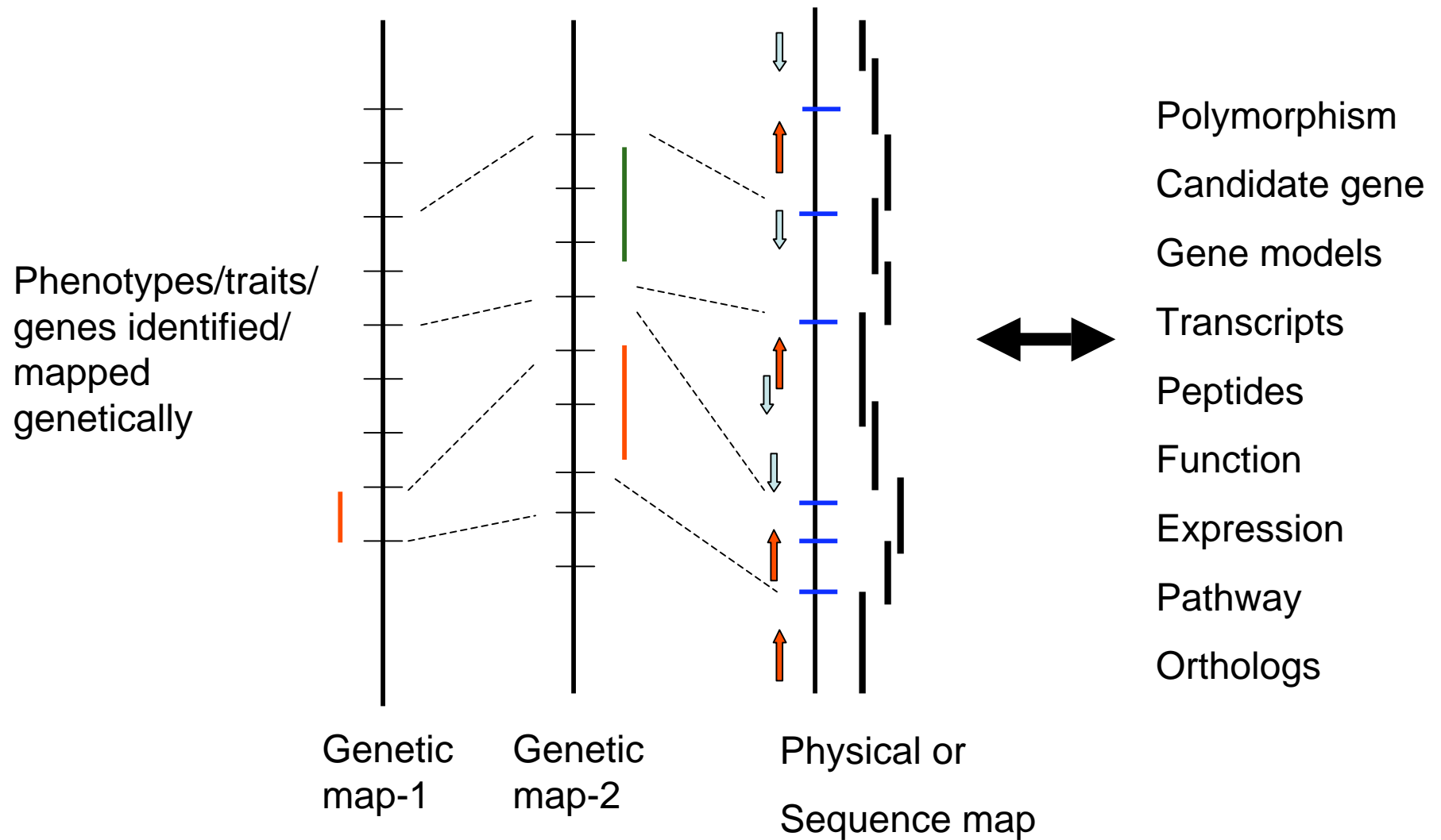


Comparative Genomics

Pankaj Jaiswal
pj37@cornell.edu

Comparative genomics





Example case

Semidwarf-1 gene

Summary for Gene: *sd1* (GR:0060842)

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


General Information	
Accession	GR:0060842
Gene Symbol	<i>sd1</i>
Gene Name	<i>semidwarf-1</i>
Gene Synonym(s)	dee-geo-woo-gen dwarf, d49, d47, green revolution gene
Species	<i>Rice</i>
Chromosome No.	1
Gene Type	CDS (Protein coding)
Has Phenotype	yes
Description	Semidwarf, resistant to lodging especially at high fertilizer level, high yielding. Elongation of lower internodes less than that of upper internodes from inhibition of cell division during elongation. Defective in biosynthetic enzyme GA20ox-2 that catalyzed the conversion of GA53 to GA20.
Phenotypic Image	<div> <p>1.</p>  <p>1. Semidwarfness of an isogenic line (<i>sd1</i>) in the 'Shiokari' background. Dwarfness is intensified in this 'early' background compared to DGWG. The mutant image was kindly provided by Dr. Kinoshita.</p> </div> <div> <p>2.</p>  <p>2. Stature of normal-type and semidwarf rice plants at ripening. Right: normal-type (Sasanishiki, a japonica cultivar). Left: semidwarf-type (isogenic line of Sasanishiki with a chromosomal segment containing <i>sd-1</i> introduced from the semidwarf-type indica cultivar Habataki). Image from Monna-2002 (DNA Research 11-17).</p> </div>
Allele	<i>sd1.1</i> , <i>sd1.2</i> , <i>sd1.3</i> (d49), <i>sd1.4</i> (SC-SRN(N)), <i>sd1.5</i> (SC-AJNT(N)), <i>sd1.6</i> (SC-CPSLO(N)), <i>sd1.7</i> (<i>sd1-a</i>), <i>sd1.8</i> (<i>sd1-h</i>)
Germplasm	T65d, Doongara, Remei, Calrose 76 (D51), CP-SLO, Deo-geo-woo-gen, Ai-Jio-Nan-Te, HS90, Jikkoku, Shiranui-1, IR8, TN1 (Taichung Native 1)

Example continued

Sequence Association	
Protein	Gramene Protein: Q8RVF5 , Q8S492
Nucleotide (DNA)	GenBank Nucleotide: AB077025 , AF465255 , AF465256 , AY114310 , U50333 Rice Ensembl Gene: LOC_Os01g66100

Map Position [View in Marker DB]				
#	Map Set Name	Linkage Group	Start Position	Stop Position
1	Cornell RFLP 2001	1	103.50 cM	104.10 cM
2	Hokkaido Morphological 2000	1	73.00 cM	73.00 cM
3	JRGP RFLP 2000	1	149.10 cM	151.00 cM
4	Gramene Annotated Nipponbare Sequence 2006	Chr. 1	38709242.00 bp	38712353.00 bp

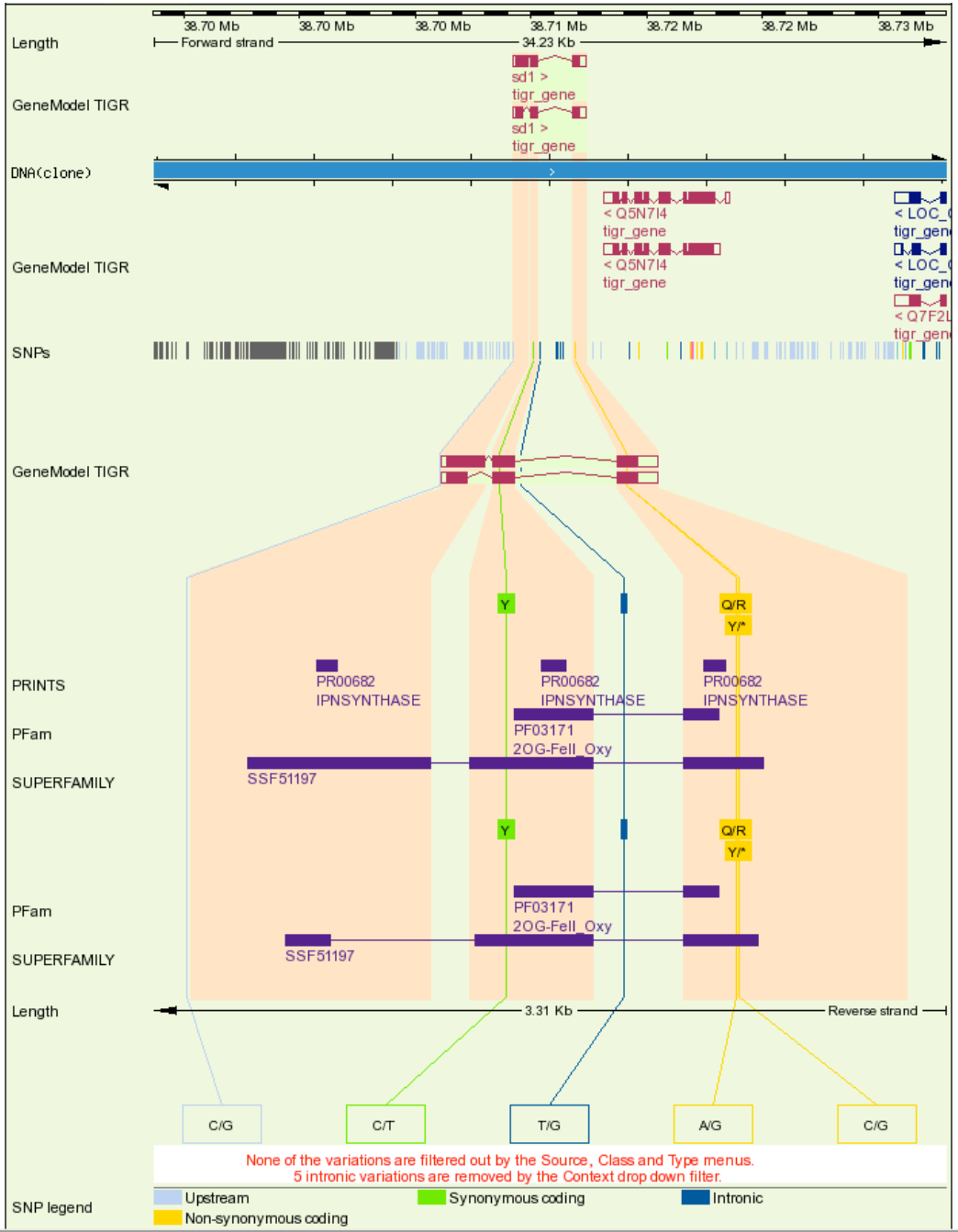
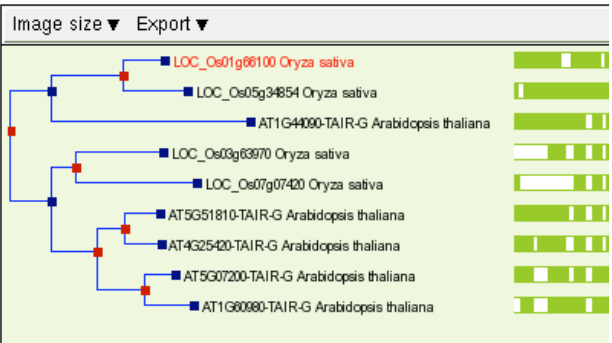
Ontology Association	
Trait	enzyme activity (TO:0000599), growth and development trait (TO:0000357), plant growth hormone sensitivity (TO:0000401), stem length (TO:0000576)
Plant Structure	stem (PO:0009047)
Plant Growth and Development Stage	A vegetative growth (PO:0007134), FR.04 fruit ripening complete (PO:0007038), inflorescence emergence from flag leaf sheath (PO:0007041), leaf production (PO:0007133), stem elongation (PO:0007089), whole plant growth stages (PO:0007033)
Cereal Plant Growth Stage	02-seedling (GRO:0007047), 04-stem elongation stage (GRO:0007048), 06-heading stage (GRO:0007044), 09-mature grain stage (GRO:0007045), A-vegetative stage (GRO:0007139), rice growth stage (GRO:0007040)
Molecular Function	gibberellin 20-oxidase activity (GO:0045544)
Biological Process	gibberellic acid biosynthesis (GO:0009686), gibberellic acid metabolism (GO:0009685), response to abiotic stimulus (GO:0009628), unidimensional cell growth (GO:0009826)
Environment	laboratory study (EO:0007255)

Reference	
DBxref	E.C. Number(s): 1.14.11.- , 1.14.11.15 Oryzabase: 470
 1. Aquino-R-C, Jennings-P-R. Inheritance and significance of dwarfism in an Indica rice variety. Crop Science.1966;6(6):551-554.	

