

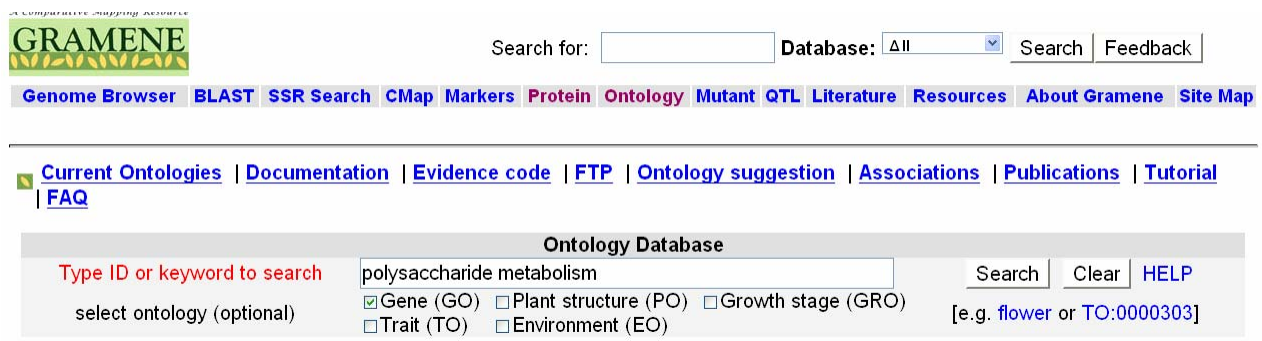
Gramene Ontology Module Exercises

Gene Ontology

Go to <http://www.gramene.org> and select “Ontology” from the navigation bar.

1a. Search for the term “polysaccharide biosynthesis” and report its GO id and its definition.

1) Enter “polysaccharide metabolism” in the Ontology Search field, as shown below.



GRAMENE

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Ontology Database

Type ID or keyword to search: polysaccharide metabolism Search Clear HELP

select ontology (optional): ☒ Gene (GO) ☐ Plant structure (PO) ☐ Growth stage (GRO) ☐ Trait (TO) ☐ Environment (EO) [e.g. flower or TO:0000303]

2) The following Summary page will result.


Summary for *polysaccharide metabolism*

Items 1 to 3 of 3

#	Term Accession	Term Name	Synonym	Definition
1	GO:0005976	polysaccharide metabolism	glycan metabolism.	The chemical reactions and physical changes involving polysaccharides (synonym:glycans), a polymer of more than about 10 monosaccharide residues joined by glycosidic linkages.
2	GO:0008653	lipopolysaccharide metabolism	None	The chemical reactions and physical changes involving lipopolysaccharides, any of a group of related, structurally complex components of the outer membrane of Gram-negative bacteria. Lipopolysaccharides consist three covalently linked regions, lipid A, core oligosaccharide, and an O side chain. Lipid A is responsible for the toxicity of the lipopolysaccharide.
3	GO:0046379	extracellular polysaccharide metabolism	None	The chemical reactions and physical changes involving polysaccharides used in extracellular structures.

Answer: The GO id is GO:0005976 and its definition is “The chemical reactions and physical changes involving polysaccharides (synonym:glycans), a polymer of more than about 10 monosaccharide residues joined by glycosidic linkages..”

1b. How many of its children have children of their own?

Select the appropriate Term accession, as shown above. The following Summary Page will result. The  symbol indicates that the tree is expandable, i.e., the children terms have children terms of their own.

Summary for GO Term: <i>polysaccharide metabolism</i> (GO:0005976)	
Term Name	polysaccharide metabolism
Synonym	glycan metabolism.
Definition	The chemical reactions and physical changes involving polysaccharides (synonym:glycans), a polymer of more than about 10 monosaccharide residues joined by glycosidic linkages.
Derivation	<ul style="list-style-type: none"> • biological process (GO:0008150) #19728  <ul style="list-style-type: none"> ◦ [i] physiological process (GO:0007582) #19354  <ul style="list-style-type: none"> ▪ [i] metabolism (GO:0008152) #10584  <ul style="list-style-type: none"> ▪ [i] macromolecule metabolism (GO:0043170) #4291  <ul style="list-style-type: none"> ▪ [i] carbohydrate metabolism (GO:0005975) #747  <ul style="list-style-type: none"> ▪ [i] polysaccharide metabolism (GO:0005976) #122  <ul style="list-style-type: none"> ▪ [i] polysaccharide biosynthesis (GO:0000271) #53  ▪ [i] polysaccharide catabolism (GO:0000272) #58  ▪ [i] glucan metabolism (GO:0006073) #69  ▪ [i] chitin metabolism (GO:0006030) #40  ▪ [i] mannan metabolism (GO:0006080) #0  ▪ [i] lipopolysaccharide metabolism (GO:0008653) #4  ▪ [i] colanic acid metabolism (GO:0046377) #0  ▪ [i] O antigen metabolism (GO:0046402) #0  ▪ [i] enterobacterial common antigen metabolism (GO:0046378) #0  ▪ [i] K antigen metabolism (GO:0046375) #0  ▪ [i] fructan metabolism (GO:0010145) #0  ▪ [i] GDP-alpha-D-mannosylchitobiosyldiphosphodolichol metabolism (GO:0046376) #0  ▪ [i] poly-N-acetyllactosamine metabolism (GO:0030309) #0  ▪ [i] alginic acid metabolism (GO:0042120) #0  ▪ [i] extracellular polysaccharide metabolism (GO:0046379) #0  ▪ [i] pectin metabolism (GO:0045488) #0  ▪ [i] xylan metabolism (GO:0045491) #0  ▪ [i] galactomannan metabolism (GO:0051069) #0  ▪ [i] 4,6-pyruvylated galactose residue metabolism (GO:0051071) #0 

Answer: All the children terms have children of their own.

1c. How many total (direct and indirect) number of proteins are associated to the GO term polysaccharide metabolism? Are there any proteins which are not directly associated to this term? If so, which child term has the greatest number of associations?

1) In the same Summary page, examine the number next to the term “polysaccharide metabolism.” That number indicates the total number of proteins associated. Then examine the number next to the children terms. Adding them together indicates the number of proteins not directly associated to the term, as shown below. However sometimes the parent term may display the number less than the actual total because same protein may have been annotated to tow of the children terms and while adding these numbers for the parents, the protein accession is counted only once.

Summary for GO Term: *polysaccharide metabolism* (GO:0005976)

Term Name	polysaccharide metabolism
Synonym	glycan metabolism.
Definition	The chemical reactions and physical changes involving polysaccharides (synonym:glycans), a polymer of more than about 10 monosaccharide residues joined by glycosidic linkages.
Derivation	<ul style="list-style-type: none"> • biological process (GO:0008150) #19728 <ul style="list-style-type: none"> ◦ [i] physiological process (GO:0007582) #19354 <ul style="list-style-type: none"> ▪ [i] metabolism (GO:0008152) #10584 <ul style="list-style-type: none"> ▪ [i] macromolecule metabolism (GO:0043170) #4291 <ul style="list-style-type: none"> ▪ [i] carbohydrate metabolism (GO:0005975) #747 <ul style="list-style-type: none"> ▪ [i] polysaccharide metabolism (GO:0005976) #122 <ul style="list-style-type: none"> ▪ [i] polysaccharide biosynthesis (GO:0000271) #53 ▪ [i] polysaccharide catabolism (GO:0000272) #53 ▪ [i] glucan metabolism (GO:0006073) #69 ▪ [i] chitin metabolism (GO:0006030) #40 ▪ [i] mannan metabolism (GO:0006080) #0 ▪ [i] lipopolysaccharide metabolism (GO:0008653) #4 ▪ [i] colanic acid metabolism (GO:0046377) #0 ▪ [i] O antigen metabolism (GO:0046402) #0 ▪ [i] enterobacterial common antigen metabolism (GO:0046378) #0 ▪ [i] K antigen metabolism (GO:0046375) #0 ▪ [i] fructan metabolism (GO:0010145) #0 ▪ [i] GDP-alpha-D-mannosylchitobiosyldiphosphodolichol metabolism (GO:0046376) #0 ▪ [i] poly-N-acetyllactosamine metabolism (GO:0030309) #0 ▪ [i] alginic acid metabolism (GO:0042120) #0 ▪ [i] extracellular polysaccharide metabolism (GO:0046379) #0 ▪ [i] pectin metabolism (GO:0045488) #0 ▪ [i] xylan metabolism (GO:0045491) #0 ▪ [i] galactomannan metabolism (GO:0051069) #0 ▪ [i] 4,6-pyruvylated galactose residue metabolism (GO:0051071) #0

2) To find the child term with the greatest number of associations, examine the Gene Product Association list, as shown below.

Answer: There are 122 proteins associated to the term 'polysaccharide metabolism'. None of the 122 proteins are directly associated to the term "polysaccharide metabolism". "chitin catabolism" has the greatest number (40) of associated proteins.

1d. Browse through the "Gene Product Symbol" column of the associations and report the protein name and gene symbol of an important cereal gene that is associated with seed/grain quality.

