

ONTOLOGY DEVELOPMENT AND INTEGRATION

Tutorial exercise: A preview

<http://www.gramene.org>



What's in a name/vocabulary?

- How do we define “cell”?
 - the basic structural and functional unit of all living organisms
 - a device that delivers an electric current as the result of a chemical reaction
 - a room where a prisoner is kept
 - any small compartment (eg. *cells* of a honeycomb)
 - a small unit serving as part of or as the nucleus of a larger political movement
- A cell can be a whole organism or a part of it

What is an Ontology?

An Ontology is a glossary of keywords arranged in a structured order or a network based on the biological concepts

- The problem:
 - Vast amounts of biological data
 - Different names/terms for the same concepts
 - Cross-species comparison is difficult
- A (part of the) solution:
 - Ontology : “a controlled vocabulary that can be applied to either all organisms or at least with in a kingdom/sub-class/family even as knowledge of phenotypes and the associated gene and their roles in cells is accumulating and changing”

What is an Ontology?

- NOT a system of nomenclature or a list of gene products/phenotypes
- It doesn't attempt to cover all aspects of biology or evolutionary relationships
- NOT a dictated standard
- NOT a way to unify databases.
- It allows the users to query the different databases using the same keywords and query strings provided those different databases have implemented the commonly adopted ontologies.

How does it work?

In Gramene we have ontologies describing three different types of biological concepts.

- **Gene Ontology (GO)** to describe a protein/gene's biochemical property
 - **Molecular Function** (e.g. transporter, enzyme)
 - Role in a **Biological Process** (e.g. photosynthesis, defense response)
 - Localization in a **Cellular Component** (e.g. plastid, cell wall)
- **Plant Ontology (PO)** to describe a protein/gene/phenotype expression
 - In a **Plant Structure** (e.g. panicle, flower, xylem, phloem)
 - At a **Growth Stage** (e.g. germination, embryo development)
- **Trait Ontology (TO)** to describe the observable feature assayed to determine the phenotype.
 - **Plant traits** (e.g. leaf color, plant height, disease resistance)

Anatomy of an ontology

- Ontology terms are composed of
 - Term name
 - Unique ID
 - Definition (more than 75% of terms defined)
 - Synonyms (optional)
 - Database references (optional)
 - Relationships to other terms in the same ontology
- 16600+ Gene Ontology terms (from [GO consortium](#))
- 400+ Trait Ontology terms (from Gramene)
- 400+ plant structure terms (from [PO consortium](#))
- 200+ cereal plant growth stages terms (from Gramene)

Each 'child term' has a unique relationship to its 'parent term'.

Instance of (is a, type of):

Used to describe the relationship between a child term that represents a specific type of a more general parent term. For example: a *caryopsis* is a type of *fruit*; a *panicle* is an *inflorescence*.

Part of:

