GRAMENE — Triticeae Resources at Gramene

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Database Data Contributors:
GrainGenes
NCBI
GenBank
BarleyBase/PlexDB
Published papers
Ensembl genomes
NASC Arabidopsis
TIGR Rice Genome annotation
TIGR GeneIndex
OMAP FPC
Uniprot/SPTrembl
MaizeGDB
Rice BAC Physical map
Sorghum Genetic and Physical maps
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SAGE
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GRIN
Panzea
Gene Ontology Consortium
Plant Ontology Consortium

Genomes – Ensemble
Maps – CMap
Markers
QTL
Diversity
Genes
Proteins
Pathways
Ontologies
Literature
Sequences – BLAST
All – GrameneMart

Search using Dropdown menu

Maps	*Triticum aestivum*	14
	Triticum turgidum	2
Markers	*Triticum aestivum*	1309013
	Triticum monococcum	10693
	Triticum turgidum subsp. durum	8988
	Triticum turgidum	1720
	Triticum turgidum subsp. dicoccoides	173
	Triticum urartu	126
	Triticum aestivum/Thinopyrum intermedium alien add	36
	Triticum baeoticum	18
	Triticum sp.	6
	Triticum aestivum x Triticum timopheevi	2
	Triticum timopheevii	1
QTL	*Triticum aestivum*	22
	Triticum turgidum	8
Diversity	3802 Wheat Markers and 48 Germplasms	
Genes	0	
Proteins	*Triticum* 3358	
Pathways	N/A	
Ontologies	*Triticum* 3370 object associations	
Literature (curated publications)	"triticum" 202 "Wheat" 961	

	Hordeum vulgare	13
	Hordeum vulgare subsp. spontaneum	334555
	Hordeum vulgare	304705
	Hordeum vulgare subsp. vulgare	42638
	Hordeum brevisubulatum	39
	Hordeum chilense	39
	Hordeum murinum subsp. leporinum	10
	Hordeum muticum	7
	Hordeum patagonicum	6
	Hordeum lechleri	5
	Hordeum stenostachys	3
	Hordeum jubatum	3
	Hordeum brachyantherum subsp. californicum	3
	Hordeum depressum	3
	Hordeum pusillum	3
	Hordeum erectifolium	3
	Hordeum roshevitzii	3
	Hordeum euclaston	3
	Hordeum bulbosum	2
	Hordeum vulgare	299
	N/A	
	0	
	Hordeum	2346
	N/A	
	Hordeum	2659 object associations
ons)	"hordeum" 228	"Barley" 718

Species Pages for eleven (11) Poaceae species: Get a summary of species data in Gramene; review general information, production and nutritional statistics, Link to research and news resources. Includes Triticum, Hordeum and Secale.

Triticum Introduction

Triticum Species Page: Introduction | Facts | Anatomy | Taxonomy | Agronomic Statistics | Research | Education | Nutrition | Recipes | News | Germplasm Resources | Gramene Statistics | Gramene Queries

Leaf 1 emerges at soil level. Photo courtesy of: Wheat:The Big Picture
Young wheat. Photo courtesy USDA Photo by: Jeff Vanuga
Wheat starting to turn Photo courtesy USDA Photo by: Jeff Vanuga
Close up ripe wheat in Minnesota Image courtesy USDA, Photo by unknown
Harvested wheat Image courtesy USDA Photo by: Gene Alexander
Global Wheat Production Map

Grown all over the world, wheat covers more of the earth's surface than any other cereal crop (1, 7, 16). However, although it takes more land space than other cereals, based on a three year average it is only the third-largest cereal crop, behind maize and rice (16). The domestication of grains and the development of agricultural lifestyles led to significant changes in people's lives, encouraging permanent settlements, the development of civilization, and trade (7, 8). Wheat's domestication produced larger grains and a more productive crop, which could not have survived in the wild and required continued intervention of farmers

DIVERSITY - With data from Haplotype Polymorphism in Polyploid Wheats and their Diploid Ancestors, this is a repository for allelic variation data of SSR, SNP and RFLP loci in rice, maize, and wheat germplasm accessions. The module also contains passport descriptions. Data can be searched using germplasm accession identifiers or marker names. Useful for germplasm management, marker assisted selection and DNA-based variety identification. The Diversity module links to advanced software search tools for filtering the data, including GDPC.

