

Using Gramene:

**A genomics and genetics resource
for rice and other grasses.**

PAG XIV

Jan 15, 2006

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Objectives

- Review Gramene datasets and tools available
- Answer biological questions using Gramene.
- Present non-transgenic ways to approach a breeding program.
- Provide hands-on experience using the database.

Assumptions

- You are working with crop plants (cereals).
- Familiar with conducting laboratory research
- Familiar with Maps
- May or may not be familiar with rice
- Have used or intend to use Gramene or another database.
- Breeders, Grad students

Accessing Gramene

To access Gramene, open your browser (such as Netscape, IE, Mozilla, or Firefox).

(If some website features don't work correctly, try using a different browser)

In the address bar type www.gramene.org and press “Enter” to open the **Gramene Home Page**.

Home Page Navigation

Only on home page,
indicates Gramene release
number being used



Click on Gramene
Logo to return to
the Home page

Select "feedback" from any page to
reference that page and open a
communication box. Use for asking
questions or giving feedback.

Home Page

The screenshot shows the Gramene website interface. At the top, the header includes the site name 'GRAMENE' with a leaf logo, the title 'Comparative Grass Genomics', the version 'v20 (Dec 2005)', and navigation links: 'Load', 'Resources', 'About', 'Help', and 'Feedback'. The main content area is divided into three columns. The left column, 'Quick Search', features a search box with the placeholder 'Find anything...' and a 'Search' button. A callout bubble points to the search box, stating: 'Quick search, found at the top of all other pages'. Below the search box is a section titled 'Have you tried...?' with a bulleted list: 'Learning to use Gramene tools and resources with the **tutorials**' and 'Gramene Tips Archive'. The middle column, 'Quick Start', lists several categories with green square icons: 'GENOMES' (Browse sequenced genomes for Rice, Maize & Arabidopsis; Look for rice/maize synteny; Narrow your search with GrameneMart; Search for sequence alignment with BLAST; search by Gene Ontology), 'PROTEINS' (Search by PFam or ProSite or Browse by Gene Ontology using GO Slim), 'MAPS' (Browse genetic or physical maps for Rice, Maize, wheat, Barley, Oats, Sorghum, and other grasses, or use the Comparative Map Viewer (CMap) to compare maps of different types and species), 'MOLECULAR MARKERS' (Use the Simple Sequence Repeat Identification Tool (SSR-IT); or search by marker type or species, including Rice, Maize, Sorghum and Others), 'TRAITS' (Search for genes or QTL database for important phenotype traits such as Rice Genes, Rice QTL, Maize QTL), 'LITERATURE' (Browse the literature on grasses and topics of interest), and 'SUBMISSION' (Submit a Rice Gene or Ontology Term to Gramene). The right column, 'Featured News', has a section titled 'Visit us at' with a bulleted list: 'Plant and Animal Genome XIV Conference, January 14-18, 2006, San Diego, CA, USA', 'Rice Technology Working Group Meeting, Feb. 26-March 5, The Woodlands, Texas, USA', and 'Breaking news on genomic research'. A callout bubble points to the 'Visit us at' section, stating: 'News about the current release and the grass genomic community is listed here'. Another callout bubble points to the 'GRAMENE' logo, stating: 'Gramene Tips give advice on using the site. The Archive'.

GRAMENE Comparative Grass Genomics v20 (Dec 2005)

[Load](#) [Resources](#) [About](#) [Help](#) [Feedback](#)

Quick Search

Find anything...

Search

Have you tried...?

- Learning to use Gramene tools and resources with the **tutorials**
- [Gramene Tips Archive](#)

Quick Start

- GENOMES:** Browse sequenced genomes for [Rice](#), [Maize](#) & [Arabidopsis](#); Look for [rice/maize synteny](#); Narrow your search with [GrameneMart](#); Search for sequence alignment with [BLAST](#); search by [Gene Ontology](#).
- PROTEINS:** Search by [PFam](#) or [ProSite](#) or Browse by Gene Ontology using [GO Slim](#).
- MAPS:** Browse genetic or physical maps for [Rice](#), [Maize](#), [wheat](#), [Barley](#), [Oats](#), [Sorghum](#), and other grasses, or use the Comparative Map Viewer ([CMap](#)) to compare maps of different types and species.
- MOLECULAR MARKERS:** Use the Simple Sequence Repeat Identification Tool ([SSR-IT](#)); or search by [marker type](#) or species, including [Rice](#), [Maize](#), [Sorghum](#) and [Others](#).
- TRAITS:** Search for [genes](#) or [QTL](#) database for important phenotype traits such as [Rice Genes](#), [Rice QTL](#), [Maize QTL](#).
- LITERATURE:** Browse the literature on grasses and topics of interest.
- SUBMISSION:** Submit a [Rice Gene](#) or [Ontology Term](#) to Gramene.

Featured News

Visit us at

- [Plant and Animal Genome XIV Conference](#), January 14-18, 2006, San Diego, CA, USA
- [Rice Technology Working Group Meeting](#), Feb. 26-March 5, The Woodlands, Texas, USA
- Breaking news on genomic research
- [Rice News Worldwide](#) from IRRI
- [Gramene News Archive](#)

Gramene Tips give advice on using the site. The Archive

Quick links help get you directly to where you want to go

News about the current release and the grass genomic community is listed here

Gramene Tips
give advice on
using the site.
The Archive
contains all tips.

Quick links help get you directly to where you want to go

News about the current release and the grass genomic community is listed here, along with a **Gramene Calendar**.

Non-home Page Navigation

This heading is on all pages except for the home page.

Title identifies the page being viewed.

Quick search, optionally select a specific database to search, enter a term to search for, and click on “search.”



Click logo to return to Home page

Dropdown Navigation Bar
(see next slides)

Easily accessible “Feedback” button on every page.

Searches



Each module has its own module-specific navigation bar below the main Gramene navigation bar.

QTL Home | Simple Search

Genomes-Ensembl

Maps-CMap

Markers

QTL

Genes

Proteins

Ontologies

Literature

Sequences-EST

All-Gramene

Tutorial | FAQ

Gramene QTL Database

Search:

creation that identifies a particular region of the genome as containing a gene (or trait) that is being measured. They are shown as intervals on a chromosome where the gene or trait is located in the mapping experiment.

QTL identified for numerous traits is on presenting the QTLs.

Module specific searches will search **ONLY** that module (the example here is the QTL module)

QTL Search or Browse Options

The user can search the QTL database using a wild card search (e.g. [seed*](#)).

- Trait name (e.g. [Seed color](#), [A](#))
- Trait symbol (e.g. [SDCL](#), [ALSI](#))
- Trait category
 - [Abiotic stress](#) | [Anatomy](#) | [Development](#) | [Disease](#) | [Growth](#) | [Quality](#) | [Sterility or fertility](#) | [Vigor](#) | [Yield](#)

Gramene Modules and tools used to **access** the **databases**. See individual module tutorials.

Genomes

The screenshot shows the GRAMENE Genome Browser interface. At the top is a green header with the GRAMENE logo and the text "Genome_browser". To the right of the logo is a search bar with a dropdown menu set to "Find anything" and a "Search" button. Below the header is a navigation bar with links: Search, Genomes, Download, Resources, About, Help, and Feedback. The "Genomes" link is highlighted, and a dropdown menu is open showing "Rice", "Maize", and "Arabidopsis". Below the navigation bar is a section titled "Gramene Genome Browser". On the left, there is a "Find" section with a dropdown menu set to "All" and a search box. On the right, there are "Help" and "Tutorial" buttons. The main content area is divided into two columns. The left column is titled "Gramene-Ensembl" and contains text about the browser being a web-based tool for plant genomes, mentioning physical maps, technology, a joint project with EBI and the Sanger Institute, and a software tool that produces and updates automatic annotations on selected eukaryotic genomes, funded by the Wellcome Trust. The right column is titled "Species in Gramene" and contains a table with three rows: "Rice-japonica" (Dec 2004, TIGR v3), "Maize" (Oct 2004, AGI), and "Arabidopsis" (May 2004, TIGR v5). Below the table is a "Links" section with buttons for "GrameneMart", "BlastView", and "Release Note".

GRAMENE Genome_browser

Find anything Search

Search Genomes Download Resources About Help Feedback

Find All

Rice
Maize
Arabidopsis

Help
Tutorial

Gramene Genome Browser

Gramene-Ensembl

Species in Gramene

| | | |
|---------------|----------|---------|
| Rice-japonica | Dec 2004 | TIGR v3 |
| Maize | Oct 2004 | AGI |
| Arabidopsis | May 2004 | TIGR v5 |

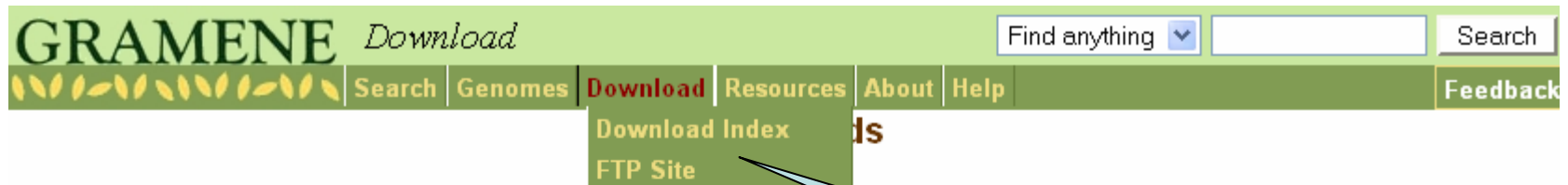
Links

GrameneMart
BlastView
Release Note

Select Genomes to access the genome browser, as well as search tools GrameneMart and BLAST Logo to return to the Home page

Select which genome to view. Also available are Rice-Maize synteny diagrams.

Downloads



FPC Physical Map (AGI)
Genetic Maps
In Silico Data
Microsatellites
Databases as tab-separated-value files
MySQL database dumps (insert statements)
Protein Data
RiceGenes Database (Archived Copy, October 2000)
Blast Databases
Software
Script to search for simple sequence repeats in FASTA-formatted DNA sequences --by S.Cartinhour
Gramene Web Site and supporting code. (live version)
Gramene Web & supporting software by anonymous CVS.

Download data or software to
install Gramene on your own
machine.

