

## **Gramene: A Resource for Comparative Grass Genomics**

RiceCAP Workshop  
DNA MARKERS, MAPPING, AND BEYOND  
6/8/06

### **What is Gramene**

- A genomic database for rice and other cereals
- A resource for comparing these genomes
- A collection of public data. Adds value to public info
  - Automated and curated relationships
  - Web displays

## A biological database :

- Is an [extensive] collection of biological data in computerized format . . .
- Is used for updating, querying and retrieving information.
- Requires communication between the user and the computer.

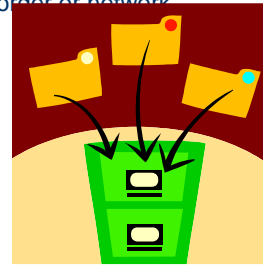


# Human-Human

## Tendency for Organization and Growth

This common vocabulary is arranged in a structured order or network based on their relationships to each other.

Kingdom: Animalia  
 Phylum: Chordata  
 Subphylum: Vertebrata  
 Class: Mammalia  
 Subclass: Theria  
 Infraclass: Eutheria  
 Order: Primates  
 Suborder: Anthropoidea  
 Superfamily: Hominoidea  
 Family: Hominidae  
 Genus: Homo  
 Species: sapiens



Facilitates global communication

# Perspectives



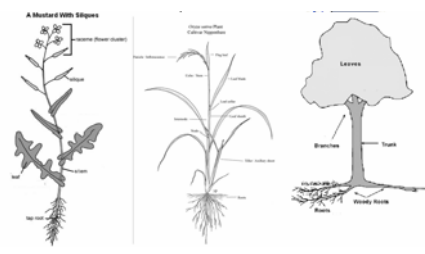
Term Name	Synonym
photoperiodism, <b>flowering</b>	photoperiodic control of <b>flowering</b> time, photoperiodic control of inflorescence development, response to daylength, <b>flowering</b> , response to nightlength, <b>flowering</b> , response to photoperiod, <b>flowering</b> .
long-day photoperiodism, <b>flowering</b>	long-day photoperiodic control of <b>flowering</b> , long-day photoperiodic control of <b>flowering</b> time, long-day photoperiodic control of inflorescence development, response to long-day, <b>flowering</b> , response to short-night, <b>flowering</b> , short-night photoperiodism, <b>flowering</b> .
short-day photoperiodism, <b>flowering</b>	long-night photoperiodism, <b>flowering</b> , response to long-night, <b>flowering</b> , response to short-day, <b>flowering</b> , short-day photoperiodic control of <b>flowering</b> , short-day photoperiodic control of <b>flowering</b> time, short-day photoperiodic control of inflorescence development.

When there is no pre-existing organizational template, our training and experience shape our language.





- Ontologies remain constant across species.



Term Name	Synonym	Definition
fruit	achene, berry, capsule, caryopsis, circumcissile capsule, cypsela, drupe, follicle, grain, kernel, legume, loculicidal capsule, lomentum, nut, PO:0020067, PO:0020068, PO:0020069, PO:0020070, PO:0020071, PO:0020072, PO:0020073, PO:0020074, PO:0020076, PO:0020077, PO:0020078, PO:0020079, PO:0020080, PO:0020082, PO:0020083, PO:0020087, PO:0020107, pod, poricidal capsule, schizocarp, septicidal capsule, septifragal capsule, silicula, siliqua, silique.	The seed-bearing structure in angiosperms, formed from the ovary after flowering.

## Development of Ontologies

- An Ontology is a “common vocabulary” used to facilitate communication between researchers and databases.
- Developed by diverse experts.
- An ontology matches classification and reasoning methods of the computer.
- Ontologies can be indexed “objectively” by a computer.
- Computers can infer new knowledge



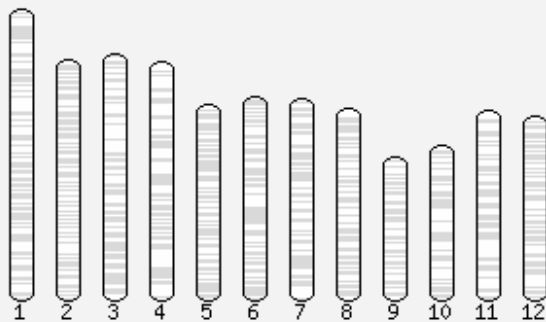
## Keys to working with a database

- What goes in is what comes out
- Knowledge grows/changes
- Interpretation is up to you
- Be persistent
- Be patient



## How does Gramene Depict the Genotype?

### Browse a Chromosome



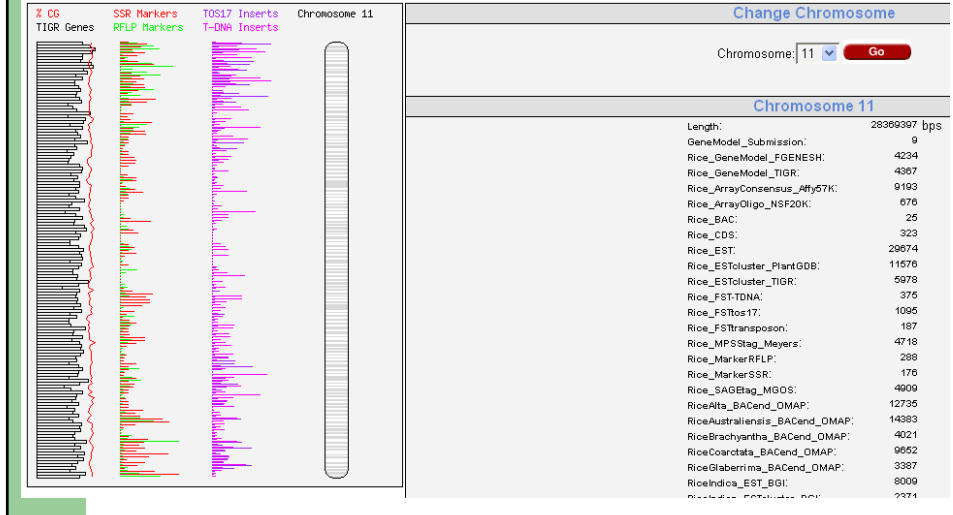
The rice genome has 12 chromosomes, with 259 - 485 mbp

Sorghum has ~1190 mbp,

Maize has ~2670 mbp.



# Rice Chromosome 11



# Map Types

Map Type: **Genetic**  
 Accession ID: genetic  
 Map Units: cM

Map Type: **QTL**  
 Accession ID: qtl  
 Map Units: cM

Map Type: **Physical**  
 Map Units: bands  
 Is Relational Only

Map Type: **Deletion**  
 Accession ID: deletion  
 Map Units: arm fraction

Map Type: **Sequence**  
 Accession ID: sequence  
 Map Units: bp

**genetic maps** - indirect estimate of the distance and order of the sequence; use markers; provide framework for genome sequencing.

**physical maps**- estimate of the true distance (base pairs); define sequence between markers; used for gene identification.

**Features:** everything that can be mapped



## Gramene Data Sets

- Markers
- QTL
- Maps
- Genes
- Proteins
- Ontologies
- Literature
- Diversity
- Pathways



## Gramene Tools

- BLAST – sequence alignment
- Gramene-Mart – data mining
- CMap – Comparative mapping
- Genome Browser – visual overview of genome



## Gramene Contributors

### Controlled Vocabulary

- TAIR
- IRRI
- MaizeGDB
- Gene Ontology Consortium
- ICIS
- INGER
- CIMMYT
- Oryzabase
- Scottish Crop Research Institute
- Plant Ontology Consortium
- Monsanto
- Pioneer

### Maps

- Cari Soderland, University of Arizona
- Rod Wing, University of Arizona
- John Mullet, Texas A & M
- Patricia Klein, Texas A & M
- Robert Klein, USDA-ARS
- Andrew Paterson, Univ of GA
- Dave Matthews, USDA-ARS
- Mary Polacco, USDA-ARS
- Maize GDB

### Sequences and Proteins

- National Center for Gene Research Chinese Academy of Sciences
- NCBI
- TIGR
- Uniprot/SPTremble
- LGB
- BGI
- Interpro
- MaizeGDB
- BarleyBase
- Orion Genomics
- NASC for the arabidopsis genome view in Ensembl.
- Cari Soderland SAGE
- GuoLiang Wang SAGE
- Blake Meyers MPSS

### QTL

- MaizeGDB
- GrainGenes

### Genes

- Oryzabase
- MaizeGDB

### Reference Databases

- Albert Mann Library, Cornell University
- TEEAL

### Software Development

- Ensembl
- Gene Ontology Consortium
- GMOD
- Pioneer

### Germplasm

- NPGS/GRIN

## Collaborators

- Ben Faga – CMap
- Bonnie Hurwitz – OMap

## SAB

- Anna M McClung
- Georgia Davis
- James H. Oard
- David Marshall
- Patricia Klein



## 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	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



# Let's go: [www.gramene.org](http://www.gramene.org)



**GRAMENE** *A Resource for Comparative Grass Genomics* v21 (May 2006)

Search Genomes Download Resources About Help Feedback

**Quick Search**

All Available

Search

Search a single module or all available modules plus online documentation.  
[Diversity](#), [Pathways](#), [BLAST](#) and [Mart](#) not available in this search.