Germplasm Accessions for Wheat

- G1812
- ICTW600161
- As01
- As02
- AL8/78
- AS75
- Langdon Clone 1
- Langdon Clone 2
- Langdon Clone 3
- Langdon Clone 4
- Langdon Clone 5
- Langdon Clone 6
- Langdon Clone 7
- Langdon Clone 8
- Langdon Clone 9
- Langdon Clone 10
- PI 428020
- PI 428027
- PI 428053
- PI 428073
- PI 428064
- PI 428082
- PI 428083
- PI 428086
- G 2944
- G 2040
- PI 166698
- PI 166305
- PI 166792
- PI 350731
- PI 410595
- IWA 10993
- Yangxian Yangqianmai
- Yecora Rojo
- PI 119325
- IWA 10940
- Chinese Spring
- 405a
- Opata85
- W7984
- RL5402
- RL5403
- RL5405
- RL5406
- CIMMYT 62052_4
- CIMMYT 62056_4
- CIMMYT 161725_0
- Sn32

Accession name	Yangxian Yangqianmai	**Collector**	33
Institute(s) holding accession		**Collection number**	
Accession number	"Shaanxi, China"	**Collection source**	
Synonym(s)	Shaanxi (5660) #26	**Collection code**	
Stock source	Shaanxi (5660) #26	**Collection/release date**	
Stock number	1	**Locality**	
Germplasm type	N/A	**City**	
Genus	Triticum	**Elevation**	
Species	aestivum	**Latitude**	NA
Subspecies		**Longitude**	NA
Subtaxa		**State/province**	Shaanxi
Taxonomy xref		**Country**	China

Experiments

There is allele data for germplasm ""Shaanxi, China"" from 1 experiment.

Title	Design	Polymorphism Type	Allele Scoring Protocol	PI(s)	Comments	Data
Haplotype polymorphism in polyploid wheats and their diploid ancestors	"Select approximately 6,000 wheat EST unigenes; Design conserved PCR primers for STS development; Use STS polymorphism to develop genome specific primers; Amplify STSs from wheat A, B and D genomes; And discovery SNPs based on aligned sequences"	SNP Sequencing	SNP detection by sequence alignments, Sequencing of direct PCR	Jan Dvorak (PI)	See http://wheat.pw.usda.gov/SNP/	Show Allele Data

Germplasm Accession Name	Subsp. & subtaxa	Country of Origin	Accession Number	Stock Number	Locus name	Genotype
IWA 10993		Iran	Iran	1	CF133109_139-3A	C
PI 350731	compactum	Austria	Austria	1	CF133109_139-3A	C
PI 166792		Turkey	Turkey	1	CF133109_139-3A	C
PI 410595	compactum	Pakistan	Pakistan	1	CF133109_139-3A	G
RL5402		Unknown	Eric Kerber	1	CF133109_139-3A	G
PI 166305	compactum	Turkey	Turkey	1	CF133109_139-3A	C
Opata85		Unknown	USA	1	CF133109_139-3A	C
PI 119325		Turkey	Turkey	1	CF133109_139-3A	C
405a	spelta	Iran	Iran	1	CF133109_139-3A	C
RL5405		Unknown	Eric Kerber	1	CF133109_139-3A	G
RL5403		Unknown	Eric Kerber	1	CF133109_139-3A	G
PI 166698		Turkey	Turkey	1	CF133109_139-3A	C
RL5406		Unknown	Eric Kerber	1	CF133109_139-3A	G
Yecora Rojo		Mexico	CIMMYT	1	CF133109_139-3A	G
Sn32		Unknown	E.R. Sears	1	CF133109_139-3A	C
PI 119325		Turkey	Turkey	1	CF133109_139-3A	C
Chinese Spring		China	China	1	CF133109_139-3A	C
W7984		Mexico	CIMMYT	1	CF133109_139-3A	G