Resources

Defines terms, abbreviations and acronyms used. Links to other on-line glossaries

Click to browse fact pages on different **grass species**

Provides **links** to other websites of interest

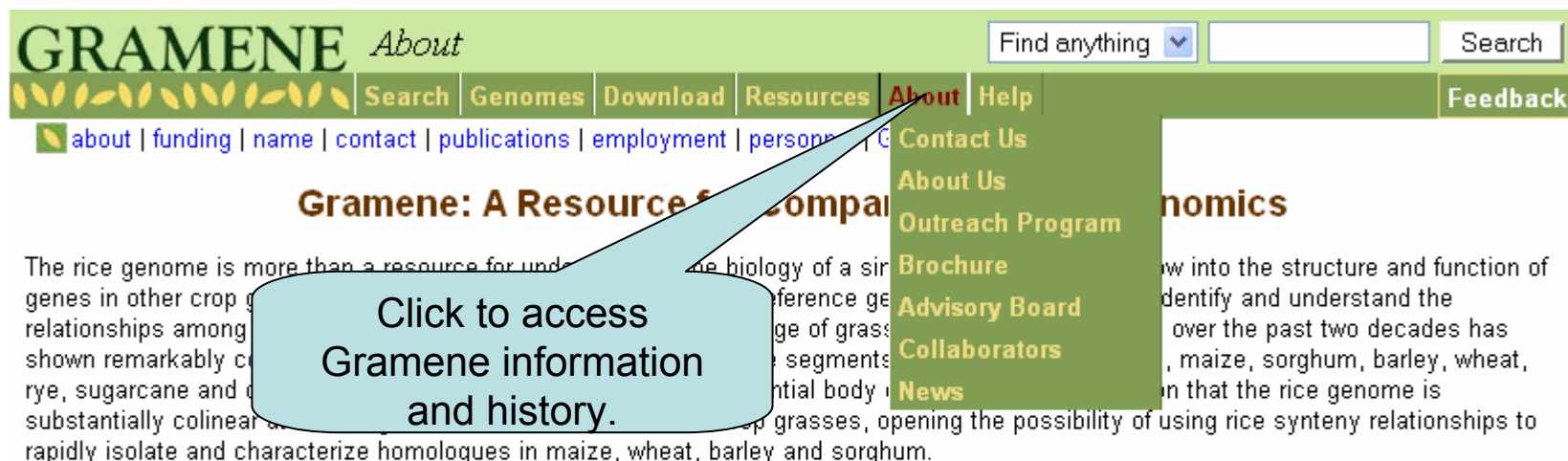
Submit a gene or ontology term to the database

Links page of **genetic newsletters** for rice

Rice Genome Sequencing Efforts

- ♦ [Rice Genome Program \(RGP\)](#)
- ♦ [US Rice Genome Sequencing](#)
- ♦ [Plant Genome Initiative at Rutgers](#)
- ♦ [Arizona Genomics Institute \(AGI\)](#)
- ♦ [Clemson University Genomics Institute \(CUGI\)](#)
- ♦ [Wisconsin Rice Genome Project](#)
- ♦ [Rice Genome Analysis, McCombie Lab, Cold Spring Harbor Laboratory](#)
- ♦ [TIGR Rice Genome Project and TIGR Rice Gene Index](#)
- ♦ [National Center for Gene Research Chinese Academy of Sciences, China](#)
- ♦ [National Center for Genetic Engineering and Biotechnology, Thailand](#)
- ♦ [Rice Genome Project in Republic of China, Taiwan](#)
- ♦ [Genoscope, France](#)
- ♦ [IRD Rice Genetics Group, France](#)
- ♦ [Monsanto Rice Genome Project](#)

About



The screenshot shows the GRAMENE website interface. At the top, the logo 'GRAMENE' is followed by the word 'About'. To the right is a search bar with the placeholder text 'Find anything' and a 'Search' button. Below the logo, a horizontal navigation bar contains links: 'Search', 'Genomes', 'Download', 'Resources', 'About', and 'Help'. A dropdown menu is open under the 'About' link, listing: 'Contact Us', 'About Us', 'Outreach Program', 'Brochure', 'Advisory Board', 'Collaborators', and 'News'. A light blue callout bubble points to the 'About' link in the navigation bar, containing the text: 'Click to access Gramene information and history.'

GRAMENE *About* Find anything Search

[Search](#) [Genomes](#) [Download](#) [Resources](#) [About](#) [Help](#) [Feedback](#)

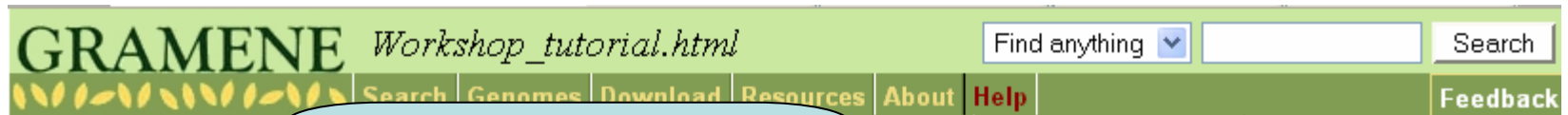
[about](#) | [funding](#) | [name](#) | [contact](#) | [publications](#) | [employment](#) | [persons](#) | [Contact Us](#)
[About Us](#)
[Outreach Program](#)
[Brochure](#)
[Advisory Board](#)
[Collaborators](#)
[News](#)

Gramene: A Resource for Comparative Genomics

The rice genome is more than a resource for understanding the biology of a single reference genome. The discovery of synteny relationships among genes in other crop grasses has shown remarkably conserved gene order over the past two decades has shown that the rice genome is substantially colinear with other crop grasses, opening the possibility of using rice synteny relationships to rapidly isolate and characterize homologues in maize, wheat, barley and sorghum.

As an information resource, Gramene's purpose is to provide added value to data sets available within the public sector to facilitate researchers' ability to leverage the rice genomic sequence to identify and understand corresponding genes, pathways and phenotypes in the crop grasses. This is achieved by building automated and curated relationships between rice and other cereals for both sequence and biology. The automated and curated relationships are queried and displayed using controlled vocabularies and web-based displays. The controlled vocabularies (Ontologies), currently being utilized include Gene ontology, Plant ontology and Trait ontology. The web-based displays for phenotypes include mutant and quantitative trait loci (QTL) modules. Sequence based relationships are displayed in the genome browser adapted from Ensembl, in the comparative map viewer (CMap), Blast databases, and protein displays.

Help



Gramene help docs and documentation

The following table is a guide to the resources available to help you answer your

There are currently **9 main modules** within Gramene. The modules are interrelated in one way to obtain information of interest. The following table provides a brief description of individual entry pages, **help documents, tutorials and guided tours**.

Searchable Frequently Asked Questions about Gramene, curation, and database modules.

Link to info on Rice gene nomenclature

Site Map
Help Documents
Release Notes
Tutorials
FAQs
Workshop Materials
Mailing Lists
Rice Gene
Ask Us

E-Lists for discussion and for announcements

General, Data
Curation,
BLAST, Maps,
Genomes,
Literature,
Genes,
Ontologies,

Footer

Images link to species
information pages

Collaborators and **funding sources**
are linked along the bottom



Information about
citing Gramene

[Copyright](#)

[About](#)

[Site Map](#)

Gramene **purpose**,
history and **people**

Provides an **overview** of
everything on the site

Gramene Modules

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.

Tutorials and Help

There are many ways to seek assistance on how to use the database.

Online Documentation and Help files

Documentation

 Documentation

[Search](#) [Genomes](#) [Download](#)

Gramene Documentation

- **Web Site Help Documents**
 - ◊ [Genomes](#)
 - ◊ [BLAST](#)
 - ◊ [Maps](#)
 - ◊ [Markers](#)
 - ◊ [Proteins](#)
 - ◊ [Ontologies](#)
 - ◊ [Genes](#)
 - ◊ [QTL](#)
- **FAQs**
 - ◊ [General](#)
 - ◊ [Data Curation](#)
 - ◊ [Genomes](#)
 - ◊ [BLAST](#)
 - ◊ [Maps](#)
 - ◊ [Markers](#)
 - ◊ [Protein](#)
 - ◊ [Ontologies](#)
 - ◊ [Genes](#)
 - ◊ [QTL](#)
 - ◊ [Literature](#)
- **Tutorials**
 - ◊ [Genomes](#)
 - ◊ [BLAST](#)
 - ◊ [Maps](#)
 - ◊ [Markers](#)
 - ◊ [Proteins](#)
 - ◊ [Ontologies](#)
 - ◊ [Genes](#)
 - ◊ [QTL](#)
 - ◊ [Literature](#)

- ◊ [How to Use Gramene](#)
- ◊ [Glossary](#)
- ◊ [Rice Gene Nomenclature](#)
- ◊ [Standard Operating Procedures](#)
 - ◊ [Documentation](#)
- ◊ [External Use](#)
 - ◊ [Linking back to Gramene](#)
 - ◊ [Installing Gramene](#)
- ◊ [Release Notes](#)

[Gene Home](#) | [Search](#) | [Submit](#) | [Help Documents](#) | [Tutorial](#) | [FAQ](#)

[Release Notes](#) | [Information Help](#) | [Search Help](#) | [Submit Help](#)

[Release Notes:](#)

Gramene Genes Database now contains 1,488 genes from rice characterized by phenotype, including around 400 genes fully annotated and 1000-1100 genes under curation. More data of genes from other cereal crops will be available in the near future.

[Top](#)

[Description of Information in Gramene Genes Database:](#)

1. For fully annotated genes, the database provides the following information:
 - ◊ **General information:**
 - **Gene name:** Traditional gene names have been used. Some gene names have been modified according to the Gene Nomenclature System.
 - **Gene symbol:** Gene symbols have been assigned, according to the Gene Nomenclature System.
 - **Gene synonym:** List of names or symbols that have been used for a specific gene.
 - **Phenotypic description:** Text defines the primary visual feature used to detect the phenotype for a particular gene to distinguish it from the wild type.
 - **Phenotypic image:** Display image(s) and text explanation of phenotypes for a particular gene, if available.
 - ◊ **Gene accession and gene product:**
 - **GenBank accession:** Provides the link to [NCBI](#), if the related GenBank accession number is available.
 - **Gene product:** Provides the link to [the Gramene Protein Database](#), if available.
 - ◊ **Allele:** Shows one or multiple allele names for a particular gene. Detailed information for the specific allele can be displayed when you click the allele name.
 - **Allele designation:** Different alleles of the same gene are distinguished by a decimal between the name of the gene and the number that follows, e.g., [gle1.1](#). The synonyms for that allele are also listed following the allele designation.
 - **Allele description:** Provided if alleles give phenotypic differences.
 - **Description of allelic interaction:** Provided if the information about the interaction with other alleles or loci is available.
 - **Study:** Provides a list of one or several studies or assays for that particular allele. Detailed information for a specific study



Glossary and FAQ

Search Genomes Download Resources About Help

Gramene Acronyms and Abbreviations

The following is a list of acronyms and abbreviations currently used in Gramene that have been defined for users. In the future, this list will grow to also include definitions of the biological and module-specific terms used in Gramene.

A B C D E F G H I J K L M N O P Q R S T U V W X Y Z

Select a letter to find terms in that category.