Transcript LOC_Os01g66100.1

Transcript	sd1 () To view all Ensembl genes linked to the name click here
Transcript information	Exons: 3 Transcript length: 1,539 bps Protein length: 511 aa [Further Transcript info] [Exon information] [Protein information]
Similarity Matches	This GeneModel TIGR entry corresponds to the Gramene_GenesDB: sd1 SPTREMBL: Q2Z277 [Target %id: 100%] Q2Z278 [Target %id: 100%] Q2Z279 [Target %id: 100%] Q2Z293 [Target %id: 100%] Q2Z294 [Target %id: 100%] Q6YLY2 [Target %id: 100%] Q8RVF5 [Target %id: 100%] RefSeq peptide predicted: XP_463540.1 [Target %id: 100%] RefSeq DNA predicted: XM_463540.1 [Target %id: 100%] EntrezGene: 3049902 TIGR_LOCUS: LOC_Os01g66100.1 Gramene_Pathway: 1.21.3.1-RXN TIGR_FN: 11971.m12718 Gramene_Pathway: GIBBERELLIN-3-BE RXN1F-101 RXN1F-162 RXN1F-163 RXN1F-164 RXN1F-167 RXN1F-168 RXN1F-169

Gene Tree for gene LOC_Os01g66100




Example continued

Sequence Association	
Protein	Gramene Protein: Q8RVF5 , Q8S492
Nucleotide (DNA)	GenBank Nucleotide: AB077025 , AF465255 , AF465256 , AY114310 , U50333 Rice Ensembl Gene: LOC_Os01g66100

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#	Map Set Name	Linkage Group	Start Position	Stop Position
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4	Gramene Annotated Nipponbare Sequence 2006	Chr. 1	38709242.00 bp	38712353.00 bp

Ontology Association	
Trait	enzyme activity (TO:0000599), growth and development trait (TO:0000357), plant growth hormone sensitivity (TO:0000401), stem length (TO:0000576)
Plant Structure	stem (PO:0009047)
Plant Growth and Development Stage	A vegetative growth (PO:0007134), FR.04 fruit ripening complete (PO:0007038), inflorescence emergence from flag leaf sheath (PO:0007041), leaf production (PO:0007133), stem elongation (PO:0007089), whole plant growth stages (PO:0007033)
Cereal Plant Growth Stage	02-seedling (GRO:0007047), 04-stem elongation stage (GRO:0007048), 06-heading stage (GRO:0007044), 09-mature grain stage (GRO:0007045), A-vegetative stage (GRO:0007139), rice growth stage (GRO:0007040)
Molecular Function	gibberellin 20-oxidase activity (GO:0045544)
Biological Process	gibberellic acid biosynthesis (GO:0009686), gibberellic acid metabolism (GO:0009685), response to abiotic stimulus (GO:0009628), unidimensional cell growth (GO:0009826)
Environment	laboratory study (EO:0007255)

Reference	
DBxref	E.C. Number(s): 1.14.11.- , 1.14.11.15 Oryzabase: 470
 1. Aquino-R-C, Jennings-P-R. Inheritance and significance of dwarfism in an Indica rice variety. Crop Science.1966;6(6):551-554.	

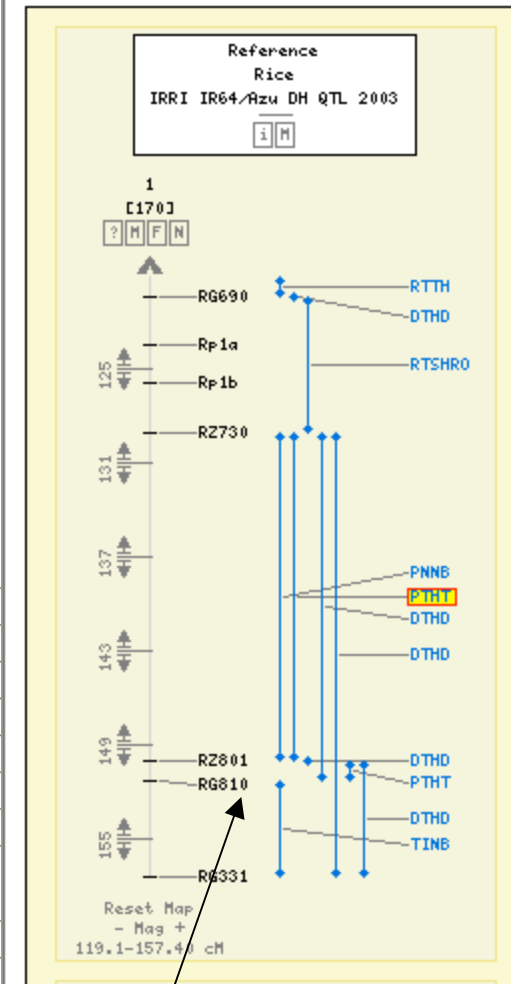
View Rice Gene "GR:0060842"

Details	Source/Library	Map Positions (3)	Associations (4)	Images (0)	
Direction	Name	Type	Species	Analysis	Assoc. Type
From	LOC_Os01g66100	Gene Model	Oryza sativa	gene_model	gene_model
From	CQAI1	QTL	Oryza sativa	curated_gene_to_qtl	IAGP
From	CQAI3	QTL	Oryza sativa	curated_gene_to_qtl	IAGP
From	CQAI6	QTL	Oryza sativa	curated_gene_to_qtl	IAGP

Details for QTL "CQAI1" (plant height)

QTL Accession ID	CQAI1		
Species	Oryza sativa (Rice)		
Trait Symbol	PTHT		
Trait Name	plant height		
Species Ontology	GR_tax:013681		
Trait Ontology	TO:0000207		
Published Symbol	sd1		
Trait Synonym(s)	PH height	PHT seedling height	
Trait Category	Vigor		
Chromosome	1		

Mappings	Species	Map Type	Map Set	Name	Map	Start	Stop	Map Links	Method
	Oryza sativa (Rice)	QTL	IRRI IR64/Azu DH QTL 2003	PTHT	1	129.1	150.1	View in Mappings DB View Comparative Map	Experimental
	Oryza sativa (Rice)	Sequence	Gramene Annotated Nipponbare Sequence 2006	CQAI1-PTHT	Chr. 1	40,894,491	40,895,246	View in Mappings DB View in Genome Browser View Comparative Map	Inferred
Comments	Plant height in cm was measured on 65th day after sowing. The plants were subjected to well watered condition by watering them every alternate day.								
DBXRefs	Gramene Literature	Hemamalini-G-S Shashidhar-H-E Hittalmani-S, Molecular marker assisted tagging of morphological and physiological traits under two contrasting moisture regimes at peak vegetative stage in rice (Oryza sativa L.), <i>Euphytica</i> , 112 (1), 2000, pp. 69-78							



Use of ontology

A controlled vocabulary with every child has one or more parent.

- [all \(all\)](#) #391761
 - [i] [trait ontology \(TO:0000387\)](#) #12358
 - [i] [anatomy and morphology related trait \(TO:0000017\)](#) #4642
 - [i] [shoot anatomy and morphology trait \(TO:0000077\)](#) #3757
 - [i] [plant height \(TO:0000207\)](#) #1482
 - [i] [seedling height \(TO:0000019\)](#) #0
 - [p] [stem length \(TO:0000576\)](#) #202
 - [i] [plant height uniformity \(TO:0001003\)](#) #5
 - [i] [stature or vigor trait \(TO:0000133\)](#) #1701
 - [i] [height related trait \(TO:0000171\)](#) #1482
 - [i] [plant height \(TO:0000207\)](#) #1482
 - [i] [seedling height \(TO:0000019\)](#) #0
 - [p] [stem length \(TO:0000576\)](#) #202
 - [i] [plant height uniformity \(TO:0001003\)](#) #5

Parent Terms (2)

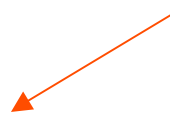
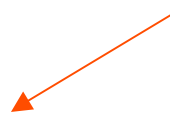
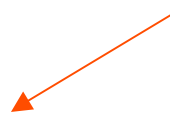
- [i] [shoot anatomy and morphology trait \(TO:0000077\)](#)
- [i] [height related trait \(TO:0000171\)](#)

Child Terms (3)

- [i] [seedling height \(TO:0000019\)](#)
- [p] [stem length \(TO:0000576\)](#)
- [i] [plant height uniformity \(TO:0001003\)](#)

Total Number of Annotations:	1465 objects, 1482 associations protein(5) gene(73) QTL(1387)
protein:	Oryza sativa (indica cultivar-group)(1) Oryza sativa (japonica cultivar-group)(4)
gene:	Oryza sativa(73)
QTL:	Avena sativa(78) Hordeum vulgare(17) Oryza sativa(1028) Pennisetum glaucum(9) Sorghum bicolor(28) Triticum aestivum(2) Zea mays(219) Zizania palustris(6)