**Have Questions...?**

- Gramene now has [tutorials](#) for every module.
- Ask questions through [Feedback](#) or [Email](#).

**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 \(SSRIT\)](#); or search by [marker type](#) or species, including [Rice \(\*Oryza sativa\*\)](#), [Maize](#), [Sorghum](#) and [Others](#).
- 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](#).

**Featured News**

- Gramene Release 21 May 2006. See the [release notes](#).
- [Pathways Module \(RiceCyc\) Released](#) **NEW**
- [Diversity Module Released](#) **NEW**
- New Publication: [Gramene: A genomics and genetics resource for rice](#).
- RTWG Gramene workshop materials are available.
- [Gramene News Archive](#)

**Visit with us at**

# Gramene Workshop

6/8/06

## Hands-On Exercise: Grain Yield after Milling

Begin on the web at [www.gramene.org](http://www.gramene.org)

### ➔ 1) Conduct a trait search for milling yield.

(At Gramene, the QTL database is searchable by trait. On the Gramene home page point your mouse to 'Search' on the menu. Click on 'QTL' in the dropdown box. Type "milling yield" in the quick search box and click submit).



You will find out that there are no results for this trait.



The QTL search for "milling yield" came up empty, therefore you have two options: Search the whole database for information on it (#2), or go to "Ontologies" to find a better term (#3).

### ➔ 2) Search all of Gramene for "milling yield".

(Use the box at the top of the page for a search of the whole database. Type “milling yield” in the ‘find anything’ search box at the top right, and click ‘search’.)

Results have turned up in the literature and other publications. Since “milling yield” is in the title of the first literature database result, it looks like a good match.

➔ a. **Select that article on milling yield and get data on published results.** (Click on ‘More info’)

**Search the Gramene Database**

Results: Literature | Newsletter & Docs

Search for (object name, identifier, or keyword):  Search

Database: All  Include Rice Genetics Newsletter & Gramene Documentation

**Literature Search Result**

Items 1-2 of 2 Page 1 of 1 Select page: 1

1. [Mei-H, Luo-L, Guo-L, Wang-Y, Yu-X, Ying-C, Li-Z](#)  
Molecular mapping of QTLs for rice **milling yield** traits. ([More info](#))  
Acta-Genetica-Sinica, 2002, vol.29, pp791-797
2. [Martinez-Bustos-F, Delgado-L-L, Victorio-M-G, Morales-S-E](#)  
Characterization of yellow rice and development of instant flours by hydrothermal process ([More info](#))  
Archivos latinoamericanos de nutricion, 1997, vol.47, pp50-56

Items 1-2 of 2 Page 1 of 1 Select page: 1

**Rice Genetics Newsletter & Documentation Search Result**

69 matches in Rice Genetic Newsletter & Documentation

Score	Document
1000	Registration of Rice Varieties1 Registration of 'Arkose' rice Registration of 'Bluebonnet' rice Registration of 'Bluebonnet 50' rice Registration of 'Blue Rose' rice Regi rice Registration of 'Calrose' rice Registration of 'Century Patna 231' rice Registration of 'Colusa' rice Registration of 'Fortuna' rice Registration of 'Improved Bluebonnet'

You should look to see what ‘associations’ there are in the database with this article. There are 3 QTL associated with this article.

➔ b. **Select the QTL for more information on them** (click on ‘QTLs (3)’)..

Search result	
Reference ID	7776
Title	Molecular mapping of QTLs for rice milling yield traits.
Source	Acta-Genetica-Sinica , 2002, 29, pp.791-797
Authors	<a href="#">Mei-H, Luo-L, Guo-L, Wang-Y, Yu-X, Ying-C, Li-Z</a>
Abstract	QTLs of three milling yield traits, including brown rice (BR, %) ,milled rice (MR, %) and head milled rice (HR, %) ,were mapped using a set of 212 Lemont/Teqing RI population, an RFLP linkage map with 182 markers and a mixed model approach (QTLMapper V1.0). The population showed continuous distributions with transgressive segregation on both sides for all traits while HR had a wider variation than BR and MR. One and four main effect QTLs were detected for MR and HR. Two QTLs for HR (QHR6 and QHR7) had large additive effects. Twelve five and sixteen pairs of digenic epistatic loci were associated with BR, MR and HR respectively. Epistasis was more important than main effect QTLs according to the mapping result. A complex relationship was observed for epistatic pairs mapped in same trait or among different traits by sharing intervals.
Cross-reference	Not available
Associated Data	<a href="#">QTLs (3)</a>

**Please note:**  
To request reprints, please contact the authors or the source/journal website. Due to copyright issues Gramene does not distribute reprints.

This will bring up a table that lists those three QTL, and following those links will provide more

information.

- ➔ c. Select the first QTL to get more information. (Click on 'AQL001'.)

Reference ID	7776	
Title	Molecular mapping of QTLs for rice milling yield traits.	
Associated QTL	Accession	Published Symbol
	<a href="#">AQL001</a>	QMr12
	<a href="#">AQL002</a>	QMr2
	<a href="#">AQL004</a>	QMr6

You will be able to select the link to learn the trait name (milled rice ratio) and to view this QTL on a map. Note that there are synonyms. The trait is called “Milled Rice Ratio”.

### QTL Detail "AQL001"

QTL Accession ID	AQL001
Species	<a href="#">Rice (GR_tax:013681)</a>
Published Symbol	QMr12
Trait Symbol	MR
Trait Name	milled rice ratio
Trait Ontology Accession	TO:0000144
Trait Synonyms	milled rice milled rice percentage
Trait Category	<a href="#">Quality</a>
Linkage Group	12
Map Position	Rice-TAMU Lem/Teq RI QTL 1995-12 (15.00-15.00 cM) [ <a href="#">View On Map</a> ]
Comments	Trait was related with grain quality.
DBXRefs	<a href="#">Gramene Literature 7776</a>

The second option to your lack of QTL search for “milling yield” is to determine if you need another ‘keyword’. Perhaps others used different vocabulary (ontologies) to describe the trait. You should ...

- ➔ 3) Conduct a search for “milling yield” in the ontologies database in order to look for other terms to consider.

*On the Gramene navigation bar point your mouse to ‘Search’ on the menu, then click on ‘Ontologies’ in the dropdown box. Type “milling yield” in the quick search box and select ‘Trait Ontology’ to narrow your search. Click ‘Search’.*

- ➔ a. Try a different term. Conduct a search for “milling ” in the ontologies database.  
➔ b. Try a different term. Conduct a search for “mill ” in the ontologies database.

Searches for “milling yield” and “milling” come up negative, but shortening our search term to simply “mill” gives us 14 results. (milled, millimeters, millet, etc), but only one – milled rice, synonym milled rice ratio – seems to be a match for milling yield.

Ontology Database					
Type ID or keyword to search		mill		Search	Clear
select ontology (optional)		<input type="checkbox"/> Gene (GO)	<input type="checkbox"/> Plant structure (PO)	<input type="checkbox"/> Growth stage (GRO)	[e.g. flower or TO:0000303]
		<input checked="" type="checkbox"/> Trait (TO)	<input type="checkbox"/> Environment (EO)	<input type="checkbox"/> Taxonomy (GR_tax)	
Summary for mill					
Items 1 to 14 of 14					
#	Term Accession	Aspect	Term Name	Synonym	Definition
1	TO:0000024	Trait	ligule length	LgL, LIGLG.	The actual measurement of ligules measured in millimeters from the base of the collar to the tip.
2	TO:0000132	Trait	basal internode diameter	BAINDIA, DBI.	Actual measurements in millimeters from the outer diameter of the culms at the basal portion of the main culm. Sample size = 3
3	TO:0000134	Trait	alkali digestion	AlkD, ALKDIG.	Is an indirect measure of gelatinization temperature. Observed by placing six milled-rice kernels in 10ml 1.7% KOH in a shallow container and arrange them so that they do not touch. Let them stand for 23hrs at 30degC temperature and score for spreading. Measure for Alkali digestion is inversely proportional to the gelatinization temperature, e.g. if alkali digestion is low, the gelatinization temperature is high.
4	TO:0000144	Trait	milled rice	milled rice ratio, MR.	No Definition Available
5	TO:0000149	Trait	seed width	kernel plumpness, kernel width, percentage of plump kernels, plump grain, plump seed, SDWD.	Determined by the actual measurement of width in millimeters as the distance across the seed (with hull).
6	TO:0000222	Trait	head rice	head milled rice, head rice ratio, HEADR.	No Definition Available
7	TO:0000266	Trait	chalky endosperm	chalkiness of endosperm, Clk.	Defines a representative milled sample for the degree (extent) of chalkiness that will best describe the sample with respect to (a) white belly, (b) white center, (c) white back.