Ad... and Biotechnology

Glossary

- Glossarist's [Biology Glossaries and Dictionaries](#)
- [Online Biology Dictionary](#)
- Bioinformatics Educational Resource's [Glossary](#)
- Access Excellence Resource Center's [Visual Library](#)
- Food and Agriculture Organization of the United Nations's [Glossary](#)
- Angiosperm Phylogeny Website's [botanical glossary](#)
- [RiceCAP glossary](#)

A

Abiotic stress
Traits related to stresses from abiotic environment, e.g., water, temperature, etc.

Abstract
A one-paragraph introduction to the main themes of an article.

Accession number
Identifier assigned to a sequence that is unique to the particular database.

ARS Agricultural Research Service
The U.S. Department of Agriculture's main in-house scientific research organization.

Alias -
Synonym or other name by which a feature may be known.

Frequently Asked Questions

General FAQ: [General Gramene](#) | [Data Curation at Gramene](#)

Module FAQ: [BLAST](#) | [Maps](#) | [Genomes](#) | [Literature](#) | [Genes](#) | [QTL](#) | [Proteins](#) | [Ontologies](#)

FAQs

Proteins Database Frequently Asked Questions

- Is there a tutorial or help section on how to use the Proteins database?
- What are some examples of scientific queries that can be answered using the Proteins database?
- Where does Gramene get its protein accessions from?
- From which grasses does Gramene have protein sets?
- Can I search the Protein database using a protein family (Pfam/Prosite) name or accession number?
- Where can I find the sequence of a given protein?
- How can I find out if a given protein is mapped to a gene from the rice genome?
- Where can I find the germplasm from where the gene encoding a given protein was isolated?
- Where can I find either the Molecular Function, Biological Process or Cellular Location of a given protein?
- What are the evidence codes used by Gramene in the Proteins database?
- Where can I find the experimental evidence that infers a gene ontology association to a protein?
- Where can I find sequence homologs from other species?
- How can I find out the protein family (PFam) to which a given protein belongs and also find all the proteins that belong to that family?
- How can I find the protein domains (Prosite) of a given protein and also find all the proteins that carry that domain?
- Where can I find the Physio-chemical features of a given protein?
- Where can I find literature citations describing a given gene or protein?
- What are the various options for downloading protein data?

Answers to Proteins Database FAQs

Is there a tutorial or help section on how to use the Proteins database?

Yes. Please refer to the Proteins [Help page](#) and [tutorials](#).

What are some examples of scientific queries that can be answered using the Proteins database?

Users can research the molecular function, biological process and cellular location of a particular rice protein, find its sequence information, orthologs from other species, examine its physio-chemical features including its amino acid composition, examine which proteins are members of the same protein family (Pfam), determine if it is an enzyme, and also determine its location in the rice genome and examine neighboring genes and features. You can determine the name of the gene, its symbol, and if known, a link to the related phenotype listed in Gramene's [Genes](#) database.

Where does Gramene get its protein accessions from?

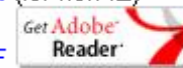
Gramene gets the rice protein accessions from [Swissprot](#).

Tutorials

- All tutorials updated
- Tutorials for all modules
- Versions to allow for different browser preferences,

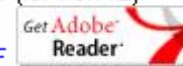
Gramene Navigation

- ♦ [PowerPoint](#) (for non-IE)
- ♦ [Adobe PDF](#)
- ♦ [Webpage](#) (for IE, Safari, Konqueror)



Gramene Overview of Modules

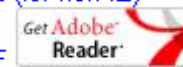
- ♦ [PowerPoint](#) (for non-IE)
- ♦ [Adobe PDF](#)
- ♦ [Webpage](#) (for IE, Safari, Konqueror)



Genomes Tutorial and Help Files

Tutorials: Select your preferred format:

- ♦ [PowerPoint](#) (for non-IE)
- ♦ [Adobe PDF](#)
- ♦ [Webpage](#) (for IE, Safari, Konqueror)



[Help Files](#)

[FAQ](#)

[Release Notes](#)

Viewing a Map - Map Detail



and Features

Map Details

Note: details appear at the bottom of the page, after the map

Tutorials

hyperlinked column headings to sort table by that column.

You can restrict the correspondence information map or map from the "Restrict by Map:" dropdown menu.

There are 488 results. Results pages can be navigated by entering a page number or clicking "next".

Click on a feature name to view the "Feature Details" page (see Step three: Gene Detail).

Step three: Gene Detail



Map and Sequence

General Info. for Gene | Allele and Germplasm | Map and Sequence Info | Associated Features

| | |
|-------------------|-----------------------------------|
| GenBank accession | GenBank: AB028603 |
| | GenBank: D38232 |
| | GenBank: AB026176 |
| | GenBank: AB026177 |
| | GenBank: AB026178 |
| Gene Product | GenBank: AB026179 |
| | GenBank: AB026180 |
| | P49083 |
| | Q43604 |

Click to view the nucleotide sequence link for each from the National Center for Biotechnology Information.

Select to view more information from Gramene's Protein database (See Protein tutorial).

Map Position

| # | Map Set Name | Linkage group | Start Position | Stop Position |
|---|-------------------------------------|---------------|----------------|---------------|
| 1 | Rice-Morph 2000 | 5 | 30.00 cM | 0.00 cM |
| 2 | Rice-JRGP RFLP 2000 | | | 0 cM |

Select to view the gene displayed in CMap (See CMap tutorial).

Home Page

GRAMENE

Comparative Grass Genomics

v20 (Dec 2005)

[Load](#) [Resources](#) [About](#) [Help](#) [Feedback](#)

Quick Search

Find anything...

Search

Quick Start

- GENOMES:** Browse sequenced genomes for [Rice](#), [Maize](#) & [Arabidopsis](#); Look for [rice/maize synteny](#); Narrow your search with [GrameneMap](#); Search for sequence alignment with [BLAST](#); search by [Gene Ontology](#).
- PROTEINS:** Search by [PFam](#) or [ProSite](#) or Browse by [Gene Ontology](#) using [GO Slim](#).
- MAPS:** Browse genetic or physical maps for [Rice](#), [Maize](#), [wheat](#), [Barley](#), [Oats](#), [Sorghum](#), and other grasses, or use the [Comparative Map Viewer \(CMap\)](#) to compare maps of different types and species.
- MOLECULAR MARKERS:** Use the Simple Sequence Repeat Identification Tool (SSR-IT), or search by [marker type](#) or species, including [Rice](#), [Maize](#), [Sorghum](#) and [Others](#).
- TRAITS:** Search for [phenotypes](#) or [traits](#) in the [QTL database](#) for important [traits](#) on [Rice](#), [Maize](#), [Sorghum](#), [Rice QTL](#), [Maize QTL](#).
- LITERATURE:** Search for [literature](#) on [Rice](#), [Maize](#), [Sorghum](#) and other grasses and topics of interest.
- SUBMISSION:** Submit a [Rice Gene](#) or [Ontology Term](#) to Gramene.

Have you tried...?

- Learning to use Gramene tools and resources with the [tutorials](#)
- [Gramene Tips Archive](#)

Featured News

- Breaking news on genomic research
- [Rice News Worldwide](#) from IRRI
- [Gramene News Archive](#)

Visit us at

- [Plant and Animal Genome XIV Conference](#), January 14-18, 2006, San Diego, CA, USA
- [Rice Technology Working Group](#), Feb. 26-Mar. 5, The World Bank, USA

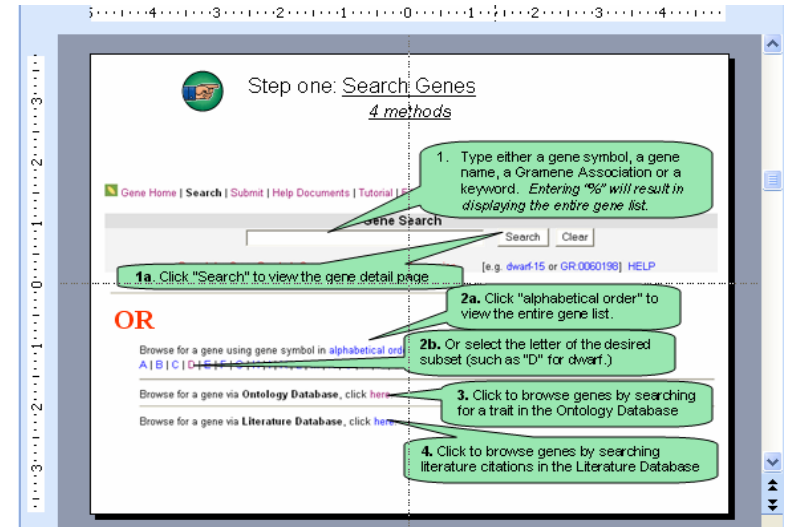
News

about the current release and the grass genomic community is listed here, along with a [Gramene Calendar](#).

Interactive links

Tutorials

- Notes pages with detailed explanations in PowerPoint presentation.



The screenshot shows the 'Step one: Search Genes' page on the Gramene website. It features a search bar with a 'Search' button and a 'Clear' button. Below the search bar, there are four numbered callouts explaining different search methods:

1. Type either a gene symbol, a gene name, a Gramene Association or a keyword. Entering "%6" will result in displaying the entire gene list.
- 1a. Click "Search" to view the gene detail page.
- 2a. Click "alphabetical order" to view the entire gene list.
- 2b. Or select the letter of the desired subset (such as "D" for dwarf.)
3. Click to browse genes by searching for a trait in the Ontology Database
4. Click to browse genes by searching literature citations in the Literature Database

The page also includes links for 'Gene Home', 'Search', 'Submit', 'Help Documents', and 'Tutorial'. Below the search bar, there are links for 'Browse for a gene using gene symbol in alphabetical order', 'Browse for a gene via Ontology Database', and 'Browse for a gene via Literature Database'.

The user can search the Gramene gene and allele database by typing a query as follows:

- Gene symbol (e.g. [dwf15](#), [sd1](#), [z1](#))
- Gene name (e.g. [dwarf-15](#), [semidwarf-1](#), [zebra-1](#))
- Gramene accession (e.g. [GR:0060198](#), [GR:0060842](#), [GR:0061047](#))
- Key word (e.g. [lesion resembling disease](#))

Option-2: Browse for a gene
The user can also do a browse search using a gene symbol, shown in alphabetical order:
The user can display all genes in the database by clicking on [alphabetical order](#).
The user can display a subset of genes by clicking on a specific character (e. g. Click [A](#)).
The user can also sort the display results by Gene symbol, Gene Name, Synonym of Gene Symbol, [Chr\(Chromosome\)](#), and [Gramene ID](#).

Option-3: Browse for a gene via Ontology Database
The user can browse genes by searching for a trait in the Ontology Database.

Exercises

- Questions and answers that are explained

3a - How many standard vocabulary (ontology) terms are associated with "drought" in the database?

3b - What ontologies are they associated with?

3c - How many contain drought in the term name?

3d - Why did some terms show up but did not contain drought in the term name, and what does this mean for you?