108	starch catabolism	Alpha-amylase isozyme 3E precursor	AMY1.4	ISS
109	starch catabolism	Alpha-amylase isozyme C precursor	AMYC	IEP ISS
110	starch catabolism	Alpha-amylase isozyme C2 precursor	AMY1.8	ISS
111	starch catabolism	Alpha-amylase precursor	AMY1.1	IEP ISS
112	starch metabolism	Starch granule-bound starch synthase	WAXY	ISS
113	starch metabolism	Granule-bound starch synthase	WAXY	ISS
114	starch metabolism	Granule-bound starch synthase	WX	IEP ISS
115	starch metabolism	Granule-bound starch synthase	WAXY	ISS
116	starch metabolism	Granule-bound starch synthase	WAXY	IEP ISS
117	starch metabolism	Granule-bound starch synthase	WX	IEP ISS
118	starch metabolism	1,4-alpha-glucan branching enzyme	SBE1	ISS
119	starch metabolism	Glucose-1-phosphate adenyltransferase small subunit, chloroplast precursor	Not available	IEP ISS
120	starch metabolism	Soluble glycogen [starch] synthase, chloroplast precursor	Not available	IEP IDA
121	starch metabolism	Granule-bound starch synthase	WAXY	ISS
122	starch metabolism	Granule-bound starch synthase	WAXY	ISS IMP

Examining the above list, scroll down the “Gene Product Symbol” column.

Answer: The name of the protein is “Granule-bound starch synthase” and its gene symbol is “WAXY.”

1e. Which GO term is directly associated with the gene found in question 1d? Click on the gene name and report its molecular function, role in biological processes, and its localization in cellular components. Is there a phenotype associated with this protein?

1) Examine the Associated Term column for the term that is directly associated, as shown below.

111	starch catabolism	Alpha-amylase precursor	AMY1.1	IEP ISS
112	starch metabolism	Starch granule-bound starch synthase	WAXY	ISS
113	starch metabolism	Granule-bound starch synthase	WAXY	ISS
114	starch metabolism	Granule-bound starch synthase	WX	IEP ISS
115	starch metabolism	Granule-bound starch synthase	WAXY	ISS

2) Then click on the gene product name. The following Protein Summary will result.

General Information about Q43012			
Name	Starch granule-bound starch synthase		
Symbol	WAXY		
Synonym(s)	GBSS, Granule-bound glycogen [starch] synthase, chloroplast precursor, Granule-bound glycogen synthase, Gss1, UDP-glycogen synthase, UDPG-glycogen synthetase, UDPG-glycogen transglucosylase, glutinous endosperm, glycogen [starch] synthetase, lycogen [starch] synthase, uridine diphosphoglucose-glycogen glucosyltransferase, waxy		
E.C. Number(s)	2.4.1.11		
Gene Symbol(s)	Wx		
Accession Numbers	GenBank	TRENBL	
	CAA45472	Q43012	
Organism(s)	Species	Cultivar	
	Oryza sativa	L.F. SPONTANEA (GRIN, IRIS)	
Phenotype	wx (glutinous endosperm)		
Comment	The Waxy (Wx) gene encodes a granule-bound starch synthase (GBSS) that plays a key role in the amylose synthesis of rice. It is expressed in the seed endosperm and pollen grains, that carry starch grains. At sub-cellular level the protein is localized in the amyloplasts. This gene undergoes alternative splicing of its transcripts suggesting that the amylose content of rice endosperm is regulated at the level of Wx transcript processing, and more specifically, at the stage of intron I excision from the Wx pre-mRNA. The alternative splicing is affected by the change in temperature. It is a single copy gene in rice.		
Associations			
Term Type	GO Term	Evidence	Evidence Code
Molecular Function	glycogen (starch) synthase activity	Gramene Ref 8047	ISS
Biological Process	starch metabolism	gramene protein : P19395	ISS
Cellular Component	amyloplast	Gramene Ref 8047	ISS
		gramene protein : P19395	ISS
	plastid	gramene protein : P19395	ISS
Keyword(s)	transglucosylase, Transferrase	Gramene Ref 7047	ISS

3) look in the phenotype section for the associated phenotype. You will notice the link to the phenotype database for more details.

Answer: The term directly related is “starch metabolism”. Its molecular function is glycogen (starch) synthase activity. Its role in the biological processes is starch metabolism and glycogen biosynthesis. It’s located in the amyloplast and plastid. The associated phenotype is “glutinous endosperm”.

Plant Ontology

2a. Go to the Ontology search section on the [Gramene Ontology page](#). Type, “plant anatomy” and search by selecting Plant Ontology (click on the check box). In the search results click on the term [plant structure \(PO:0009011\)](#) and report how many major classes of plant structures are listed. Also tell us the names of parts of a “sporophyte”. Hint: the symbol [i] stands for Instance of and [p] stands for Part of.

1) Enter “plant anatomy” in the Ontology Search field and select Plant Ontology, as shown below.

Search for: Database:

[Genome Browser](#) [BLAST](#) [SSR Search](#) [CMap](#) [Markers](#) [Protein](#) [Ontology](#) [Mutant](#) [QTL](#) [Literature](#) [Resources](#) [About Gramene](#) [Site Map](#)

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Ontology Database

Type ID or keyword to search: [HELP](#)

select ontology (optional)

☐ Gene (GO) ☒ Plant structure (PO) ☐ Growth stage (GRO)

☐ Trait (TO) ☐ Environment (EO)

[e.g. [flower](#) or [TO:0000303](#)]

2) The following Summary will result. Select “plant structure” as shown below. \

Summary for plant structure

Items 1 to 3 of 3

#	Term Accession	Term Name	Synonym	Definition
1	obsolete_plant structure	obsolete_plant structure	None	No Definition Available
2	PO:0006300	obsolete plant structure	None	The instances of this parent term are those anatomical terms which have become obsolete.
3	PO:0009011	plant structure	None	Any morphological or anatomical feature of a plant.

3) The following summary will result. Those terms with a [i] indicate a “instance of.”

Summary for PO Term: *plant structure* (PO:0009011)

Term Name	plant structure
Definition	Any morphological or anatomical feature of a plant.
Derivation	

- [plant ontology \(PO:0009075\)](#) #812
 - [i] [plant structure \(PO:0009011\)](#) #812
 - [i] [cell \(PO:0009002\)](#) #24
 - [i] [gametophyte \(PO:0009004\)](#) #2
 - [i] [sporophyte \(PO:0009003\)](#) #788
 - [i] [tissue \(PO:0009007\)](#) #73

4) Click on sporophyte to find various parts and instances of this plant structure.

Summary for PO Term: *sporophyte* (PO:0009003)

Term Name	sporophyte
Definition	A diploid plant, or phase of a life cycle, that bears spores formed by meiosis.
Derivation	<ul style="list-style-type: none"> • plant ontology (PO:0009075) #812 <ul style="list-style-type: none"> ◦ [i] plant structure (PO:0009011) #812 <ul style="list-style-type: none"> ▪ [i] sporophyte (PO:0009003) #788 <ul style="list-style-type: none"> ▪ [p] infructescence (PO:0006342) #155 ▪ [i] seed (PO:0009010) #155 ▪ [p] root (PO:0009005) #9 ▪ [p] shoot (PO:0009006) #627

Answer: The major classes of plant structures are cell, gametophyte, sporophyte and tissue. The root, shoot and infructescence are parts of sporophyte.

2b. Is [seed \(PO:0009010\)](#) a Part of [p] or an Instance of [i] sporophyte ?

Examining the same Summary Page, check to see if there is a [p] or [i] in front of the term “seed.”

Summary for PO Term: *sporophyte* (PO:0009003)

Term Name	sporophyte
Definition	A diploid plant, or phase of a life cycle, that bears spores formed by meiosis.
Derivation	<ul style="list-style-type: none"> • plant ontology (PO:0009075) #812 <ul style="list-style-type: none"> ◦ [i] plant structure (PO:0009011) #812 <ul style="list-style-type: none"> ▪ [i] sporophyte (PO:0009003) #788 <ul style="list-style-type: none"> ▪ [p] infructescence (PO:0006342) #155 ▪ [i] seed (PO:0009010) #155 ▪ [p] root (PO:0009005) #9 ▪ [p] shoot (PO:0009006) #627

Answer: Seed is an instance of a sporophyte.

2c. Click on the term seed (PO:0009010) and report the names and id's of its two immediate parents. Also tell the types of relationships does it have with them. Hint: In a simple hierarchy, seed was always a part of fruit, but Ontology can represent its multiple lineages.

Select “seed,” as shown above. The following Summary will result.