Transcript LOC_Os01g66100.1

Transcript	sd1 () To view all Ensembl genes linked to the name click here .																				
Transcript information	Exons: 3 Transcript length: 1,539 bps Protein length: 389 residues [Further Transcript info] [Exon information] [Protein information]																				
Similarity Matches	<p>This GeneModel TIGR entry corresponds to the following database identifiers:</p> <table><tr><td>Gramene_GenesDB:</td><td>sd1</td></tr><tr><td>SPTREMBL:</td><td>Q2Z277 [Target %id: 68; Query %id: 99] [Search GO] Q2Z278 [Target %id: 68; Query %id: 99] [Search GO] Q2Z279 [Target %id: 68; Query %id: 99] [Search GO] Q2Z293 [Target %id: 68; Query %id: 99] [Search GO] Q2Z294 [Target %id: 68; Query %id: 99] [Search GO] Q6YLX2 [Target %id: 99; Query %id: 99] [Search GO] Q8RVF5 [Target %id: 100; Query %id: 100] [Search GO]</td></tr><tr><td>RefSeq peptide predicted:</td><td>XP_463540.1 [Target %id: 100; Query %id: 100]</td></tr><tr><td>RefSeq DNA predicted:</td><td>XM_463540.1 [Target %id: 76; Query %id: 100]</td></tr><tr><td>EntrezGene:</td><td>3049902</td></tr><tr><td>TIGR_LOCUS:</td><td>LOC_Os01g66100.1</td></tr><tr><td>Gramene_Pathway:</td><td>1.21.3.1-RXN</td></tr><tr><td>TIGR_FN:</td><td>11971.m12718</td></tr><tr><td>Gramene_Pathway:</td><td>GIBBERELLIN-3-BETA-DIOXYGENASE-RXN  RXN1F-101 RXN1F-162 RXN1F-163 RXN1F-164 RXN1F-167 RXN1F-168 RXN1F-169 RXN1F-99</td></tr><tr><td>TIGR_GeneIndex:</td><td>TC276131 [Target %id: 99; Query %id: 99]</td></tr></table>	Gramene_GenesDB:	sd1	SPTREMBL:	Q2Z277 [Target %id: 68; Query %id: 99] [Search GO] Q2Z278 [Target %id: 68; Query %id: 99] [Search GO] Q2Z279 [Target %id: 68; Query %id: 99] [Search GO] Q2Z293 [Target %id: 68; Query %id: 99] [Search GO] Q2Z294 [Target %id: 68; Query %id: 99] [Search GO] Q6YLX2 [Target %id: 99; Query %id: 99] [Search GO] Q8RVF5 [Target %id: 100; Query %id: 100] [Search GO]	RefSeq peptide predicted:	XP_463540.1 [Target %id: 100; Query %id: 100]	RefSeq DNA predicted:	XM_463540.1 [Target %id: 76; Query %id: 100]	EntrezGene:	3049902	TIGR_LOCUS:	LOC_Os01g66100.1	Gramene_Pathway:	1.21.3.1-RXN	TIGR_FN:	11971.m12718	Gramene_Pathway:	GIBBERELLIN-3-BETA-DIOXYGENASE-RXN  RXN1F-101 RXN1F-162 RXN1F-163 RXN1F-164 RXN1F-167 RXN1F-168 RXN1F-169 RXN1F-99	TIGR_GeneIndex:	TC276131 [Target %id: 99; Query %id: 99]
Gramene_GenesDB:	sd1																				
SPTREMBL:	Q2Z277 [Target %id: 68; Query %id: 99] [Search GO] Q2Z278 [Target %id: 68; Query %id: 99] [Search GO] Q2Z279 [Target %id: 68; Query %id: 99] [Search GO] Q2Z293 [Target %id: 68; Query %id: 99] [Search GO] Q2Z294 [Target %id: 68; Query %id: 99] [Search GO] Q6YLX2 [Target %id: 99; Query %id: 99] [Search GO] Q8RVF5 [Target %id: 100; Query %id: 100] [Search GO]																				
RefSeq peptide predicted:	XP_463540.1 [Target %id: 100; Query %id: 100]																				
RefSeq DNA predicted:	XM_463540.1 [Target %id: 76; Query %id: 100]																				
EntrezGene:	3049902																				
TIGR_LOCUS:	LOC_Os01g66100.1																				
Gramene_Pathway:	1.21.3.1-RXN																				
TIGR_FN:	11971.m12718																				
Gramene_Pathway:	GIBBERELLIN-3-BETA-DIOXYGENASE-RXN  RXN1F-101 RXN1F-162 RXN1F-163 RXN1F-164 RXN1F-167 RXN1F-168 RXN1F-169 RXN1F-99																				
TIGR_GeneIndex:	TC276131 [Target %id: 99; Query %id: 99]																				

***O. sativa japonica* Reaction: 1.14.11.15**

Cross-Species Comparison

Superclasses: [EC-Reactions](#) -> [1 -- Oxidoreductases](#) -> [1.14 -- Acting on paired donors, with incorporation or reduction of](#) -> [1.14.11 -- With 2-oxoglutarate as one donor, and incorporation of one](#)

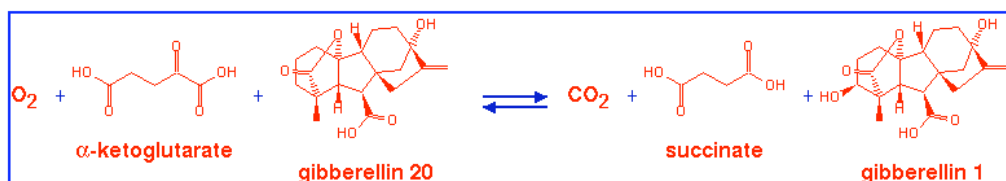
[Gibberellin 20 oxidase 1, putative, expressed : LOC_Os07q07420.1](#)

[Gibberellin 20 oxidase 2, putative, expressed : LOC_Os05q34854.1](#)

[Gibberellin 20 oxidase 2, putative, expressed : LOC_Os01q66100.1](#)

[Gibberellin 20 oxidase 1, putative, expressed : LOC_Os03q63970.1](#)

[oxidoreductase, 2OG-Fe oxygenase family protein, expressed : LOC_Os01q08220.1](#)



The reaction direction shown, that is, $A + B \rightleftharpoons C + D$ versus $C + D \rightleftharpoons A + B$, is in accordance with the Enzyme Commission system.

Cross-Species Comparison: 1.14.11.15: $O_2 + \alpha$ -ketoglutarate + gibberellin 20 = CO_2 + succinate + gibberellin 1

Note: In addition to reflecting differences in biology among different organisms, these statistics and data will also reflect differences in the level of curation and data availability and completeness among different organisms.

Organism	Enzymes and Genes	Pathways
Arabidopsis thaliana, Strain columbia COL	gibberellin 3-beta-dioxygenase : AT4G21690 gibberellin 3-beta-dioxygenase : AT1G80340 gibberellin 3-beta-dioxygenase : AT1G80330 gibberellin 3-beta-dioxygenase / gibberellin 3β-hydroxylase : AT1G15550	None
O. sativa japonica Nipponbare	Gibberellin 20 oxidase 1, putative, expressed / gibberellin 3-beta-dioxygenase activity / gibberellin 20-oxidase activity : LOC_Os07q07420.1 Gibberellin 20 oxidase 2, putative, expressed / gibberellin 3-beta-dioxygenase activity / gibberellin 20-oxidase activity : LOC_Os05q34854.1 Gibberellin 20 oxidase 2, putative, expressed / gibberellin 3-beta-dioxygenase activity / gibberellin 20-oxidase activity / response to abiotic stimulus : LOC_Os01q66100.1 Gibberellin 20 oxidase 1, putative, expressed / gibberellin 20-oxidase activity : LOC_Os03q63970.1 oxidoreductase, 2OG-Fe oxygenase family protein, expressed / gibberellin 3-beta-dioxygenase : LOC_Os01q08220.1	None

Where do we find all these information

Several Model organism genomics databases

Gramene, TAIR, MaizeGDB, Flybase, Zfin, MGI, etc.

National and International database repositories

- NCBI
- UniProt, Swissprot
- EBI
- DDBJ

Specialized research databases

- Gene Ontology
- Plant Ontology
- Ensembl

Website : <http://www.gramene.org>

GRAMENE

A Resource for Comparative Grass Genomics

v23 (November 2006)

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- 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.
- MARKERS:** Search for Genetic markers (RFLPs, SSRs, etc.), DNA Probes (Primers, Overgos, etc.), Genomic Regions (Clones, FPContigs, etc.), and Sequences (GSSs, ESTs, etc.); Use the Simple Sequence Repeat Identification Tool ([SSRIT](#)); or search by 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](#).
- GENETIC DIVERSITY** **NEW** : Search for SNP and SSR allelic variation on loci of [rice](#), [maize](#), and [wheat](#) germplasms.
- BIOCHEMICAL PATHWAYS** **NEW** : Search for ALL the rice pathways on [starch metabolism](#) or get an overview of the [metabolic network](#). Compare [rice](#) and [Arabidopsis](#) pathway datasets.
- LITERATURE:** Search the literature for your friends and topics of interest.
- SUBMISSION:** Submit a [Rice Gene](#) or [Ontology Term](#) to Gramene.

Gramene is a curated, open-source, web-accessible data resource for comparative genome analysis in the grasses. Our goal is to facilitate the study of cross-species homology relationships using information derived from public projects involved in genomic and EST sequencing, protein structure and function analysis, genetic and physical mapping, interpretation of biochemical pathways, gene and QTL localization and descriptions of phenotypic characters and mutations.

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- NEW** [Gramene November Newsletter](#)
- [Rice News Worldwide](#) from IRRI

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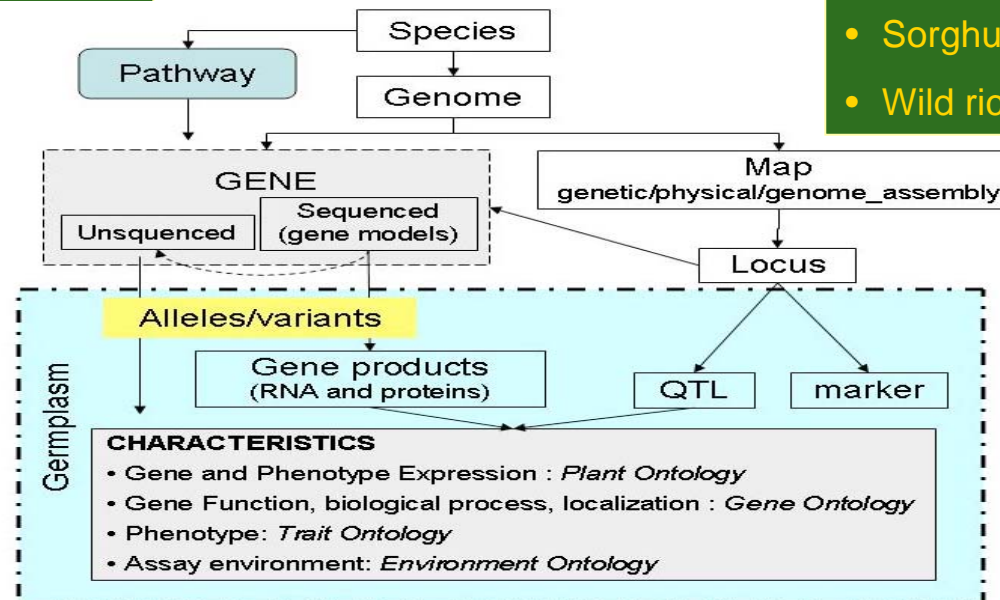
Genomes:

(Sequence/FPC maps)

- Oryza sativa
- Oryza rufipogon
- Zea mays
- Arabidopsis thaliana
- Organelles (plastid and mitochondrion)

Species:

