

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

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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	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 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.
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.

[[Top](#)]

Allele	RMg16.1 (Pita, Pi4a) , RMg16.2 (Pita 2) , RMg16.3 (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				
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4	Rice-CNHZAU Zhe97/Wuy2 QTL 2004	12	55.40 cM	59.00 cM

[[Top](#)]

Associated Feature (Evidence Code: TAS IAGP)	
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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)	PI-TA		
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  
MAPAVSASQGVIMRSLTSKLDLLLLQPPEPPPPAQPSS  
YYLLVEPPSDTAPPPDSTAACWAKEVRELSYDVDDFL  
KMISSMIARLRGELNRRRWIADEVTLFSARVKEAIRR  
REDSAGNERRRFSLSTFGMDDAAVHGQLVGRDISMQK  
GKTTLATEFYRLHGRRLD  
DRLLETIRTHLQDKRYFI  
YNSEHIIKIDPLGDDVSS  
FKSQLLDGMQQWNHIQKSLTTSNLKKNPTLQGMQVL  
DYIIRKANLVRQWMAEGFINSIENKVMEEVAGNYFDE  
HHMVLNFIRCKSIEENFSITLDHSQTTVRHADKVRRL  
MAFFGQVKCMPSIADYRLLRVLILCFWADQEKTSYDL  
EKIQGLQHLQTLEADARATAVLLDIVHTQCLLHLRLV  