Summary for PO Term: seed (PO:0009010)

Term Name	seed
Definition	A propagating organ formed in the reproductive cycle of gymnosperms and angiosperms, derived from the ovule and enclosing an embryo.
Derivation	

- [plant ontology \(PO:0009075\)](#) #812
 - [\[i\] plant structure \(PO:0009011\)](#) #812
 - [\[i\] sporophyte \(PO:0009003\)](#) #788
 - [\[i\] seed \(PO:0009010\)](#) #155
 - [\[p\] embryo \(PO:0009009\)](#) #31
 - [\[p\] anil \(PO:0009090\)](#) #0
 - [\[p\] aniloid \(PO:0019022\)](#) #0
 - [\[p\] coma \(PO:0020061\)](#) #0
 - [\[p\] endosperm \(PO:0009089\)](#) #47
 - [\[p\] hilum \(PO:0020063\)](#) #0
 - [\[p\] perisperm \(PO:0020058\)](#) #0
 - [\[p\] seed chalaza \(PO:0006333\)](#) #0
 - [\[p\] seed coat \(PO:0009088\)](#) #23
 - [\[p\] seed funicle \(PO:0006332\)](#) #0
 - [\[p\] seed micropyle \(PO:0006334\)](#) #0
 - [\[p\] seed operculum \(PO:0019024\)](#) #0
 - [\[p\] seed raphe \(PO:0006331\)](#) #0
 - [\[p\] tracheid bar \(PO:0019026\)](#) #0
 - [\[p\] infructescence \(PO:0006342\)](#) #155
 - [\[p\] fruit \(PO:0009001\)](#) #155
 - [\[i\] seed \(PO:0009010\)](#) #155
 - [\[p\] embryo \(PO:0009009\)](#) #31
 - [\[p\] anil \(PO:0009090\)](#) #0
 - [\[p\] aniloid \(PO:0019022\)](#) #0
 - [\[p\] coma \(PO:0020061\)](#) #0
 - [\[p\] endosperm \(PO:0009089\)](#) #47
 - [\[p\] hilum \(PO:0020063\)](#) #0
 - [\[p\] perisperm \(PO:0020058\)](#) #0
 - [\[p\] seed chalaza \(PO:0006333\)](#) #0
 - [\[p\] seed coat \(PO:0009088\)](#) #23
 - [\[p\] seed funicle \(PO:0006332\)](#) #0
 - [\[p\] seed micropyle \(PO:0006334\)](#) #0
 - [\[p\] seed operculum \(PO:0019024\)](#) #0
 - [\[p\] seed raphe \(PO:0006331\)](#) #0
 - [\[p\] tracheid bar \(PO:0019026\)](#) #0

Answer: The two immediate parents are sporophyte (PO:0009003) and fruit (PO:0009001). Seed is an instance ([i] of sporophyte and is part of [p] fruit.

2d. On the same page, report how many phenotypes are associated with the term “seed” (PO:0009010). Hint: Examine the number following the term id.

In the same Summary, examine the number next to “seed.”

Summary for PO Term: sporophyte (PO:0009003)

Term Name	sporophyte
Definition	A diploid plant, or phase of a life cycle, that bears spores formed by meiosis.
Derivation	

- [plant ontology \(PO:0009075\)](#) #812
 - [\[i\] plant structure \(PO:0009011\)](#) #812
 - [\[i\] sporophyte \(PO:0009003\)](#) #788
 - [\[p\] infructescence \(PO:0006342\)](#) #155
 - [\[i\] seed \(PO:0009010\)](#) #155
 - [\[p\] root \(PO:0009005\)](#) #9
 - [\[p\] shoot \(PO:0009006\)](#) #627

Answer: 155 phenotype genes are associated with the term “seed.”

2e. With the answer from 2d, report how many phenotype genes in total are associated to the children terms of seed (PO:0009010). Also explain why this number is not the same as you see next to the term seed (PO:0009010). Hint: There are two types of associations in the ontology: direct associations, which are directly associated to the term for which a phenotype has been characterized and indirect associations, which a term gets from its children terms by virtue of a parent-child relationship. This means anything associated to the child is also associated to its parent and to its grandparent.

In the same Summary, add the numbers located next to “seed’s” children.

Answer: A total of 101 phenotype genes are associated with the children terms of seed. This is not the same number as shown next to the term “seed” because there are certain genes that are directly associated to the term “seed” and are not associated to its children terms.

Summary for PO Term: seed (PO:0009010)

Term Name: seed
Definition: A propagating organ formed in the reproductive cycle of gymnosperms and angiosperms, derived from the ovule and enclosing an embryo.
Derivation:

- plant ontology (PO:0009075) #812
 - plant structure (PO:0009011) #812
 - sporophyte (PO:0009003) #788
 - seed (PO:0009010) #155
 - embryo (PO:0009009) #31
 - anil (PO:0009090) #0
 - ariloid (PO:0019022) #0
 - coma (PO:0020061) #0
 - endosperm (PO:0009089) #47
 - hilum (PO:0020063) #0
 - perisperm (PO:0020058) #0
 - seed chalaza (PO:0006333) #0
 - seed coat (PO:0009018) #23
 - seed funicle (PO:0006334) #0
 - seed micropyle (PO:0006334) #0
 - seed operculum (PO:0019024) #0
 - seed raphe (PO:0006331) #0
 - tracheid bar (PO:0019026) #0

2f. On the same page, go to the phenotype association section and click on display all button. After it downloads the list, sort by “associated gene name” and click on the indirectly associated gene [agravitropism-1](#) and report:

- What does the description say about this gene?
- Name the germplasm where it was identified.
- What are the associated traits?
- At what growth stages were the traits assayed?
- In what plant parts (anatomy) were the traits assayed?

1) On the same Summary Page, scroll to the bottom and select “Display All,” as shown below.

NOTICE: Please be patient! It will take a while to display all the associations!

Phenotype Association (155 records found)

Download Display All

2) Select the term “agravitropism,” as shown below.

Phenotype Association (155 records found)					Download
#	Associated Term (sort)	Associated Gene Name (sort)	Gene Symbol (sort)	Evidence Codes	
1	embryo	agravitropism-1	agr1	TAS	
2	embryo	Awn-7	An7	TAS	
3	embryo	apical displacement-1	apd1	TAS	
4	embryo	club-shaped embryo-1	cle1	TAS	
5	embryo	Dominant hybrid lethal-1	Dhl1	TAS, IAGP	
6	embryo	Dominant hybrid lethal-2	Dhl2	TAS, IAGP	
7	embryo	depressed palea-1	dp1	TAS, IAGP	

3) The following Mutant Summary page will result. Examine the individual rows and columns for the requested information.

Summary for Rice Mutant: *agravitropism-1* (GR:0060019)

Gene Name	agravitropism-1
Gene Symbol	agr1
Phenotypic Description	Abnormal germination, embryo with shrunken shoot and root. Seedlings have various morphological and histological abnormalities of leaves and roots, loss of gravitropism.

[Top]

Allele	agr1.1
Germplasm	odm24

[Top]

Associated Feature		Sort by TO Accs (default)	Sort by Developmental Stage		
#	Trait	Developmental Stage	Anatomy Location	Evidence Code	
1	leaf related trait	02-seedling	leaf	TAS	
2	root related trait	02-seedling	root	TAS	
3	embryo related trait	01-germination	embryo	TAS	
4	embryo related trait	01-germination	embryo	TAS	

[Top]

Answer: a) Abnormal germination, embryo with shrunken shoot and root. Seedlings have various morphological and histological abnormalities of leaves and roots, loss of gravitropism.

b) Odm24

c) leaf related trait , root related trait, embryo related trait

d) 02-seedling, 01-germination

e) leaf, root, embryo

3a. Return to the Ontology Search page. Search for the term plant growth stage (GRO:0007199) and report how many organisms the growth stages are listed for.

1) Enter “plant growth stage” in the search field, as shown below.

Ontology Database			
Type ID or keyword to search	plant growth stage ontology	Search	Clear
select ontology (optional)	<input type="checkbox"/> Gene (GO) <input type="checkbox"/> Plant structure (PO) <input checked="" type="checkbox"/> Growth stage (GRO) <input type="checkbox"/> Trait (TO) <input type="checkbox"/> Environment (EO)	[e.g. flower or TO:0000303]	
		HELP	

2) The following Summary will result. Then select the rice growth stage (GRO:0007040)

Summary for *plant growth stage ontology*

Items 1 to 1 of 1

#	Term Accession	Term Name	Synonym	Definition
1	GRO:0007199	plant growth stage ontology	None	Ontology of the growth stages in various cereal crops.

Summary for Gramene Term: *plant growth stage ontology* (GRO:0007199)

Term Name plant growth stage ontology

Definition Ontology of the growth stages in various cereal crops.

Derivation

- [cereal plant ontology \(GRO:0080001\)](#) #1332
 - [i] [plant growth stage ontology \(GRO:0007199\)](#) #1332
 - [i] [maize growth stage \(GRO:0007002\)](#) #0
 - [i] [rice growth stage \(GRO:0007040\)](#) #1332
 - [i] [sorghum growth stage \(GRO:0007124\)](#) #0
 - [i] [wheat, barley and oat growth stage \(GRO:0007156\)](#) #0

Answer: From six organisms: Barley, Oat, Wheat, Maize, Rice, and Sorghum. Of which wheat, barley and oat have the same growth stage ontology.