➔ c. Select the Trait Accession for ‘milled rice ratio.’ (Click on “TO:0000144”)

Ontologies show relationships between terms, and this reflects that milled rice (ratio) is an example of seed quality, which is an example of a quality trait. There are 8 QTL that are associated with this trait, which we will come back to in a minute.

First, however, you should know that sometimes it can be helpful to explore related terms so that we can consider other terms to search for.

➔ d. Select the parent term of milled rice. (Click on “seed quality (TO:0000162).”)

Summary for TO Term: milled rice (TO:0000144)	
Term Name	milled rice
Synonym	milled rice ratio, MR.
Aspect	Trait
Derivation	<ul style="list-style-type: none"> <li>• <a href="#">trait ontology (TO:0000387) #10679</a> <ul style="list-style-type: none"> <li>◦ [i] <a href="#">quality trait (TO:0000597) #963</a> <ul style="list-style-type: none"> <li>▪ [i] <a href="#">seed quality (TO:0000162) #907</a> <ul style="list-style-type: none"> <li>▪ [i] <a href="#">milled rice (TO:0000144) #8</a></li> </ul> </li> </ul> </li> </ul> </li> </ul>
Parent Term (1)	<ul style="list-style-type: none"> <li>• [i] <a href="#">seed quality (TO:0000162)</a></li> </ul>
Total Number of Annotations:	8 objects, 8 associations
QTL:	8 <a href="#">oryza sativa QTL</a>

More terms are revealed that are also associated with seed quality. Many of these will also affect milling yield, so in further research you may wish to explore some of these other options.

➔ 4) For now, go back to “milled rice (TO:0000144)” and select the link to the 8 associated QTL. (Use the Browser “back” button, or simply click on ‘milled rice’) click on ‘8 oryza sativa QTL.’)

- [trait ontology \(TO:0000387\) #10679](#) +
  - [i] [quality trait \(TO:0000597\) #963](#) +
    - [i] [seed quality \(TO:0000162\) #907](#)
      - [milled rice \(TO:0000144\) #8](#)
      - [i] [head rice \(TO:0000222\) #17](#)
      - [i] [seed viability \(TO:0000345\) #130](#) +
      - [i] [brown rice ratio \(TO:0000375\) #4](#)
      - [i] [cracked grain percentage \(TO:0000381\) #14](#)
      - [i] [grain color \(TO:0000385\) #0](#)
      - [i] [grain size \(TO:0000397\) #0](#)
      - [i] [grain thickness \(TO:0000399\) #0](#)
      - [i] [grain width \(TO:0000402\) #19](#)
      - [i] [seed shattering \(TO:0000473\) #21](#)
      - [i] [seed shape \(TO:0000484\) #212](#) +
      - [i] [seed color \(TO:0000486\) #40](#) +
      - [i] [seed composition based quality trait \(TO:0000488\) #220](#) +
      - [i] [endosperm quality \(TO:0000587\) #58](#) +
      - [i] [seed density \(TO:0000612\) #79](#)
      - [i] [groat percentage \(TO:0000613\) #36](#)
      - [i] [crushed grain percentage \(TO:0000618\) #2](#)
      - [i] [seed fertility \(TO:0000639\) #1](#)
      - [i] [cooking or brewing quality \(TO:0000667\) #135](#) +
      - [i] [bran percentage \(TO:0000672\) #6](#)
      - [i] [starch yield \(TO:0000697\) #14](#)

You will receive a table with information about these 8 QTL.

➔ 5) Learn how these QTL were identified. (Click on ‘IAGP’ in the “Evidence” column.)

**Term *milled rice* ( TO:0000144 ) Associations**

Items 1 to 8 of 8

Term Name	Object Type	Object Accession ID	Object Symbol	Object Name	Object Synonyms	Object Species	Evidence
milled rice	QTL	AQFU013	MR	milled rice ratio	mr5	Oryza sativa	<a href="#">IAGP</a>
milled rice	QTL	AQEE012	MR	milled rice ratio		Oryza sativa	<a href="#">IAGP</a>
milled rice	QTL	AQFU049	MR	milled rice ratio		Oryza sativa	<a href="#">IAGP</a>
milled rice	QTL	CGR3	MR	milled rice ratio		Oryza sativa	<a href="#">IAGP</a>
milled rice	QTL	AQL001	MR	milled rice ratio	QMr12	Oryza sativa	<a href="#">IAGP</a>
milled rice	QTL	AQFU014	MR	milled rice ratio	mr7	Oryza sativa	<a href="#">IAGP</a>
milled rice	QTL	CGR2	MR	milled rice ratio		Oryza sativa	<a href="#">IAGP</a>
milled rice	QTL	AQFU048	MR	milled rice ratio		Oryza sativa	<a href="#">IAGP</a>

The evidence for these QTL being associated with milled rice ratio is strong, based on experiments showing an association between the QTL and the phenotype (*see below*) (as opposed to another form of evidence, such as a non-traceable author statement.)

**IAGP \*inferred by association of genotype from phenotype**

- Polymorphism or segregation of genetic markers eg. isozymes, RFLPs (Random Fragment Length Polymorphism), RAPDs (Random amplified polymorphic DNA), AFLPs (Amplified Fragment Length Polymorphism), SNPs (Single Nucleotide Polymorphisms), Microsatellite markers or SSR (Simple Sequence Repeats), TD (Transposon Display).
- Polymorphism or segregation of physical markers eg. FISH, centromeric, heterochromatic regions, chromosomal banding patterns.
- Detection of polymorphisms in segregating plant material derived from Bi-parental crosses eg. F2 lines, F3 families, Back cross populations, viz., BC1, BC2 etc. ; Doubled Haploid lines (DH), Recombinant Inbred Lines (RIL).
- Detection of polymorphisms in genetic stocks, e.g., Near Isogenic Lines (NIL), Introgression Lines (IL), Radiation Hybrids (RH), Cytogenetic Stocks (CG), i.e., trisomics, aneuploids, etc.

➔ **6) For this exercise, select AQFU049.** (In most cases you may wish to review all 8 of these QTL to learn what data is known about them.)

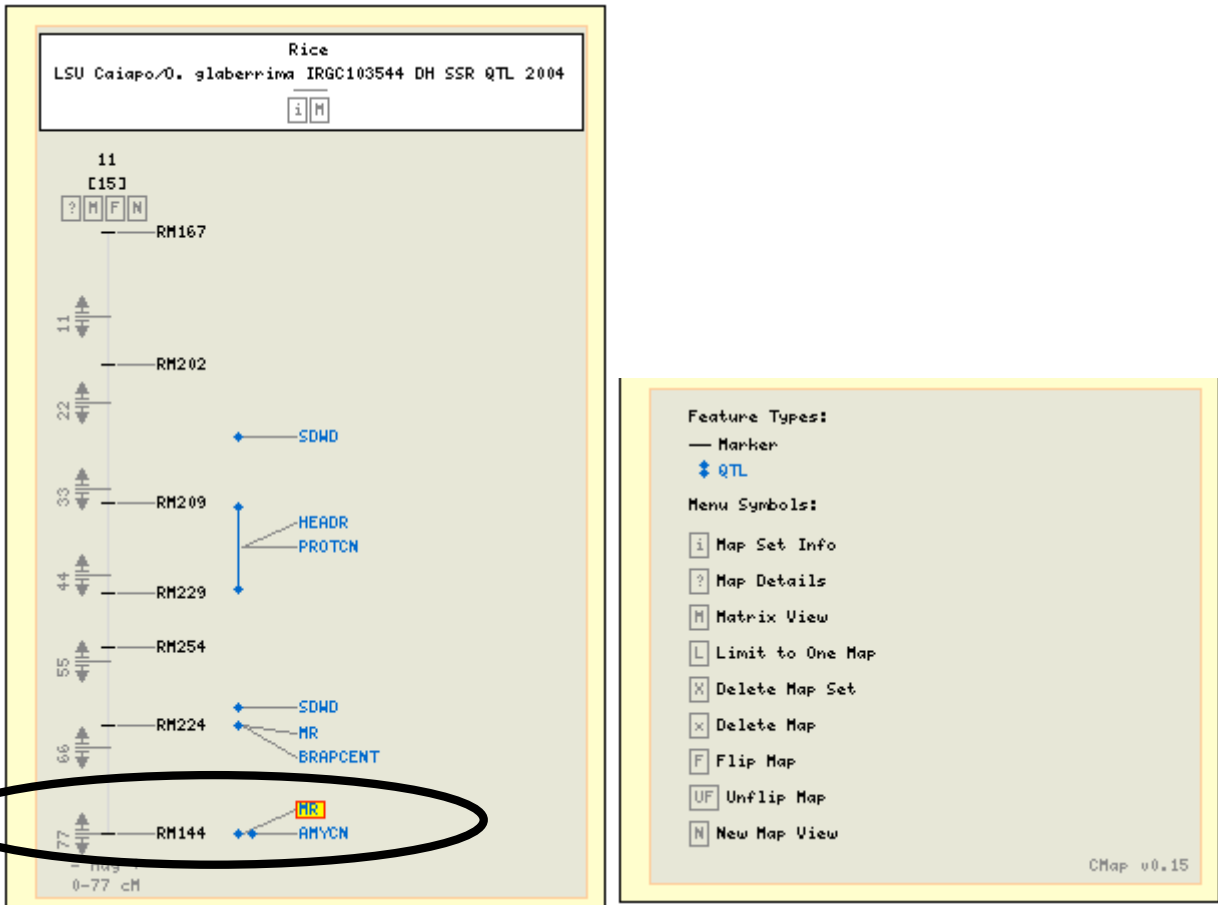
Once again you can see that this is a rice QTL for milled rice ratio. You can also learn that it is on chromosome 11. If you would like more reference information for this QTL you should select the literature reference link, since it is different than the previous article we reviewed.

