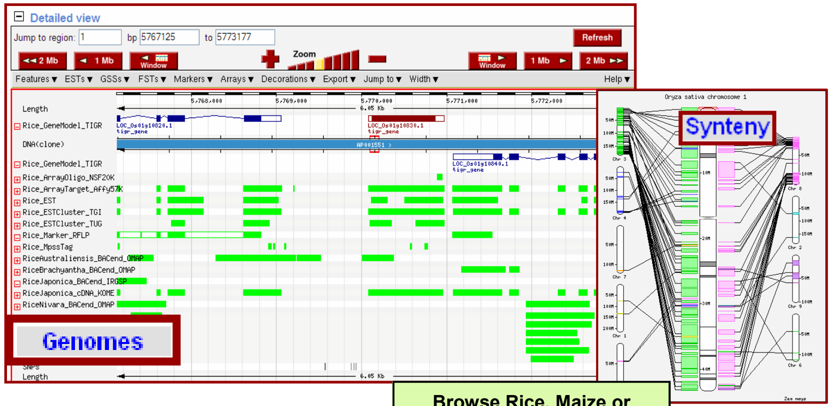
Web site

www.gramene.org

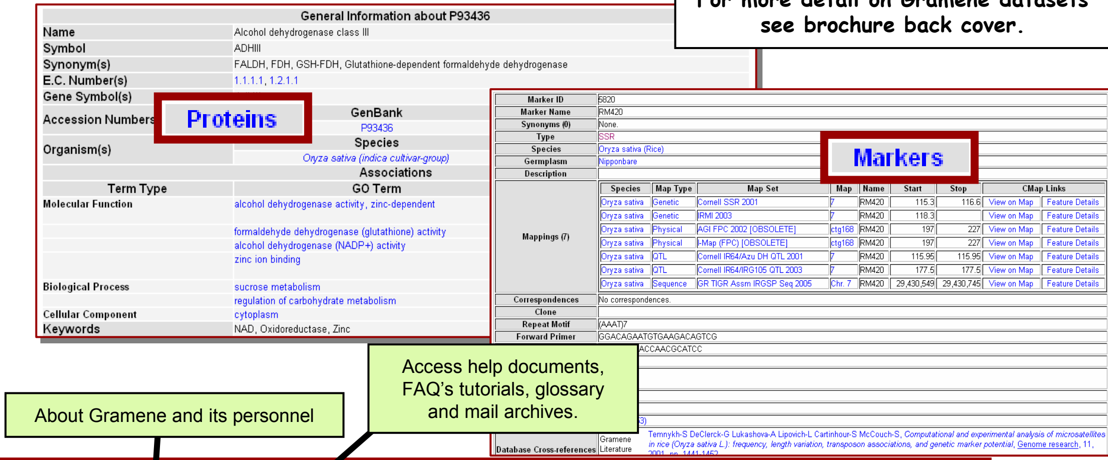
Contact

gramene@gramene.org

For more detail on Gramene datasets see brochure back cover.



Browse Rice, Maize or Arabidopsis genomes



General Information about P93436	
Name	Alcohol dehydrogenase class III
Symbol	ADHIII
Synonym(s)	FALDH, FDH, GSH-FDH, Glutathione-dependent formaldehyde dehydrogenase
E.C. Number(s)	1.1.1.1, 1.2.1.1
Gene Symbol(s)	
Accession Numbers	GenBank P93436
Organism(s)	Species Oryza sativa (indica cultivar-group)
	Associations
Term Type	GO Term
Molecular Function	alcohol dehydrogenase activity, zinc-dependent
	formaldehyde dehydrogenase (glutathione) activity
	alcohol dehydrogenase (NADP+) activity
	zinc ion binding
Biological Process	sucrose metabolism
	regulation of carbohydrate metabolism
Cellular Component	cytoplasm
Keywords	NAD, Oxidoreductase, Zinc

Marker ID	5820
Marker Name	RM420
Synonyms (0)	None.
Type	SSR
Species	Oryza sativa (Rice)
Germplasm	Nipponbare
Description	

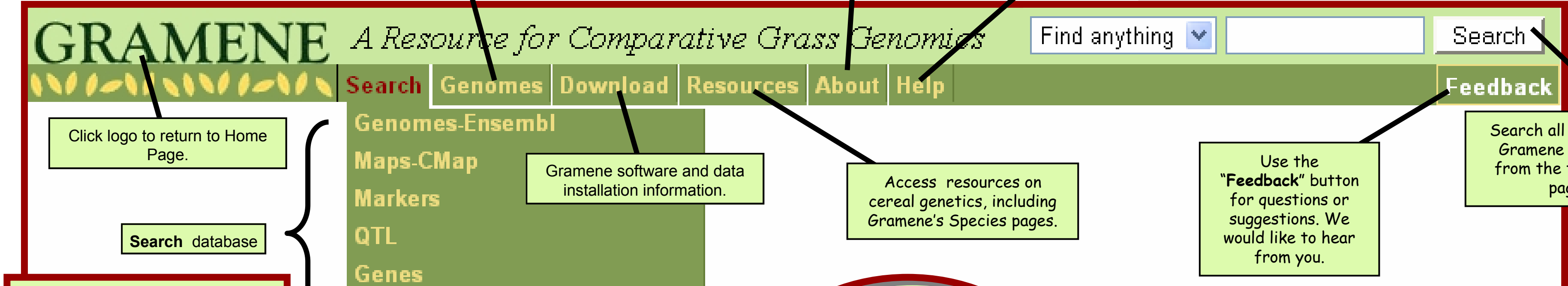
Mappings (7)