MARKERS: This is a key database at Gramene. The Markers Module contains all map sets, maps, and mappings, and should be considered to be the primary source for information about maps and markers of various types. The exact information displayed depends on the marker type, but all markers will display the marker name, synonyms, source species, and a listing of map positions. Markers also links to several SSR Marker resources, including The Simple Sequence Repeat Identification Tool, the Panel of 50 standard SSR markers used by the Generation Challenge Program for rice diversity analysis, the Table of SSR Primers from McCouch et al. (2002), and several other documents and resources.

View Wheat EST "BF485510"

Details | Source/Library | Sequence | Map Positions (4) | Associations

Name	Wheat pre-anthesis spike cDNA library
Center Name:	
Center Project:	
Development Stage:	Adult plant
Tissue Type:	Spike before anthesis
Cell Type:	
Cell Line:	
Sex:	
Comments:	
Plant Ontology:	
Growth Ontology:	
Environment Ontology:	

Details | Source/Library | Sequence | Map Positions (4) | Associations (1) | Images (0)

ID	1406598
Name	GENBANK_ACCESSION BF485510
Synonyms (2)	GENBANK_GI 11568811 GENBANK_VERSION BF485510.1
Type	EST
Species	Triticum aestivum (Wheat)
Germplasm	Chinese Spring
Description	WHE2312_H02_P04ZS Wheat pre-anthesis spike cDNA clone WHE2312_H02_P04, mRNA sequence.
Clone	WHE2312_H02_P04
Comment	Contact: Olin Anderson US Department of Agriculture, A Service, Pacific West Area, Western Regional Research Street, Albany, CA 94710, USA Tel: 5105595773 Fax: 5 oandersn@pw.usda.gov Sequence have been trimmed t and low quality sequence with phred score less than 20 Stratagene SK primer.
Date Created	2000-12-06
Date Updated	2000-12-06
Lab Host	E. coli SOLR
Map	
Note	Vector: Lambda Uni-ZAP XR, excised phe were grown in the greenhouse. Whole spik yellow anther were collected and total RNA cDNA library was made, and the cDNA clo pBluescript phagemids in the TJ Close lab (Close, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors).
Origin	
Ref Authors	Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. a
Ref Location	Unpublished (2000)
Ref Medline	
Ref Pubmed	
Ref Title	The structure and function of the expressed portion of the w anthesis spike cDNA library
Ref Year	2000

Details | Source/Library | Sequence | Map Positions (4) | Associations (1) | Images (0)

Direction	Name	Type	Species	Analysis	Assoc. Type
To	BF485510	EST Cluster	Triticum aestivum	gss_poaceae	shared_synonym

Details | Source/Library | Sequence | Map Positions (4) | Associations (1) | Images (0)

```
ATTGTCACCGGCCTGCAGGGCCAGCCACCAGCAGACCACCCTCACGGTTA
CCCATTCCTCGCTTCGGTTAGGGACAATGTGCTTGCTTGTGCCAAGCATT
TCGTAGGGGATGGTGGCACTGACAAGGGTATCAACGAGGGGAATGCGGGG
GGGTGACCANAANATTTGGAGAGGATCCACACGAAACCATACCCGGGGGG
GTATAGCTCAAGGGGTGGCGACAGTCATGGCATCCTACTCTCAATGGAAT
GGGGAGCCGTTACATGCCAGCCGTCATTTGCTCACAGATGTTCTAAAGGG
CAAGTTACGCTTCCAGGGGTTTGTGGTGTCAGACTGGGAGGGTATTGACA
```

Details | Source/Library | Sequence | Map Positions (4) | Associations (1) | Images (0)