3b. Follow the links on rice growth stages and report the definition and id of the “08 dough stage” in rice.

1) Select “rice growth stage” from the Summary page shown above. And keep on scrolling up to the view until you reach C-embryo stage (GRO:0007141). You will see 08-dough stage as one of the instances of reproductive stages of rice.

2) The following Summary will result.

Summary for Gramene Term: *08-dough stage* (GRO:0007042)

Term Name 08-dough stage

Synonym rice growth stage-8.

Definition One of the ripening stages when endosperm starts hardening

Derivation

- [cereal plant ontology \(GRO:0080001\)](#) #2144
 - [i] [plant growth stage ontology \(GRO:0007199\)](#) #1332
 - [i] [rice growth stage \(GRO:0007040\)](#) #1332
 - [i] [rice plant growth stage \(GRO:0007001\)](#) #1332
 - [i] [C-embryo stage \(GRO:0007141\)](#) #479
 - [i] [08-dough stage \(GRO:0007042\)](#) #133
 - [i] [8.1-dough stage \(GRO:0007152\)](#) #0
 - [i] [8.2-hard dough stage \(GRO:0007154\)](#) #0

Answer: The definition is “One of the ripening stages when endosperm starts hardening.” The id is GRO:0007042

3c. How many “brittle culm” genes are associated with “dough stage” in rice?

Select “Display All” at the bottom of the above Summary page. The following list will result.