**a. View the map for “AQFU049”** (Click on “View on Map”)

**QTL Detail "AQFU049"**

QTL Accession ID	AQFU049
Species	<a href="#">Rice (GR_tax:013681)</a>
Published Symbol	NA
Trait Symbol	MR
Trait Name	milled rice ratio
Trait Ontology Accession:	<a href="#">TO:0000144</a>
Trait Synonym(s)	milled rice milled rice percentage
Trait Category	<a href="#">Quality</a>
Linkage Group	11
Map Position	Rice-LSU Caiapo/IRGC103544 QTL 2004-11 (77.00-77.00 cM) <a href="#">[View On Map]</a>
Comments	This locus was found to have significant interaction with another locus, AQFU048.
DBXRefs	<a href="#">Gramene Literature 8212</a>

Notice that the QTL is highlighted as “MR”, and is located near Marker RM144. You may also find it interesting to learn that it is also co-located with the QTL AMYCN, which is a QTL for amylose content.



Clicking on any of the features on the map will link you to the detail page for that feature.

➔ 7) **View “RM144” marker detail information.** (Click on ‘RM144’)

We can see that this marker has been mapped to several different maps and map types. However, you are still in the maps module (look at the module heading to know which module you are in) and you want to get to the markers module.

- ➔ a. Go to the markers module detail page. (Select the first “View *Oryza sativa* SSR marker “RM144” in Marker DB” to view the marker in the markers module.)



## Feature "RM144"

**Feature Name:** RM144

**Aliases:** N/A

**Accession ID:** alg2004a-97

**Feature Type:** Marker

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

**Map:** Rice-LSU Caiapo/O. glaberrima IRGC103544 DH SSR QTL 2004-11

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

**Start:** 77.00 cM

**Stop:** 77.00 cM

**Cross-references:** [\[ View Marker Details \]](#)

[\[ View Oryza sativa SSR marker "RM144" in Marker DB \]](#)

[\[ View Oryza sativa SSR marker "RM144" in Marker DB \]](#)

[\[ View "RM144" in Genome Browser \]](#)

Correspondences						
Feature	Map	Map Type	Aliases	Evidence Type	Actions	
RM144	Rice-Class I SSR (93-11) 2005-11	Sequence	AUT27367, RM27367	Automated name-based	<a href="#">[ Correspondence Details ]</a>	<a href="#">[ View On Map ]</a> <a href="#">[ Comparative View ]</a>
RM144	Rice-Class I SSR (IRGSP) 2005-11	Sequence	AUT27367, RM27367	Automated name-based	<a href="#">[ Correspondence Details ]</a>	<a href="#">[ View On Map ]</a> <a href="#">[ Comparative View ]</a>
RM144	Rice-Class I SSR (TIGR) 2005-11	Sequence	AUT27367, RM27367	Automated name-based	<a href="#">[ Correspondence Details ]</a>	<a href="#">[ View On Map ]</a> <a href="#">[ Comparative View ]</a>
RM144	Rice-I-Map (FPC) [OBSOLETE]-ctg248	Physical	None	Automated name-based	<a href="#">[ Correspondence Details ]</a>	<a href="#">[ View On Map ]</a> <a href="#">[ Comparative View ]</a>
RM144	Rice-Cornell SSR 2001-11	Genetic	None	Automated name-based	<a href="#">[ Correspondence Details ]</a>	<a href="#">[ View On Map ]</a> <a href="#">[ Comparative View ]</a>
RM144	Rice-Cornell SSR 2001-11	Genetic	None	Automated name-based	<a href="#">[ Correspondence Details ]</a>	<a href="#">[ View On Map ]</a> <a href="#">[ Comparative View ]</a>
RM144	Rice-IRMI 2003-11	Genetic	None	Automated name-based	<a href="#">[ Correspondence Details ]</a>	<a href="#">[ View On Map ]</a> <a href="#">[ Comparative View ]</a>
RM144	Rice-IRMI 2003-11	Genetic	None	Automated name-based	<a href="#">[ Correspondence Details ]</a>	<a href="#">[ View On Map ]</a> <a href="#">[ Comparative View ]</a>

You are now in the Markers Database. (look at the module heading)

## Markers Search

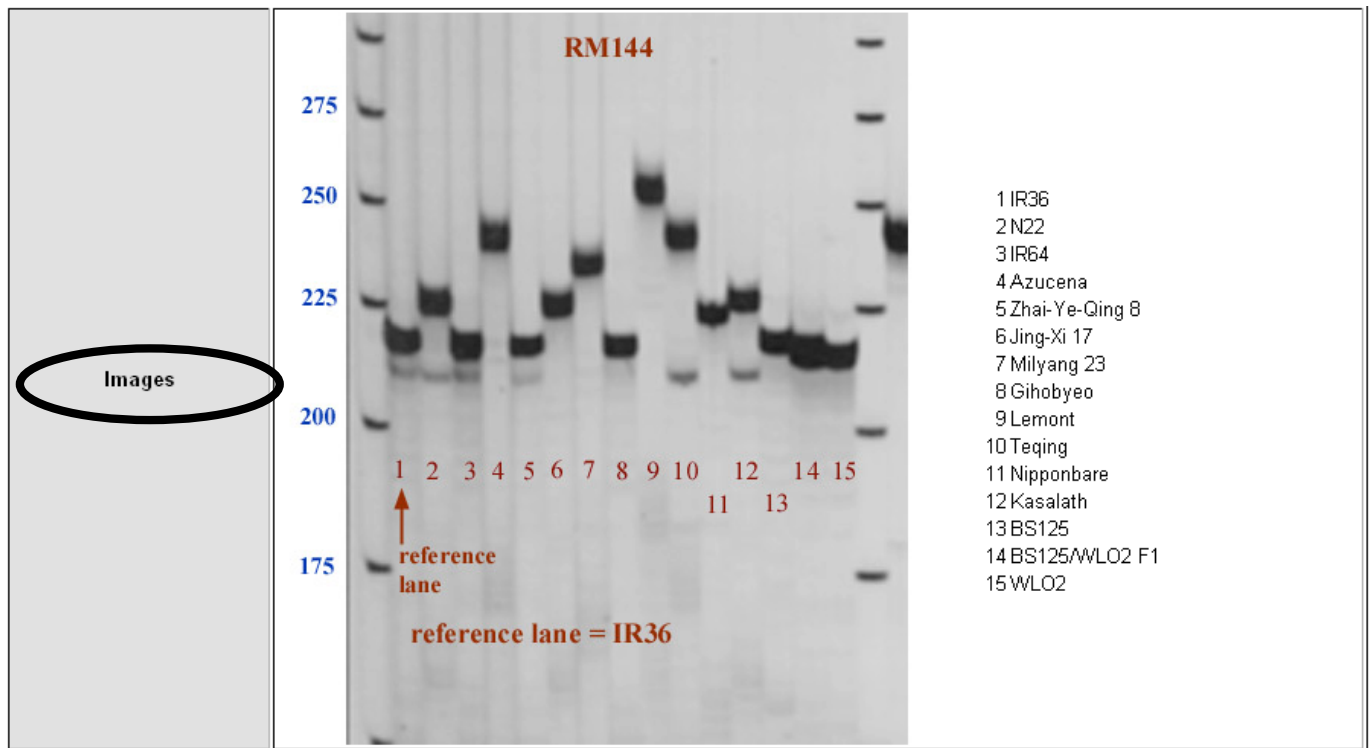
Marker Name:  Marker Type:  Species:

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

- ➔ **8) Notice the following:**
- ➔ **a. Forward and Reverse Primers** – these are the primary defining characteristics of the SSR markers that make it unique. You need to know this if you want to synthesize the primer for yourself.
  - ➔ **b. Anneal Temperature** – need to know this to program the PCR
  - ➔ **c. Expected PCR Product size** – approximate size of the band that you should expect to see
  - ➔ **d. Genome Positions** – click to see marker displayed in the genome browser.
  - ➔ **e. Images** – May or may not be available. The images gives a better idea of the range of band sizes on representative germplasm. If you don't see a band in the expected size you may need to adjust your PCR conditions.

