

GRAMENE QTL DATA MODULE

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ABSTRACT:

We continue to curate and develop the QTL data module within Gramene. The current release of the QTL database (V24) houses trait and map position information for more than 11,000 QTL. Out of them, around 1,700 are maize QTL, including both those integrated from MaizeGDB and maize drought resistance QTL curated internally by Gramene. Gramene uses traits, Trait Ontology (TO), and Plant Ontology (PO) (both Plant Structure and Plant Growth and Development Stage) to define, organize, cluster, and search the QTL. Each QTL's detail includes ontology terms, map position, and links to Gramene's Markers and Maps modules. This assists researchers to retrieve associated feature information for a QTL and perform multiple map or species comparisons. Together, with other modules within Gramene, QTL can be utilized as a starting point for maize researchers developing scientific hypotheses and discovering candidate genes. Users are encouraged to participate in the improvement of the QTL search through suggestions for search utilities and visual displays, as well as direct data submission and curation.

View Maize RFLP "CSU690"

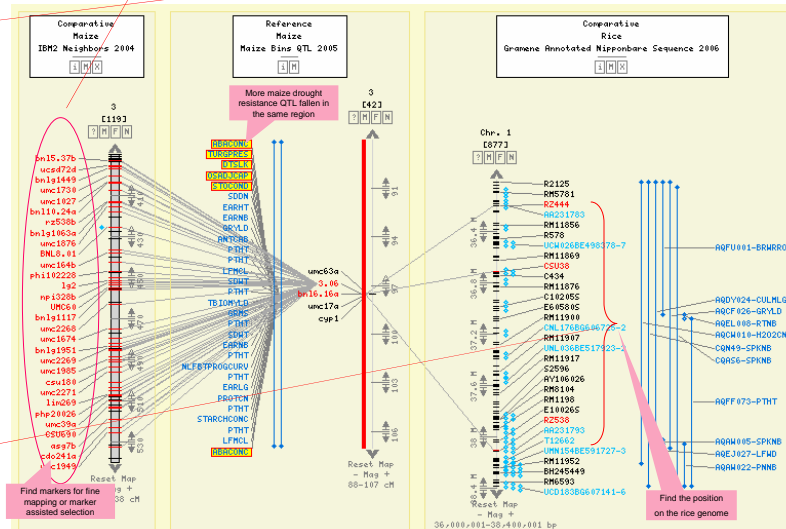
Details	Source/Library	Map Positions (4)	Associations (5)	Image
ID	4278			
Name	CSU690			
Synonyms (4)	CSU690E5 GENBANK_ACCESSION MAIZEGDB_PROBE	csuh00690 AA072460 p-csu690		
Type	RFLP			
Species	Zea mays subsp. mays (Maize)			
Germplasm	Unknown			
Description				
DNA Treatment				
Source Type				
Source Tissue				
Source Treatment				
Vector				

Using Markers to find marker detailed info and associated features

Details	Source/Library	Map Positions (4)	Associations (5)	Images (0)	
Direction	Name	Type	Species	Analysis	Assoc. Type
To	AA072460	EST	Zea mays	gss_poaceae	shared_synonym
To	AA072460	EST Cluster	Zea mays	gss_poaceae	shared_synonym
To	SO0160	OVERGO	Zea mays	SO0_OVERGO	related_probe
From	AA072460	EST	Zea mays	gss_poaceae	shared_synonym
From	Bin 3.06	Maize Bin	Zea mays subsp. mays	bin_marker	bin_marker

Details	Source/Library	Map Positions (4)	Associations (5)	Images (0)			
Species	Map Typ	Map Set	Name/Map	Start	Stop	Map Links	Comment
<i>Sorghum bicolor</i> (sorghum)	Genetic	Paterson 2003	CSU690 A	03.9 cM		View Comparative Map	
Zea mays (Maize)	Genetic	IMZ neighbors	CSU690 3	439.9 cM		View Comparative Map	
		IMZ2 Neighbors 2014	CSU690 3	510.93 cM		View Comparative Map	
		UMC 1998	CSU690 3	107.3 cM		View Comparative Map	

Using CMap to compare QTL with other map/map sets



QTL basic Information

Details for QTL "AQFS428" (osmotic adjustment capacity)