Species	Map Type	Map Set	Map	Name	Start	Stop	CMap Links	
Oryza sativa	Genetic	Cornell SSR 2001	7	RM420	115.3	116.6	View on Map	Feature Details
Oryza sativa	Genetic	IRMI 2003	7	RM420	118.3		View on Map	Feature Details
Oryza sativa	Physical	AGI FPC 2002 [OBSOLETE]	ctg168	RM420	197	227	View on Map	Feature Details
Oryza sativa	Physical	I-Map (FPC) [OBSOLETE]	ctg168	RM420	197	227	View on Map	Feature Details
Oryza sativa	QTL	Cornell IR64/Azu DH QTL 2001	7	RM420	115.95	115.95	View on Map	Feature Details
Oryza sativa	QTL	Cornell IR64/IRG105 QTL 2003	7	RM420	177.5	177.5	View on Map	Feature Details
Oryza sativa	Sequence	GR TIGR Assm IRGSP Seq 2005	Chr. 7	RM420	29,430,549	29,430,745	View on Map	Feature Details

Correspondences	No correspondences.
Clone	
Repeat Motif	(AAAT)7
Forward Primer	GGACAGAATGTGAAGACAGTCG
	ACCAACGCATCC
Database Cross-references	Gramene Literature: Temnykh-S DeClerck-G Lukashova-A Lipovich-L Cartinhour-S McCouch-S, *Computational and experimental analysis of microsatellites in rice (Oryza sativa L.): frequency, length variation, transposon associations, and genetic marker potential*, Genome research, 11, 2001, pp. 1441-1452

About Gramene and its personnel

Access help documents, FAQ's tutorials, glossary and mail archives.



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

Click logo to return to Home Page.

Search database

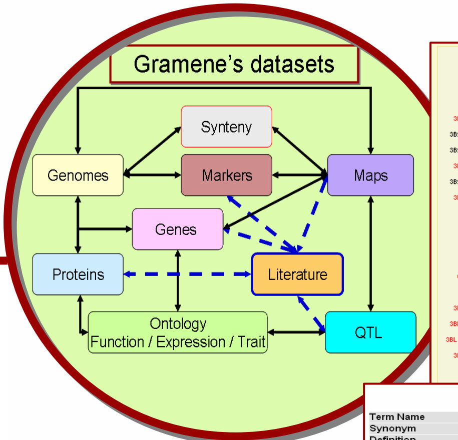
Gramene software and data installation information.

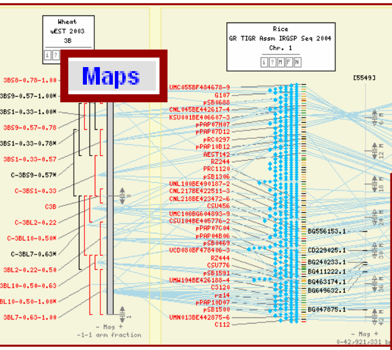
Access resources on cereal genetics, including Gramene's Species pages.

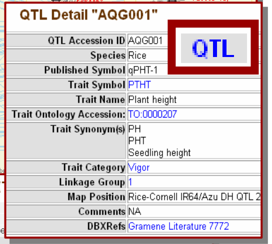
Use the "**Feedback**" button for questions or suggestions. We would like to hear from you.

Search all or a single Gramene database from the top of any page.

Web site
www.gramene.org





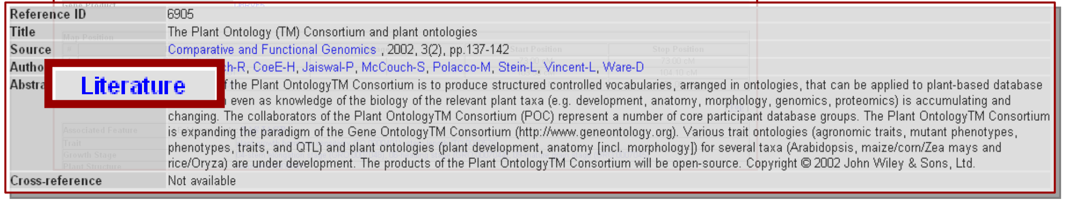


QTL Detail "AQG001"