View Wheat EST "BF485510"

Species	Map Type	Map Set	Name	Map	Start	Stop	Map Links	Comments
Oryza sativa (Rice)	Sequence	Gramene Annotated Nipponbare Sequence 2006	BF485510	Chr. 5	21,986,093 bp	21,986,145 bp	View in Genome Browser	
			15% EST sequence aligns (53/362bp)					
			BF485510	Chr. 5	21,986,243 bp	21,986,307 bp	View in Genome Browser	
			18% EST sequence aligns (65/362bp)					
			BF485510	Chr. 5	21,986,367 bp	21,986,479 bp	View in Genome Browser	
			31% EST sequence aligns (113/362bp)					
			BF485510	Chr. 5	21,986,621 bp	21,986,670 bp	View in Genome Browser	
			14% EST sequence aligns (50/362bp)					

Currently in Database

Type	Count		Type	Count	
Clone	2,561,808	Search	AFLP	8,150	Search
EST	4,459,675	Search	Breakpoint interval	303	Search
EST Cluster	1,325,127	Search	Centromere	49	Search
Gene Primer	19	Search	deletion	895	Search
GSS	4,750,481	Search	FPC	22,651	Search
mRNA	142,037	Search	Gene	9,764	Search
other_dna	30,601	Search	Gene Model	95,297	Search
OVERGO	16,964	Search	insertion	686	Search
Primer	5,398	Search	Maize Bin	100	Search
STS	2,234	Search	QTL	11,210	Search
			RAPD	174	Search
			RFLP	17,739	Search
			SSR	14,762	Search
			SSR Primer Pair	16,883	Search
			Undefined	68,879	Search

13,561,886 total

Map Sets 1 to 14 of 14

Map Type	Species	Map Set Name	CMap Accession	Num. of Maps	
Deletion	Triticum aestivum	wEST 2003	west	21	View
Genetic	Triticum aestivum	Composite 2004	apr2004a	29	View
Genetic	Triticum aestivum	Consensus SSR 2004	sod2004a	21	View
Genetic	Triticum aestivum	Cornell Synthetic/Opata 1995	cu-sxo-1995	21	View
Genetic	Triticum aestivum	Wheat genes - 1993	hag1993a	21	View
QTL	Triticum aestivum	AAFCCRC Wuhan1/ Marin QTL 2003	sod2003a	4	View
QTL	Triticum aestivum	Cheyenne/Wichita RI RFLP QTL 1999	shm1999a	1	View
QTL	Triticum aestivum	Geneva/Augusta RI RFLP QTL 2000	kha2000a	1	View
QTL	Triticum aestivum	Synthetic/Opata RI RFLP/SSR QTL 1995	nej1995a	21	View
QTL	Triticum aestivum	UMN ND2603/Butte QTL 2003	lis2003b	1	View
QTL	Triticum aestivum	UMN Sumai/Stoa QTL 1999	wab1999a	2	View
QTL	Triticum aestivum	UMN Sumai/Stoa QTL 2003	lis2003a	1	View
QTL	Triticum aestivum	Wheat composite QTL 2004	apr2004b	29	View
QTL	Triticum aestivum	WL711/HD29 KBunt SSR QTL 2003	sus2003a	1	View

PROTEINS: Find a protein and its sequence; Determine its cellular location and function (each associated reference is supported with an evidence code, suggesting the type of experiment/assertions used in inferring the association). Explore protein families.