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  
MAPAVSASQGVIMRSLTSKLDLLLLQPPEPPPPAQPSSLRKGERKKILLRGLRHL  
YYLLVEPPSDTAPPPDSTAACWAKEVRELSYDVDDFLDELTTQLLHHRGGGDSSTA  
KMISSMIARLRGELNRRRWIADEVTLFSARVKEAIRRQESYHLGRRTSSSRPREEVD
```

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

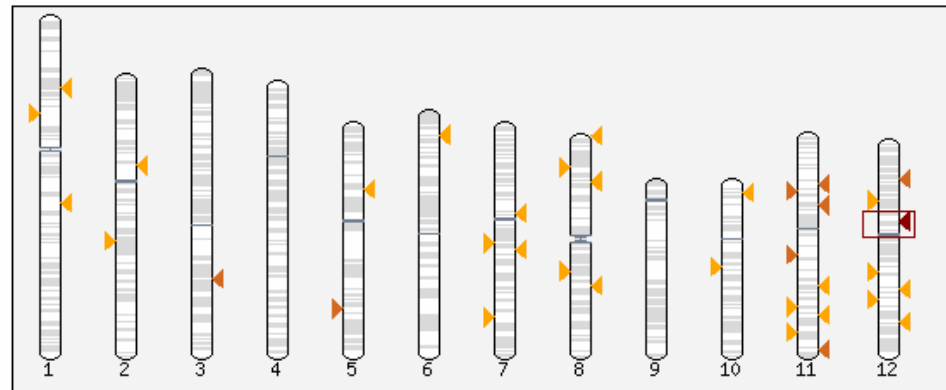
Genomic sequence
Peptides (TIGR gene models)

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>The diagram illustrates the protein sequence from 0 to 928 amino acids. Key features include the NB-ARC domain (approx. 160-480 aa), two SUPERFAMILY domains (SSF52540 and SSF52058), and a PRINTS domain (DISEASERSIST). A peptide sequence is highlighted in pink from 0 to 320 aa. SNPs are marked along the sequence, with a legend indicating green for Synonymous and pink for Non-Synonymous mutations.</p>
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

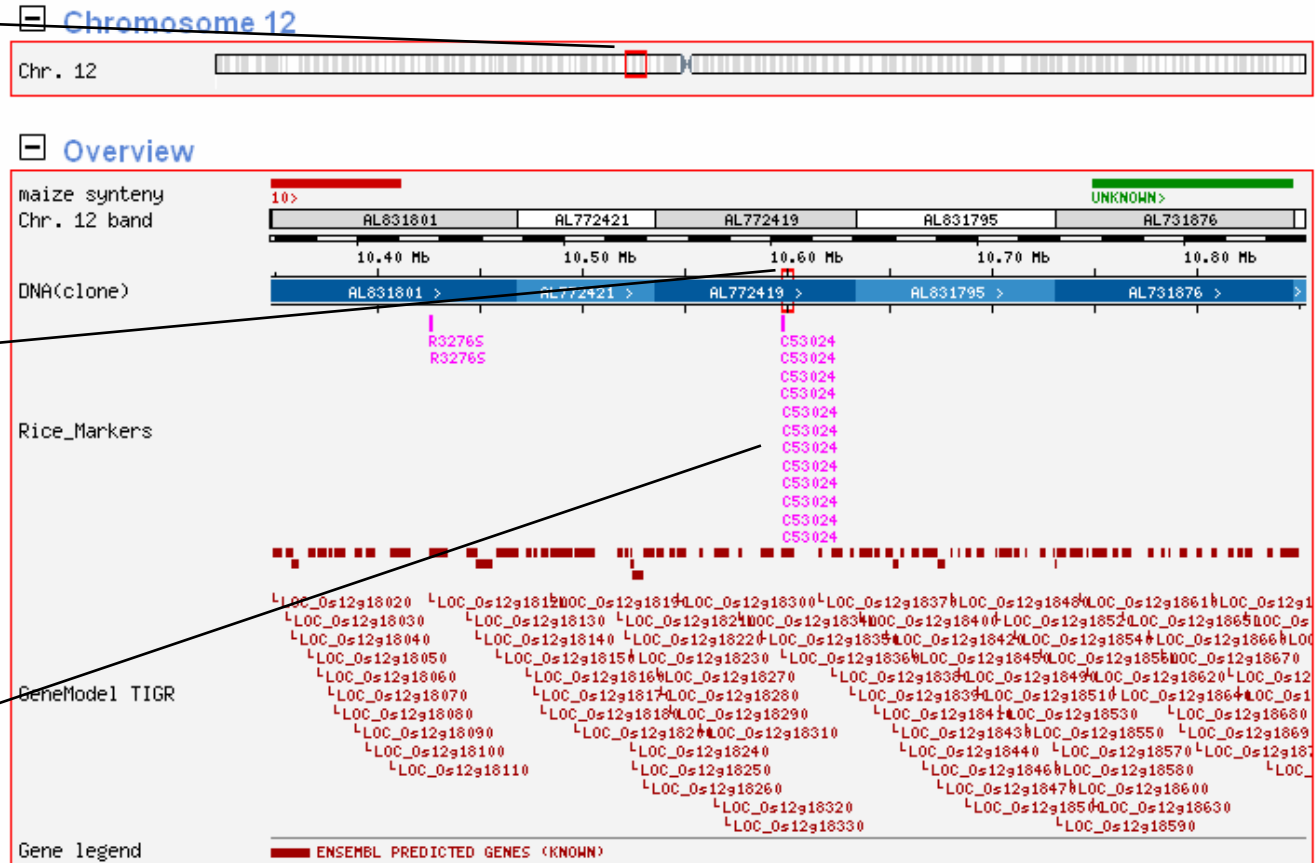
Ensembl Gene Report page provides information about the identity, base pair location on the chromosome, description, and structure.

Genome Browser Overview

Red window on chromosome indicates region shown in “Overview”.

Red window on
“Overview” indicates
region shown in
“Detailed View”.