## View Rice SSR marker "RM144"

<b>Marker ID</b>	6083								
<b>Marker Name</b>	RM144								
<b>Synonyms (1)</b>	X67711 (GENBANK_ACCESSION)								
<b>Type</b>	SSR								
<b>Species</b>	Oryza sativa (Rice)								
<b>Germplasm</b>	Nipponbare								
<b>Library</b>	UNKNOWN								
<b>Description</b>									
<b>Mappings (12)</b>	<b>Species</b>	<b>Map Type</b>	<b>Map Set</b>	<b>Map</b>	<b>Name</b>	<b>Start</b>	<b>Stop</b>	<b>CMap Links</b>	
	Oryza sativa (Rice)	Genetic	IRMI 2003	11	RM144	117.3		<a href="#">View on Map</a>	<a href="#">Feature Details</a>
	Oryza sativa (Rice)	QTL	M202/IR50 UCD QTL 2003	11	RM144	91.5	91.5	<a href="#">View on Map</a>	<a href="#">Feature Details</a>
	Oryza sativa (Rice)	QTL	Cornell IR64/Azu DH QTL 2001	11	RM144	123.2	123.2	<a href="#">View on Map</a>	<a href="#">Feature Details</a>
	Oryza sativa (Rice)	QTL	IRRI RD23/Olong F2 QTL 2003	11	RM144	175	175	<a href="#">View on Map</a>	<a href="#">Feature Details</a>
	Oryza sativa (Rice)	QTL	TKU Integrated QTL 2002	11	RM144	131.5	131.5	<a href="#">View on Map</a>	<a href="#">Feature Details</a>
	Oryza sativa (Rice)	QTL	CNZU IR1552/Azu RI QTL 2003	11	RM144	17.6	17.6	<a href="#">View on Map</a>	<a href="#">Feature Details</a>
	Oryza sativa (Rice)	Genetic	Cornell SSR 2001	11	RM144	123.2		<a href="#">View on Map</a>	<a href="#">Feature Details</a>
	Oryza sativa (Rice)	QTL	CNZU IR1552/Azu RI QTL 2004	11	RM144	17.6	17.6	<a href="#">View on Map</a>	<a href="#">Feature Details</a>
	Oryza sativa (Rice)	QTL	NDSU EM93/SS18 BC QTL 2004	11	RM144	160.3	160.3	<a href="#">View on Map</a>	<a href="#">Feature Details</a>
	Oryza sativa (Rice)	Physical	I-Map (FPC) [OBSOLETE]	ctg248	RM144	3	43	<a href="#">View on Map</a>	<a href="#">Feature Details</a>
	Oryza sativa (Rice)	Sequence	GR TIGR Assm IRGSP Seq 2005	Chr. 11	RM144	28,158,704	28,158,928	<a href="#">View on Map</a>	<a href="#">Feature Details</a>
Oryza sativa (Rice)	Sequence	GR TIGR Assm IRGSP Seq 2005	Chr. 11	RM144	28,158,704	28,158,928	No CMap Feature Accession		
<b>Correspondences</b>	No correspondences.								
<b>Clone</b>									
<b>Repeat Motif</b>	(ATT)11								
<b>Forward Primer</b>	TGCCCTGGCGCAAATTTGATCC								
<b>Reverse Primer</b>	GCTAGAGGAGATCAGATGGTAGTGCATG								
<b>Anneal Temperature</b>	65								
<b>Expected PCR Product Size</b>	237								
<b>Remarks</b>									
<b>Sequence Source</b>									
<b>Genome Positions</b>	RM144 (89706) RM144 (89703)								
<b>Database Cross-references</b>	Gramene Literature <a href="#">Temnykh-S Park-W-D Ayres-N-M Cartinhour-S Hauck-N Lipovich-L Cho-Y-G Ishii-T McCouch-S-R, Mapping and genome organization of microsatellite sequences in rice (Oryza sativa L.), Theoretical and applied genetics, 100, 2000, pp. 697-712</a>								



➡ 9) **Return to the Cmap view in #6 (click the browser's 'Back' button two times.)**

➡ 10) **Compare this map to a genetic map and a sequence map to see what other features may be in the same region.**

- *Genetic maps will give a general order to surrounding features, but do not offer the exact sequence and distance.*
- *\*\*Underneath the map select "Show additional options menu" and check "yes" for "Collapse overlapping features". This will speed up your results time\*\**
- *Underneath the map click on 'Show Reference Menu.' We will put the genetic map on the left, and the sequence map on the right.*
- *Under the left heading select the 'Select Map Set' menu to open a list of maps with comparisons. Click on "Genetic: Rice – Cornell SSR 2001 [7]" (7 comparisons are on chromosome 11). If there were more than one chromosome with correlations you would need to select the ones you wanted to compare.*
- *Under the right heading select the 'Select Map Set' menu to open a list of maps with comparisons. Click on "Sequence: Rice – Gramene Annot Seq 2006 [8]".*
- *Click on 'Redraw Map.'*

Ref Map Start:   
 Ref Map End:   
 Current Map Sets: Rice-LSU Caiapo/IRGC103544 QTL 2004 (Ref.)  
 Min. No. Correspondences for Left Slot:   
 Min. No. Correspondences for right Slot:   
 Min. No. Correspondences for the menu:

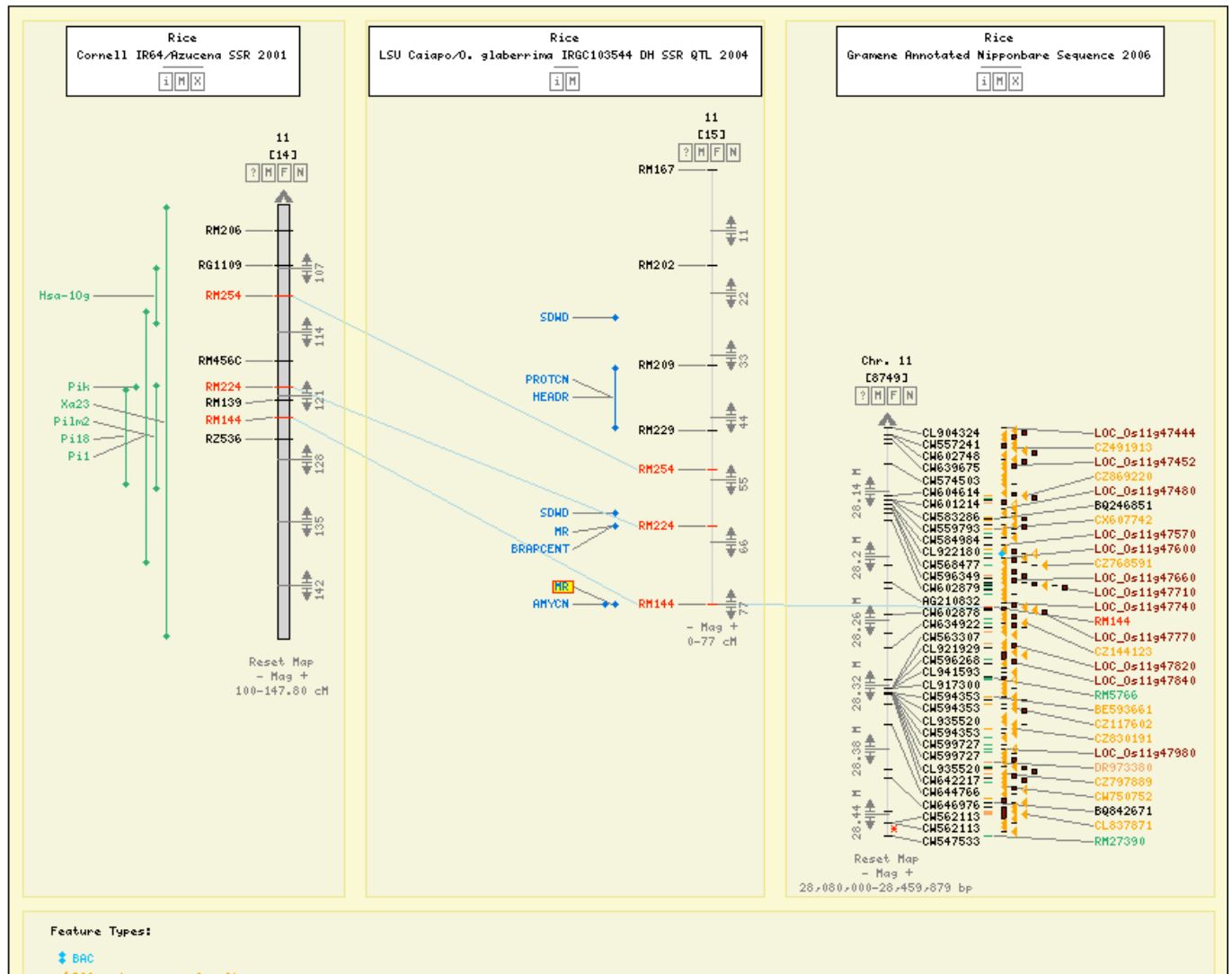
Comparative Maps (Left):