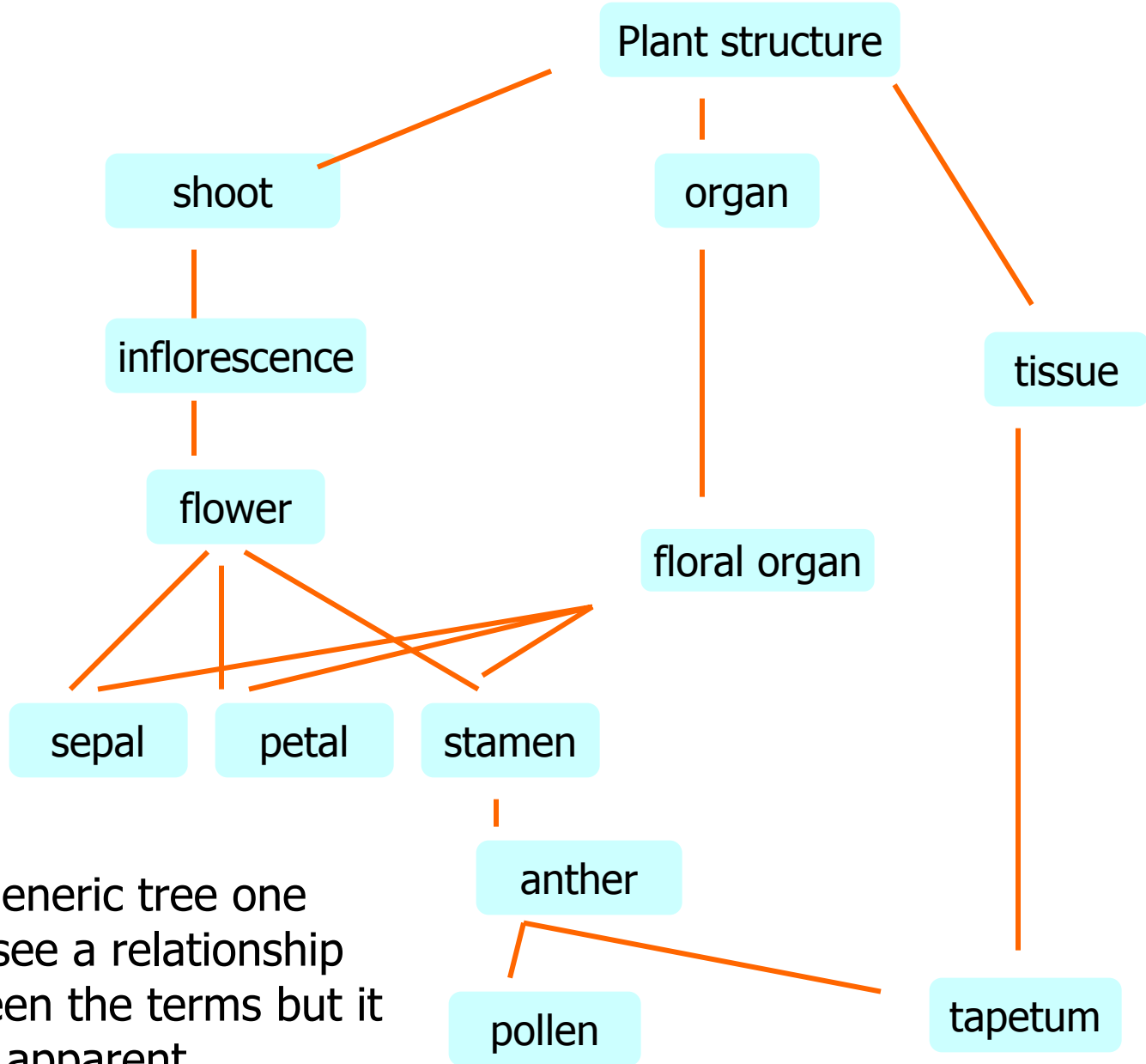
Used to indicate the relationship between a child term that is a part of the parent term. For example: the *ectocarp* is a part of the *pericarp*, which in turn is part of the *fruit*.

Develops from: (used only in plant structure ontology)

Used to describe the relationship between a child term that develops from its parent term. For example: the *root hair* develops from *trichoblast*