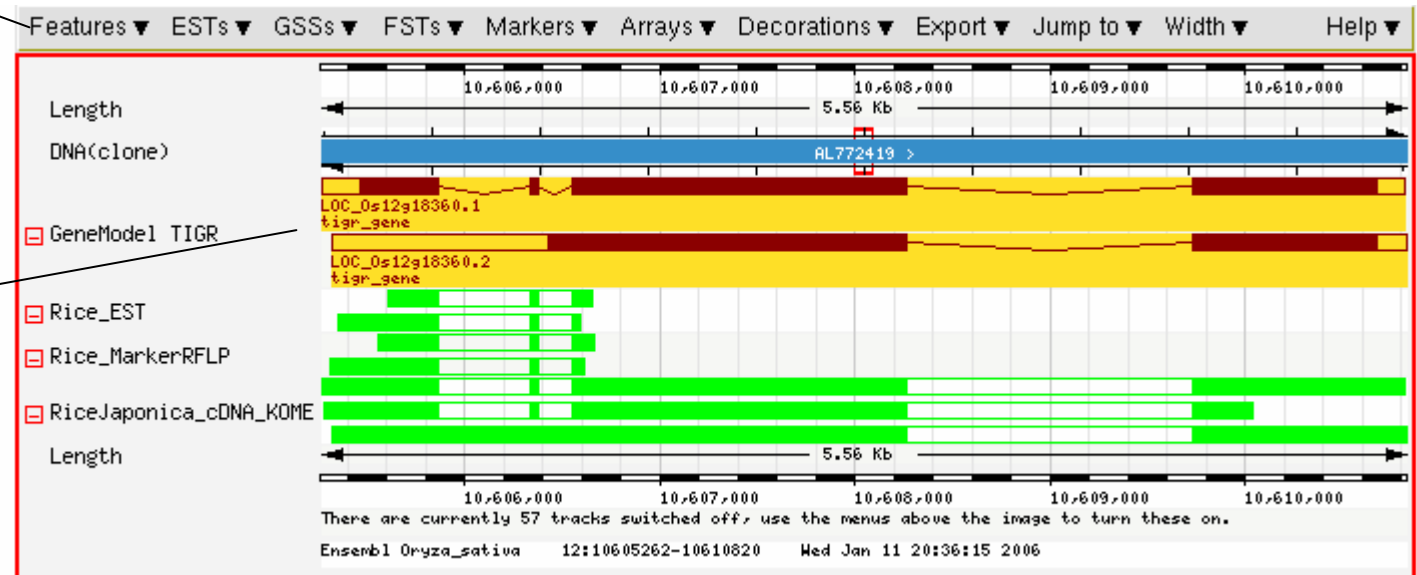
Nearest rice marker.



Genome Browser Detailed View

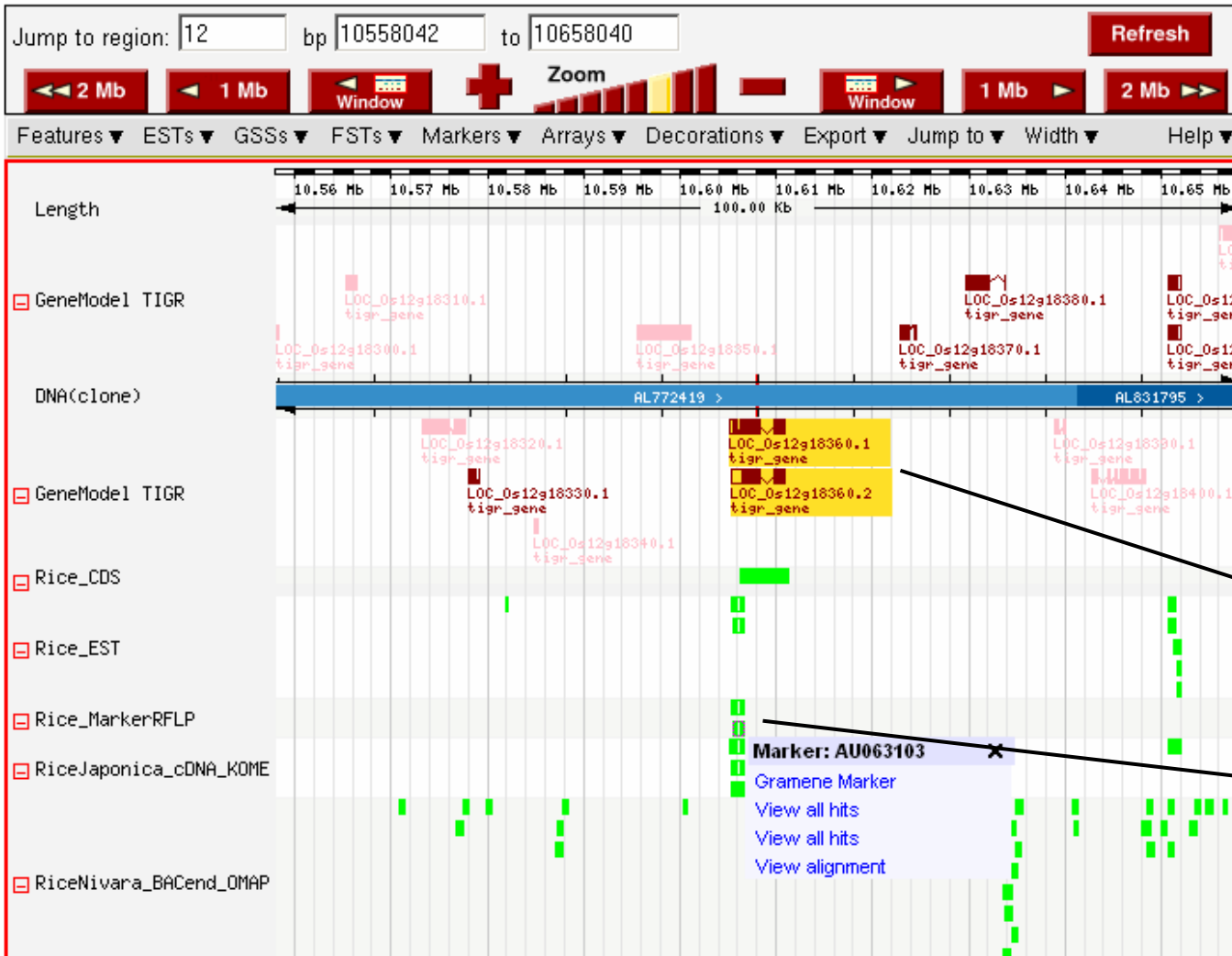
Choose additional tracks from the popup menu.

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](#).