Comparative Maps (Right):

Format: Name [total correspondences to slot, Max correspondences to single map]  
 hint: To save time, select the desired options before redrawing the map.

You will see that the marker that is associated with your QTL is also located near several other markers and some interpolated genes. Once again, following those links will provide more information that may or may not be useful or interesting to you.

- ➔ **11) Use the CMAP tools to alter the view.**
- a. **Crop the maps to magnify the view** (*Click on the arrows for cropping.*)
  - b. **Use “options” and “additional options” menus.** (*Located below the map image. Click on ‘Show Options Menu’ and ‘Show Additional Options Menu’*)



Hide Options Menu

Highlight Features: "AQFU049"

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"/>
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 type="radio"/>
	<input type="button" value="Check All"/>	<input type="button" value="Check All"/>	<input type="button" value="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"/>	<input type="text" value="0"/>
Insilico	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="text" value="0"/>
Name-based	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="text" value="0"/>
	<input type="button" value="Check All"/>	<input type="button" value="Check All"/>			

Aggregate Correspondences:  No  1 Line  2 Lines  Cluster

Number of Clusters (if clustering):  2  3  4

Total Magnification:

(Hide Options Menu)

Hide **Additional Options Menu**

Image Size:  Tiny  Small  Medium  Large

Font Size:  Small  Medium  Large

Image Type:  PNG  JPEG  GIF  SVG \*

Show Labels:  None  Landmarks  All

Collapse Overlapping Features:  No  Yes

Draw Maps Using Same Scale:  No  Yes

Correspondence lines drawn to:  Feature  Map

Stack the Reference Maps:  No  Yes

Clean View (no navigation buttons):  No  yes

Clickable Image:  Default  Omit Features  Omit All Buttons

View Intra-Slot Correspondences:  No  yes

Aggregate evidence types separately:  No  yes

Menu Order of Comparative Maps:  Predefined Order  Number of Correspondences

Ignore Image Map Sanity Check:  No  Yes

(Hide Additional Options Menu)

➔ 12) **View RM144 in the Rice Genome Browser** (Click on the ‘RM144’ on the map to open the maps feature page. Under ‘Cross-References’ select [View “RM144” in Genome Browser]. This will open a page with where you need to click on the location. Select “**Location [28158704 - 28158928 bps](#)**”.

### Chromosome Map Marker RM144

<b>Marker Location</b>	Location <b>28158704 - 28158928 bps</b> on chromosome 11 [Export Data]
<b>Marker Type</b>	SSR (Simple Sequence Repeat)
<b>Marker Synonyms</b>	Cmap : RM144 RM144
<b>Marker Primers</b>	Marker RM144 primers are not in the database

(You May use “Export the data” to get this information in text format, but selecting the location bps (base pairs) will show you the same information in a diagram, which can aid in understanding the data.) It may take a few moments for the results to load in your browser, but the first thing you will notice is that this marker is located at one end of chromosome 11.

The “overview” diagram identifies other features mapped to this area, including synteny with other species. This view is magnified from the chromosome view, so along the blue DNA bar is a box indicating the selected area on the chromosome view.

Red boxes indicate the part of genome being viewed in the next image.



The detailed view is once again magnified from the overview, and zooms in to cover only the area in the selected section of the chromosome. It can be customized to provide information of interest to you by changing the magnification, genomic area, features and decorations through the menus at the top of the display box.

Zoom in/out to a desired level of

Click on a feature to open menu options

Features! Those above your sequence are on the forward strand, ones below are on the reverse strand

Select options to customize the view.

Detailed view

Jump to region: 11 bp 28148704 to 28168928 Refresh

Features ESTs GSSs FSTs Markers Arrays Decorations Export Jump to Width Help

Length 28.15 Mb 28.15 Mb 28.15 Mb 28.16 Mb 28.16 Mb 28.16 Mb 28.16 Mb 28.16 Mb 28.17 Mb 28.17 Mb

GeneModel TIGR LOC\_0s11g47740 -> tigr\_gene LOC\_0s11g47760 -> tigr\_gene LOC\_0s11g47770 -> tigr\_gene

DNA(clone) RC134045

GeneModel TIGR LOC\_0s11g47750 tigr\_gene LOC\_0s11g47780 tigr\_gene

Rice\_ArrayConsensus\_Affy57K

Rice\_EST

Rice\_ESTcluster\_PlantGDB

Rice\_ESTcluster\_TIGR

Rice\_MarkerRFLP

Rice\_MarkerSSR

RiceIndica\_EST\_BGI

RiceIndica\_ESTcluster\_BGI

RiceJaponica\_BACend\_OMAP

RiceJaponica\_cDNA\_KOME

RiceRufipogon\_BACend\_OMAP

SNPs

Length 28.15 Mb 28.15 Mb 28.15 Mb 28.16 Mb 28.16 Mb 28.16 Mb 28.16 Mb 28.16 Mb 28.16 Mb 28.17 Mb 28.17 Mb

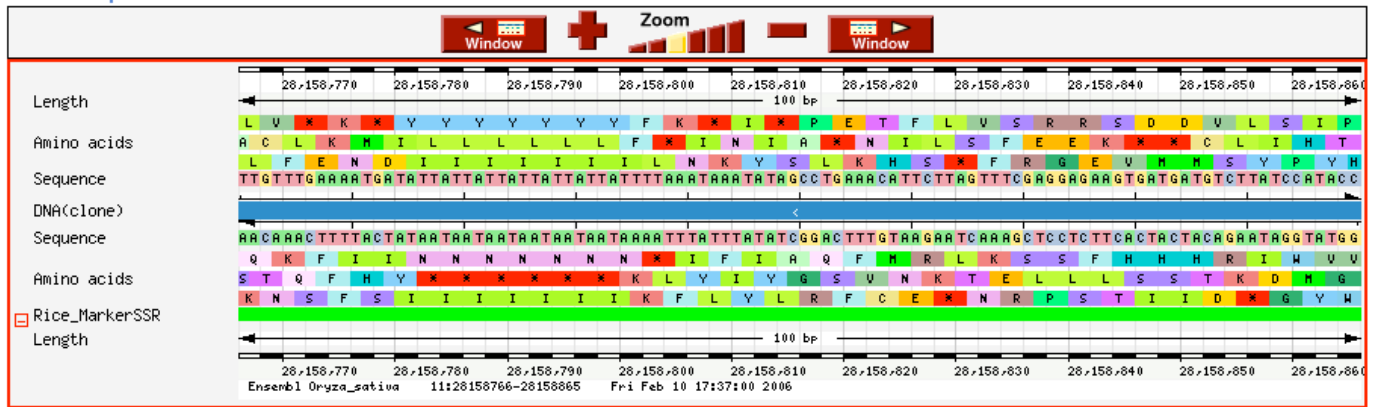
There are currently 59 tracks switched off; use the menus above the inset to turn these on.

Ensembl Orzyza\_sativa 11:28148704-28168928 Fri Feb 10 17:36:58 2006

Finally, at the bottom of this page you will find the Basepair View. This diagram shows the sequence and the possible codon sequences for this section.



Basepair view



13) You may wish to examine the alleles in your germplasm, and begin by viewing RM144 in the Diversity database. (*Go to Diversity, search for RM144 in markers*)

**GRAMENE Diversity** Find anything  Search

Search Genomes Download Resources About Help Feedback

Diversity Home | Germplasm Search | Molecular Diversity Search | Gene/Locus Search | Phenotype Search | GDCP Browser | Help | Tutorial | FAQ

### Gramene: Genetic Diversity Database

Search for:  Search in:  Species:

Similarity Search

E.g., IRGC 3575, RA4969, Basmati 1, RM22.