3a - There are 13 results for "drought" in the ontology search.

3b - These are associated with Gene Ontology (GO), Trait Ontology (TO) and Cereal Plant Growth Stages Ontology (GRO)

3c - 7 term names contain the word "drought"

3d - Terms other than those with "drought" in the name are associated with drought, and it's important to explore other terms possibly associated with drought, such as leaf rolling.

Summary for drought

Items 1 to 13 of 13

| # | Term Accession | Term Name | Synonym | Definition |
|----|----------------|---|---|--|
| 1 | GO:009744 | Biological Process response to water deprivation | response to dehydration, response to drought , response to thirst. | A change in state or activity of an organism (in terms of movement, secretion, gene expression, enzyme production, etc.) as a result of prolonged deprivation of water. |
| 2 | GO:009633 | Biological Process drought tolerance | None | OBSOLETE (was not defined before being made obsolete). |
| 3 | GO:009619 | Biological Process drought recovery | None | A change in state or activity of an organism (in terms of movement, secretion, gene expression, enzyme production, etc.) as a result of prolonged deprivation of water that restores that organism to a normal (non-stressed) condition. |
| 4 | GO:0042630 | Biological Process behavioral response to water deprivation | behavioral response to drought , behavioral response to thirst, behavioural response to water deprivation. | A change in the behavior of an organism as a result of a deprivation of water. |
| 5 | GO:0042631 | Biological Process cellular response to water deprivation | cellular response to drought , response to drought . | A change in the state or activity of a cell (in terms of enzyme production, gene expression, etc.) as a result of a prolonged deprivation of water. |
| 6 | TO:000165 | Trait leaf rolling | LFRL | Leaf rolling is a feature observed in response to drought or water stress. It precedes leaf drying stage. |
| 7 | TO:000155 | Trait drought susceptibility index | drought sensitivity index, DRSD, DRSSD, DSI. | The index is calculated as, DSI = (1-Yds/Yns), where Yds and Yns are mean yields of a given genotype in drought susceptible (DS) and non-susceptible (NS) environments respectively. |
| 8 | TO:000188 | Trait drought sensitivity | drought susceptibility, DRs, DRSN. | Drought sensitivity is highly interactive with crop phenology, plant growth prior to stress, and timing, duration, and intensity of drought stress. For many crops, it takes at least 2 rainless weeks to cause marked differences in drought sensitivity during the vegetative stage and at least 7 rainless days during the reproductive stage to cause severe drought injury. Leaf rolling precedes leaf drying during drought . Repeated ratings are recommended through progress of the drought . |
| 9 | TO:000276 | Trait drought tolerance | drought resistance, DRTL. | Becoming tolerant to drought like conditions of minimal or no water content in environment or high salt stress due to flash flooding in coastal areas. |
| 10 | TO:000394 | Trait drought related trait | desiccation related trait. | No Definition Available |
| 11 | TO:000458 | Trait drought recovery | DRR. | Scores are taken after 10 days following soaking rain or watering. Indicate the degree of stress before recovery. |
| 12 | TO:000555 | Trait leaf rolling time | LFRLTM. | Measure time taken by the leaf to roll completely under drought or water stress. |
| 13 | GRO:0007022 | Growth Stage 6.02-silking | silking growth stage-5.2, R1, silk emergence. | Silks (styles) emerge from the husks at the ear tip. Normally the first silks appear slightly after anthesis begins, but this interval can be delayed by drought or other stresses. Silks of spikelets at the base of the ear emerge prior to those from more apical spikelets. |

Direct Assistance

| | |
|------------------|--|
| Email | gramene@gramene.org |
| Feedback buttons | On every web page |
| Listserve | •Gramene listserve |
| Archived Online | •Announce listserve |

TASKS

- Map a cloned rice blast resistance gene to its putative location in the rice genome
- Compare its position to that of other mapped resistance genes

What do we already know ?

- The rice disease resistance gene *Pi-ta*
- Genetically mapped to chromosome 12 Rybka et al. (1997)
- It has also been sequenced Bryan et al. (1997).



MPMI Vol. 10, No. 4, 1997, pp. 517–524. Publication no. M-1997-0404-01R. © 1997 The American Phytopathological Society

High Resolution Mapping of the *Indica*-Derived Rice Blast Resistance Genes II. *Pi-ta*² and *Pi-ta* and a Consideration of Their Origin

Krystyna Rybka,^{1,2} Masaru Miyamoto,^{1,3,4} Ikuo Ando,⁵ Akira Saito,¹ and Shinji Kawasaki^{1,6}

¹National Institute of Agrobiological Resources (NIAR), Kan'non-dai, Tsukuba, Ibaraki 305, Japan; ²Plant Breeding and Acclimatization Institute, Radzikow, Blonie, Poland; ³Institute of Plant Biotechnology

The Plant Cell, Vol. 12, 2033–2045, November 2000, www.plantcell.org © 2000 American Society of Plant Physiologists

A Single Amino Acid Difference Distinguishes Resistant and Susceptible Alleles of the Rice Blast Resistance Gene *Pi-ta*

Gregory T. Bryan,^{1,2} Kun-Sheng Wu,^{1,3} Leonard Farrall, Yulin Jia,⁴ Howard P. Hershey, Sean A. McAdams, Kristina N. Faulk, Gail K. Donaldson, Renato Tarchini,⁵ and Barbara Valent⁶

DuPont Agricultural Products, P.O. Box 80402, Wilmington, Delaware 19880-0402

The rice blast resistance (*R*) gene *Pi-ta* mediates gene-for-gene resistance against strains of the fungus *Magnaporthe grisea* that express avirulent alleles of *AVR-Pita*. Using a map-based cloning strategy, we cloned *Pi-ta*, which is linked to the centromere of chromosome 12. *Pi-ta* encodes a predicted 928-amino acid cytoplasmic receptor with a centrally


Gramene Literature

Literature search

Search for publications:

[e.g. [Wessler SR](#) , [rice genome](#) , [Rice Genetics Newsletter](#)]

Search result

| | |
|-----------------|---|
| Reference ID | 385 |
| Title | tA single amino acid difference distinguishes resistant and susceptible alleles of the rice blast resistance gene Pi-ta |
| Source | The Plant cell , 2000, 12, pp.2033-2046 |
| Authors | Bryan-G-T , Wu-K-S , Farrall-L , Jia-Y , Hershey-H-P , McAdams-S-A , Faulk-K-N , Donaldson-G-K , Tarchini-R , Valent-B |
| Abstract | <p>The rice blast resistance (R) gene Pi-ta mediates gene-for-gene resistance against strains of the fungus <i>Magnaporthe grisea</i> that express avirulent alleles of AVR-Pita. Using a map-based cloning strategy, we cloned Pi-ta, which is linked to the centromere of chromosome 12. Pi-ta encodes a predicted 928-amino acid cytoplasmic receptor with a centrally localized nucleotide binding site. A single-copy gene, Pi-ta shows low constitutive expression in both resistant and susceptible rice. Susceptible rice varieties contain pi-ta(-) alleles encoding predicted proteins that share a single amino acid difference relative to the Pi-ta resistance protein: serine instead of alanine at position 918. Transient expression in rice cells of a Pi-ta(+) R gene together with AVR-Pita(+) induces a resistance response. No resistance response is induced in transient assays that use a naturally occurring pi-ta(-) allele differing only by the serine at position 918. Rice varieties reported to have the linked Pi-ta(2) gene contain Pi-ta plus at least one other R gene, potentially explaining the broadened resistance spectrum of Pi-ta(2) relative to Pi-ta. Molecular cloning of the AVR-Pita and Pi-ta genes will aid in deployment of R genes for effective genetic control of rice blast disease.</p> |
| Cross-reference |  |
| URLs | http://www.plantcell.org/cgi/content/full/12/11/2033 |
| Associated Data | Proteins (2) Genes (1) |

| Reference ID | 385 | | | | |
|-----------------|--|-----------|------|------------|----------------------------------|
| Title | tA single amino acid difference distinguishes resistant and susceptible alleles of the rice blast resistance gene Pi-ta | | | | |
| Associated Gene | <table><tr><th>Accession</th><th>Name</th></tr><tr><td>GR:0060627</td><td>Magnaporthe grisea resistance-ta</td></tr></table> | Accession | Name | GR:0060627 | Magnaporthe grisea resistance-ta |
| Accession | Name | | | | |
| GR:0060627 | Magnaporthe grisea resistance-ta | | | | |

View Gramene record for *Pita* gene from rice

Summary for Rice Gene: *Magnaporthe grisea* resistance-ta (GR:0060627)

| | |
|------------------------|----------------------------------|
| Gene Name | Magnaporthe grisea resistance-ta |
| Gene Symbol | <i>Pita</i> |
| Gene Synonym | RMg16, Pi4a, Pita2 |
| Phenotypic Description | Resistant to rice blast disease. |

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| | |
|-----------|---|
| Allele | <i>RMg16.1</i> (Pita, Pi4a), <i>RMg16.2</i> (Pita 2), <i>RMg16.3</i> (Pita n) |
| Germplasm | K1, Nakei 212, Pi No. 1, Pi No. 4, Tadukan-1, Yashiro-mochi |

[[Top](#)]

| | |
|-------------------|--|
| GenBank accession | AF207842([NCBI]), AY196754([NCBI] [Gramene Genomes]) |
| Gene Product | Q84UB1 , Q9AY26 |

| Map Position | | | | |
|--------------|---|---------------|----------------|---------------|
| # | Map Set Name | Linkage group | Start Position | Stop Position |
| 1 | Rice-Morph 2000 | 12 | 16.00 cM | 26.00 cM |
| 2 | Rice-Cornell RFLP 2001 | 12 | 33.20 cM | 63.80 cM |
| 3 | Rice-JRGP RFLP 2000 | 12 | 32.60 cM | 63.20 cM |
| 4 | Rice-CNHZAU Zhe97/Wuy2 QTL 2004 | 12 | 55.40 cM | 59.00 cM |

[[Top](#)]

| | |
|--------------------|--|
| Associated Feature | (Evidence Code: TAS IAGP) |
| Trait | leaf blast disease resistance (TO:0000468) |
| Growth Stage | 02-seedling (GRO:0007047) , 03-tillering stage (GRO:0007049) , 04-stem elongation stage (GRO:0007048) , 05-booting stage (GRO:0007148) , 06-heading stage (GRO:0007044) , 07-milk stage (GRO:0007046) , 08-dough stage (GRO:0007042) , 09-mature grain stage (GRO:0007045) |
| Plant Structure | inflorescence (PO:0009049) , leaf (PO:0009025) , node (PO:0020141) , stem (PO:0009047) |
| Biological Process | response to fungi (GO:0009620) |