- Rice (Oryza)
- Maize (Zea)
- Wheat (Triticum)
- Barley (Hordeum)
- Oat (Avena)
- Foxtail millet (Setaria)
- Pearl millet (Pennisetum)
- Rye (Secale)
- Sorghum (Sorghum)
- Wild rice (Zizania)



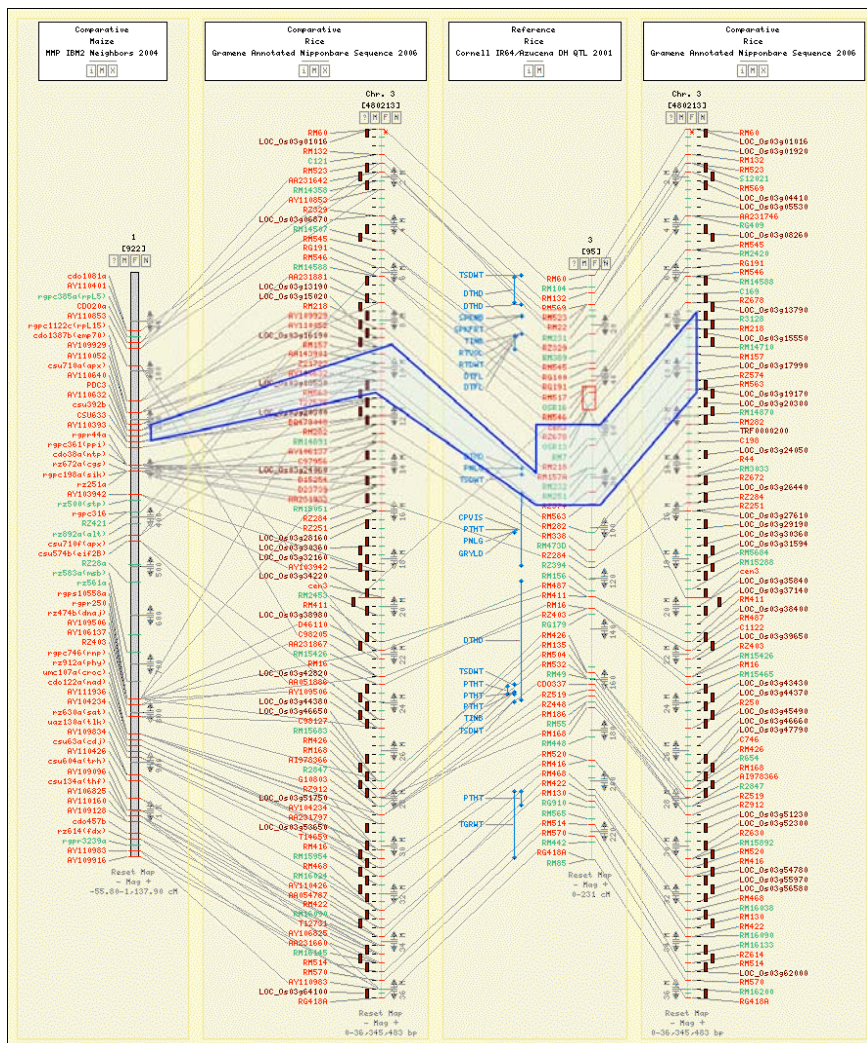
Comparative maps (CMap)

Map details

Type	Maps
Sequence	5
Physical	16
Genetic	39
QTL	112
Deletion	1
Maize Bin	1

Map Set Name:	INDIR IR58025/O. rufipogon BC SSR QTL 2005				[Show Only This Set]
Abbreviated Name:	INDIR IR58025/O. rufipogon BC				[Download Map Set Data]
Accession ID:	map2005a				[View Map Set In Matrix]
Species:	Oryza sativa (Rice)				[View Species Info]
Map Type:	QTL				[View Map Type Info]
Map Units:					
Published On:	N/A				
Description:	<p>The mapping population is a set of 251 interspecific BC2 testcross progeny IR58025A/O. rufipogon//IR580325B//IR58025B//KMR3. IR 58025A was a commercial cms line and was used as a recurrent parent. IR 58025A grows to a height of 80 cm and is characterized by having long grain type and early maturity along with good milling and eating qualities. The O. rufipogon accession, IC22015, collected from Kerala, India, and maintained at DRR was used as a donor parent. A total of 80 polymorphic microsatellite markers separated by an average distance of 15.37 cM were used to analyze the 251 testcross progeny and construct the linkage map.</p>				
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]
	5	[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]
[Display All Maps in Viewer]					

CMap allows genetic, physical and sequence maps to be aligned. e.g. a QTL map in rice aligned to the corresponding regions of the annotated rice genome and the genetic map of maize



<i>Avena sativa</i>	3
<i>Hordeum vulgare</i>	13
<i>Oryza alta</i>	1
<i>Oryza australiensis</i>	1
<i>Oryza brachyantha</i>	1
<i>Oryza coarctata</i>	1
<i>Oryza glaberrima</i>	1
<i>Oryza granulata</i>	1
<i>Oryza minuta</i>	1
<i>Oryza nivara</i>	1
<i>Oryza officinalis</i>	1
<i>Oryza punctata</i>	1
<i>Oryza ridleyi</i>	1
<i>Oryza rufipogon</i>	1
<i>Oryza sativa</i>	102
<i>Oryza sativa x Oryza eichingeri</i>	1
<i>Oryza sativa x Oryza longistaminata</i>	2
<i>Oryza sativa x Oryza rufipogon</i>	1
<i>Pennisetum glaucum</i>	9
<i>Secale cereale</i>	1
<i>Setaria italica</i>	1
<i>Sorghum bicolor</i>	6
<i>Triticum aestivum</i>	14
<i>Triticum turgidum</i>	2
<i>Zea mays</i>	19
<i>Zizania palustris</i>	1

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:

* eg. [development](#), [vegetative*](#), [VGTM](#), [QTL*](#), [AQEZ001](#). Or [view help](#).

QTL Annotations

Items 1 to 25 of 60.			
		Page 1	of 3. Next
Trait Name	Trait Symbol	TO Accession	Number of QTL
abscisic acid concentration	ABACONC	TO:0000478	46 View
aluminum sensitivity	ALSN	TO:0000354	11 View
cell membrane stability	CELMBSTB	TO:0000467	9 View
cold tolerance	COLDTL	TO:0000303	31 View
deep root dry weight	DRTDWT	TO:0000081	41 View
deep root to shoot ratio	DRTSHRO	TO:0000092	18 View
drought sensitivity index	DRSN	TO:0000155	18 View
drought susceptibility index	DRSID	TO:0000155	4 View
drought tolerance	DRTL	TO:0000276	23 View
dry mass	DMASS	TO:0000352	10 View

Trait categories	Rice	Maize	Wheat	Oat	Barley	Sorghum	Pearl millet	Foxtail millet	Wild rice (Zizania)	All species	Number of traits
Abiotic stress	666	113					17			796	59
Anatomy	1,214	217				41	31		16	1519	70
Biochemical	159	200			20					379	34
Biotic stress	402	6	11	53	45		24			541	16
Development	899	274		54	23	18	35		6	1309	17
Quality	589	143	7	88	17	1			8	853	57
Sterility or fertility	484									484	11
Vigor	1,694	233		78		14	15	65	9	2108	19
Yield	2,022	495		102		19	162		2	2802	32
All	8129	1681	18	375	105	93	284	65	41	10791	315

Genetic Diversity database

Species	rice	corn	wheat
# of germplasms	626	1800	48
# of loci	542	1400	3802
# of SSR loci	542	520	none
# of SNP loci	none	897	3802

Genetic Diversity database contains SSR and SNP allelic data and passport descriptions for rice, maize and wheat germplasms. It also holds phenotypic data for maize. It is modeled on GDPDM schema.

GRAMENE Diversity

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[Diversity Home](#) | [Germplasm Search](#) | [Molecular Diversity Search](#) | [Gene/Locus Search](#) | [Phenotype Search](#) | [Advanced Search](#) | [Help](#) | [Tutorial](#) | [FAQ](#) | [Release Notes](#)

Allele data for germplasm "BOV 492" from the experiment "MEG_1998-2003 Genotyping".

[Search Again](#)

Items 1 to 25 of 96.
 1 of 4 | [Next](#)

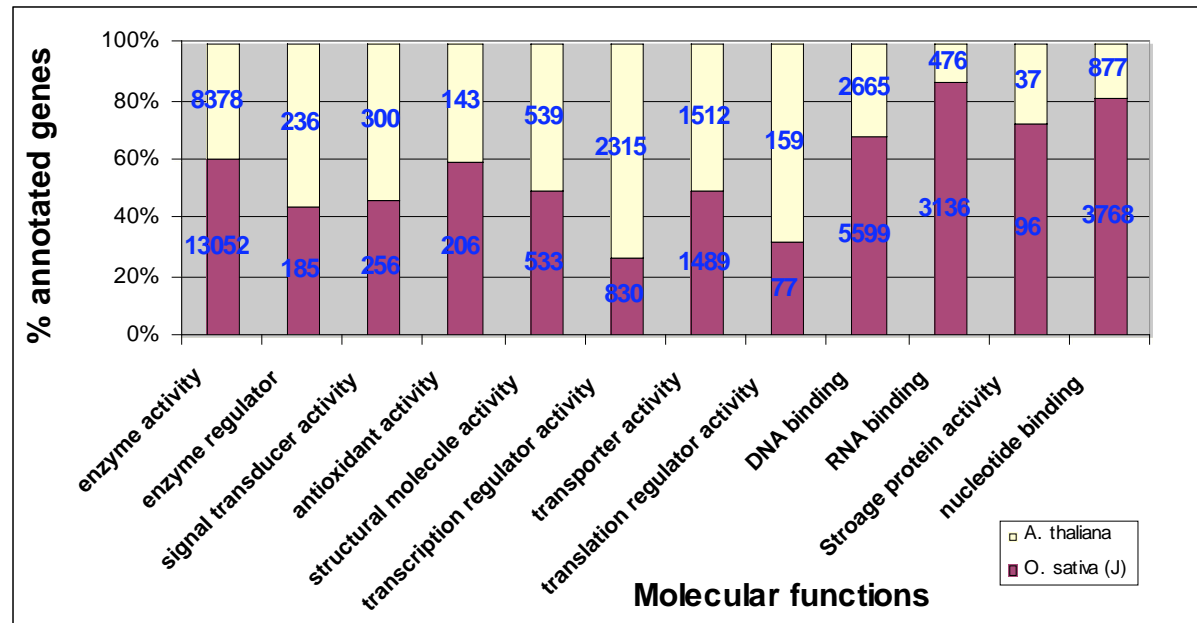
Germplasm Accession Name	Subsp. & subtaxa	Country of Origin	Accession Number	Stock Number	Locus name	Genotype	View All Genotypes on Marker
BOV 492	mays	BOLIVIA		77/78 T-9	nc004	148, 156	All Genotypes On "nc004"
BOV 492	mays	BOLIVIA		77/78 T-9	nc009	111, 111	All Genotypes On "nc009"
BOV 492	mays	BOLIVIA		77/78 T-9	dupssr14	76, 92	All Genotypes On "dupssr14"
BOV 492	mays	BOLIVIA		77/78 T-9	phi017	113, 113	All Genotypes On "phi017"
BOV 492	mays	BOLIVIA		77/78 T-9	phi021	94, 102	All Genotypes On "phi021"
BOV 492	mays	BOLIVIA		77/78 T-9	phi024	180, 183	All Genotypes On "phi024"
BOV 492	mays	BOLIVIA		77/78 T-9	dupssr28	147, 147	All Genotypes On "dupssr28"
BOV 492	mays	BOLIVIA		77/78 T-9	phi031	198, 200	All Genotypes On "phi031"