Gramene Genetic Diversity database contains SSR and SNP allelic data and passport descriptions for rice, maize and wheat germplasm. It also holds phenotypic data for maize. The database can be searched by germplasm accession number, accession name and marker/locus name. For example in the rice database, you can search for IRGC 3575, PI 400604, RA4969, RM22. Please specify the species of your interest from pull-down menu before you press the submit button. For search tips, please read the [help document](#).

The ultimate goal is to make this database a source of rice, maize, and wheat bio-information from/for evolutionary, domestication, association, and genetic diversity studies. It also could be useful for potential applications such as germplasm management, marker assisted selection and DNA-based variety identification.

For more complex queries, you can use [The Genomic Diversity and Phenotype Connection \(GDCP\) Browser](#). Click [here](#) to download and get documentation how to use the GDCP Browser.

We welcome your questions, comments and suggestions. Please use the feedback button on the top of the pages to send us your remarks.

For data summary of the database, click [here](#).

Your results will look like:

Diversity Home | Germplasm Search | Molecular Diversity Search | Gene/Locus Search | Phenotype Search | GDCP Browser | Help | Tutorial | FAQ

### View Marker "RM144"

There is allele data for locus "RM144" from 1 experiment.

Title	Design	Polymorphism Type	Allele Scoring Protocol	Producer	Originator	Comments
<a href="#">Genetic structure and diversity in Oryza sativa L.</a>	234 rice accessions from wide geographical regions of the world	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 Genotyper 2.5 software.	McCouch Lab	McCouch/Tai	Prediction of population structure was model-based (STRUCTURE) and based on data from 169 genomic SSRs. For more information, see the paper by <a href="#">Garris et al., 2005</a> .

[ Search for RM144 in Gramene's Marker Database ]

Select the

Click for experiment info

to view all the data for RM144.

Click for allele data

## Allele data for marker "RM144" from the experiment "Genetic structure and diversity in Oryza sativa L.".

[Search Again](#)

Germplasm Accession Number	Germplasm Accession Name	Locus name	Genotype	View All Genotypes on Germplasm
RA4877	Dourado Agulha	RM144	250	<a href="#">All Genotypes On "Dourado Agulha"</a>
RA4878	Khao Dawk Mali 105	RM144	220	<a href="#">All Genotypes On "Khao Dawk Mali 105"</a>
RA4879	CO25	RM144	220	<a href="#">All Genotypes On "CO25"</a>
RA4881	Sintane Diofor	RM144	220	<a href="#">All Genotypes On "Sintane Diofor"</a>
RA4882	Kotobuki Mochi	RM144	247	<a href="#">All Genotypes On "Kotobuki Mochi"</a>
RA4883	Pin Kaeo	RM144	220	<a href="#">All Genotypes On "Pin Kaeo"</a>
RA4884	DA7	RM144	268	<a href="#">All Genotypes On "DA7"</a>
RA4885	DA9	RM144	212, 244	<a href="#">All Genotypes On "DA9"</a>
RA4886	DA5	RM144	247	<a href="#">All Genotypes On "DA5"</a>
RA4887	DA13	RM144	220	<a href="#">All Genotypes On "DA13"</a>
RA4888	Pankhari 203	RM144	235	<a href="#">All Genotypes On "Pankhari 203"</a>
RA4889	PTB9	RM144	220	<a href="#">All Genotypes On "PTB9"</a>
RA4890	DA1A	RM144	220	<a href="#">All Genotypes On "DA1A"</a>
RA4891	FR13 A	RM144	220	<a href="#">All Genotypes On "FR13 A"</a>
RA4892	Makalioka-34	RM144	244	<a href="#">All Genotypes On "Makalioka-34"</a>
	Chitraj ( DA23 )	RM144	229	<a href="#">All Genotypes On "Chitraj ( DA23 )"</a>
RA4893	T1T1	RM144	226	<a href="#">All Genotypes On "T1T1"</a>
RA4894	N12	RM144	274	<a href="#">All Genotypes On "N12"</a>
RA4895	CO18	RM144	220	<a href="#">All Genotypes On "CO18"</a>
RA4896	Baguamon 14	RM144	220	<a href="#">All Genotypes On "Baguamon 14"</a>
RA4897	RTS12	RM144	220	<a href="#">All Genotypes On "RTS12"</a>
RA4898	Hsia-Chioh-Keh-Tu	RM144	247	<a href="#">All Genotypes On "Hsia-Chioh-Keh-Tu"</a>
RA4899	EH-1A-Chiu	RM144	286	<a href="#">All Genotypes On "EH-1A-Chiu"</a>
RA4900	Shuang-Chiang	RM144	247	<a href="#">All Genotypes On "Shuang-Chiang"</a>
RA4901	Davao	RM144	235	<a href="#">All Genotypes On "Davao"</a>

Comparing the alleles of each parent can help determine which allele is in your germplasm. In this example, look at Lemont and Teqing germplasms. All the known markers will be listed, along with their genotype.

### 14) Biochemical Pathways – An example for biochemists:

Go to the Genes database, and search for Wx. Locate the gene ID. Copy and paste this ID (LOC\_) into the search box for Pathways.

#### Summary for Gene: wx (GR:0061010)

[General Info](#) | [Sequence Association](#) | [Map Position](#) | [Ontology Association](#) | [References](#)

General Information				
Accession	GR:0061010			
Gene Symbol	wx			
Gene Name	glutinous endosperm			
Gene Synonym(s)	UDP-glycogen synthase, GBSS, Granule-bound starch synthase, Waxy, chloroplast precursor, glycogen [starch] synthase, Granule-bound glycogen synthase, UDPG-glycogen transglucosylase, uridine diphosphoglucose-glycogen glucosyltransferase, glycogen [starch] synthetase, waxy, Granule-bound glycogen [starch] synthase, UDPG-glycogen synthetase			
Species	Rice			
Chromosome No.	6			
Gene Type	CDS (Protein coding)			
Has Phenotype	yes			
Description	The Waxy (Wx) gene encodes a granule-bound starch synthase (GBSS) that plays a key role in the amylose synthesis of rice. It is expressed in the seed endosperm and pollen grains, that carry starch grains. At sub-cellular level the protein is localized in the amyloplasts. This gene undergoes alternative splicing of its transcripts suggesting that the amylose content of rice endosperm is regulated at the level of Wx transcript processing, and more specifically, at the stage of intron I excision from the Wx pre-mRNA. The alternative splicing is affected by the change in temperature. It is a single copy gene in rice. The phenotype shows white and non-translucent endosperm which turns brown to the iodine staining.			
Sequence Association				
Protein	Gramene Protein: <a href="#">GZD6</a> , <a href="#">Q94LY7</a> , <a href="#">Q9S7U4</a> , <a href="#">Q9SB03</a> , <a href="#">Q9XHN9</a>			
Nucleotide (DNA)	GenBank Nucleotide: <a href="#">AF031162</a> , <a href="#">AF141954</a> , <a href="#">AF141955</a> Rice Ensemble Gene: <a href="#">LOC_Os06g04200</a>			
Map Position				
#	Map Set Name	Linkage Group	Start Position	Stop Position
1	Cornell BS125/2/BS125AVLO2 RFL	6	6.70 cM	6.70 cM
2	JRGP Nipponbare/Kasalath RFLP	6	8.20 cM	8.20 cM
3	Hokkaido Morphological 2000	6	22.00 cM	22.00 cM
4	Cornell BS125/2/BS125AVLO2 RFL	6	-1.50 cM	-1.50 cM
5	IGCN ZhaiYeQing 8/JingXi 17 19	6	5.70 cM	5.70 cM
6	IGCN Oryza sativa/Oryza eichin	6	0.00 cM	0.00 cM
Ontology Association				
Trait	glutinous endosperm ( <a href="#">TO:0000098</a> )			
Plant Structure	endosperm ( <a href="#">PO:0009089</a> )			
Cellular Component	amyloplast ( <a href="#">GO:0009501</a> ), amyloplast starch grain ( <a href="#">GO:0009568</a> ), plastid ( <a href="#">GO:0009536</a> )			
Molecular Function	glycogen (starch) synthase activity ( <a href="#">GO:0004373</a> )			
Biological Process	starch metabolism ( <a href="#">GO:0005962</a> )			
Reference				

There are two ways to begin a search on Pathways. Either click on the large red button at the top of the page, or select your species on the right hand side of the page.:

**GRAMENE Pathway** Find anything

Search Genomes Download Resources About Help

Tutorial | FAQ | Help

### RiceCyc home and Biochemical pathways

Click here to SEARCH and BROWSE the pathways

#### About pathways

The Pathway tool is a web-based tool for viewing gene annotations mapped to various biochemical pathways in plants, rice (*Oryza sativa*) and *Arabidopsis thaliana* and bacteria *E. coli*.

