A Comparative mapping resource



GRAMENE QTL DATA MODULE

Junjian Ni¹, Immanuel V. Yap¹, Pankaj Jaiswal¹, Edward S. Buckler³, Ken Youens-Clark², Claire Hebbard¹, Anuradha Pujar¹, Terry M. Casstevens³, Peter J. Bradbury³, Liya Ren², Wei Zhao², Isaak Yosief Tecle¹, Dean Ravenscroft¹, Chih-Wei Tung¹, Shulamit Avraham², Will Spooner², Sharon Wei², Payan Canaran², Chengzhi Liang², Doreen H. Ware², Lincoln D. Stein², Susan R. McCouch¹

Comparative Maize

IBM2 Neighbors 2004

1 Department of Plant Breeding, Cornell University, Ithaca, New York, 14853, USA 2 Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA 3 USDA-ARS, Institute for Genomic Diversity, Cornell University, Ithaca, New York, 14853, USA

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.

iew Maize RELP "CSU690"										
			De	etails / So	ource/Lib	irary Map	Positions (+) Asso	ociations (5) I	mages (0)
Details Source/Library Map	Position	ns (4) Associations (5) I	mage	. /			-			
ID	47	78		irection	Name	Туре	Spec	ies	Analysis	Assoc. Type
Name	CS	10690	7	0	AA072460	EST	Zea mays		gss_poaceae	shared_synonym
	0	SUE90E5 csub00E90	7	0	AA072460	EST Cluster	r Zea mays		gss poaceae	shared synonym
Synonyms (4)		GENBANK_ACCESSION B A4072460 MAIZEGDB_PROBE p-csu680		0	SOG0160	OVERGO	Zea mays		SOG_OVERGO	related_probe
				rom	AA072460	EST	Zea mays		gss poaceae	shared synonym
Туре	RF	UP	/ F	rom	Bin 3.06	Maiza Bin	Zee maye cut	en may	e hin markar	hin marker
Species	Ze	a mays subsp. mays (Maize)		om	Bill 3.00	Maize Dill	Izea mays suc	op. may	5 Din_marker	bin_marker
Germplasm	Un	known								
Description			Atom D					- 1		
DNA Treatment		Details Source/Librar	ry Map P	ositions ((+) ASSO	ciations (5	5) Images (0)		
Source Type		Species	Map Ty	/n M	lan Set	Name	Mar Star	Stop	Man Links	s Comment
Source Tissue		Carl State	Concelle	0		0.011000	02.0		New Occupient	
Source Treatment		Sorgnum bicolor (sorgnum)	Genetic	Paterso	n 2003	050690	A 00.9 cl	n	view Comparative	мар
Vector		Zea mays (Ma/ze)	Genetic	IBM nei	ghbors	CSU690	3 439.9 cl	1	View Comparative	Map

UMC 1998

Reference

Using Markers to find marker detailed info and associated features



Details for QTL "AQFS428" (osmotic adjustment capacity)

QTL Accession ID	AQFS428		One maize C	Ti related								
Species	Zea mays subsp. mays	with drought resistance										
Trait Symbol	OSADJCAP											
Trait Name	osmotic adjustment cap	acity										
Published Symbol	qosmp2	op heize										
Trait Synonym(s)	OA osmotic potential				esmotic a	djustme	nt					
Trait Category	Abiotic stress											
Chromosome	3											
	Species Map Type		Map Set		Name	Мар	Start	Stop		Map Links		Method
Mappings	Zea mays (Maize)	Maize Bins (DTL 2005	OSADJCAP	3	87	108.3	Vie Viev	w in Mappings r Comparative	DB Experimental		
	Ter	rm Type			Te	rm				Evidence	F	teference
	Trait Ontology		osmotic adjustment capacity (TO.0000507)							KOP.	Gramene Lit. 9421	
Related Ontologies	Plant Structure		alant structure	10		Gramene Lit. 11453						
	Plant Growth and Dev	e s	plant growth an	10		Gramene Lit. 11453						
	Species Ontology	1	Zea mays (GR_tax:014450)						SM Gramene Lit. 9421			
Comments	This QTL was originally of evaluate osmotic adjustr	curated in Maizel ment capacity an	GDB Database d used for QTL	and the QTL analysis.	map position was	displaye	d on the r	naize bin	s map. O	ismotic potent	ial was m	teasured to
DBXRefs	Gramene Literatur	Quarrie-SA St physiological t	teed-A Lebreto traito, Fiziol Ra	n-C Gulli-M Ca est. 41, 1994,	elestani C Marmiro pp. 565-571	II-N, QT	(, analysis	of ABA (roductio	n in wheat and	(maize a	nd associated
Derritorio	MaizeGDB 102644											