#	Associated Term (sort)	Associated Gene Name (sort)	Gene Symbol (sort)	Evidence Codes
1	O8-dough stage	Activator for anthocyanin pigmentation	Ap	TAS, IAGP
2	O8-dough stage	adaxialized leaf-1	adl1	TAS
3	O8-dough stage	adaxialized leaf-2	adl2	TAS
4	O8-dough stage	Awn-1	An1	TAS
5	O8-dough stage	Awn-2	An2	TAS, IAGP
6	O8-dough stage	Awn-3	An3	TAS, IAGP
7	O8-dough stage	Awn-4	An4	TAS, IAGP
8	O8-dough stage	awn-5	an5	TAS, IAGP
9	O8-dough stage	Awn-6	An6	TAS
10	O8-dough stage	Awn-7	An7	TAS
11	O8-dough stage	awn-8	an8	TAS, IAGP
12	O8-dough stage	awn-9	an9	TAS, IAGP
13	O8-dough stage	awn-10	an10	TAS, IAGP
14	O8-dough stage	awn-11	an11	TAS, IAGP
15	O8-dough stage	awn-12	an12	TAS, IAGP
16	O8-dough stage	awn-13	an13	TAS, IAGP
17	O8-dough stage	awn-14	an14	TAS, IAGP
18	O8-dough stage	awn-15	an15	TAS, IAGP
19	O8-dough stage	awn-16	an16	TAS, IAGP
20	O8-dough stage	awn-17	an17	TAS, IAGP
21	O8-dough stage	awn-18	an18	TAS, IAGP
22	O8-dough stage	awn-19	an19	TAS, IAGP
23	O8-dough stage	awn-20	an20	TAS, IAGP
24	O8-dough stage	awn-21	an21	TAS, IAGP
25	O8-dough stage	awn-22	an22	TAS, IAGP
26	O8-dough stage	awn-23	an23	TAS, IAGP
27	O8-dough stage	awn-24	an24	TAS, IAGP
28	O8-dough stage	awn-25	an25	TAS, IAGP
29	O8-dough stage	awn-26	an26	TAS, IAGP
30	O8-dough stage	awn-27	an27	TAS, IAGP
31	O8-dough stage	awn-28	an28	TAS, IAGP
32	O8-dough stage	awn-29	an29	TAS, IAGP
33	O8-dough stage	awn-30	an30	TAS, IAGP
34	O8-dough stage	awn-31	an31	TAS, IAGP
35	O8-dough stage	awn-32	an32	TAS, IAGP
36	O8-dough stage	awn-33	an33	TAS, IAGP
37	O8-dough stage	awn-34	an34	TAS, IAGP
38	O8-dough stage	awn-35	an35	TAS, IAGP
39	O8-dough stage	awn-36	an36	TAS, IAGP
40	O8-dough stage	awn-37	an37	TAS, IAGP
41	O8-dough stage	awn-38	an38	TAS, IAGP
42	O8-dough stage	awn-39	an39	TAS, IAGP
43	O8-dough stage	awn-40	an40	TAS, IAGP
44	O8-dough stage	awn-41	an41	TAS, IAGP
45	O8-dough stage	awn-42	an42	TAS, IAGP
46	O8-dough stage	awn-43	an43	TAS, IAGP
47	O8-dough stage	awn-44	an44	TAS, IAGP
48	O8-dough stage	awn-45	an45	TAS, IAGP
49	O8-dough stage	awn-46	an46	TAS, IAGP
50	O8-dough stage	awn-47	an47	TAS, IAGP
51	O8-dough stage	awn-48	an48	TAS, IAGP
52	O8-dough stage	awn-49	an49	TAS, IAGP
53	O8-dough stage	awn-50	an50	TAS, IAGP
54	O8-dough stage	awn-51	an51	TAS, IAGP
55	O8-dough stage	awn-52	an52	TAS, IAGP
56	O8-dough stage	awn-53	an53	TAS, IAGP
57	O8-dough stage	awn-54	an54	TAS, IAGP
58	O8-dough stage	awn-55	an55	TAS, IAGP
59	O8-dough stage	awn-56	an56	TAS, IAGP
60	O8-dough stage	awn-57	an57	TAS, IAGP
61	O8-dough stage	awn-58	an58	TAS, IAGP
62	O8-dough stage	awn-59	an59	TAS, IAGP
63	O8-dough stage	awn-60	an60	TAS, IAGP
64	O8-dough stage	awn-61	an61	TAS, IAGP
65	O8-dough stage	awn-62	an62	TAS, IAGP
66	O8-dough stage	awn-63	an63	TAS, IAGP
67	O8-dough stage	awn-64	an64	TAS, IAGP
68	O8-dough stage	awn-65	an65	TAS, IAGP
69	O8-dough stage	awn-66	an66	TAS, IAGP
70	O8-dough stage	awn-67	an67	TAS, IAGP
71	O8-dough stage	awn-68	an68	TAS, IAGP
72	O8-dough stage	awn-69	an69	TAS, IAGP
73	O8-dough stage	awn-70	an70	TAS, IAGP
74	O8-dough stage	awn-71	an71	TAS, IAGP
75	O8-dough stage	awn-72	an72	TAS, IAGP
76	O8-dough stage	awn-73	an73	TAS, IAGP
77	O8-dough stage	awn-74	an74	TAS, IAGP
78	O8-dough stage	awn-75	an75	TAS, IAGP
79	O8-dough stage	awn-76	an76	TAS, IAGP
80	O8-dough stage	awn-77	an77	TAS, IAGP
81	O8-dough stage	awn-78	an78	TAS, IAGP
82	O8-dough stage	awn-79	an79	TAS, IAGP
83	O8-dough stage	awn-80	an80	TAS, IAGP
84	O8-dough stage	awn-81	an81	TAS, IAGP
85	O8-dough stage	awn-82	an82	TAS, IAGP
86	O8-dough stage	awn-83	an83	TAS, IAGP
87	O8-dough stage	awn-84	an84	TAS, IAGP
88	O8-dough stage	awn-85	an85	TAS, IAGP
89	O8-dough stage	awn-86	an86	TAS, IAGP
90	O8-dough stage	awn-87	an87	TAS, IAGP
91	O8-dough stage	awn-88	an88	TAS, IAGP
92	O8-dough stage	awn-89	an89	TAS, IAGP
93	O8-dough stage	awn-90	an90	TAS, IAGP
94	O8-dough stage	awn-91	an91	TAS, IAGP
95	O8-dough stage	awn-92	an92	TAS, IAGP
96	O8-dough stage	awn-93	an93	TAS, IAGP
97	O8-dough stage	awn-94	an94	TAS, IAGP
98	O8-dough stage	awn-95	an95	TAS, IAGP
99	O8-dough stage	awn-96	an96	TAS, IAGP
100	O8-dough stage	awn-97	an97	TAS, IAGP
101	O8-dough stage	awn-98	an98	TAS, IAGP
102	O8-dough stage	awn-99	an99	TAS, IAGP
103	O8-dough stage	awn-100	an100	TAS, IAGP
104	O8-dough stage	awn-101	an101	TAS, IAGP
105	O8-dough stage	awn-102	an102	TAS, IAGP
106	O8-dough stage	awn-103	an103	TAS, IAGP
107	O8-dough stage	awn-104	an104	TAS, IAGP
108	O8-dough stage	awn-105	an105	TAS, IAGP
109	O8-dough stage	awn-106	an106	TAS, IAGP
110	O8-dough stage	awn-107	an107	TAS, IAGP
111	O8-dough stage	awn-108	an108	TAS, IAGP
112	O8-dough stage	awn-109	an109	TAS, IAGP
113	O8-dough stage	awn-110	an110	TAS, IAGP
114	O8-dough stage	awn-111	an111	TAS, IAGP
115	O8-dough stage	awn-112	an112	TAS, IAGP
116	O8-dough stage	awn-113	an113	TAS, IAGP
117	O8-dough stage	awn-114	an114	TAS, IAGP
118	O8-dough stage	awn-115	an115	TAS, IAGP
119	O8-dough stage	awn-116	an116	TAS, IAGP
120	O8-dough stage	awn-117	an117	TAS, IAGP
121	O8-dough stage	awn-118	an118	TAS, IAGP
122	O8-dough stage	awn-119	an119	TAS, IAGP
123	O8-dough stage	awn-120	an120	TAS, IAGP
124	O8-dough stage	awn-121	an121	TAS, IAGP
125	O8-dough stage	awn-122	an122	TAS, IAGP
126	O8-dough stage	awn-123	an123	TAS, IAGP
127	O8-dough stage	awn-124	an124	TAS, IAGP
128	O8-dough stage	awn-125	an125	TAS, IAGP
129	O8-dough stage	awn-126	an126	TAS, IAGP
130	O8-dough stage	awn-127	an127	TAS, IAGP
131	O8-dough stage	awn-128	an128	TAS, IAGP
132	O8-dough stage	awn-129	an129	TAS, IAGP
133	O8-dough stage	awn-130	an130	TAS, IAGP
134	O8-dough stage	awn-131	an131	TAS, IAGP
135	O8-dough stage	awn-132	an132	TAS, IAGP
136	O8-dough stage	awn-133	an133	TAS, IAGP
137	O8-dough stage	awn-134	an134	TAS, IAGP
138	O8-dough stage	awn-135	an135	TAS, IAGP
139	O8-dough stage	awn-136	an136	TAS, IAGP
140	O8-dough stage	awn-137	an137	TAS, IAGP
141	O8-dough stage	awn-138	an138	TAS, IAGP
142	O8-dough stage	awn-139	an139	TAS, IAGP
143	O8-dough stage	awn-140	an140	TAS, IAGP
144	O8-dough stage	awn-141	an141	TAS, IAGP
145	O8-dough stage	awn-142	an142	TAS, IAGP
146	O8-dough stage	awn-143	an143	TAS, IAGP
147	O8-dough stage	awn-144	an144	TAS, IAGP
148	O8-dough stage	awn-145	an145	TAS, IAGP
149	O8-dough stage	awn-146	an146	TAS, IAGP
150	O8-dough stage	awn-147	an147	TAS, IAGP
151	O8-dough stage	awn-148	an148	TAS, IAGP
152	O8-dough stage	awn-149	an149	TAS, IAGP
153	O8-dough stage	awn-150	an150	TAS, IAGP
154	O8-dough stage	awn-151	an151	TAS, IAGP
155	O8-dough stage	awn-152	an152	TAS, IAGP
156	O8-dough stage	awn-153	an153	TAS, IAGP
157	O8-dough stage	awn-154	an154	TAS, IAGP
158	O8-dough stage	awn-155	an155	TAS, IAGP
159	O8-dough stage	awn-156	an156	TAS, IAGP
160	O8-dough stage	awn-157	an157	TAS, IAGP
161	O8-dough stage	awn-158	an158	TAS, IAGP
162	O8-dough stage	awn-159	an159	TAS, IAGP
163	O8-dough stage	awn-160	an160	TAS, IAGP
164	O8-dough stage	awn-161	an161	TAS, IAGP
165	O8-dough stage	awn-162	an162	TAS, IAGP
166	O8-dough stage	awn-163	an163	TAS, IAGP
167	O8-dough stage	awn-164	an164	TAS, IAGP
168	O8-dough stage	awn-165	an165	TAS, IAGP
169	O8-dough stage	awn-166	an166	TAS, IAGP
170	O8-dough stage	awn-167	an167	TAS, IAGP
171	O8-dough stage	awn-168	an168	TAS, IAGP
172	O8-dough stage	awn-169	an169	TAS, IAGP
173	O8-dough stage	awn-170	an170	TAS, IAGP
174	O8-dough stage	awn-171	an171	TAS, IAGP
175	O8-dough stage	awn-172	an172	TAS, IAGP
176	O8-dough stage	awn-173	an173	TAS, IAGP
177	O8-dough stage	awn-174	an174	TAS, IAGP
178	O8-dough stage	awn-175	an175	TAS, IAGP
179	O8-dough stage	awn-176	an176	TAS, IAGP
180	O8-dough stage	awn-177	an177	TAS, IAGP
181	O8-dough stage	awn-178	an178	TAS, IAGP
182	O8-dough stage	awn-179	an179	TAS, IAGP
183	O8-dough stage	awn-180	an180	TAS, IAGP
184	O8-dough stage	awn-181	an181	TAS, IAGP
185	O8-dough stage	awn-182	an182	TAS, IAGP
186	O8-dough stage	awn-183	an183	TAS, IAGP
187	O8-dough stage	awn-184	an184	TAS, IAGP
188	O8-dough stage	awn-185	an185	TAS, IAGP
189	O8-dough stage	awn-186	an186	TAS, IAGP
190	O8-dough stage	awn-187	an187	TAS, IAGP
191	O8-dough stage	awn-188	an188	TAS, IAGP
192	O8-dough stage	awn-189	an189	TAS, IAGP
193	O8-dough stage	awn-190	an190	TAS, IAGP
194	O8-dough stage	awn-191	an191	TAS, IAGP
195	O8-dough stage	awn-192	an192	TAS, IAGP
196	O8-dough stage	awn-193	an193	TAS, IAGP
197	O8-dough stage	awn-194	an194	TAS, IAGP
198	O8-dough stage	awn-195	an195	TAS, IAGP
199	O8-dough stage	awn-196	an196	TAS, IAGP
200	O8-dough stage	awn-197	an197	TAS, IAGP
201	O8-dough stage	awn-198	an198	TAS, IAGP
202	O8-dough stage	awn-199	an199	TAS, IAGP
203	O8-dough stage	awn-200	an200	TAS, IAGP
204	O8-dough stage	awn-201	an201	TAS, IAGP
205	O8-dough stage	awn-202	an202	TAS, IAGP
206	O8-dough stage	awn-203	an203	TAS, IAGP
207	O8-dough stage	awn-204	an204	TAS, IAGP
208	O8-dough stage	awn-205	an205	TAS, IAGP
209	O8-dough stage	awn-206	an206	TAS, IAGP
210	O8-dough stage	awn-207	an207	TAS, IAGP
211	O8-dough stage	awn-208	an208	TAS, IAGP
212	O8-dough stage	awn-209	an209	TAS, IAGP
213	O8-dough stage	awn-210	an210	TAS, IAGP
214	O8-dough stage	awn-211	an211	TAS, IAGP
215	O8-dough stage	awn-212	an212	TAS, IAGP
216	O8-dough stage	awn-213	an213	TAS, IAGP
217	O8-dough stage	awn-214	an214	TAS, IAGP
218	O8-dough stage	awn-215	an215	TAS, IAGP
219	O8-dough stage	awn-216	an216	TAS, IAGP
220	O8-dough stage	awn-217	an217	TAS, IAGP
221	O8-dough stage	awn-218	an218	TAS, IAGP
222	O8-dough stage	awn-219	an219	TAS, IAGP
223	O8-dough stage	awn-220	an220	TAS, IAGP
224	O8-dough stage	awn-221	an221	TAS, IAGP
225	O8-dough stage	awn-222	an222	TAS, IAGP
226	O8-dough stage	awn-223	an223	TAS, IAGP
227	O8-dough stage	awn-224	an224	TAS, IAGP
228	O8-dough stage	awn-225	an225	TAS, IAGP
229	O8-dough stage	awn-226	an226	TAS, IAGP
230	O8-dough stage	awn-227	an227	TAS, IAGP
231	O8-dough stage	awn-228	an228	TAS, IAGP
232	O8-dough stage	awn-229	an229	TAS, IAGP
233	O8-dough stage	awn-230	an230	TAS, IAGP
234	O8-dough stage	awn-231	an231	TAS, IAGP
235	O8-dough stage	awn-232	an232	TAS, IAGP
236	O8-dough stage	awn-233	an233	TAS, IAGP
237	O8-dough stage	awn-234	an234	TAS, IAGP
238	O8-dough stage	awn-235	an235	TAS, IAGP
239	O8-dough stage	awn-236		

Trait Ontology

5a. Go to the Ontology search section on the [Gramene Ontology page](#) and search for “trait ontology.” How many major categories (except obsolete) of traits are there and which one has the greatest number of associations?

1) On the Ontology search page, enter “trait ontology,” as shown below.