Genome browser for sequence and FPC maps

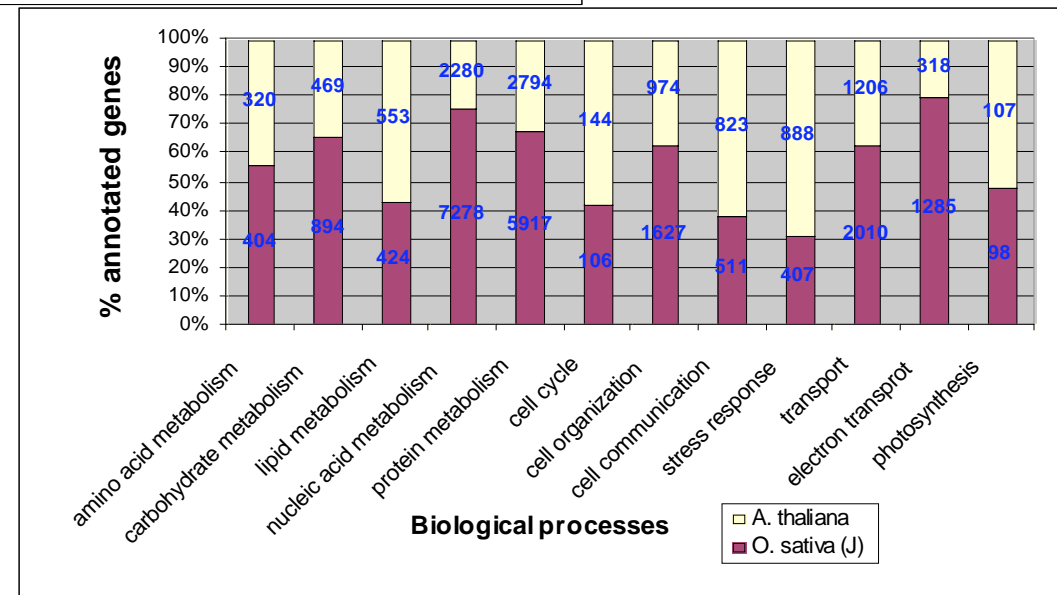
The screenshot shows the GRAMENE Genome Browser interface. At the top, the logo "GRAMENE" is followed by "Genome_browser". To the right is a search bar with the text "Find anything" and a "Search" button. Below this is a navigation bar with links: Search, Genomes, Species, Download, Resources, About, Help, and Feedback. A "Find in Genomes" section contains a dropdown menu set to "All" and a "Search" button. On the left, a "Browser Links" sidebar includes "Genomes Home", "Genomes Help", "Switch Species", and an "e!mpowered" logo. The main content area is titled "browse a genome" and features three columns: "Oryzae", "Other Poaceae", and "Other". Under "Oryzae", there are links for *Oryza sativa* (rice) [TIGR 4] and *Oryza rufipogon* (red rice) [OMAP OR_CBa]. Under "Other Poaceae", there is a link for *Zea mays* (maize) [Agarose Oct04]. Under "Other", there is a link for *Arabidopsis thaliana* [TAIR 6]. At the bottom, an "About Gramene-Ensembl" section explains that the browser is built on Ensembl technology and provides a brief description of the Ensembl project, which is a joint effort between EMBL, EBI, and the Sanger Institute, funded by the Wellcome Trust.

It provides information on gene models, aligned cDNAs, ESTs, unigenes, BAC clones, BAC ends, markers, FSTs, SNPs, QTL, orthologs and the syntenic regions.

Protein annotations from Sequenced genomes



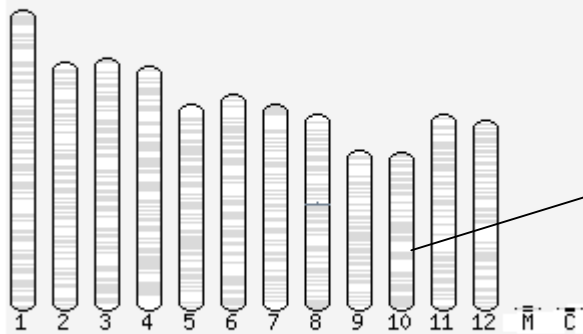
About 65% of the genes have some kind of functional annotation and expression information



Genome browser (e.g. rice)

Entry Points

Browse by Chromosome

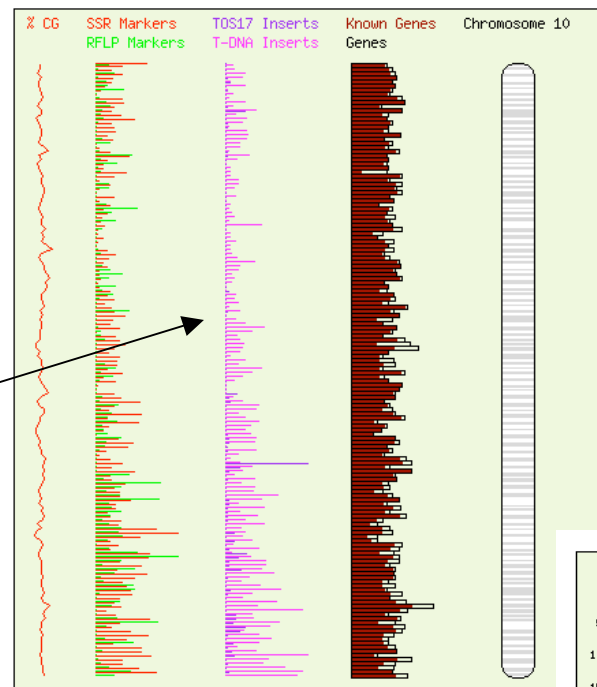


Lookup a Chromosome Location

Chr: from -

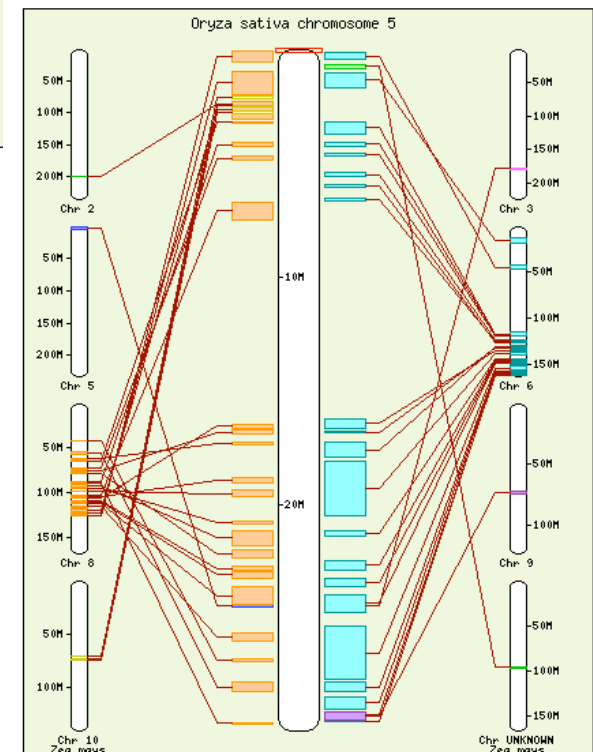
Rice Synteny Vs Maize FPC Map

- Rice Chr 1 vs. Maize
- Rice Chr 2 vs. Maize
- Rice Chr 3 vs. Maize
- Rice Chr 4 vs. Maize
- Rice Chr 5 vs. Maize**
- Rice Chr 6 vs. Maize
- Rice Chr 7 vs. Maize
- Rice Chr 8 vs. Maize
- Rice Chr 9 vs. Maize
- Rice Chr 10 vs. Maize
- Rice Chr 11 vs. Maize
- Rice Chr 12 vs. Maize



Click on the image above to zoom into that point

Rice chr-10
overview



Synteny view

Manually curated Genes and alleles

GRAMENE Genes Find anything

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[Gene Home](#) | [Search](#) | [Submit](#) | [Help](#) | [Tutorial](#) | [FAQ](#)

Gene Search

Search for *: Search in: Gene Type: Species: Has Phenotype: ☐

[Browse by Ontology Database](#) [Trait](#) [Plant Structure](#) [Growth Stage](#)

Items 1 to 25 of 2

Species	Gene Symbol	Gene Name	Synonyms	TO	GRO	GO	EO	Chr. No.	Gene Type	Accession
Rice	Bph1	Brown planthopper resistance-1		brown planthopper resistance	shoot, LP.06 six leaves visible, 2 formation of axillary shoot, leaf production, leaf, LP.05 five leaves visible	03-tillering stage, 02-seedling	response to insect	12	Not sequenced	GR:0060089
Rice	Bph10	Brown planthopper resistance-10	Brown planthopper resistance introduced from <i>Oryza australiensis</i>	brown planthopper resistance	shoot, leaf production, leaf	02-seedling	response to insect	12	Not sequenced	GR:0060098
Rice	Bph11	Brown planthopper resistance-11	Brown planthopper resistance, Bph(t)*	brown planthopper resistance	root, A vegetative growth		response to insect	9	Not sequenced	GR:0060099
Rice	bph12	Brown planthopper resistance-12	brown planthopper resistance-11, bph, bph11	brown planthopper resistance	root, A vegetative growth		response to insect	3	Not sequenced	GR:0060100

Total gene number	8783
# Maize genes	6676
# Rice genes	2104
# Sorghum genes	3
# genes with sequence information	637
# genes with protein information	371
# genes with map position	4054

Total allele number	553
Total references used for the gene curation	
# of Literature references	2067
# of MaizeGDB references	6676
# of Oryzabase references	1040
# of miRNbase references (micro RNAs)	182

Protein dataset


[Proteins](#)

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[About](#)
[Help](#)