Trait Ontology Browser

Summary for TO Term: *leaf blast disease resistance* (TO:0000468)

| | |
|------------------------------|---|
| Term Name | leaf blast disease resistance |
| Synonym | BI, LFBLRS. |
| Aspect | Trait |
| Definition | Causal agent: Magnaporthe grisea (Pyricularia oryzae - the imperfect/anamorphic stage name). |
| External References | GR:pj IRRI:SES |
| Derivation | <ul style="list-style-type: none">• trait ontology (TO:0000387) #10679 +<ul style="list-style-type: none">◦ [i] stress trait (TO:0000164) #1489 +<ul style="list-style-type: none">▪ [i] biotic stress trait (TO:0000179) #541 +<ul style="list-style-type: none">▪ [i] crop damage resistance trait (TO:0000236) #541 +<ul style="list-style-type: none">▪ [i] microbial damage resistance (TO:0000242) #384 +<ul style="list-style-type: none">▪ [i] disease resistance trait (TO:0000112) #384 +<ul style="list-style-type: none">▪ [i] fungal disease resistance (TO:0000439) #250 +<ul style="list-style-type: none">▪ [i] blast disease (TO:0000074) #209 +<ul style="list-style-type: none">▪ [i] leaf blast disease resistance (TO:0000468) #127 |
| Parent Term (1) | <ul style="list-style-type: none">• [i] blast disease (TO:0000074) |
| Total Number of Annotations: | 127 objects, 127 associations |
| gene: | 44 oryza genes |
| QTL: | 83 oryza sativa QTL |

View Gramene record for *Pita* gene from rice

Summary for Rice Gene: *Magnaporthe grisea* resistance-ta (GR:0060627)

| | |
|------------------------|----------------------------------|
| Gene Name | Magnaporthe grisea resistance-ta |
| Gene Symbol | <i>Pita</i> |
| Gene Synonym | RMg16, Pi4a, Pita2 |
| Phenotypic Description | Resistant to rice blast disease. |

[[Top](#)]

| | |
|-----------|---|
| Allele | <i>RMg16.1</i> (Pita, Pi4a), <i>RMg16.2</i> (Pita 2), <i>RMg16.3</i> (Pita n) |
| Germplasm | K1, Nakei 212, Pi No. 1, Pi No. 4, Tadukan-1, Yashiro-mochi |

[[Top](#)]

| | |
|-------------------|--|
| GenBank accession | AF207842([NCBI]), AY196754([NCBI] [Gramene Genomes]) |
| Gene Product | Q84UB1 , Q9AY26 |

| Map Position | | | | |
|--------------|---|---------------|----------------|---------------|
| # | Map Set Name | Linkage group | Start Position | Stop Position |
| 1 | Rice-Morph 2000 | 12 | 16.00 cM | 26.00 cM |
| 2 | Rice-Cornell RFLP 2001 | 12 | 33.20 cM | 63.80 cM |
| 3 | Rice-JRGP RFLP 2000 | 12 | 32.60 cM | 63.20 cM |
| 4 | Rice-CNHZAU Zhe97/Wuy2 QTL 2004 | 12 | 55.40 cM | 59.00 cM |

[[Top](#)]

| Associated Feature (Evidence Code: TAS IAGP) | |
|--|--|
| Trait | leaf blast disease resistance (TO:0000468) |
| Growth Stage | 02-seedling (GRO:0007047) , 03-tillering stage (GRO:0007049) , 04-stem elongation stage (GRO:0007048) , 05-booting stage (GRO:0007148) , 06-heading stage (GRO:0007044) , 07-milk stage (GRO:0007046) , 08-dough stage (GRO:0007042) , 09-mature grain stage (GRO:0007045) |
| Plant Structure | inflorescence (PO:0009049) , leaf (PO:0009025) , node (PO:0020141) , stem (PO:0009047) |
| Biological Process | response to fungi (GO:0009620) |

Pita gene product record


[General Information](#) |
 [Associations](#) |
 [Similarity to Other Proteins](#) |
 [Features](#) |
 [References Used for Curation](#) |
 [FASTA Sequence](#)

| General Information about Q84UB1 | | | |
|------------------------------------|---|---|---------------------|
| Name | Pi-ta protein | | |
| Symbol | Pi-ta | | |
| Synonym(s) | Not available | | |
| E.C. Number(s) | Not available | | |
| Gene Name(s) | <i>PI-TA</i> | | |
| Best hits to TIGR rice gene models | Click here to generate a BLASTP query | | |
| Accession Numbers | GenBank | TREMBL | |
| | AA045178.1 | Q84UB1 | |
| Organism(s) | Species | Cultivar | |
| | Oryza sativa (japonica cultivar-group) | Tsuyake (GRIN , IRIS) | |
| Phenotype | Pita (Magnaporthe grisea resistance-ta) | | |
| Comment | Protein does not confer resistance to M. grisea. Has serine at residue 918. Resistant allele is protein accession Q9AY26, which has alanine at residue 918. | | |
| Associations | | | |
| Term Type | Term | Evidence | Evidence Code |
| Molecular Function | ATP binding (GO:0005524) | InterPro IPR002182 | IEA |
| Biological Process | apoptosis (GO:0006915) | InterPro IPR002182 | IEA |
| | defense response (GO:0006952) | gramene.literature 385 | IMP |
| | | InterPro IPR000767 | IEA |
| Cellular Component | plastid (GO:0009536) | gramene.literature 7047 | ISS |
| Keywords | Not available | | |

Gramene Blast Search

```
>tr|Q84UB1|Q84UB1_ORYSA Pi-ta protein  
MAPAVSASQGVIMRSLTSKLD SLLQPPPEPPPAQPS  
YYLLVEPPSDTAPPPDSTAACWAKEVRELSYDVDDFL  
KMISSMIARLRGELNRRRWIAD E VTLFSARVKEAIRR  
REDSAGNERRRFSLSTFGMDDAAVHGQLVGRDISMQK  
GKTTLATEFYRLHGRRLD  
DRLLETIRTHLQDKRYFI  
YNSEHIIKIDPLGDDVSS  
FKSQLLDGMQQWNHIQKSLTTSNLKKNPTLQGMQVL  
DYIIRKANLVRQWMAEGFINSIENKVMEEVAGNYFDE  
HHMVLNFIRCKSIEENFSITLDHSQTTVRHADKVRRL  
MAFFGQVKCMPSIADYRLLRVLILCFWADQEKTSYDL  
EKIQGLQHLQTL EADARATAVLLDIVHTQCLLHLRLV  
NNLRILNIAVMQISQDDLDTLKGLGSLTALSLLVRTA  
APCMTFVEGAMPVQRLNLRFNANEFKQYDSKETGLE  
EVESALRTAIRKHPTPSTLMVDIQWVDWIFGAEGRDL  
QGLLSFFLSLPWLLSLPSMHLQPDLMIV
```

Copy sequence

Enter the Query Sequence

Either Paste sequences (max 10) in FASTA or plain text:

```
>tr|Q84UB1|Q84UB1_ORYSA Pi-ta protein - Oryza sativa (jap  
MAPAVSASQGVIMRSLTSKLD SLLQPPPEPPPAQPS SLRKGERKKILLRGLRHL  
YYLLVEPPSDTAPPPDSTAACWAKEVRELSYDVDDFLDELTTQLLHHRGGGDSSTA  
KMISSMIARLRGELNRRRWIAD E VTLFSARVKEAIRRQESYHLGRRTSSSRPREEVD
```

Or Upload a file containing one or more FASTA sequences

Or Enter an existing ticket ID:

- ☐ dna queries
☒ peptide queries

Select the databases to search against

Select species
Use 'ctrl' key to select multiple species

Poaceae
Rice
Rice_alta

- ☐ dna database
☒ peptide database

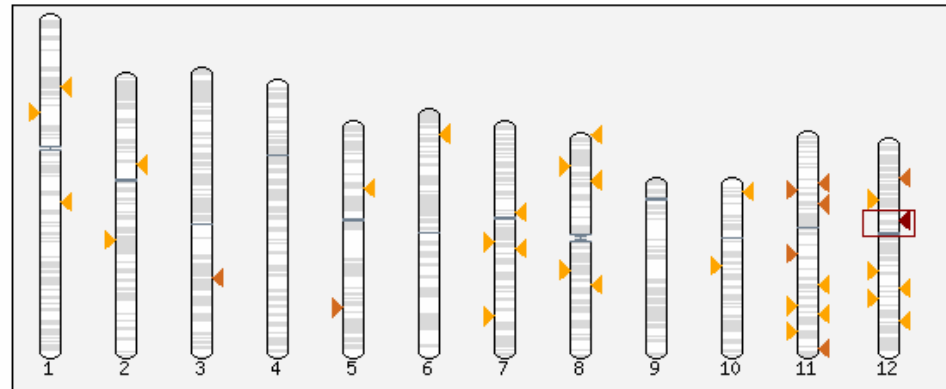
Genomic sequence
Peptides (TIGR gene models)

Select the Search Tool

BLASTP

BLAST Search Results

▼ Alignment Locations vs. Karyotype (click arrow to hide)



Key (%ID): 0 - 20 20 - 40 40 - 60 60 - 80 80 - 100

► Alignment Locations vs. Query (click arrow to view)

▼ Alignment Summary (click arrow to hide)

Select rows to include in table, and type of sort
(Use the 'ctrl' key to select multiples)

refresh

Query
off
Name
Start

Subject
off
Name
Start

Chromosome
off
Name
Start

Clone
off
Name
Start

Stats
off
Score
E-val

Sort By
>Score
<E-val
>E-val

| Links | Query Start End Ori | Subject Name | Start End Ori | Chromosome Name Start End Ori | Stats Score E-val %ID Length |
|---|------------------------|-------------------------|---------------|----------------------------------|---------------------------------|
| [A] [S] [G] [C] | 81 928 + | LOC_Os12g18360.2 | 8 928 + | Chr:12 10606425 10610433 - | 6731 0. 94.58 848 |
| [A] [S] [G] [C] | 81 896 + | LOC_Os12g18360.1 | 8 893 + | Chr:12 10606358 10610433 - | 6561 0. 95.59 816 |
| [A] [S] [G] [C] | 201 747 + | LOC_Os05g40150.1 | 174 723 + | Chr:5 23396933 23397779 - | 2121 9.0e-204 51.51 563 |
| [A] [S] [G] [C] | 197 747 + | LOC_Os11g45750.1 | 263 815 + | Chr:11 27137406 27139699 - | 2051 2.5e-210 49.83 576 |


Ensembl protein report

Tigr_gene Protein Report

Ensembl Protein Report page, which provides information about the identity, description, and structure of the protein.