General Information | Associations | Similarity to Other Proteins | Features | FASTA Sequence

General Information about P58272

Accession	P58272	
Name	Translation initiation factor IF-1, chloroplast	
Symbol	infA	
Synonym(s)	Not available	
E.C. Number(s)	Not available	
Gene Name(s)	*INFA*	
Organelle	Chloroplast	
Best hits to TIGR rice gene models	Click here to generate a BLASTP query	
Accession Numbers	**GenBank**	**SWISSPROT**
	BAB47068.1	P58272
Database references	**GrainGenes** AB042240	
Organism(s)	**Species**	**Cultivar**
	Triticum aestivum	Chinese Spring (GRIN)
Keywords	Chloroplast, Initiation factor, Protein biosynthesis	

Similarity to Other Proteins

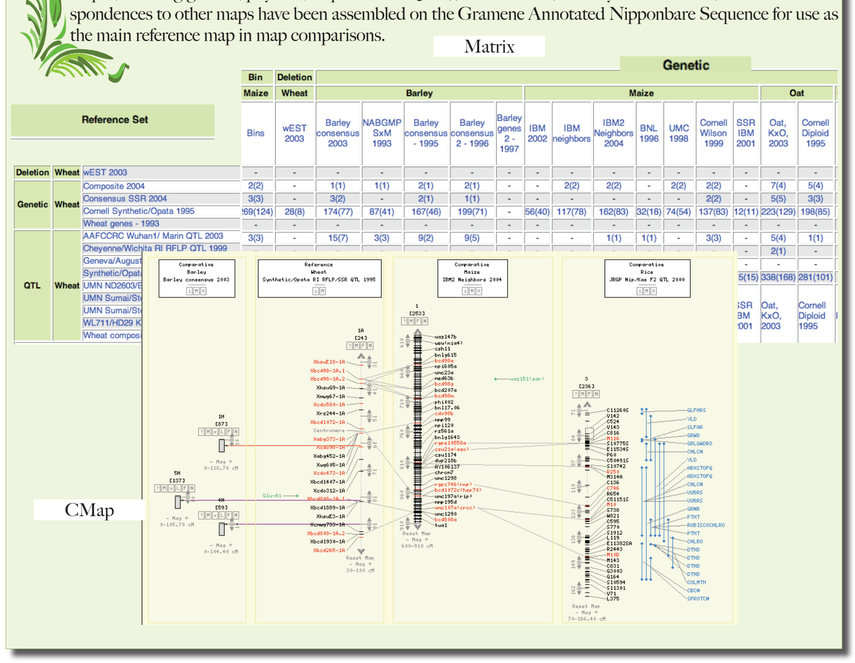
Viridiplantae Green plants
-Embryophyles (plants)
-Magnoliophytes (flowering plants)
-Monocots | Grasses | Rice | Maize | Sorghum | Wheat | Barley | Rye | Oat | Sugarcane
-Dicots | Brassicaceae | Arabidopsis | Fabaceae (Legumes) | Solanaceae | Cucurbitaceae
Others : Fungi | Metazoa
3D protein structures : Sequence Annotated by Structure (SAS)

Protein Features

Pfam (Infor)	PF01176; eIF-1a	All Members of this Family
Prosite (Infor)	PS50832; S1_IF1_TYPE	Sequence info. not available All Members of this Family
Physio-chemical features	P58272	
ProtoMap (Info)	IF1C_WHEAT	

MAPS/CMAP: All visualizations in the CMap views (map sets, maps, features, and correspondences) are generated from the Markers Module. To view correlations and genetic colinearity between and within species you may search, view, and compare mapped genes, markers, QTL and clones using various types of maps (including genetic, physical, sequence and QTL); All features (and only those features) that have correspondences to other maps have been assembled on the Gramene Annotated Nipponbare Sequence for use as the main reference map in map comparisons.

Matrix



CMap

Search by Trait Category:
Abiotic stress | Anatomy | Biochemical | Biotic stress | Development | Quality | Sterility or fertility | Vigor | Yield

GR_tax:014341) Assoc

QTL: Use this module to find qualitative trait locus (QTL) associated with traits from major cereal crops. QTL for rice, sorghum, pearl millet, foxtail millet and wild rice have been curated in-house from research publications. Other QTL (roughly 1/6 of the QTL) have been imported from MaizeGDB and GrainGenes.