QTL Accession ID	AQFS428	One maize QTL related with drought resistance							
Species	Zea mays subsp. mays (Maize)								
Trait Symbol	OSADJCAP								
Trait Name	osmotic adjustment capacity								
Published Symbol	qomq2								
Trait Synonym(s)	DA	osmotic adjustment							
Trait Category	Abiotic stress								
Chromosome	3								
Mappings	Species	Map Type	Map Set	Name	Map	Start	Stop	Map Links	Method
	Zea mays (Maize)	QTL	Maize Bins QTL 2005	OSADJCAP	3	87	108.3	View in Mappings DB View Comparative Map	Experimental
Related Ontologies	Term Type	Term	Evidence	Reference					
	Trait Ontology	osmotic adjustment capacity (TO:000507)	WQIP	Gramene L1: 9421					
	Plant Structure	plant structure (PO:000011)	IC	Gramene L1: 11453					
	Plant Growth and Development Stage	plant growth and development stages (PO:0009012)	IC	Gramene L1: 11453					
	Species Ontology	Zea mays (GR_tax014450)	SM	Gramene L1: 9421					
Comments	This QTL was originally curated in MaizeGDB Database and the QTL map position was displayed on the maize bins map. Osmotic potential was measured to evaluate osmotic adjustment capacity and used for QTL analysis.								
DBXRefs	Gramene Literature	Guanne SA, Sreed-A-Labron C, Gull M, Calatrano C, Mammiroli N. QTL analysis of ABA production in wheat and maize and associated physiological traits. <i>Euphytica</i> . 41, 1994, pp. 555-571							
	MaizeGDB	102644							

Using Mart to find candidate gene list and filter them with GO terms

Gene Model	Coordinates	GO Term	Description
37537699	37543973	LOC_Os01g65070.G0.0006278	RNA-dependent DNA replication
37537699	37543973	LOC_Os01g65070.G0.0006277	DNA binding
37537699	37543973	LOC_Os01g65070.G0.0006310	RNA recombination
37537699	37543973	LOC_Os01g65070.G0.0006295	chromatin
37537699	37543973	LOC_Os01g65070.G0.0006362	chromatin binding
37537699	37543973	LOC_Os01g65070.G0.0006363	nucleus
37537699	37543973	LOC_Os01g65070.G0.0006333	chromatin assembly or disassembly
37537699	37543973	LOC_Os01g65070.G0.0006191	aspartic-type endopeptidase activity
37537699	37543973	LOC_Os01g65070.G0.0006293	proteolysis
37549662	37555957	LOC_Os01g64980.G0.0006372	RNA binding
37549662	37555957	LOC_Os01g64980.G0.0006384	RNA-directed DNA polymerase activity
37549662	37555957	LOC_Os01g64980.G0.0006270	RNA-dependent DNA replication
37549662	37555957	LOC_Os01g64980.G0.0006376	nucleic acid binding
37549662	37555957	LOC_Os01g64980.G0.0006452	ribonuclease H activity
37549662	37555957	LOC_Os01g64980.G0.0006361	sugar porter activity
37549662	37555957	LOC_Os01g64980.G0.0006401	phosphoenolpyruvate-dependent sugar phosphotransferase activity
37559356	37561500	LOC_Os01g65090.G0.0006372	structural constituent of ribosome
37559356	37561500	LOC_Os01g65090.G0.0006522	intracellular
37559356	37561500	LOC_Os01g65090.G0.0006540	ribosome
37559356	37561500	LOC_Os01g65090.G0.0006411	protein biosynthesis
37559356	37561500	LOC_Os01g65090.G0.0006412	ribosome
37559356	37561500	LOC_Os01g65090.G0.0006413	structural constituent of ribosome
37559356	37561500	LOC_Os01g65090.G0.0006414	ribosome
37559356	37561500	LOC_Os01g65090.G0.0006415	protein biosynthesis
37559356	37561500	LOC_Os01g65090.G0.0006416	hydrolase activity, hydrolyzing O-glycosyl covalent bonds
37559356	37561500	LOC_Os01g65090.G0.0006417	carbohydrate metabolism
37559356	37561500	LOC_Os01g65090.G0.0006418	hydrolase activity, hydrolyzing O-glycosyl covalent bonds
37559356	37561500	LOC_Os01g65090.G0.0006419	carbohydrate metabolism
37559356	37561500	LOC_Os01g65090.G0.0006420	electron transporter activity
37559356	37561500	LOC_Os01g65090.G0.0006421	iron ion binding
37559356	37561500	LOC_Os01g65090.G0.0006422	electron transport

Using Genome Browser to compare other features



Candidate gene detail view