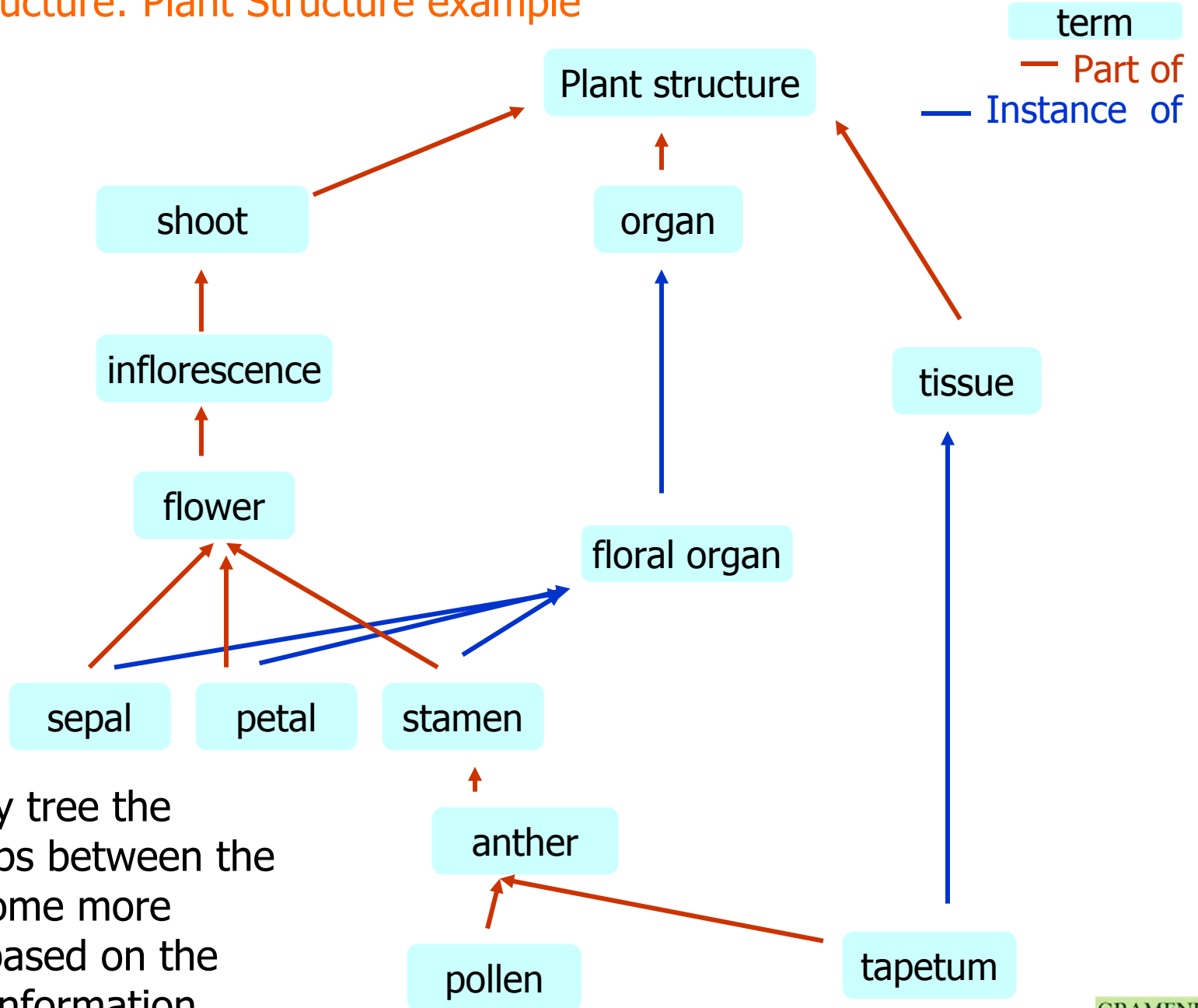
Ontology Structure: Plant structure example