Ontology Database	
Type ID or keyword to search	<input type="text" value="trait ontology"/> <input type="button" value="Search"/> <input type="button" value="Clear"/> HELP
select ontology (optional)	<input type="checkbox"/> Gene (GO) <input type="checkbox"/> Plant structure (PO) <input type="checkbox"/> Growth stage (GRO) <input checked="" type="checkbox"/> Trait (TO) <input type="checkbox"/> Environment (EO) [e.g. flower or TO:0000303]

2) The following Summary will result will result. After this click on the term with id: TO:0000387 (Trait Ontology)

Summary for TO Term: *trait ontology* (TO:0000387)

Term Name	trait ontology
Synonym	TO.
Derivation	
<ul style="list-style-type: none"> • trait ontology (TO:0000387) #786 <ul style="list-style-type: none"> ◦ [i] biochemical trait (TO:0000277) #94 ◦ [i] fertility or sterility trait (TO:0000392) #36 ◦ [i] yield related trait (TO:0000371) #3 ◦ [i] plant anatomy and morphology related trait (TO:0000017) #482 ◦ [i] plant development related trait (TO:0000357) #139 ◦ [i] quality related trait (TO:0000597) #119 ◦ [i] stature or vigor related trait (TO:0000133) #58 ◦ [i] stress related trait (TO:0000164) #211 	

Answer: There are eight major categories of traits. They are [biochemical trait](#) (TO:0000277) , [fertility or sterility trait](#) (TO:0000392), [yield related trait](#) (TO:0000371), [plant anatomy and morphology related trait](#) (TO:0000017), [plant development related trait](#) (TO:0000357), [quality related trait](#) (TO:0000597), [stature or vigor related trait](#) (TO:0000133), and [stress related trait](#) (TO:0000164).

5b. How many phenotype genes are associated with the trait endosperm color?

In the same Summary Page, select “Display All” at the bottom of the page. The following list will result.

286	embryo related trait	globular embryo-1	gle1	TAS
287	embryo related trait	apical displacement-1	apd1	TAS
288	endosperm color	amylose extender-1	ae1	TAS
289	endosperm color	Red pericarp and seed coat	Rd	TAS, IAGP
290	endosperm color	amylose extender-2	ae2	TAS
291	endosperm color	Rice R gene (Anthocyanin biosynthesis)-a	Ra	TAS, IAGP
292	endosperm color	Rice R gene-b	Rb	TAS, IAGP
293	endosperm color	Brown pericarp and seed coat	Rc	TAS, IAGP
294	endosperm color	amylose extender-3	ae3	TAS
295	endosperm quality (sensu Poaceae)	amylose extender-1	ae1	TAS
296	endosperm quality (sensu Poaceae)	reduced embryo-3	re3	TAS

Answer: There are seven phenotype genes associated with the trait term endosperm color (TO:0000487).

5c. What linkage group is the gene *Rice R gene (Anthocyanin biosynthesis)-a* located on?

1) In the same summary page, select *Rice R gene*, as shown below.

286	embryo related trait	globular embryo-1	gle1	TAS
287	embryo related trait	apical displacement-1	apd1	TAS
288	endosperm color	amylose extender-1	ae1	TAS
289	endosperm color	Red pericarp and seed coat	Rd	TAS, IAGP
290	endosperm color	amylose extender-2	ae2	TAS
291	endosperm color	<u>Rice R gene (Anthocyanin biosynthesis)-a</u>	Ra	TAS, IAGP
292	endosperm color	Rice R gene-b	Rb	TAS, IAGP
293	endosperm color	Brown pericarp and seed coat	Rc	TAS, IAGP
294	endosperm color	amylose extender-3	ae3	TAS
295	endosperm quality (sensu Poaceae)	amylose extender-1	ae1	TAS
296	endosperm quality (sensu Poaceae)	reduced embryo-3	re3	TAS

2) The following Mutant Summary will result.

Summary for Rice Mutant: *Rice R gene (Anthocyanin biosynthesis)-a* (GR:0060719)

Gene Name	Rice R gene (Anthocyanin biosynthesis)-a
Gene Symbol	Ra
Phenotypic Description	One rice R gene. An active homologue with extensive homology with other R genes. Located at a position on chromosome 4 previously shown to be in synteny with regions of maize chromosomes 2 and 10 that contain the B and R loci, respectively. Ra gene can activate the anthocyanin pathway.

Answer: The gene *Rice R gene (Anthocyanin biosynthesis)-a* is located on linkage group 4 (evidence *Rice-Cornell RFLP 2001*).

6. Return to the Ontology search page. Name the two trait categories to which the trait “amylose to amylopectin ratio” belongs.

Enter the term “amylose to amylopectin ratio” in the main Ontology search field. The following Summary will result.

Summary for TO Term: *amylose to amylopectin ratio* (TO:0000372)

Term Name	amylose to amylopectin ratio
Synonym	AMYAMYPTRO.
Definition	Ratio of amount of amylose to amylopectin content.
Derivation	<ul style="list-style-type: none"> • trait ontology (TO:0000387) #780 <ul style="list-style-type: none"> ◦ [i] biochemical trait (TO:0000277) #93 <ul style="list-style-type: none"> ▪ [i] metabolite content related trait (TO:0000281) #94 <ul style="list-style-type: none"> ▪ [i] carbohydrate content (TO:0000291) #19 <ul style="list-style-type: none"> ▪ [i] amylopectin content (TO:0000097) #0 <ul style="list-style-type: none"> ▪ [i] amylose to amylopectin ratio (TO:0000372) #0 ▪ [i] amylose content (TO:0000196) #19 <ul style="list-style-type: none"> ▪ [i] amylose to amylopectin ratio (TO:0000372) #0 ◦ [i] quality related trait (TO:0000597) #119 <ul style="list-style-type: none"> ▪ [i] seed quality (TO:0000162) #104 <ul style="list-style-type: none"> ▪ [i] seed composition based quality trait (TO:0000488) #39 <ul style="list-style-type: none"> ▪ [i] carbohydrate composition related trait (TO:0000489) #31 <ul style="list-style-type: none"> ▪ [i] amylopectin content (TO:0000097) #0 <ul style="list-style-type: none"> ▪ [i] amylose to amylopectin ratio (TO:0000372) #0

Answer: The trait [amylose to amylopectin ratio \(TO:0000372\)](#) belongs to two categories: [biochemical trait \(TO:0000277\)](#) and [quality related trait \(TO:0000597\)](#).

7a. Return to the Ontology search field. Name the major trait categories of which “stem length” is an instance of.

Enter “stem length” in the main Ontology search field. The following Summary page will result.

Summary for TO Term: *stem length* (TO:0000576)

Term Name	stem length
Definition	Measure from soil surface to highest point on stem.
Derivation	<ul style="list-style-type: none"> • trait ontology (TO:0000387) #789 <ul style="list-style-type: none"> ◦ [i] plant development related trait (TO:0000357) #139 <ul style="list-style-type: none"> ▪ [i] stem length (TO:0000576) #53 <ul style="list-style-type: none"> ▪ [i] culm length (TO:0000309) #39 ▪ [i] internode length (TO:0000145) #14 ◦ [i] stress related trait (TO:0000164) #211 <ul style="list-style-type: none"> ▪ [i] abiotic stress related trait (TO:0000168) #129 <ul style="list-style-type: none"> ▪ [i] stem length (TO:0000576) #53 <ul style="list-style-type: none"> ▪ [i] culm length (TO:0000309) #39 ▪ [i] internode length (TO:0000145) #14 ◦ [i] plant anatomy and morphology related trait (TO:0000017) #482 <ul style="list-style-type: none"> ▪ [i] shoot related trait (TO:0000077) #240 <ul style="list-style-type: none"> ▪ [i] stem related trait (TO:0000361) #90 <ul style="list-style-type: none"> ▪ [i] stem length (TO:0000576) #53 <ul style="list-style-type: none"> ▪ [i] culm length (TO:0000309) #39 ▪ [i] internode length (TO:0000145) #14 ◦ [i] stature or vigor related trait (TO:0000133) #38 <ul style="list-style-type: none"> ▪ [i] height related trait (TO:0000171) #56 <ul style="list-style-type: none"> ▪ [i] plant height (TO:0000207) #56 <ul style="list-style-type: none"> ▪ [i] stem length (TO:0000576) #53 <ul style="list-style-type: none"> ▪ [i] culm length (TO:0000309) #39 ▪ [i] internode length (TO:0000145) #14

Answer: The trait [stem length \(TO:0000576\)](#) is an instance of four trait categories. The categories are [plant development related trait \(TO:0000357\)](#), [stress related trait \(TO:0000164\)](#), [plant anatomy and morphology related trait \(TO:0000017\)](#), and [stature or vigor related trait \(TO:0000133\)](#).

7b. Name the dwarf genes associated with stem length's child term "internode length."

On the same Summary page, scroll down the list of Phenotype Associations.

37	culm length	reduced culm number-6	rcn6	TAS
38	culm length	semidwarf-1	sd1	TAS, IAGP
39	culm length	Dwarf-44	Dwf44	TAS, IAGP
40	internode length	accelerated overgrowth of internode	ao	TAS
41	internode length	dwarf-1	dwf1	TAS, IAGP
42	internode length	dwarf-9	dwf9	TAS
43	internode length	dwarf-10	dwf10	TAS, IAGP
44	internode length	dwarf-24	dwf24	TAS, IAGP
45	internode length	dwarf-25	dwf25	TAS, IAGP

Answer: There are 5 dwarf genes associated with the trait term internode length. They are dwarf-1, dwarf-9, dwarf-10, dwarf-24, dwarf-25.