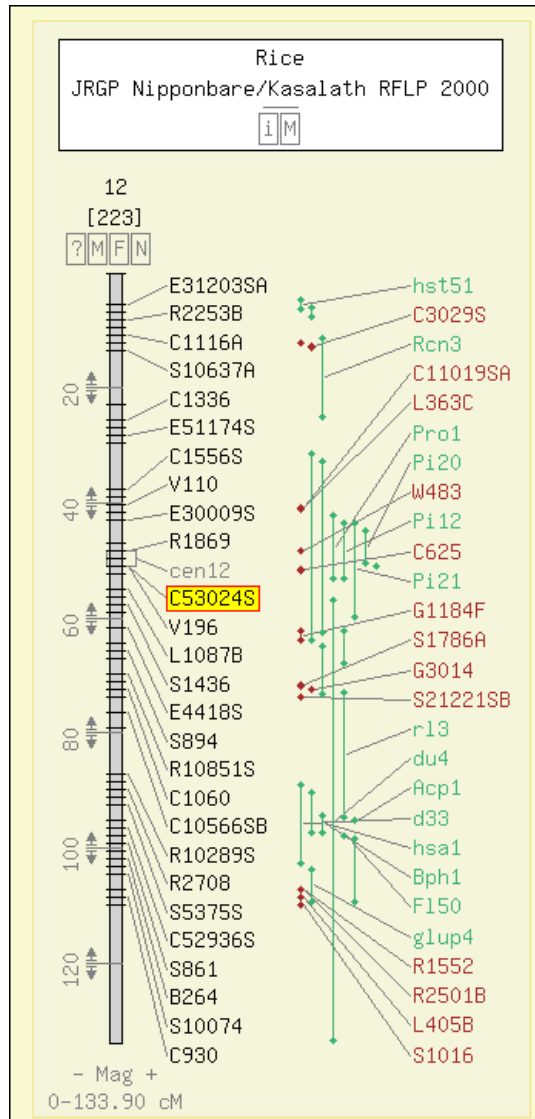
Marker ID	12780
Marker Name	C53024
Synonyms (4)	AU063103 C53024S
Type	RFLP
Species	Oryza sativa (Rice)
Germplasm	Unknown
Description	

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

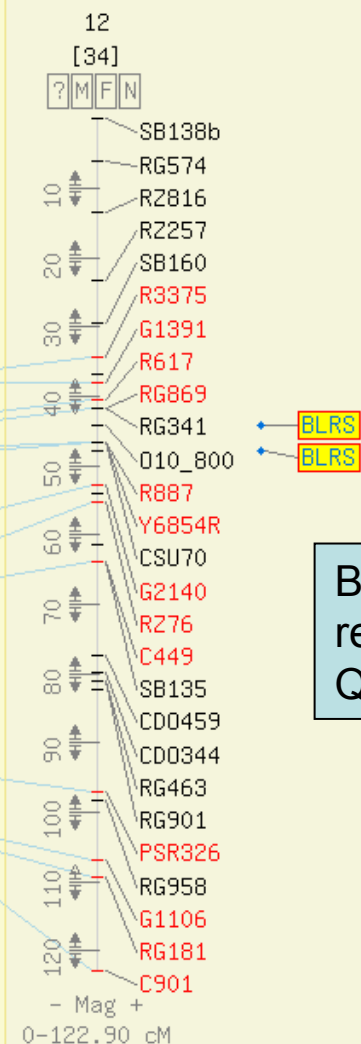