| | |
|--------------------------|--|
| Peptide | LOC_Os12g18360.2 (TIGR_LOCUS ID) |
| Tigr_gene Translation ID | LOC_Os12g18360.2 |
| Tigr_gene Translation | This peptide is a product of gene LOC_Os12g18360 [Transcript Information] [Exon Information] |
| Description | NB-ARC domain, putative |
| Prediction Method | This gene was annotated by TIGR through a process of automatic and manual curation. |
| GO | The following GO terms have been mapped to this entry via InterProScan: GO:0005524 [ATP binding] IEA GO:0006915 [apoptosis] IEA GO:0006952 [defense response] IEA GO:0042829 [defense response to pathogen] IEA |
| InterPro | IPR002182 NB-ARC - [View other genes with this domain] IPR000767 Disease resistance protein - [View other genes with this domain] |
| Protein Features | <p>Diagram illustrating protein features and annotations along the sequence (Scale in aa: 0 to 928).</p> <ul style="list-style-type: none"> SUPERFAMILY: SSF52540 (approx. 240-480 aa), SSF52058 (approx. 560-800 aa). Prints: DISEASERSIST (approx. 240-480 aa). Pfam Domain: NB-ARC (approx. 240-480 aa). Low complexity: Indicated by yellow bars at approx. 40-80 aa and 920-960 aa. Peptide: Represented by a purple bar from 0 to 928 aa. SNPs: Green squares indicate Synonymous SNPs (approx. 160, 780 aa); pink squares indicate Non-Synonymous SNPs (approx. 140, 180 aa). |
| Export Data | Export peptide data in EMBL, GenBank or FASTA |

Ensembl Gene Report

| | |
|----------------------|--|
| Gene | LOC_Os12g18360 (TIGR_LOCUS ID) |
| Ensembl Gene ID | LOC_Os12g18360 |
| Genomic Location | View gene in genomic location: 10605262 - 10610820 bp (10.6 Mb) on chromosome 12 This gene is located in sequence: AL772419 |
| Description | NB-ARC domain, putative |
| Prediction Method | This gene was annotated by TIGR through a process of automatic and manual curation. |
| Sequence Markup | View genomic sequence for this gene with exons highlighted |
| Export Data | Export gene data in EMBL, GenBank or FASTA |
| SNP information | View information about variations on this gene. |
| Transcript Structure | <p>1: LOC_Os12g18360.1 (LOC_Os12g18360.1) [Transcript information] [Exon information] [Protein information]</p> <p>2: LOC_Os12g18360.2 (LOC_Os12g18360.2) [Transcript information] [Exon information] [Protein information]</p> <p>Features ▼</p>  |

Gene Model id
TIGR gene Id

Location of *Pi-ta* gene
on the rice genome

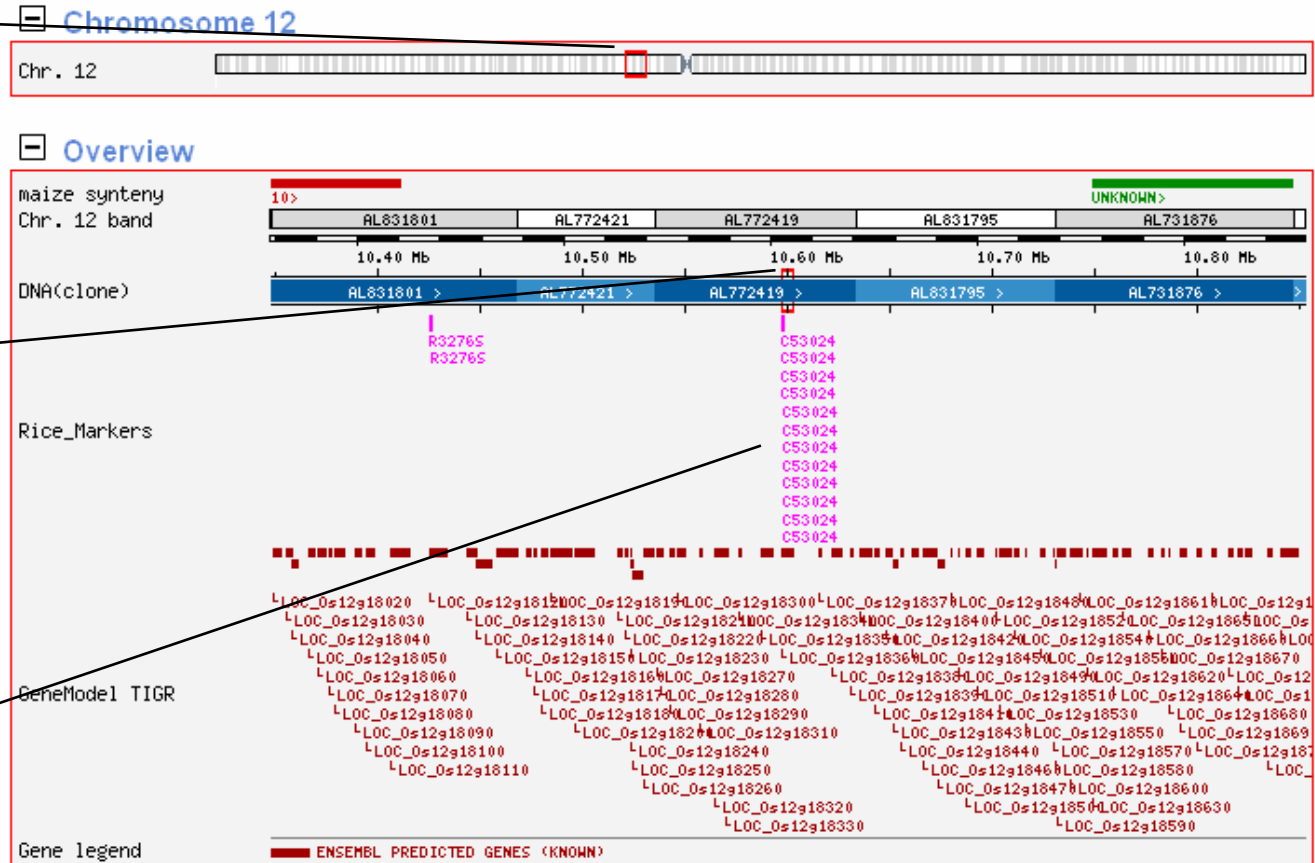
Ensembl Gene Report page provides information about the identity, base pair location on the chromosome, description, and structure.

Genome Browser Overview

Red window on chromosome indicates region shown in "Overview".

Red window on "Overview" indicates region shown in "Detailed View".

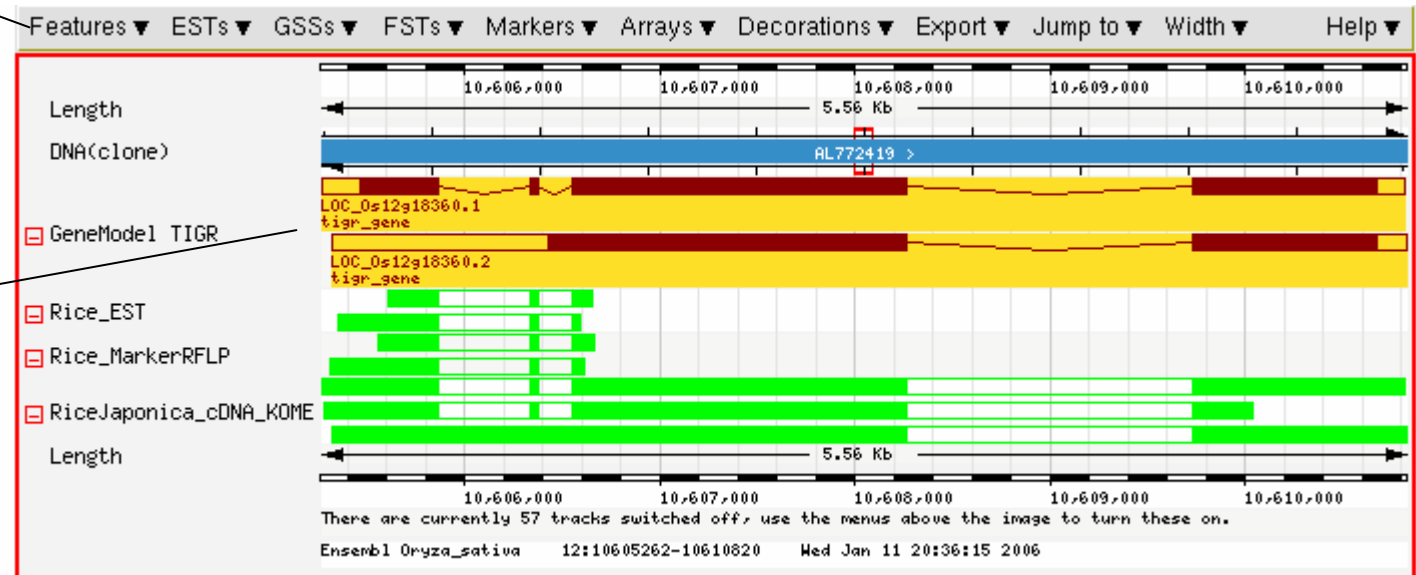
Nearest rice marker.



Genome Browser Detailed View

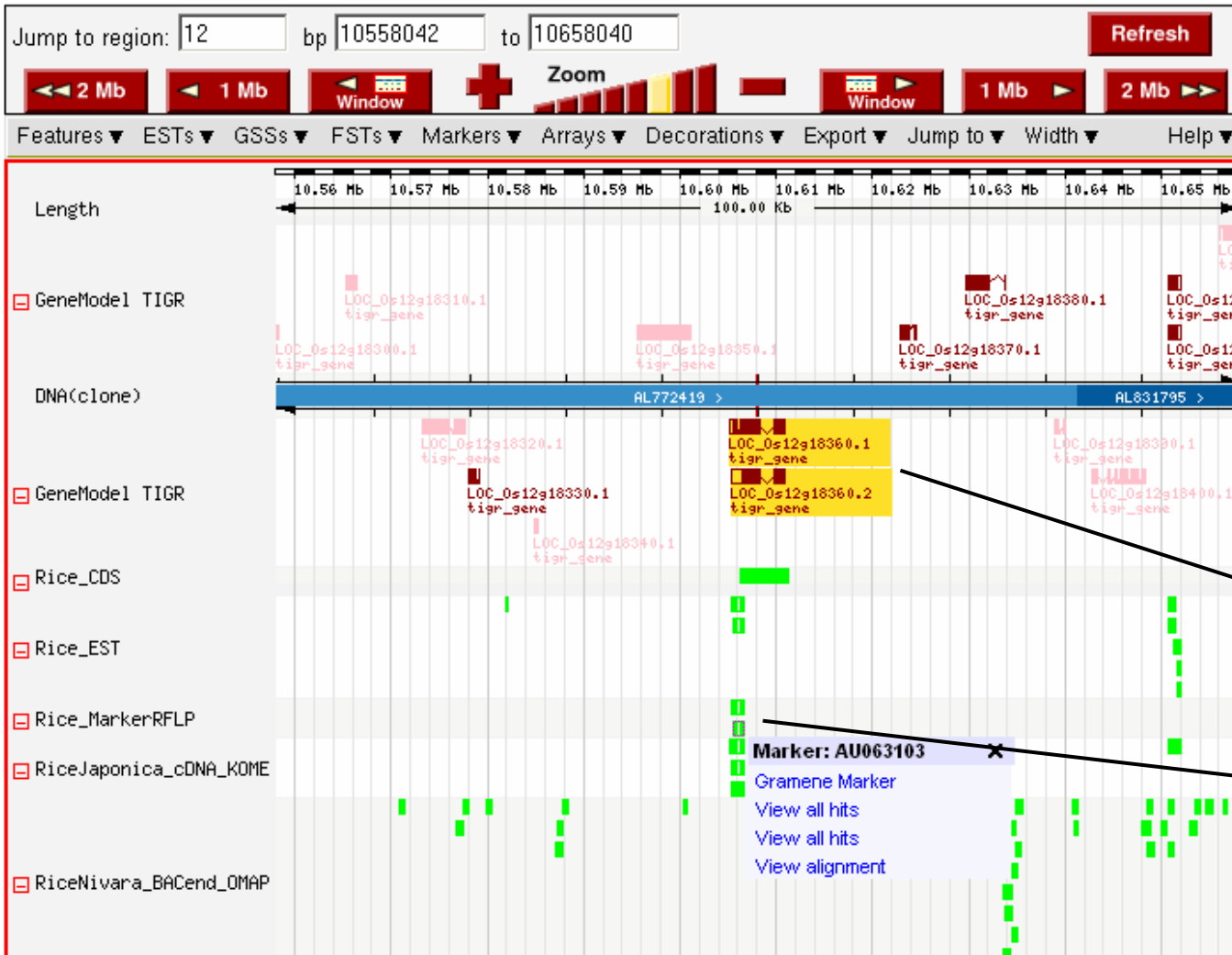
Choose additional tracks from the popup menu.