term



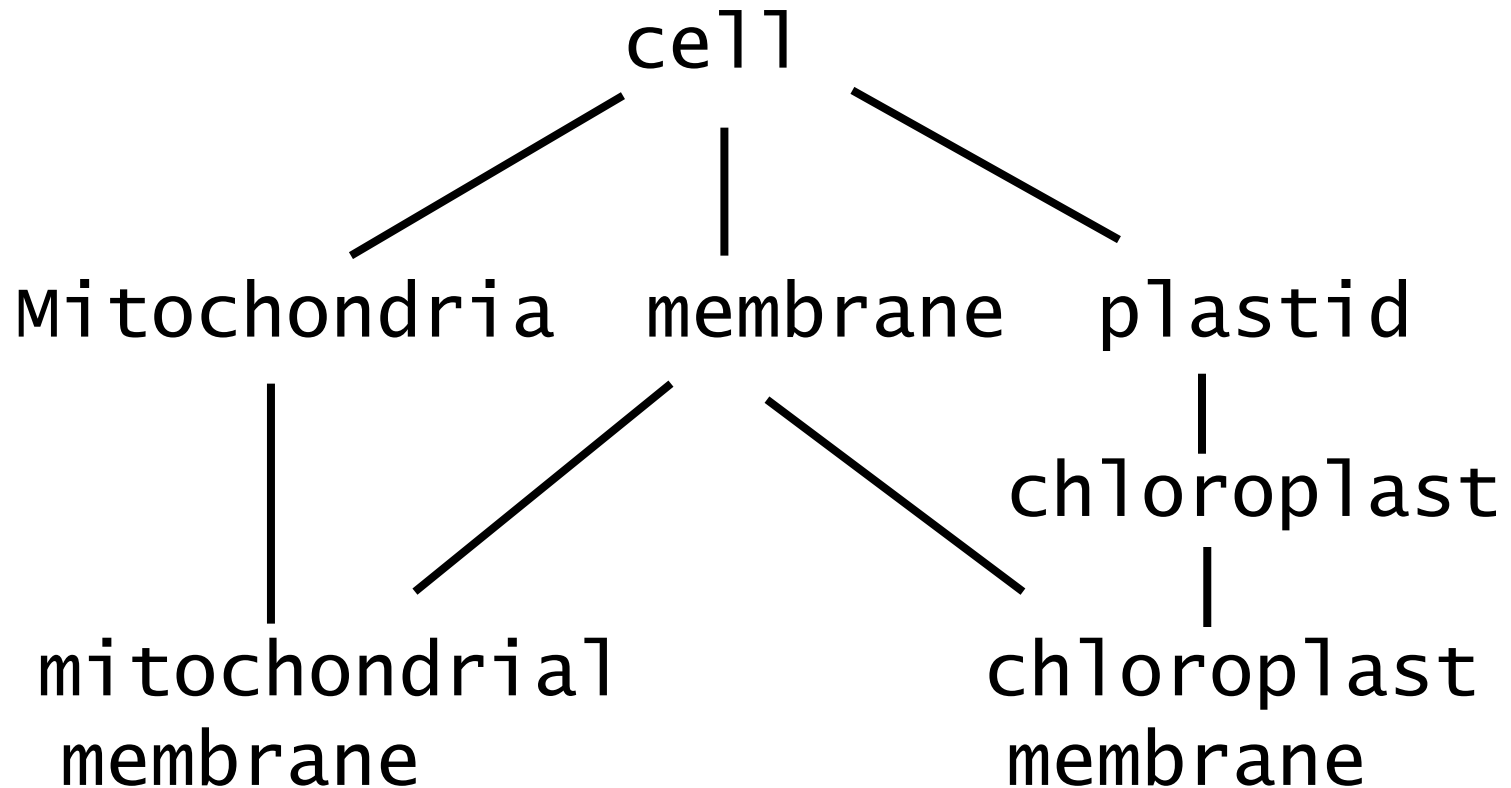
In a generic tree one does see a relationship between the terms but it is not apparent.