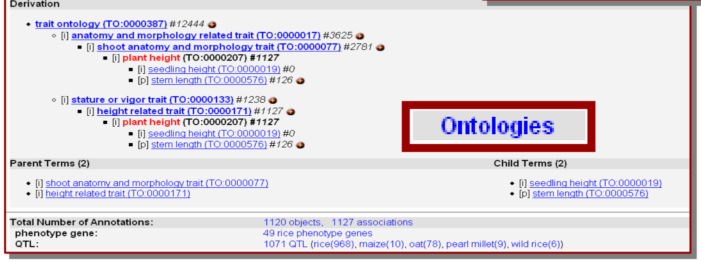
QTL Accession ID	AQG001
Species	Rice
Published Symbol	qPHT-1
Trait Symbol	PTHT
Trait Name	Plant height
Trait Ontology Accession:	TO:0000207
Trait Synonym(s)	PH PHT Seedling height
Trait Category	Vigor
Linkage Group	1
Map Position	Rice-Cornell IR64/Azu DH QTL 2
Comments	NA
DBXRefs	Gramene Literature 7772

Summary for Rice Gene: *semidwarf-1* (GR:0060842)

Gene Name	semidwarf-1
Gene Symbol	*sd1*
Gene Synonym	d47, d49, dee-geo-woo-gen dwarf
Phenotypic Description	Semidwarf, resistant to lodging especially at high fertilizer level, high yielding. Elongation of lower internodes less than that of upper internodes from inhibition of cell division during elongation. Defective in biosynthetic enzyme GA20ox-2 that catalyzed the conversion of GA53 to GA20.
Phenotypic Image	1 . Semidwarfness of an isogenic line (sd1) in the 'Shiokari' background. Dwarfness is intensified in this 'early' background compared to DGWG. The mutant image was kindly provided by Dr. Kinoshita. 2 . Stature of normal-type and semidwarf rice plants at ripening. Right: normal-type (Sasanishiki, a japonica cultivar). Left: semidwarf-type (isogenic line of Sasanishiki with a chromosomal segment containing sd-1 introduced from the semidwarf-type indica cultivar Habataki). Image from Monna-2002 (DNA Research 11-17).
Allele	*sd1*.1, *sd1*.2, *sd1*.3 (d49), *sd1*.4 (SC-SRN(N), *sd1*.5 (SC-AJNT(N)), *sd1*.6 (SC-CPSLO(N)), *sd1*.7 (sd1-a), *sd1*.8 (sd1-h)
Germplasm	Ai-Jio-Nan-Te, CP-SLO, Calrose 76 (D51), Deo-geo-woo-gen, Doongara, HS90, IR8, Jikkoku, Remei, Shiranui-1, T65d, TN1 (Taichung Native 1)
GenBank accession	AB077025([NCBI] [Gramene Genomes]), AF465255([NCBI] [Gramene Genomes]), AF465256([NCBI] [Gramene Genomes]), AY114310([NCBI] [Gramene Genomes]), U50333([NCBI] [Gramene Genomes])



Reference ID	6905
Title	The Plant Ontology (TM) Consortium and plant ontologies
Source	Comparative and Functional Genomics , 2002, 3(2), pp.137-142
Autho	h-R, CoeE-H, Jaiswal-P, McCouch-S, Polacco-M, Stein-L, Vincent-L, Ware-D
Abstra	f the Plant OntologyTM Consortium is to produce structured controlled vocabularies, arranged in ontologies, that can be applied to plant-based database even as knowledge of the biology of the relevant plant taxa (e.g. development, anatomy, morphology, genomics, proteomics) is accumulating and changing. The collaborators of the Plant OntologyTM Consortium (POC) represent a number of core participant database groups. The Plant OntologyTM Consortium is expanding the paradigm of the Gene OntologyTM Consortium (http://www.geneontology.org). Various trait ontologies (agronomic traits, mutant phenotypes, phenotypes, traits, and QTL) and plant ontologies (plant development, anatomy [incl. morphology]) for several taxa (Arabidopsis, maize/corn/Zea mays and rice/Oryza) are under development. The products of the Plant OntologyTM Consortium will be open-source. Copyright © 2002 John Wiley & Sons, Ltd.
Cross-reference	Not available



Summary for TO Term: *plant height* (

Term Name	plant height
Synonym	Ht, PTHT.
Definition	actual measurement of plant height from soil surface to the highest point in plant as ide

Derivation

- trait ontology (TO:0000387) *#12444*
  - [i] anatomy and morphology related trait (TO:0000017) *#3625*
    - [i] shoot anatomy and morphology trait (TO:0000077) *#2781*
      - [i] plant height (TO:0000207) *#1127*
        - [i] seedling height (TO:0000019) *#0*
        - [p] stem length (TO:0000576) *#126*
  - [i] stature or vigor trait (TO:0000133) *#1238*
    - [i] height related trait (TO:0000171) *#1127*
      - [i] plant height (TO:0000207) *#1127*
        - [i] seedling height (TO:0000019) *#0*
        - [p] stem length (TO:0000576) *#126*

Parent Terms (2)

- [i] shoot anatomy and morphology trait (TO:0000077)
- [i] height related trait (TO:0000171)

Child Terms (2)

- [i] seedling height (TO:0000019)
- [p] stem length (TO:0000576)

Total Number of Annotations:	1120 objects, 1127 associations
phenotype gene:	49 rice phenotype genes
QTL:	1071 QTL (rice(968), maize(10), oat(78), pearl millet(9), wild rice(6))