Transcription units from TIGR gene models.



Pi-ta Gene Neighborhood

Detailed view



Genes mapped to + strand.

Genes mapped to - strand.

Putative *Pi-ta* gene models

Click to get the popup menu. Click "Gramene Marker" to go to marker database.

Marker Database

Search results for all markers matching "AU063103."

Click to view
marker details.

Marker Name: Marker Type: Species:

E.g., "AG020731,AG020732", "rm*", Oat RFLP markers like "CDO*", or view [help](#).

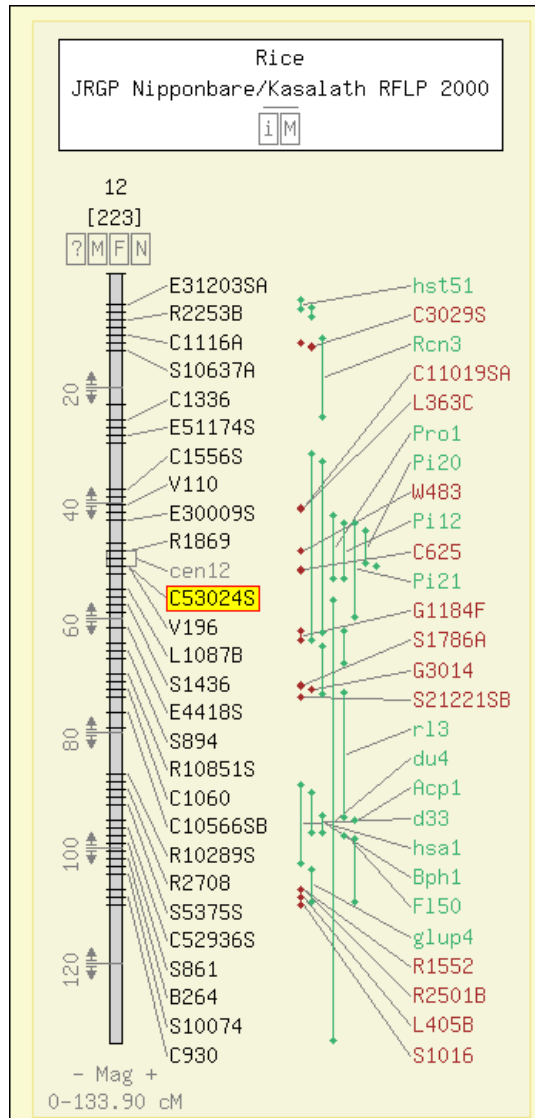
| | |
|--------------|-------------------------------------|
| Marker ID | 12780 |
| Marker Name | C53024 |
| Synonyms (4) | AU063103 C53024S |
| Type | RFLP |
| Species | Oryza sativa (Rice) |
| Germplasm | Unknown |
| Description | |

| Markers 1 to 2 of 2 | | | |
|-----------------------------------|--|--|----------------------|
| Marker Name | Marker Synonyms | Species | Marker Type |
| C53024 | AU063103, AU085774, C53024S, C53024_1A | Oryza sativa | RFLP |
| AU063103 | 7219947, AU063103.1, AU063103.2 | Oryza sativa (japonica cultivar-group) | EST |
| [Download Data] | | | |

| Mappings (8) | Species | Map Type | Map Set | Map | Name | Start | Stop | CMap Links | |
|--------------|------------------------------|----------|-----------------------------|---------|---------|------------|------------|-----------------------------|---------------------------------|
| | Oryza sativa | Genetic | JRGP RFLP 2000 | 12 | C53024S | 50.4 | | View on Map | Feature Details |
| | Oryza sativa | Physical | AGI FPC 2002 [OBSOLETE] | ctg255 | C53024S | 651 | 665 | View on Map | Feature Details |
| | Oryza sativa | Physical | I-Map (FPC) [OBSOLETE] | ctg255 | C53024S | 651 | 665 | View on Map | Feature Details |
| | Oryza sativa | QTL | JRGP Nip/Kas F2 QTL 2000 | 12 | C53024S | 50.4 | 50.4 | View on Map | Feature Details |
| | Oryza sativa | Sequence | GR TIGR Assm IRGSP Seq 2005 | Chr. 12 | C53024 | 10,605,312 | 10,606,607 | View on Map | Feature Details |
| | Oryza sativa | Sequence | GR TIGR Assm IRGSP Seq 2005 | Chr. 12 | C53024 | 10,605,312 | 10,606,607 | View on Map | Feature Details |
| | Oryza sativa | Sequence | GR TIGR Assm IRGSP Seq 2005 | Chr. 12 | C53024 | 10,605,555 | 10,606,663 | View on Map | Feature Details |
| | Oryza sativa | Sequence | GR TIGR Assm IRGSP Seq 2005 | Chr. 12 | C53024 | 10,605,555 | 10,606,663 | View on Map | Feature Details |

Click to view
marker on map.

CMap Comparative Map Viewer



Feature Types:

- ☐ Centromere
- ☒ Interpolated Gene
- ☒ Low LOD marker
- ☐ Marker

Menu Symbols:

- ☒ Map Set Info
- ☐ Map Details
- ☒ Matrix View
- ☐ Limit to One Map
- ☒ Delete Map Set
- ☒ Delete Map
- ☐ Flip Map
- ☐ Unflip Map
- ☐ New Map View

CMap v0.15

Map Set Info

Map Set Info "JRGP RFLP 2000"

[\[Show All Map Sets \]](#)

Items 1 to 1 of 1.

| | | | | | |
|----------------------------|---|--------------------------------|---------------------------------|-----------------------------------|--|
| Map Set Name: | JRGP Nipponbare/Kasalath RFLP 2000 | | | | [Show Only This Set] |
| Abbreviated Name: | JRGP RFLP 2000 | | | | [Download Map Set Data] |
| Accession ID: | jrgp-rflp-2000 | | | | [View Map Set In Matrix] |
| Species: | Oryza sativa (Rice) | | | | [View Species Info] |
| Map Type: | Genetic | | | | [View Map Type Info] |
| Map Units: | cM | | | | |
| Published On: | 23 October, 2002 | | | | |
| Description: | This is an updated version of the map reported by Kurata et al. (1994) and Harushima et al. (1998) . It uses an F ₂ population of 186 plants from a cross between the cultivars Nipponbare (japonica) and Kasalath (indica). A total of 3267 markers were located covering 1530.4 cM. Marker names ending with the letter 'S' indicate that the 3' UTR of a cDNA fragment was used as a probe rather than the whole insert. The centromere position of chromosome 10 has been updated to reflect the new estimate given by Cheng et al. (2001) . | | | | |
| Parental Germplasm: | Nipponbare | | | | |
| Parental Germplasm: | Kasalath | | | | |
| Maps: | 1 | [Map Viewer] | [Map Details] | [Matrix Viewer] | [Download Map Data] |
| | 2 | [Map Viewer] | [Map Details] | [Matrix Viewer] | [Download Map Data] |
| | 3 | [Map Viewer] | [Map Details] | [Matrix Viewer] | [Download Map Data] |
| | 4 | [Map Viewer] | [Map Details] | [Matrix Viewer] | [Download Map Data] |
| | 5 | [Map Viewer] | [Map Details] | [Matrix Viewer] | [Download Map Data] |
| | 6 | [Map Viewer] | [Map Details] | [Matrix Viewer] | [Download Map Data] |
| | 7 | [Map Viewer] | [Map Details] | [Matrix Viewer] | [Download Map Data] |
| | 8 | [Map Viewer] | [Map Details] | [Matrix Viewer] | [Download Map Data] |
| | 9 | [Map Viewer] | [Map Details] | [Matrix Viewer] | [Download Map Data] |
| | 10 | [Map Viewer] | [Map Details] | [Matrix Viewer] | [Download Map Data] |
| | 11 | [Map Viewer] | [Map Details] | [Matrix Viewer] | [Download Map Data] |
| | 12 | [Map Viewer] | [Map Details] | [Matrix Viewer] | [Download Map Data] |

CMap – Add comparative maps

☐ Hide Comparison Menu

Ref Map Start:

Ref Map End:

Current Map Sets: Rice-JRGP RFLP 2000 (Ref.)