Ontology Structure: Plant Structure example



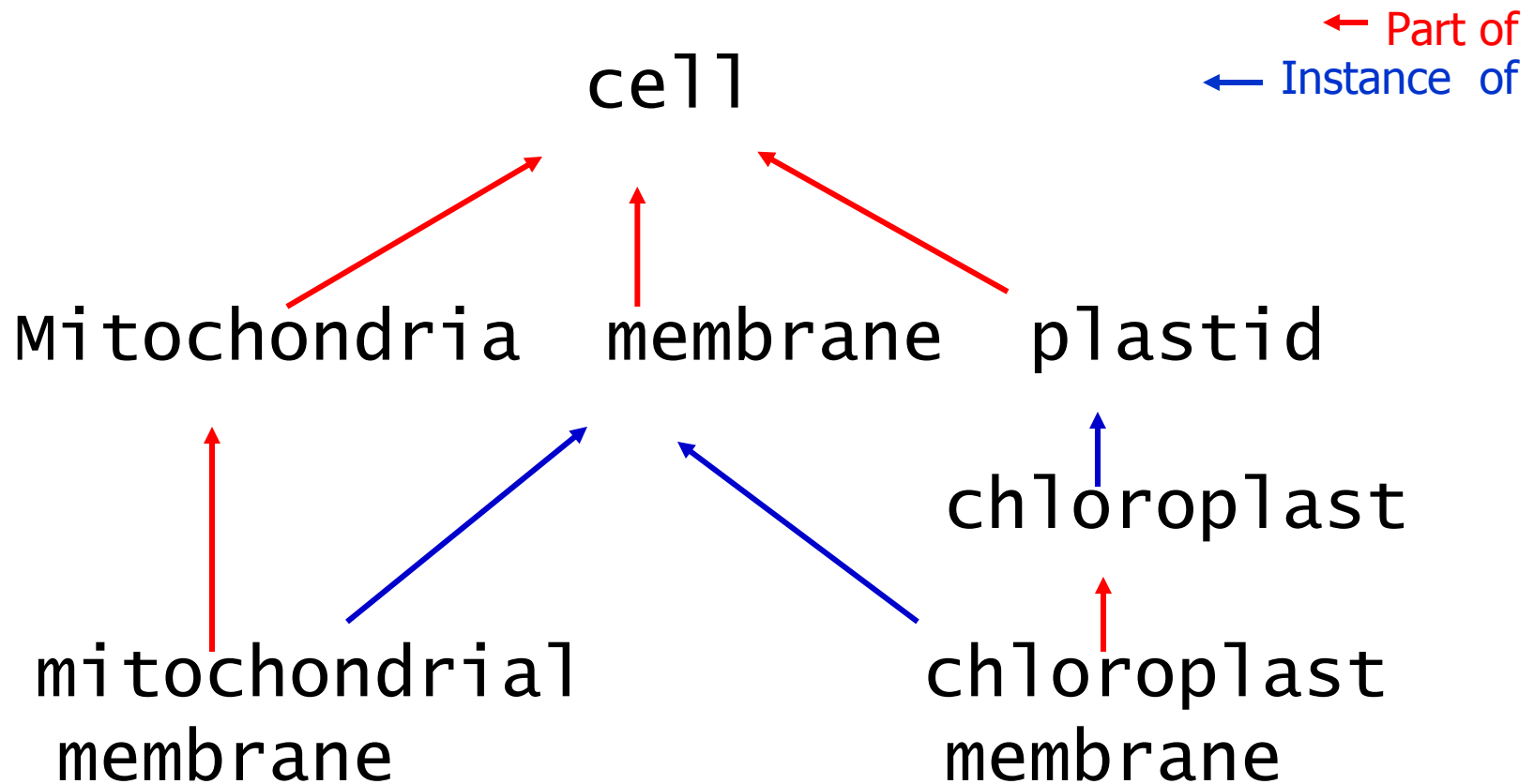
In ontology tree the relationships between the terms become more apparent based on the biological information