Details for QTL "AQGU008" (ear

QTL Accession ID	AQGU008
Species	Triticum aestivum (Wheat)
Trait Symbol	EARNB
Trait Name	ear number
Published Symbol	QSpsm.sha-3A
Trait Synonym(s)	ENO ear number per plant ears per plant
Trait Category	Yield
Chromosome	3A

Species	Map Type	Map Set	Name	Map	Start	Stop	Map Links	Method
Triticum aestivum (Wheat)	QTL	Cheyenne/Wichita RI RFLP QTL 1999	EARNB	3A	85.1	91.1	View in Mappings DB View Comparative Map	Experimental

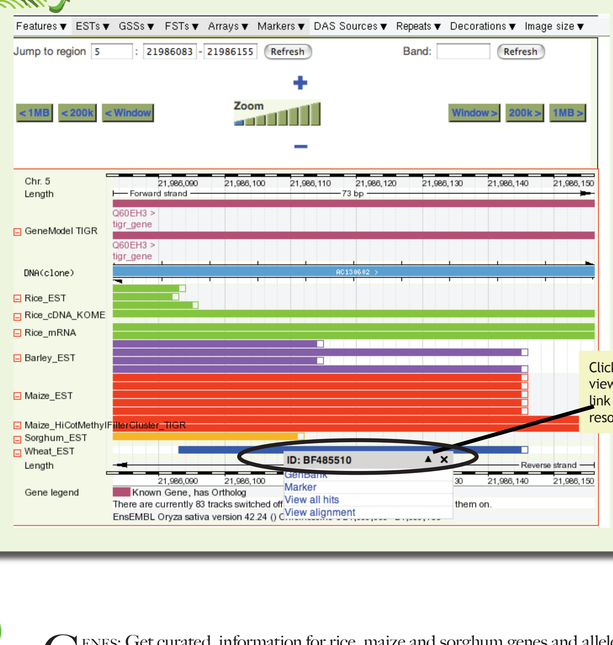
Related Ontologies: Term Type	Term	Evidence	Reference
Trait Ontology	ear number (TO:0000443)	IAGP	Gramene Lit. 11301
Plant Structure	inflorescence (PO:0009049)	IC	Gramene Lit. 11453
Plant Growth and Development Stage	inflorescence emergence from flag leaf sheath (PO:0007041)	IC	Gramene Lit. 11453
Species Ontology	Triticum aestivum (GR_tax:014341)	SM	Gramene Lit. 11301

Comments	This QTL was originally curated in GrainGenes Database.
DBXRefs	**Gramene Literature** Shah-M-M Gill-K-S Baenziger-P-S Yen-Y Kaeppler-S-M Ariyarathne-H-M, *Molecular mapping of loci for agronomic traits on chromosome 3A of bread wheat.*, Crop Science, 39, 1999, pp. 1728-1732 **GrainGenes** QSpsm.sha-3A

Object Accession ID	Object Symbol	Object Name
AQFO006	DONCONC	deoxynivalenol concentration
AQFO002	DONCONC	deoxynivalenol concentration
AQHB001	DSRS	disease resistance
AQGU008	EARNB	ear number
AQHA001	FGDSRS	fungal disease resistance
AQHC001	FGDSRS	fungal disease resistance
AQGU001	GRNB	grain number
AQGU006	GRNB	grain number
AQGU004	GRNB	grain number
AQGU007	PTHT	plant height
AQGU002	PTHT	plant height
AQGU005	SDWT	seed weight
AQGU003	SDWT	seed weight
AQFO005	Ta_FUSHEADBTRS	wheat fusarium head blight resistance
AQFG001	Ta_FUSHEADBTRS	wheat fusarium head blight resistance
AQFO001	Ta_FUSHEADBTRS	wheat fusarium head blight resistance
AQFI002	Ta_FUSHEADBTRS	wheat fusarium head blight resistance
AQFI001	Ta_FUSHEADBTRS	wheat fusarium head blight resistance
AQFO004	Ta_FUSHEADBTRS	wheat fusarium head blight resistance
AQFO003	Ta_FUSHEADBTRS	wheat fusarium head blight resistance
AQFG002	Ta_FUSHEADBTRS	wheat fusarium head blight resistance
AQGT001	VDSRS	viral disease resistance