Min. No. Correspondences for Left Slot:

Min. No. Correspondences for right Slot:

Min. No. Correspondences for the menu:

Comparative Maps (Left):

Genetic : Rice - Cornell RFLP 2001 [33]

== ALL ==

11 [2,2]

12 [31,31]

Comparative Maps (Right):

QTL : Rice - CIRAD IR64/Azu DH QTL 2003 [32]

== ALL ==

2 [2,2]

4 [2,2]

10 [2,2]

11 [2,2]

12 [24,24]

Format: Name [Total correspondences to slot, Max correspondences to single map]

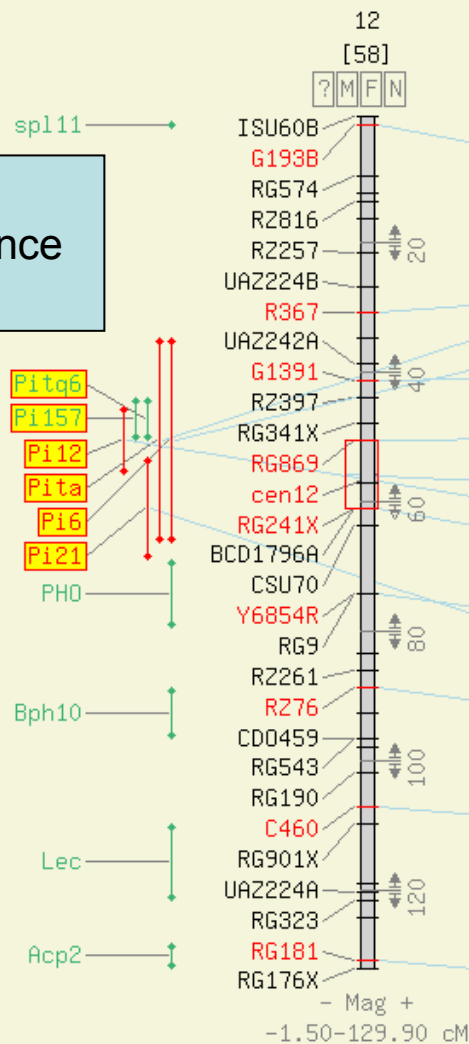
hint: To save time, select the desired options before redrawing the map.

(Hide Comparison Menu)

Rice
Cornell BS125/2/BS125/WL02 RFLP 2001

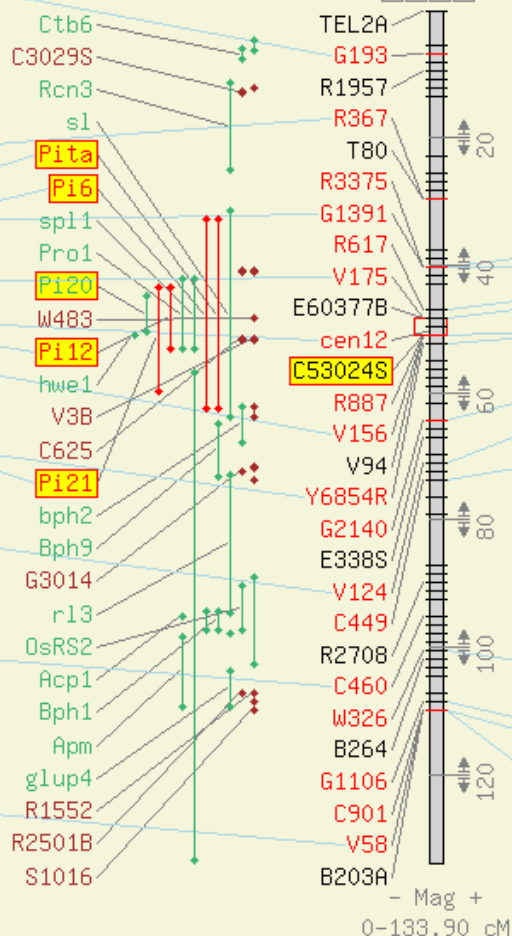
i M X

Blast
resistance
genes



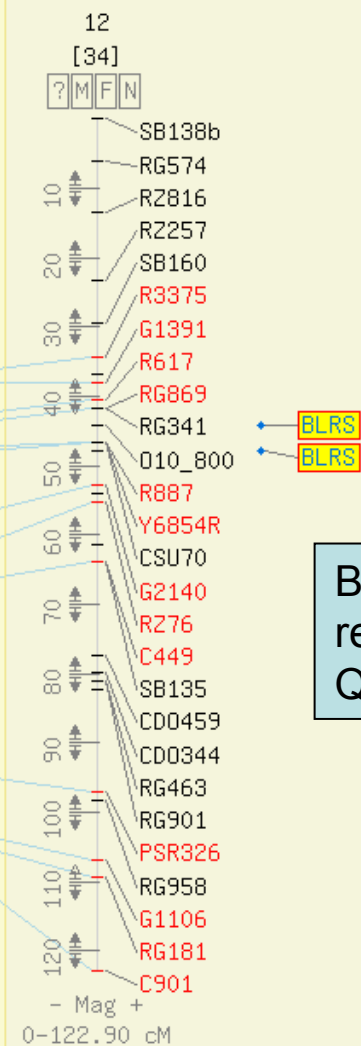
Rice
JRGP Nipponbare/Kasalath RFLP 2000

i M



Rice
CIRAD IR64/Azucena DH RFLP QTL 2003

i M X



Blast
resistance
QTL

CMap Options

☐ Hide Options Menu

Redraw Map

Reset

Highlight Features: "C53024S" Pita Pitq6 Pi157 Pi12 Pi6 Pi21 Pi2

Feature Types:

| Feature | Ignore | Display if Correspondence | Always Display |
|-------------------|-----------------------|---------------------------|----------------------------------|
| Centromere | <input type="radio"/> | <input type="radio"/> | <input checked="" type="radio"/> |
| Interpolated Gene | <input type="radio"/> | <input type="radio"/> | <input checked="" type="radio"/> |
| Low LOD marker | <input type="radio"/> | <input type="radio"/> | <input checked="" type="radio"/> |
| Marker | <input type="radio"/> | <input type="radio"/> | <input checked="" type="radio"/> |
| QTL | <input type="radio"/> | <input type="radio"/> | <input checked="" type="radio"/> |
| Default | <input type="radio"/> | <input type="radio"/> | <input checked="" type="radio"/> |
| | Check All | Check All | Check All |

Include Correspondence Types:

| Evidence | Ignore | Use | Less Than Score | Greater Than Score | Score |
|----------------------|-----------------------|----------------------------------|-----------------------|-----------------------|-------|
| Automated name-based | <input type="radio"/> | <input checked="" type="radio"/> | <input type="radio"/> | <input type="radio"/> | 0 |
| Insilico | <input type="radio"/> | <input checked="" type="radio"/> | <input type="radio"/> | <input type="radio"/> | 0 |
| Name-based | <input type="radio"/> | <input checked="" type="radio"/> | <input type="radio"/> | <input type="radio"/> | 0 |
| | Check All | Check All | | | |

Aggregate Correspondences: ☒ No ☐ 1 Line ☐ 2 Lines ☐ Cluster

Number of Clusters (if clustering): ☒ 2 ☐ 3 ☐ 4

Total Magnification: Original Magnification ▼

Redraw Map

Reset

(Hide Options Menu)

CMap Feature Details

Feature "BLRS"

Feature Name: BLRS

Aliases: Blast disease resistance

[\[View Alias Details \]](#)

Accession ID: AQCT008

Feature Type: QTL

[\[View Feature Type Info \]](#)

Map: Rice-CIRAD IR64/Azucena DH RFLP QTL 2003-12

[\[View Map Details \]](#)

Start: 44.30 cM

Stop: 44.30 cM

Correspondences

No correspondences to show.

QTL Search

| QTL Search | | | |
|---|---|--|--|
| Search by Trait Category: | | | |
| Abiotic stress Anatomy Biochemical Biotic stress Development Quality Sterility or fertility Vigor Yield | | | |
| OR | | | |
| Search for *: | Search in: | Species: | |
| <input type="text" value="AQCT008"/> | <input type="text" value="-All Fields-"/> | <input type="text" value="-All Species-"/> | <input type="button" value="Submit"/> <input type="button" value="Reset"/> |
| * eg, development , vegetative* , VGTM , QTL* , CQA11 . Or view help . | | | |

| Items 1 to 1 of 1 | | | | | | | | | |
|-----------------------------------|--------------------------|--------------------------------|---------------|----------------|--------------|------------------|------------------|------------------------------------|----------------|
| [Download Data] | | | | | | | | | |
| Species Name | Trait Name | Trait Synonyms | Linkage Group | Trait Category | Trait Symbol | Published Symbol | QTL Accession ID | Map | Position |
| Rice | blast disease resistance | blast field resistance, bla... | 12 | Biotic stress | BLRS | Pi-31(t) | AQCT008 | Rice-CIRAD IR64/Azu DH QTL 2003-12 | 44.30-44.30 cM |

QTL Details

QTL Detail "AQCT008"

| | |
|----------------------------------|---|
| QTL Accession ID | AQCT008 |
| Species | Rice (GR_tax:013681) |
| Published Symbol | Pi-31(t) |
| Trait Symbol | BLRS |
| Trait Name | blast disease resistance |
| Trait Ontology Accession: | TO:0000074 |
| Trait Synonym(s) | blast field resistance blast resistance |
| Trait Category | Biotic stress |
| Linkage Group | 12 |
| Map Position | Rice-CIRAD IR64/Azu DH QTL 2003-12 (44.30-44.30 cM) [View On Map] |
| Comments | This locus conferring resistance to blast isolates, PH68 and CD69, was mapped at chromosomal locations where several resistance genes to blast, Pi-6(t), Pi-157, Pi-ta, and Pi-ta2, had been reported previously. |
| DBXRefs | Gramene Literature 7970 |

I work with a cereal other than rice

- Search traits in rice.
- Look for synteny in your species using CMap.

I'm getting few or no hits with my search...

- Use the Ontologies module.
- There may be varying names (synonyms) for a single trait.
- Related terms may offer new ideas for searches.

Future Plans for Gramene

- QTL to sequence Map
- Diversity
- Pathways

Exercises:

- What questions do you have about using Gramene?

Personnel

| | | |
|---------------------------|---------------------------|--|
| PI Team | Lincoln Stein, Ph.D | PI, Database design and software development |
| | Susan R. McCouch , Ph.D. | Co-PI, rice data curation |
| | Doreen Ware, Ph.D. | Co-PI, Comparative genome analysis |
| | Pankaj Jaiswal, Ph.D | Co-PI; Proteins, Ontologies, QTL |
| | Ed Buckler, Ph.D | Co-PI, Diversity, Maize |
| Biological Curation | Junjian Ni, Ph.D. | Genes, QTL |
| | Immanuel Yap, Ph.D. | Maps, Markers, QTL |
| | Isaak Yosief Tecle, Ph.D. | Germplasm, Genetic Diversity |
| | Dean Ravenscroft, Ph.D. | Pathways |
| Bioinformatics Developers | Steven Schmidt | Gramene Genome Database & Browser |
| | Ken Youens-Clark | Comparative Maps, QTL, Markers, Diversity |
| | Shulamit Avraham (Shuly) | Database Management |
| | Liya Ren | Proteins, Literature, Ontologies, Genes |
| | William Spooner, Ph.D. | Genome Browser, Gramene Blast & Mart |
| | Payan Canaran | Protein Annotation Pipeline |
| | Sharon Wei | Gramene Pipeline and Genome Browser |
| | Terry Casstevens | Diversity |
| Coordinators | Chengzhi Liang, Ph.D | Project Management, Gene Build |
| | Claire Hebbard | Outreach Coordinator |