8a. Return to the Ontology search field. Name the two planthopper resistance traits.

Enter "planthopper resistance" in the main Ontology search field. The following Summary will result.

Summary for planthopper resistance

Items 1 to 2 of 2.

#	Term Accession	Term Name	Synonym	Definition
1	TO:0000424	brown planthopper resistance	BPH, BPHRS.	Causal agent: Nilaparvata lugens (also Nilaparvata lugens). Symptoms: partial to pronounced yellowing and increasing severity of stunting. Extreme signs are wilting to death of plants. Infested areas in the field may be patchy
2	TO:0000205	white-backed planthopper resistance	WBPH, WBPHRS.	Causal agent: Sagotella furcifera. Symptoms: partial to pronounced yellowing and increasing severity of stunting. Extreme signs are wilting and death of plants. Infested areas in the field may be patchy. (similar to the symptoms of whitebacked planthopper)

Answer: The two traits are brown planthopper resistance (TO:0000424) and white-backed planthopper resistance (TO:0000205).

8b. Report how many genes are associated with each one of these traits.

Select each of the planthopper resistance term accessions, as shown above. The following summaries will result.

Summary for TO Term: *brown planthopper resistance* (TO:0000424)

Term Name	brown planthopper resistance
Synonym	BPH, BPHRS.
Definition	Causal agent: Nilaparvata lugens (also Nilaparvata lugens). Symptoms: partial to pronounced yellowing and increasing severity of stunting. Extreme signs are wilting to death of plants. Infested areas in the field may be patchy
Derivation	<ul style="list-style-type: none"> • trait ontology (TO:0000387) #789 <ul style="list-style-type: none"> ◦ [i] stress related trait (TO:0000164) #211 <ul style="list-style-type: none"> ▪ [i] biotic stress related trait (TO:0000179) #82 <ul style="list-style-type: none"> ▪ [i] crop damage resistance trait (TO:0000236) #82 <ul style="list-style-type: none"> ▪ [i] animal damage resistance (TO:0000054) #13 <ul style="list-style-type: none"> ▪ [i] insect damage resistance (TO:0000261) #13 <ul style="list-style-type: none"> ▪ [i] brown planthopper resistance (TO:0000424) #13

Summary for TO Term: *white-backed planthopper resistance* (TO:0000205)

Term Name	white-backed planthopper resistance
Synonym	WBPH, WBPHRS.
Definition	Causal agent: Sagotella furcifera. Symptoms: partial to pronounced yellowing and increasing severity of stunting. Extreme signs are wilting and death of plants. Infested areas in the field may be patchy. (similar to the symptoms of whitebacked planthopper)
Derivation	<ul style="list-style-type: none"> • trait ontology (TO:0000387) #789 <ul style="list-style-type: none"> ◦ [i] stress related trait (TO:0000164) #211 <ul style="list-style-type: none"> ▪ [i] biotic stress related trait (TO:0000179) #82 <ul style="list-style-type: none"> ▪ [i] crop damage resistance trait (TO:0000236) #82 <ul style="list-style-type: none"> ▪ [i] animal damage resistance (TO:0000054) #13 <ul style="list-style-type: none"> ▪ [i] insect damage resistance (TO:0000261) #13 <ul style="list-style-type: none"> ▪ [i] white-backed planthopper resistance (TO:0000205) #0 <ul style="list-style-type: none"> ▪ [i] white-backed planthopper egg mortality (TO:0000569) #0

Answer: The trait [brown planthopper resistance \(TO:0000424\)](#) has 13 genes associated with it and the white-backed has 0.

Annotation exercises

Exercise-1

Please read the following abstract published on a rice semidwarfing gene and answer the questions that will help in its annotation.

ABSTRACT: ref: DNA Res. 2002 Feb 28;9(1):11-7.

A rice **semidwarfing gene**, **sd-1**, known as the "green revolution gene," was isolated by positional cloning and revealed to encode **gibberellin 20-oxidase**, the key enzyme in the **gibberellin biosynthesis** pathway. Analysis of 3477 segregants using several PCR-based marker technologies, including cleaved amplified polymorphic sequence, derived-CAPS, and single nucleotide polymorphisms revealed 1 ORF in a 6-kb candidate interval. Normal-type rice cultivars have an identical sequence in this region, consisting of 3 exons (558, 318, and 291 bp) and 2 introns (105 and 1471 bp). **Dee-Geo-Woo-Gen**-type **sd-1** mutants have a 383-bp deletion from the genome (278-bp deletion from the expressed sequence), from the middle of exon 1 to upstream of exon 2, including a 105-bp intron, resulting in a frame-shift that produces a termination codon after the deletion site. The radiation-induced **sd-1** mutant **Calrose 76** has a 1-bp substitution in exon 2, causing an amino acid substitution (Leu [CTC] to Phe [TTC]). Expression analysis suggests the existence of at least one more locus of gibberellin 20-oxidase which may prevent **severe dwarfism** from developing in **sd-1** mutants.

Use the highlighted terms to answer the following.

9a. What is the name of the rice gene mentioned in the above abstract?

Answer: semidwarfing gene, green revolution gene

9b. What is the gene symbol suggested by the authors?

Answer: sd-1

9c. What is the name of the enzyme (protein) encoded by this gene?

Answer: gibberellin 20-oxidase

9d. Name the rice germplasms from where the mutant gene was isolated.

Answer: Dee-Geo-Woo-Gen and Calrose 76

9e. Using the Gene Ontology search, suggest the following characteristics of this gene by providing the GO terms and their respective id's.

- a. Molecular function
- b. Biological process

Answer: a) gibberellin 20-oxidase activity (GO:0045544)
b) gibberellic acid biosynthesis (GO:0009686) and gibberellic acid mediated signaling (GO:0009740)

9f. Find the Trait Ontology terms and their ids representing the traits observed in the phenotype.

Answer: plant height (TO:0000207) and gibberellic acid sensitivity (TO:0000166)

See an example at http://www.gramene.org/db/protein/protein_search?acc=Q8S492

Exercise-2

Gene actions of QTLs affecting several agronomic traits resolved in a recombinant inbred rice population and two testcross populations.

Mei HW, Luo LJ, Ying CS, Wang YP, Yu XQ, Guo LB, Paterson AH, Li ZK.

Theor Appl Genet. 2003 Jun;107(1):89-101. Epub 2003 Apr 30.
PMID: 12721635

To understand the types of gene action controlling seven quantitative traits in rice, QTL mapping was performed to dissect the main effect (M-QTLs) and digenic epistatic (E-QTLs) QTLs responsible for the trait performance of 254 recombinant inbred lines (RILs) of "Lemont/Teqing", and two testcross (TC) F(1) populations derived from these RILs. The correlation analyses reveal a general pattern, i.e. trait heritability in the RILs was negatively correlated to trait heterosis in the TC hybrids. A large number of M-QTLs and E-QTLs affecting seven traits, including **heading date (HD)**, **plant height (PH)**, **flag leaf length (FLL)**, **flag leaf width (FLW)**, **panicle length (PL)**, **spikelet number per panicle (SN)** and **spikelet fertility (SF)**, were identified and could be classified into two predominant groups, additive QTLs detected primarily in the RILs, and overdominant QTLs identified exclusively in the TC populations. There is little overlap between QTLs identified in the RILs and in the TC populations. This result implied that additive gene action is largely independent from non-additive gene action in the genetic control of quantitative traits of rice. The detected E-QTLs collectively explained a much greater portion of the total phenotypic variation than the M-QTLs, supporting prior findings that epistasis has played an important role in the genetic control of quantitative traits in rice. The implications of these results to the development of inbred and hybrid cultivars were discussed.

Phrase from abstract	Trait Ontology term	Trait Ontology id
heading date (HD)	Days to Heading	TO:0000137
plant height (PH)	Plant Height	TO:0000207

flag leaf length (FLL)	Leaf length	TO:0000135
flag leaf width (FLW)	Leaf width	TO:0000370
panicle length (PL)	Panicle length	TO:0000040
spikelet number per panicle (SN)	spikelet number	TO:0000456
spikelet fertility (SF)	spikelet fertility	TO:0000180

Annotation exercise on Expression libraries

Term: Sporophyte
Id: [PO:0009003](#)

Term: Leaf
Id: [PO:0009025](#)

Term: Inflorescence
Id: [PO:0009049](#)
Synonym: Panicle

Term: Sporophyte
Id: [PO:0009003](#)
Growth stage:
Term::
Id: [GRO:0007047](#)

Term: Shoot apical meristem
Id: [PO:0020148](#)

dbEST Libraries for *Oryza sativa*

Show entries with at least sequences

[Collapse All](#) | [Expand All](#)

Tissue	Lib. ID	Library Name	Sequences
All plant	Lib. 10901	Rice Uni Zap Library	29
Leaf	Lib. 9652	Drought stress (leaf)	5615
	Lib. 1010	Rice cDNA from immature leaf including apical meristem	2680
	Lib. 9651	Drought stress (root)	200
Panicle	Lib. 499	Rice panicle at flowering stage	6502
	Lib. 535	Rice panicle at ripening stage	3056
	Lib. 1009	Rice panicle shorter than 3cm	2899
Panicle shorter than 3cm	Lib. 14641	rice panicle shorter than 3cm	1
Seedlings	Lib. 11160	Rice cold stress germination cDNA library	3080
Shoot apical meristem			

<http://www.ncbi.nlm.nih.gov/UniGene/lbrowse2.cgi?TAXID=4530&CUTOFF=0>

The Plant Ontology terms for Plant structure (PO) (anatomy) and the growth stages (GRO) terms are suggested for use in defining the descriptors for expression libraries or the tissue samples that were used in these experiments.