The pathways for rice (RiceCyc) were curated by Gramene. The rice genes and their annotation used in this analyses were based on release 4 of the TIGR's-assembly of *Oryza sativa japonica* cv. Nipponbare genome sequenced by IRGSP.

#### Your favorite rice pathways

Auxin metabolism	Photosynthesis
Brassinosteroid metabolism	Respiration
Cytokinin metabolism	TCA cycle
Gibberellin metabolism	Secondary metabolic pathways
Ethylene biosynthesis from methionine	Starch biosynthesis

#### Pathways in Gramene

Species	Source	Overview#	Summary	Pathway comparison
<b>RICE</b> <i>Oryza sativa japonica</i> cv. Nipponbare	Gramene, <b>RiceCyc</b> 1.0		<a href="#">view</a>	<a href="#">Arabidopsis E. coli</a>
<b>ARABIDOPSIS *</b> <i>Arabidopsis thaliana</i> strain Columbia	TAIR, <b>AraCyc</b> 2.5		<a href="#">view</a>	<a href="#">Rice E. coli</a>
<b>E. COLI *</b> <i>Escherichia coli</i> strain K-12 MG1655	SRI, <b>EcoCyc</b> 9.5		<a href="#">view</a>	<a href="#">Rice Arabidopsis</a>

\* Not curated by Gramene. # click on icons to visit the overview

#### Useful links to pathway tool

Compare data sets from the three species for reactions, pathways, compounds and proteins [Compare](#)

**GRAMENE**

[ [Pathway Home](#) ]

### Pathway Tools Query Page

This form provides several different mechanisms for querying Pathway/Genome Databases.

**Select a dataset:**

- Query:**
- Browse Ontology:**
- Choose from a list of all:**
- Links to summary information about the selected organism:**
  - Summary page for dataset
  - Cellular Overview [Diagram/Omics Viewer](#)
  - History of updates to this dataset
  - PathoLogic Pathway Analysis (not available for *E. coli* or MetaCyc)
- Comparative Analysis**

Generate summary tables that compare various properties across one or more selected organisms.

[Help](#) [Advanced Query Form](#) [Pathway Tools Home](#) [Feedback](#)

Pathway Tools version 9.5

***O. sativa japonica* Gene: [LOC\\_Os06g04200.1](#)**

Synonyms: wx , glutinous endosperm , GBSS , UDP-glycogen synthase , Granule-bound starch synthase , chloroplast precursor , glycogen [starch] synthase , Granule-bound glycogen synthase , UDPG-glycogen transglucosylase , uridine diphosphoglucose-glycogen glucosyltransferase , glycogen [starch] synthetase , UDPG-glycogen synthetase , Granule-bound glycogen [starch] synthase , waxy

Superclasses: [UNCLASSIFIED](#)

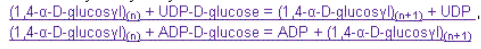
Chromosome: Chromosome 6

Map Position: 1,765,890 -> 1,769,651 (nucleotides) 5.6514 (centisomes) [click for genome browser]

Sequence Length: 3762 bp / 1253 AAs

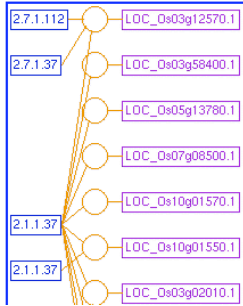
Products: [Granule-bound starch synthase 1](#), [chloroplast precursor](#), [putative](#), [expressed](#) / [starch metabolism](#)

Reactions Catalyzed by Enzymes:

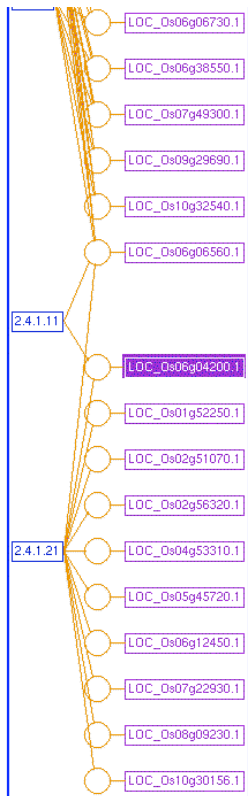


Pathways Involving Enzymes: [starch biosynthesis](#), [glycogen biosynthesis](#)

Gene-Reaction Schematic: [?](#)

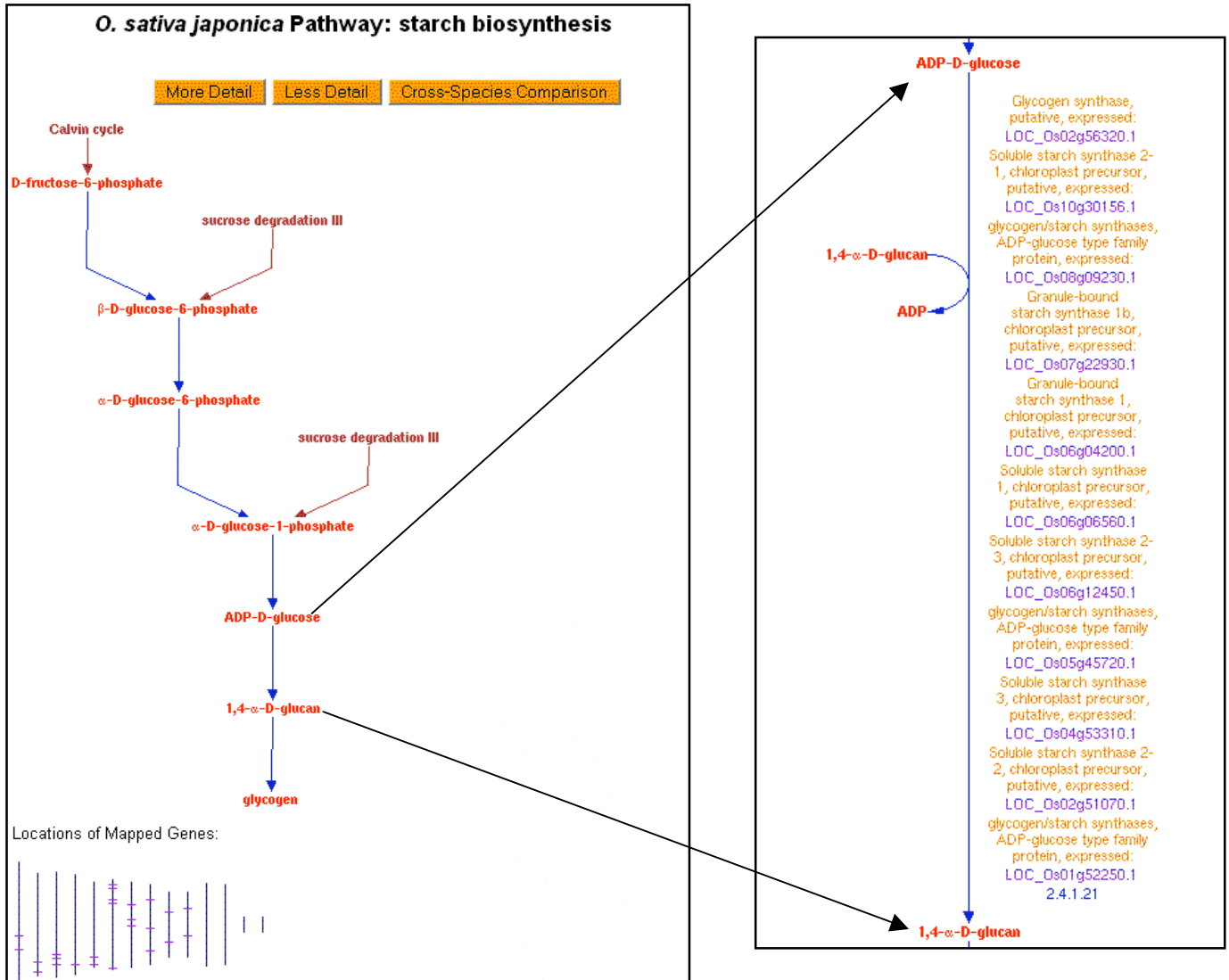


Select the “Starch Biosynthesis” link as one example of where this gene is involved in a biochemical pathway.



Unification Links: [Gramene](#) [Ensembl](#): [LOC\\_Os06g04200](#)

Gene Local Context (to scale): [?](#)



In this exercise you have simply begun to learn what Gramene can do. For more complete details on all the features available from each module, review the module tutorials available on the web.

Use the feedback button at the top of every page to submit private questions to the Gramene team. The appropriate person will get back to you. For public discussion, join the Gramene listserve.

Thank you!

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Or use the Feedback button at the top of every page on the Gramene website [www.gramene.org](http://www.gramene.org)