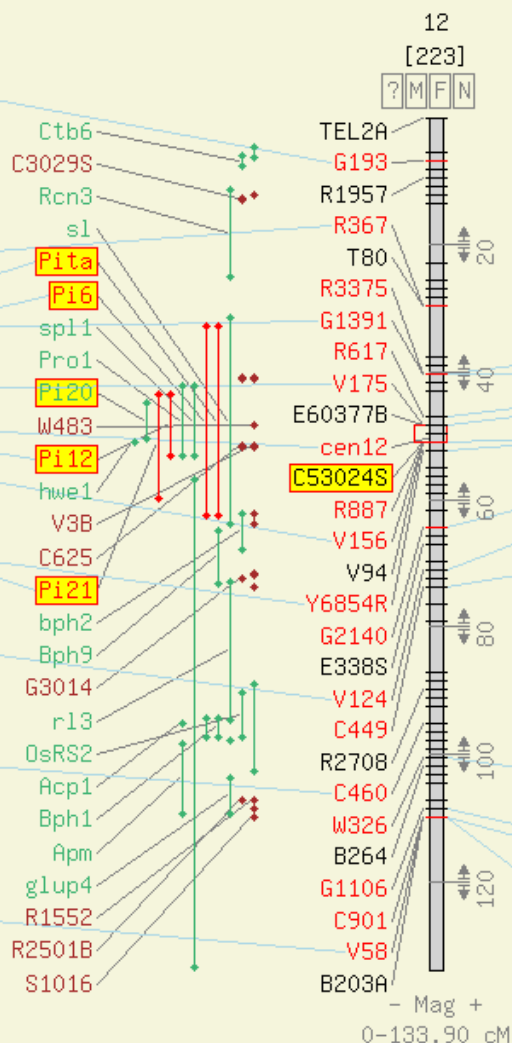
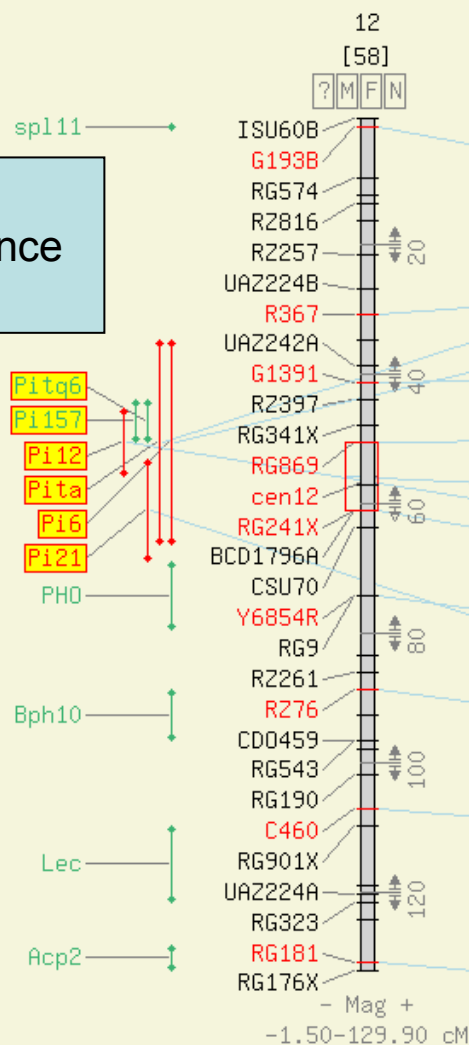
Rice
JRGP Nipponbare/Kasalath RFLP 2000

i M

Rice
CIRAD IR64/Azucena DH RFLP QTL 2003

i M X

Blast
resistance
genes



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