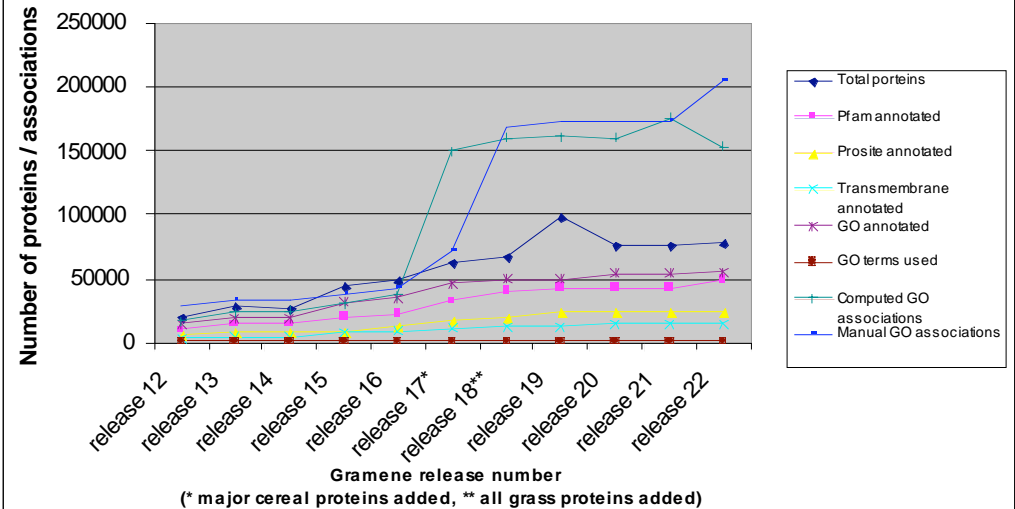
[Protein Home](#) |
 [Advanced Search](#) |
 [Search by Pfam or PROSITE](#) |
 [Browse by GO Slim](#) |
 [Documents](#) |
 [Tutorial](#) |
 [FAQ](#) |
 [Help](#)

Protein Search

Search for: Search in: Species:

Items 1 to 25 of 281. Page			
Accession No.	Names/Symbols/Synonyms	Organism (cultivar)	Evidence codes
P27935	Alpha-amylase isozyme 2A precursor AMY1.5 1,4-alpha-D-glucan glucanohydrolase A	<i>Oryza sativa (japonica cultivar-group)</i> (M202)	IEP ISS RCA TAS
P27932	Alpha-amylase isozyme 3A precursor AMY1.2 1,4-alpha-D-glucan glucanohydrolase A	<i>Oryza sativa (japonica cultivar-group)</i> (M202)	IEP ISS RCA TAS
P27937	Alpha-amylase isozyme 3B precursor AMY1.6 1,4-alpha-D-glucan glucanohydrolase A	<i>Oryza sativa (japonica cultivar-group)</i> (M202)	IEP ISS RCA TAS
P27939	Alpha-amylase isozyme 3C precursor AMY1.7 1,4-alpha-D-glucan glucanohydrolase AMY3B	<i>Oryza sativa (japonica cultivar-group)</i> (M202)	IEP ISS RCA TAS
P27933	Alpha-amylase isozyme 3D precursor AMY1.3 1,4-alpha-D-glucan glucanohydrolase AMY3D	<i>Oryza sativa (japonica cultivar-group)</i> (M202)	RCA IEP ISS TAS
P27934	Alpha-amylase isozyme 3E precursor AMY1.4 1,4-alpha-D-glucan glucanohydrolase AMY3E	<i>Oryza sativa (japonica cultivar-group)</i> (M202)	IEP ISS RCA TAS

Total proteine number	93712
# Swissprot	2508
# TrEMBL	91204
# rice (<i>Oryza</i>)	78405
# corn (<i>zea</i>)	4400
# of taxons (genus) from Poaceae (grasses)	340
# with Pfam annotation	50800
# with Prosite	28500
# with Gene Ontology	63842
# with Transmembrane domains	17800



Pathway database

	RiceCyc	AraCyc
Pathways	324	197
Enzymatic Reactions	1687	1298
Transport Reactions	5	4
Polypeptides	43172	5061
Protein Complexes	4	109
Enzymes	10387	2917
Transporters	62	13
Compounds	1265	1071



The Pathway database is a comprehensive resource for gene annotations, maps, and sequences. It includes data for rice (*Oryza sativa*) and Arabidopsis (*Arabidopsis thaliana*).

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
Jasmonic acid biosynthesis	Pentose phosphate pathways
Salicylic acid biosynthesis	ALL pathways

In order to promote exciting new discoveries on biochemical pathways in rice, the current version of RiceCyc presents the complete predicted set and not just the curated pathways.

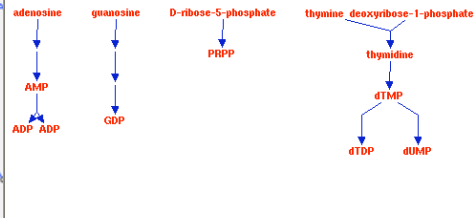
Since the functions of many of the rice genes are either provided by homology and HMM based predictions or unknown, many of the pathways might be incomplete or may contain errors. The manual curation of pathways is an ongoing process at Gramene and we

Pathways in Gramene				
Species	Source	Overview [#]	Summary	Pathway comparison
RICE <i>Oryza sativa japonica</i> cv. Nipponbare	Gramene, RiceCyc 1.1		view	Arabidopsis E.coli
ARABIDOPSIS * <i>Arabidopsis thaliana</i> strain Columbia	TAIR, AraCyc 2.5		view	Rice E.coli
E. COLI * <i>Escherichia coli</i> strain K-12 MG1655	SRI, EcoCyc 9.5		view	Rice Arabidopsis
* Not curated by Gramene. # click on icons to visit the overview				

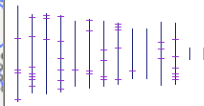
Useful links to pathway tools	
Compare data sets from the three species for reactions, pathways, compounds and proteins	Compare
Map your microarray expression, proteomics, metabolomics and other datasets on Pathway overview diagrams	Omics viewer
Details on pathway visualization [Help document]	Help
Learn how to use the tool	Tutorial
Still have questions, consult the frequently asked questions section	FAQs
Want your own copy of the RiceCyc? Download from our ftp archive. <i>For Arabidopsis and E. coli pathways please visit AraCyc and EcoCyc project sites.</i>	Download

O. sativa japonica Pathway: salvage pathways of purine and pyrimidine nucleotides

More Detail Cross-Species Comparison



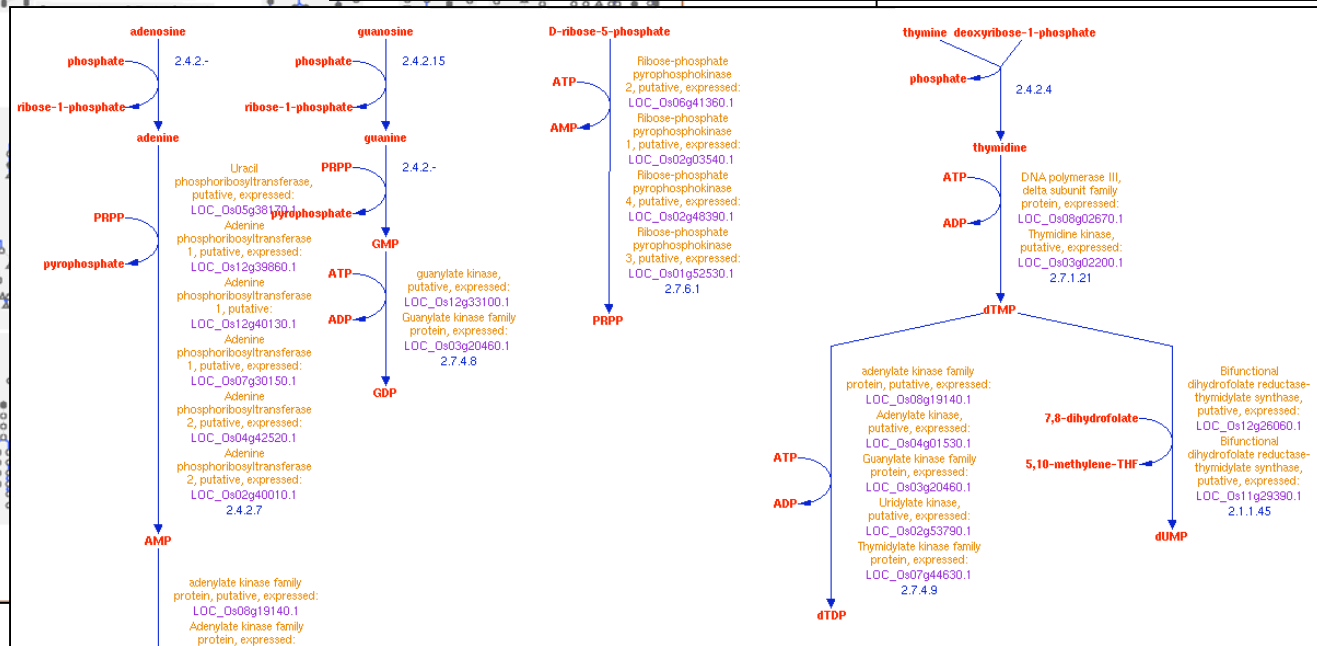
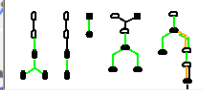
Locations of Mapped Genes:



Synonyms: purine and pyrimidine metabolism

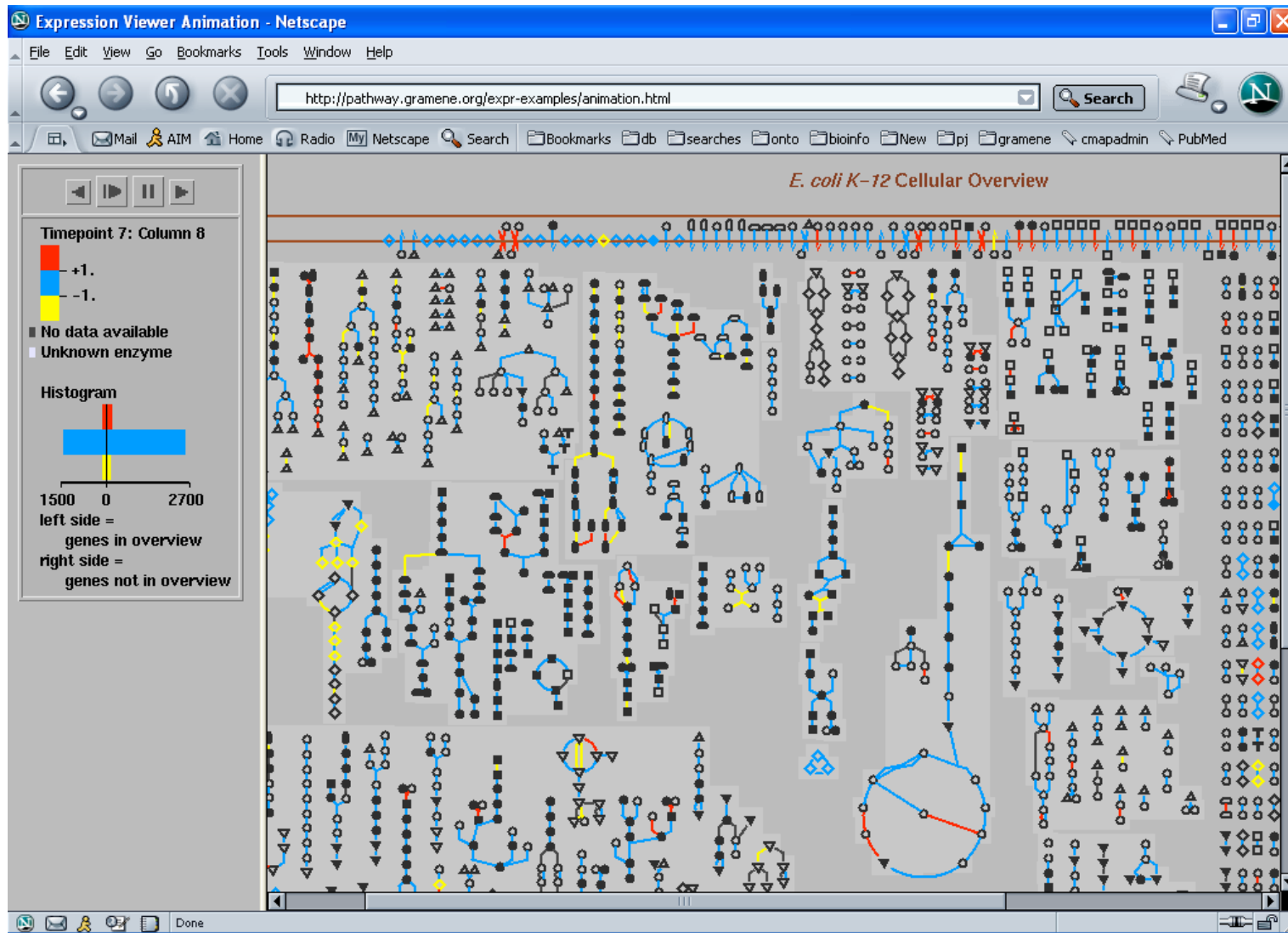
Superclasses: [Biosynthesis](#) -> [Nucleosides and Nucleotides](#)

Pathway Evidence Glyph:



A Single gene expression experiment

Pathway OMICS viewer paints the pathway with your microarray data



A time series gene expression experiment

Types of 'BUD' !