Ontology Structure: Cellular component example from GO



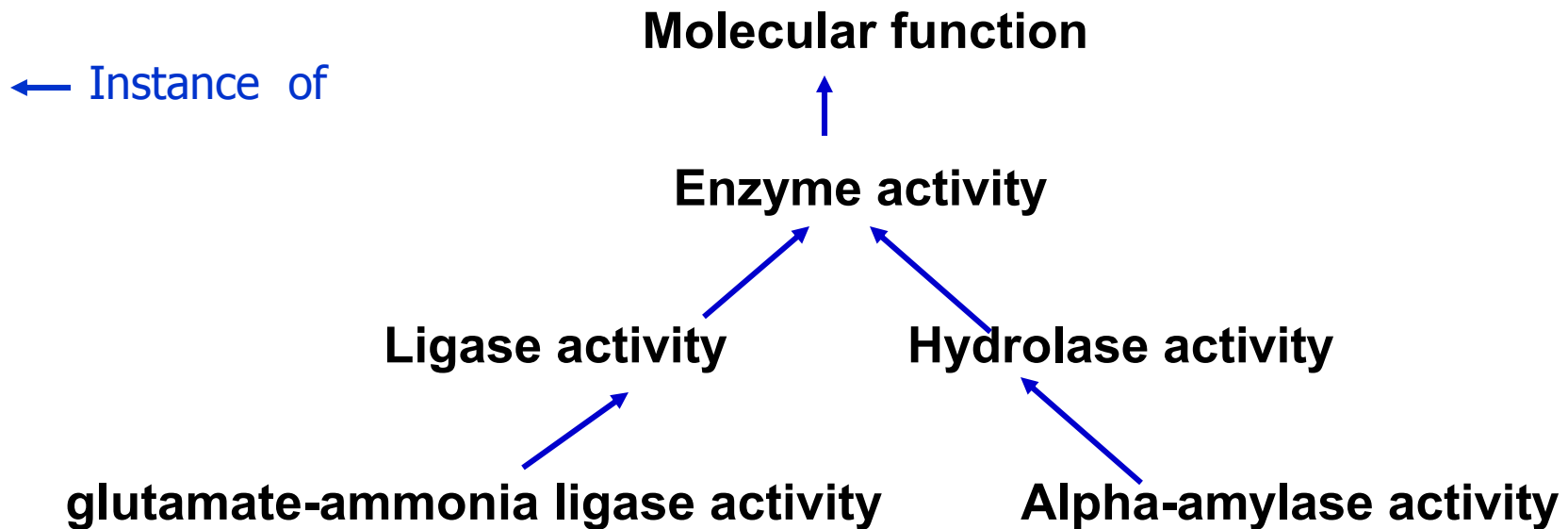
Similarly, in a generic tree one does see a relationship between the cellular component terms but it is NOT clear how they are related. This becomes important because if a user does not know about all the detail components of an organelle he/she will not be able to search/find all the appropriate annotations to a parent organ. The information remains scattered with no single way to find them all or cluster them.

Ontology Structure: Cellular component example from GO



Whereas if the relationship types are established, then it is easy to browse up or down in a tree based on the biological knowledge. Lower down in the tree are finer components, whereas as we go upwards the gross level components are organized.

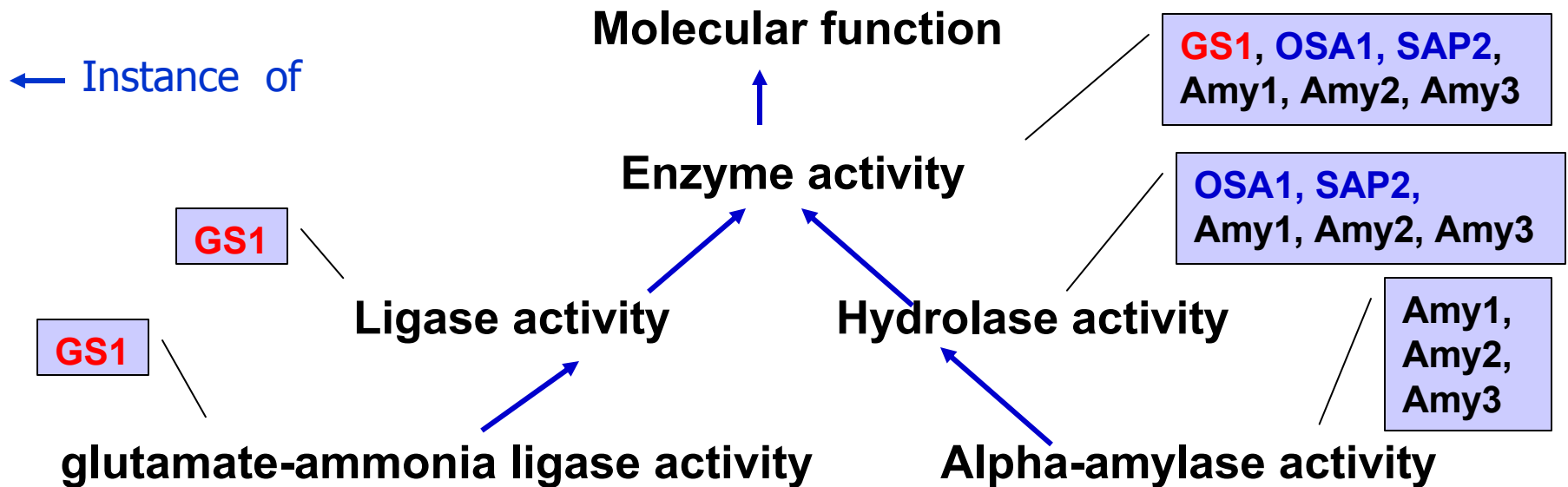
Ontology Structure: Molecular function example from GO