Items 1 to 22 of 22

GENOMES: The Genome Browser allows users to browse assembled genomes and their associated gene models. Feature mappings are taken from the Marker and Protein DBs. Further cross-genome analyses provide data on syntenic blocks and gene paralogs/orthologs. The list of genomes is growing, and includes the Rice-Japonica (*Oryza sativa*), *Oryza rufipogon*, Maize (*Zea mays*) and Arabidopsis (*Arabidopsis thaliana*) genomes and organelles.



LITERATURE: Articles associated with data, as well as several other of interest, are in the literature module. Find articles about genes, proteins, QTL, markers, or ontologies and link to that information in the database. Gramene can't provide the full article, but when available there is a link to the online-resource, which may be available to you depending upon the permissions of your institution.

Search result	
Reference ID	11301
Title	Molecular mapping of loci for agronomic traits on chromosome 3A of bread wheat.
Source	Crop Science , 1999, 39, pp.1728-1732
Authors	Shah-M-M, Gill-K-S, Baenziger-P-S, Yen-Y, Kaeppler-S-M, Ariyarathne-H-M
Abstract	Not available.
Cross-reference	Not available
Associated Data	QTLs (8) CMap Map Set (1)

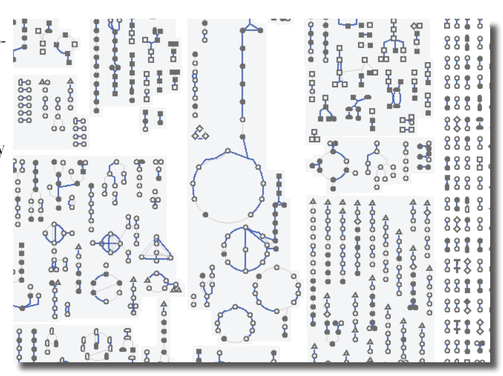
GENES: Get curated information for rice, maize and sorghum genes and alleles associated with important phenotypes and functions. Rice genes have been curated in-house from publications, and maize genes have been imported from MaizeGDB. For other species you may search genes in the Markers Database.

Summary for Gene: *d1* (GR:0060184)

General Info | Allele and Germplasm | Sequence Association | Map Position | Ontology Association | References

General Information	
Accession	GR:0060184
Gene Symbol	*d1*
Gene Name	*dwarf-1*
Gene Synonym(s)	dw1, daikoku dwarf, G-protein alpha subunit, GA1, GP-alpha-1, Guanine nucleotide-binding protein alpha-1 subunit, RGA1
Species	*Rice*
Chromosome No.	5
Gene Type	CDS (Protein coding)
Has Phenotype	yes
Description	A typical small grain dwarf type with short and stout stems, short, sinuate but broad leaves with dark green color, erect and compact panicles and small, round floral glumes. Internodes are thick and sometimes the second internode does not elongate.
Phenotypic Image	1. 1. Dwarf type of an isogenic line (d1) in the 'Shiokari' background. 2. 2. A panicle with small. round grains due to the pleiotropy of d1. 3.

PATHWAYS - The RiceCyc database integrates the latest genomic data with functional descriptions of metabolic pathways. This allows the user to visualise predicted rice metabolic pathways and aids them in the analyses of gene and protein expression. Through the use of the RiceCyc Omics viewer the user is able to paint their own microarray and proteomics research data onto the metabolic network of the organism; this allows for visualisation of metabolic pathway across multiple datasets. The RiceCyc database is manually curated and incorporates new rice information as it comes to fruition. Researchers will be able to search for closely related rice orthologues of their gene and species of interest.



BLAST: Search for DNA and peptide sequence similarities with rice and several other major cereal crops. Refine your results, or view HSP in the genome browser.