Maize Maize Bins QTL 2005 Rice Gramene Annotated Nipponbare Sequence 2006 iHX iМ More maize drought esistance QTL fallen in the same region

CSU690 3

BM2 Neighbors 2004 CSU690

Using CMap to compare QTL with other map/map sets

510.93 cN

107.3 cM

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Tip 5

Gene Dete

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

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elect the dataset for this qu	ery		Tutorial
Rice Gene Models (TIGR	√4)	~	Summary
37537699	37543973	LOC_0s01s64070/GO.0	005278 RNA-dependent DNA replication
37637699	37543973	LOC 0x01x64070/GO/0	003677 DNA binding
37637699	37543973	LOC_0s01g64070/GO:0	006310 DNA recombination
37537699	37543973	LOC_0s0164070/GO/0	000785 chromatin
37637699	37543973	LOC_0401464070/GO:0	003682 chromatin binding
37637699	37543973	LOC_0s01g64070/GO/0	005634 nucleus
37537699	37543973	LOC_0s01g64070/GO.0	006333 chromatin assembly or disassembly
37637699	37543973	LOC_0x01y64070 GO 0	004190 aspartic-type endopeptidase activity
37537699	37543973	LOC_0:01g64070/GO:0	006508 proteolysis
37549567	37555857	LOC_0:01:64080/GO:0	003723 RNA binding
37649667	37555857	LOC_0x01y64080/GO/0	003964 RNA directed DNA polymerase activity
37549567	37555857	LOC_0:01g64080/GO:0	006278 RNA dependent DNA replication
37549567	37555857	LOC_0:01g64080/GO:0	003676 nucleic acid binding
37549567	37555857	LOC_0s01g64080/GO/0	004523 nibonuclease H activity
37649567	37555857	LOC_0401464080/GO:0	005351 sugar porter activity
37549567	37555857	LOC_0:01g64080 GO:0	009401 phosphoenolpyruvate-dependent sugar phi
37558355	37561500	LOC_0s01g64090/GO/0	003735 structural constituent of ribosome
37558355	37561500	LOC_0+01g64090/GO-0	005622 intracellular
37558356	37561500	LOC_0s01g64090/GO/0	005840 nbosome
37668366	37561500	LOC_0:01:64090/GO.0	006412 protein biosynthesis
37668366	37561500	LOC_0:01:64090 GO 0	003735 structural constituent of ribosome
37558356	37561500	LOC_0:01g64090/GO:0	005622 intracellular
37658356	37561500	LOC_0:01g64090/GO.0	005840 nbosome
37668366	37561500	LOC_0x01x64090/GO/0	005412 protein biosynthesis
37562630	37564055	LOC_0:01g64100/GO:0	004553 hydrolase activity, hydrolyzing O-glycosyl
37662630	37564055	LOC_0s01g64100/GO:0	005975 carbohydrate metabolism
37566432	37567624	LOC_0s01g64110/GO.0	004553 hydrolase activity, hydrolyzing O-glycosyl
37566432	37567624	LOC_0:01g64110/GO:0	005975 carbohydrate metabolism
37568006	37568936	LOC_0s01g64120GO/0	005489 electron transporter activity
37568006	37568936	LOC_0s01g64120/GO/0	005506 iron ion binding
37568006	37568936	LOC 0x01x64120/GO/0	006118 electron transport



Candidate gene detail view

36,000,001-38,400,001 b

art under and

for LOC_0a01pl229

on the rice genome

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