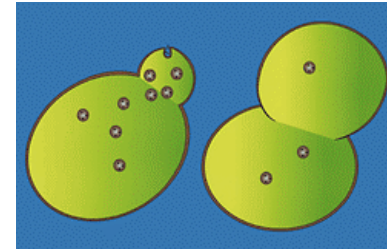
Vegetative bud



Flower bud



Tooth bud



Yeast bud

Image source:

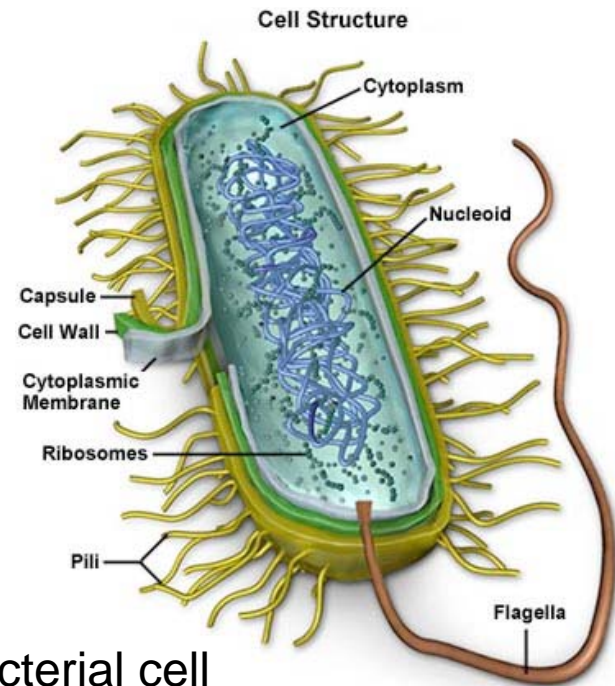
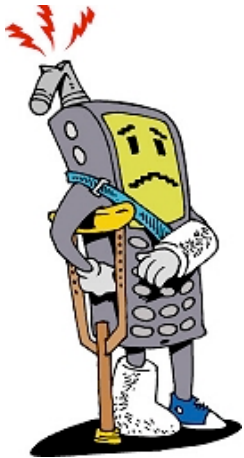
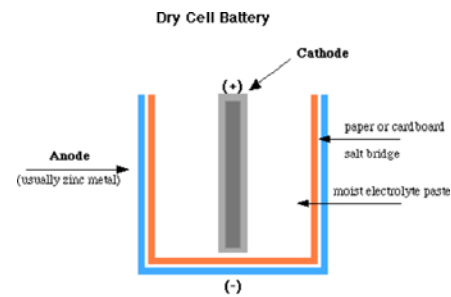
<http://www.berkeley.edu/news/media/releases/2002/09/images/2yeast.gif>

<http://www.technovelgy.com/graphics/content/tooth-thumb.jpg>

<http://165.234.175.12/photos/Angiosperms/Juglans%20nigra%20bud.jpg>

http://www.daylilies.org/ahs_dictionary/bud.jpg

Types of 'CELL'!



Bacterial cell

Image source:

http://www.rupertshoney.co.za/rh/images/bees_on_combthb.jpg

<http://homepage.mac.com/matterworks/phoneear.jpg>

<http://www.singleton-associates.org/gifs/cell.jpg>

What is an Ontology ?

Ontologies resemble faceted taxonomies but use richer semantic relationships among terms and attributes, as well as strict rules about how to specify terms and relationships.

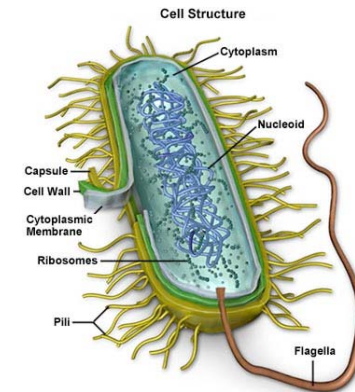
Since ontologies do more than just control a vocabulary, they are thought of as knowledge representation.

The oft-quoted definition of ontology is "the specification of one's conceptualization of a knowledge domain."

Definitions in the Ontology

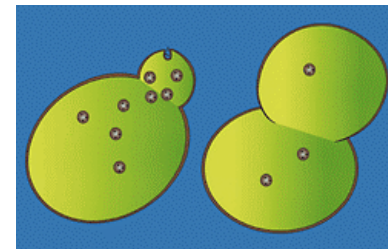
Cell:

The basic structural and functional unit of all organisms. Includes the plasma membrane and any external encapsulating structures such as the cell wall and cell envelope.

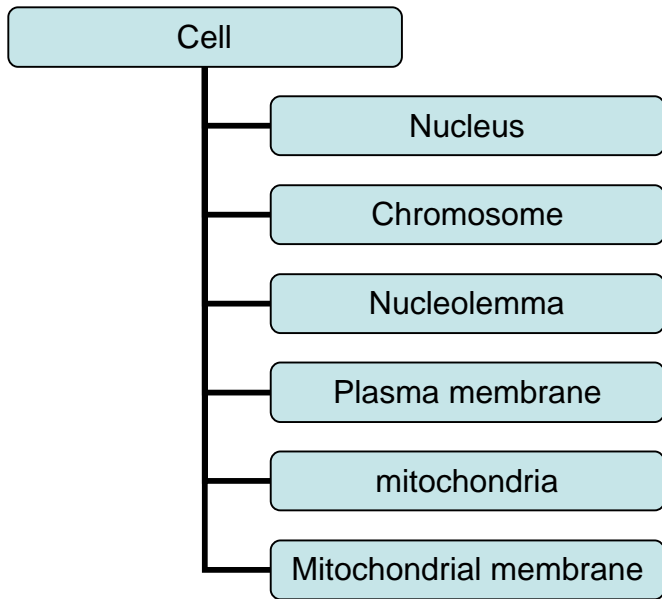


Bud:

A daughter cell of an organism that reproduces by budding; formed by pinching off part of the parent cell.