Library Browser - Netscape

http://www.ncbi.nlm.nih.gov/UniGene/lbrowse2.cgi?TAXID=4530&CUTOFF=0

EBI Databases Nucleotide for

Lib. ID	Library Name	Sequences
Lib. 10221	Oryza sativa Zhong A strain stem	2
Unclassified 169 Libraries		
Lib. 15105	Oryza sativa library (Han B)	21289
Lib. 9824	Oryza sativa mature leaf library induced by M.grisea	15139
Lib. 79	Rice callus	13388
Lib. 12928	OSJNEb	10471
Lib. 9822	Endosperm library from Oryza sativa (10 days after anthesis)	9990
Lib. 12931	OSJNEa	9585
Lib. 14239	OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)	9392
Lib. 12926	OSJIEb	9377
Lib. 12930	OSJNEd	8990
Lib. 12925	OSJIEa	8914
Lib. 307	Rice green shoot	7986
Lib. 12929	OSJNEc	7898
Lib. 12932	OSJNEf	7172
Lib. 193	Rice shoot	7154
Lib. 1073	Rice Immature Seed Lambda ZAPII cDNA Library	6730
Lib. 14231	Rice etiolated leaf plasmid cDNA library (14ETL)	6454
Lib. 16654	Rice flower lambda phage cDNA library (FLO)	5988
Lib. 14243	AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)	5740
Lib. 14242	Rice callus plasmid cDNA library (NACL)	5696
Lib. 14233	Rice leaf plasmid cDNA library I (30DGS)	5624
Lib. 14238	ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)	5483
Lib. 12927	OSJNEa	5389
Lib. 101	Rice root	5247
Lib. 12215	IRRI clones	5124
Lib. 14234	Rice leaf plasmid cDNA library II (7LEAF)	5114
Lib. 12423	IRRI Drought Stress Panicle Library	4581
Lib. 16652	Salt treated rice leaf lambda phage cDNA library (14Salt)	3917
Lib. 961	Rice callus cDNA	3507
Lib. 4938	OA	3075
Lib. 9823	Stem library from Oryza sativa (3-5 leaf stage)	2830
Lib. 14244	Regenerated callus lambda phage cDNA library (RCL1)	2631
Lib. 1746	Oryza sativa mature leaf Nipponbare	2323
Lib. 8844	Rice callus (2001)	2260
Lib. 14235	ABF3-overexpressing transgenic rice lambda phage cDNA library (ABF1)	2202
Lib. 14240	OsHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN)	2193
Lib. 14241	AtJMT-overexpressing transgenic rice lambda phage cDNA library	2170

Often the description is not sufficient to infer the information about the plant structure. For this try to click the hyperlinked **Lib_number** (e.g. Lib. 12928) and the detail page refers to the tissue and organ types

<http://www.ncbi.nlm.nih.gov/UniGene/lbrowse2.cgi?TAXID=4530&CUTOFF=0>

UniGene Library - Netscape

http://www.ncbi.nlm.nih.gov/UniGene/lbrowse2.cgi?TAXID=4530&CUTOFF=0

NCBI UniGene

ORGANIZED VIEW OF THE TRANSCRIPTOME

PubMed Nucleotide Protein Genome Structure Popset Taxonomy

Search UniGene [Go] [Clear]

Limits PreviewIndex History Clipboard Details

NCBI OSJNEb (dbEST Library ID:12928)

Organism: Oryza sativa (japonica cultivar-group)

Developmental stage: 3 week

Cultivar: Nipponbare

Tissue: **Leaf**

Vector: pBluescript KS+ (Plasmid)

Lab host: DH10B

Cloning sites: EcoRI, XhoI

Library Description
24 hrs after inoculation with Rice Blast (Che 86061)

Sequence Submitters
Rod Wing
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ 85721-0088, USA

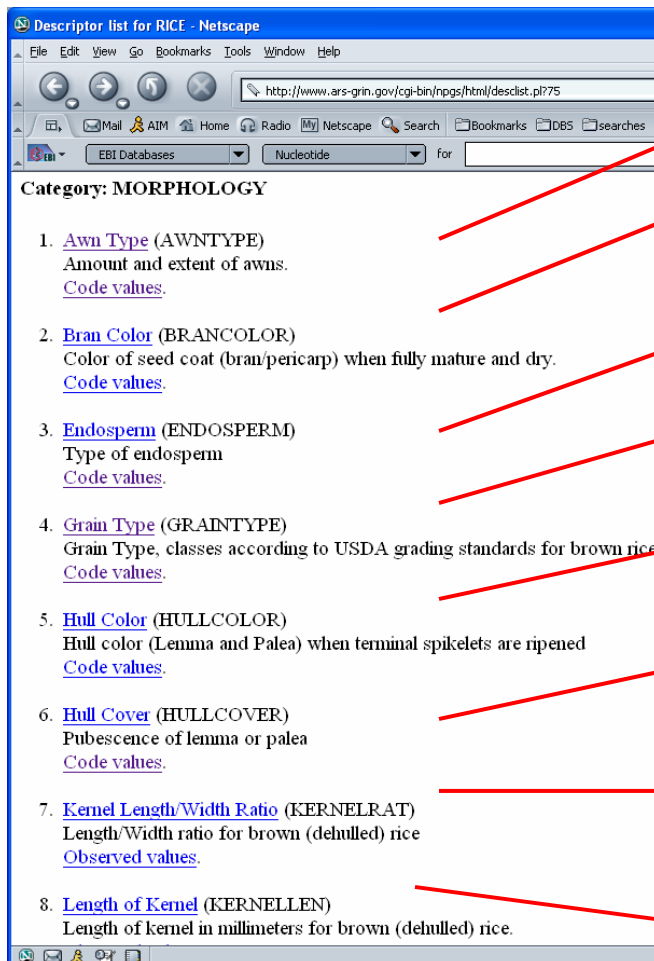
Distribution of member sequences in UniGene
9990 of the 10471 sequences from this library have been classified into 3005 UniGene entries

Transcripts per million	EST count	UniGene Entry
32150	318	Os.9330
13140	130	Os.7947

Transcribed locus, moderately similar to NP_181241.1 Arabidopsis thaliana At2g37040 gene
Endo-1,3;1,4-beta-glucanase

Term: Leaf
Id: [PO:0009025](#)

Listing of Germplasm stocks in ARS-GRIN databases. Can be listed/categorized based on trait evaluations, with a mapping to the Trait Ontology (TO) terms



Term: Awn length
Id: [TO:0000072](#)

Term: Seed coat color
Id: [TO:0000190](#)

Term: endosperm quality (sensu Poaceae)
Id: [TO:0000150](#)

Term: grain length
Id: [TO:0000395](#)

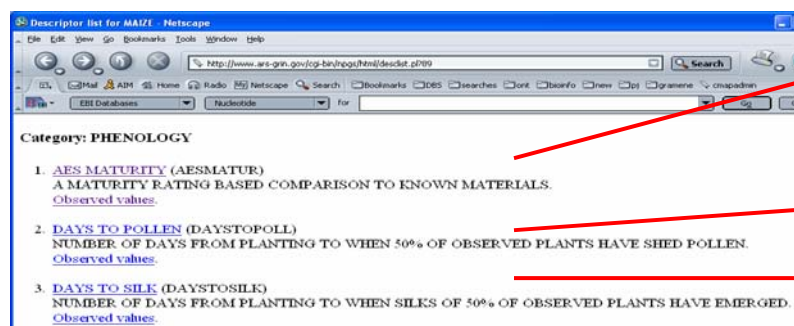
Term: lemma and palea color
Id: [TO:0000264](#)

Term: lemma and palea pubescence
Id: [TO:0000417](#)

Term: seed length to width ratio
Id: [TO:0000411](#)

Term: seed length
Id: [TO:0000146](#)

<http://www.ars-grin.gov/cgi-bin/npgs/html/desclist.pl?75>



Term: days to maturity
Id: [TO:0000469](#)

Term: male flowering
Id: [TO:0000365](#)

Term: female flowering
Id: [TO:0000359](#)

<http://www.ars-grin.gov/cgi-bin/npgs/html/desclist.pl?89>