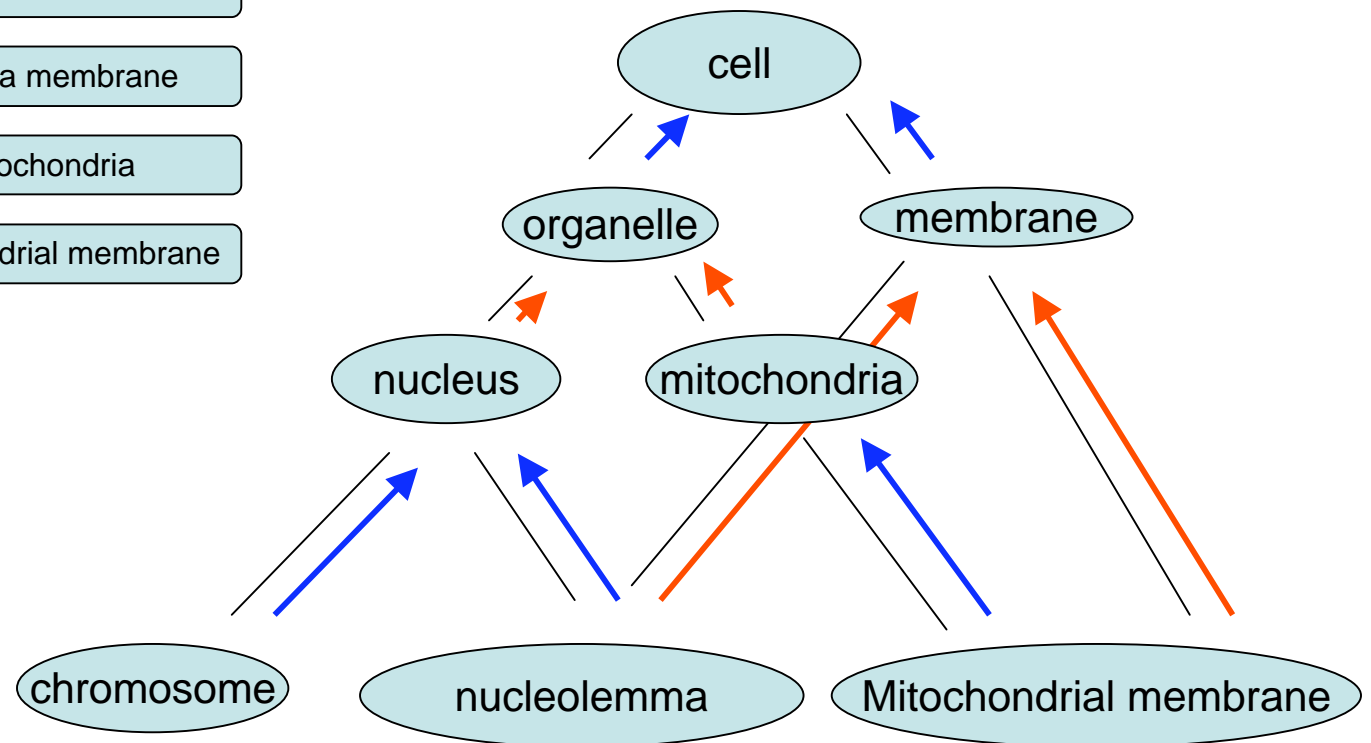


Term to term relationships



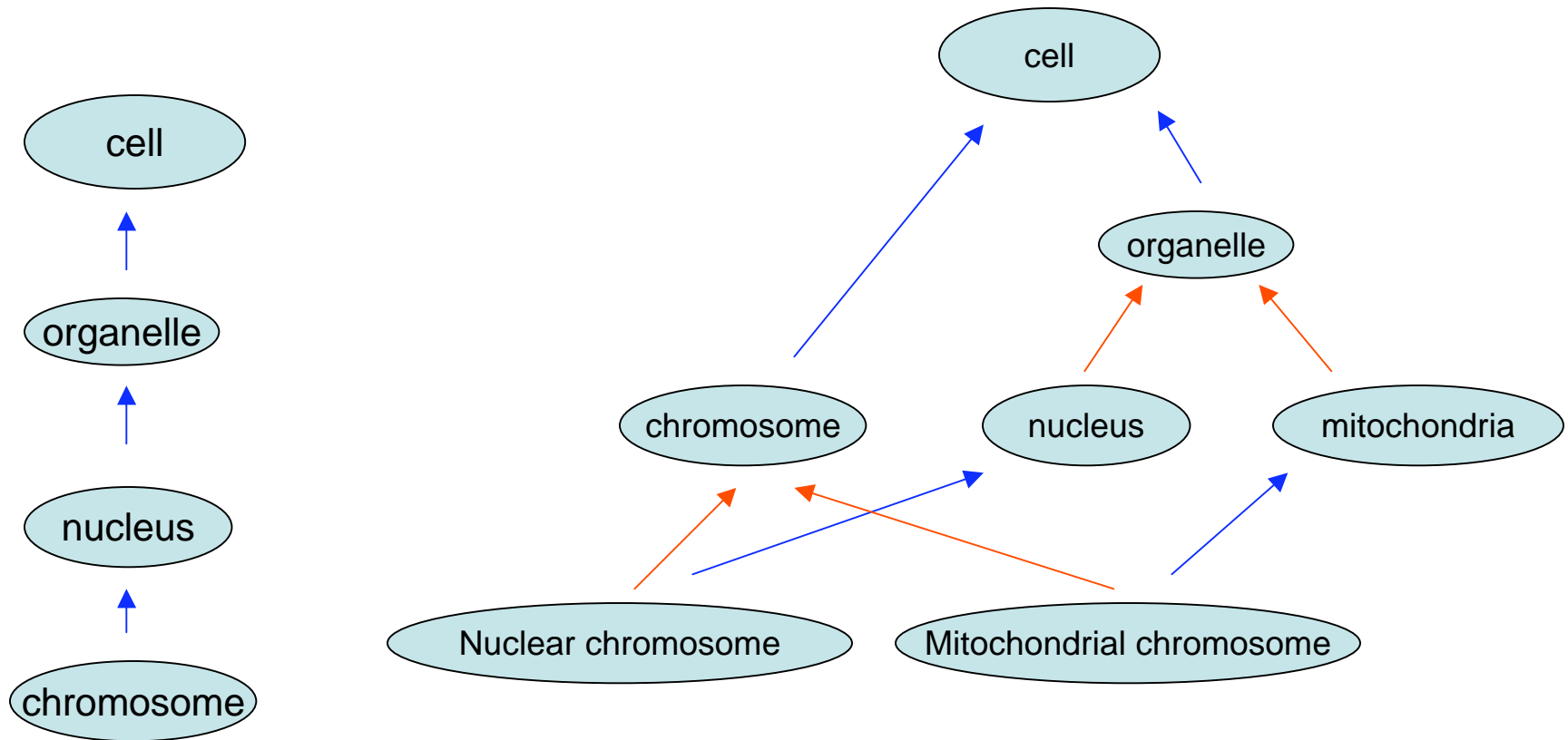
Simple hierarchy

An Ontology



[Arrows] Red: is-a (subtype/instance) Blue: part-of (component)

Conflicts and resolution



This is fine in Eukaryote cell.

What about the prokaryote cell?

There is no nucleus in it.

Two new subtypes of 'chromosome' created for specific location/source

Red: is-a (subtype/instance) Blue: part-of (component)

Gene Ontology [www.geneontology.org]

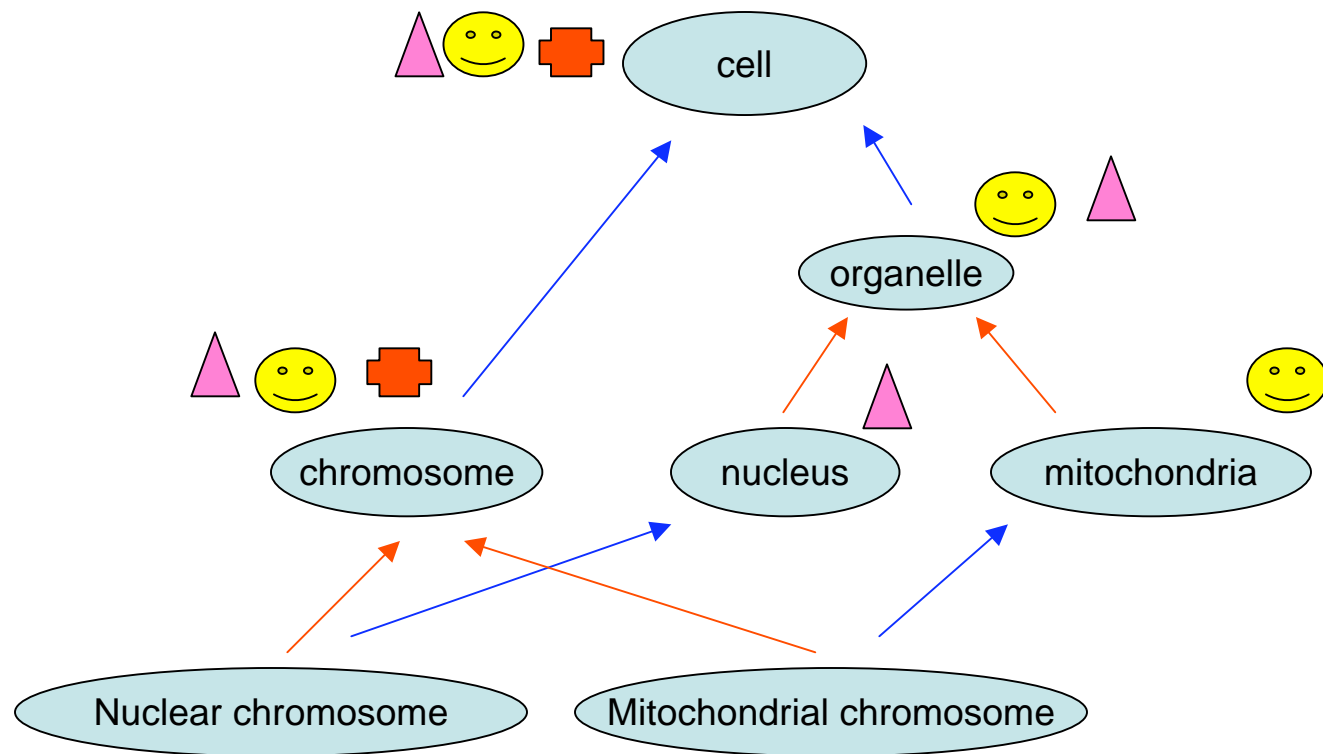
Gene Ontology provides a controlled vocabulary on three domains to describe a gene's characteristics:

Its **Molecular function(s)**

Role in a **Biological process(es)**

Location in **Cellular component(s)**

Associations and Query convenience



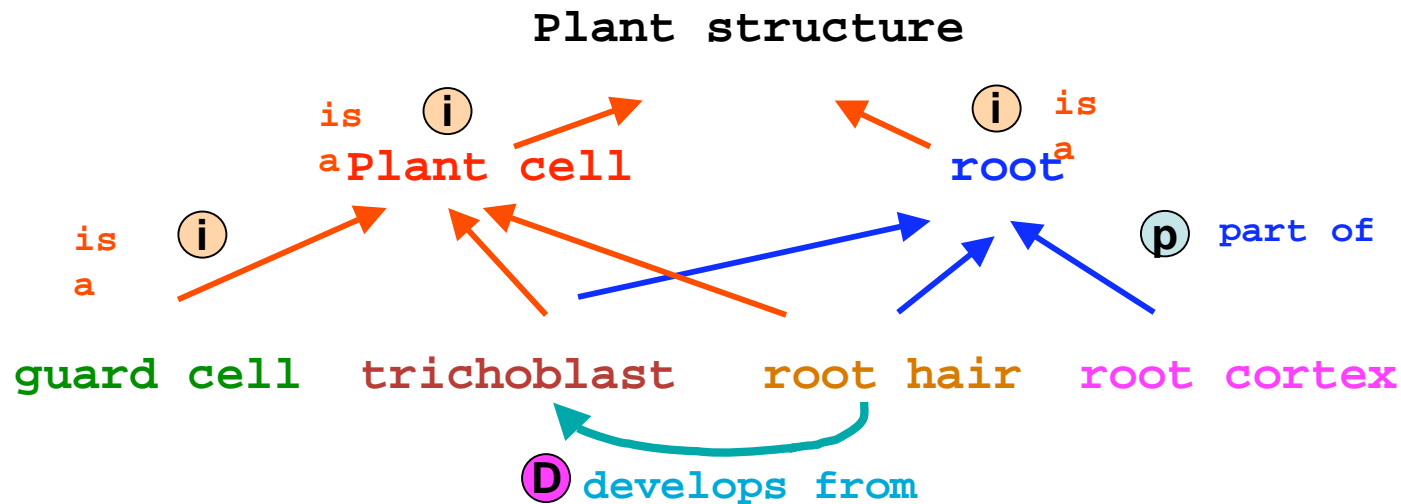
Direct associations from child term percolate to parent and grandparent as indirect associations.



Genes

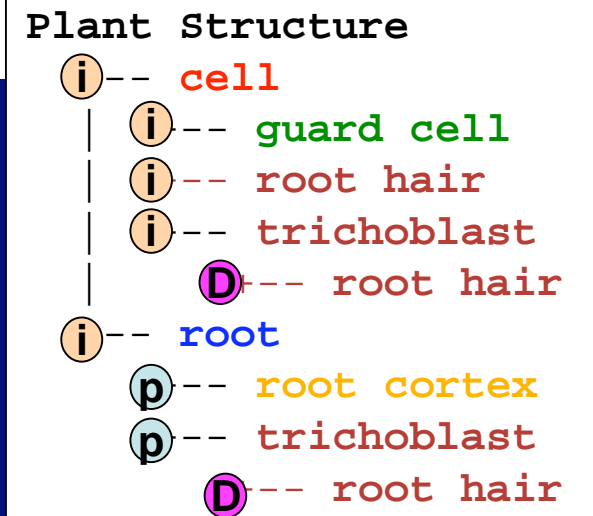
[arrows] Red: is-a (subtype/instance) Blue: part-of (component)

Plant Ontology example (www.plantontology.org)



Statement looks like

- Trichome, root hair, root cortex are part of root
- Trichoblast, root hair and guard cell are instances of cell
- Root hair develops from trichoblast
- Cell and root are instances of plant structure



Ontology resources

- OBO foundry of biological ontologies
[obo.sf.net]
- Gene ontology [www.geneontology.org]
- Plant ontology [www.plantontology.org]
- Trait ontology
[www.gramene.org/plant_ontology/]
- ChEBI (chemical ontology)
[www.ebi.ac.uk/chebi/]