Summary for GO Term: *alpha-amylase activity* (GO:0004556)

Term Name	alpha-amylase activity
Definition	Catalysis of the endohydrolysis of 1,4-alpha-D-glucosidic linkages in polysaccharides containing three or more 1,4-alpha-linked D-glucose units.
Derivation	<ul style="list-style-type: none">• Gene Ontology (GO:0003673) #46169 ◦ [p] molecular_function (GO:0003674) #13432 <ul style="list-style-type: none">▪ [i] catalytic activity (GO:0003824) #6179 <ul style="list-style-type: none">▪ [i] hydrolase activity (GO:0016787) #1765 <ul style="list-style-type: none">▪ [i] hydrolase activity, acting on glycosyl bonds (GO:0016798) #231 <ul style="list-style-type: none">▪ [i] hydrolase activity, hydrolyzing O-glycosyl compounds (GO:0004553) #229 <ul style="list-style-type: none">▪ [i] amylase activity (GO:0016160) #22 <ul style="list-style-type: none">▪ [i] alpha-amylase activity (GO:0004556) #15

How ontology helps find your favorite gene/phenotype?



As one moves upwards in a tree, the associations (based on annotations) from the children terms are accumulated by the parent terms based on their relationship. Thus you see two types of associations

Direct associations: which are exact finer level association to a ontology term. e.g. *Amy* genes are directly associated to Alpha-amylase activity.

Indirect association: which are accumulated by the parents from their children terms. e.g. *Amy* genes are indirectly associated to Alpha-amylase activity, because it is an instance of hydrolase activity.

Thus if a user enters the ontology search/browse using the hydrolase activity, the results will return not only the *OSAI* and *SAPI* genes that are directly associated to this term but also the indirectly associated *Amy* genes. From this point onwards the user has an option to find the finer level of annotations by going downwards in the tree or get a collective info at gross level by going upwards.

Ontology Structure: Biological process example with associations

Summary for GO Term: *photosynthesis, light reaction* (GO:0019684)

Term Name	photosynthesis, light reaction
Derivation	<ul style="list-style-type: none"> • Gene Ontology (GO:0003673) #46169 + <ul style="list-style-type: none"> ◦ [p] biological process (GO:0008150) #11570 + <ul style="list-style-type: none"> ▪ [i] physiological processes (GO:0007582) #11356 + <ul style="list-style-type: none"> ▪ [i] photosynthesis (GO:0015979) #45 + <ul style="list-style-type: none"> ▪ [p] photosynthesis, light reaction (GO:0019684) #6 <ul style="list-style-type: none"> ▪ [p] NADP+ reduction (GO:0009780) #0 ▪ [p] photosynthetic electron transport (GO:0009767) #0 + ▪ [p] photosynthesis light harvesting (GO:0009765) #4 + ▪ [p] photosynthetic phosphorylation (GO:0009777) #0 + ▪ [p] photosynthetic water oxidation (GO:0009781) #0 ▪ [p] primary charge separation (GO:0009766) #0 + ▪ [p] regulation of photosynthesis, light reaction (GO:0042548) #0 + ▪ [i] metabolism (GO:0008152) #6182 + <ul style="list-style-type: none"> ▪ [i] energy pathways (GO:0006091) #132 + <ul style="list-style-type: none"> ▪ [i] photosynthesis, light reaction (GO:0019684) #6 <ul style="list-style-type: none"> ▪ [p] NADP+ reduction (GO:0009780) #0 ▪ [p] photosynthetic electron transport (GO:0009767) #0 + ▪ [p] photosynthesis light harvesting (GO:0009765) #4 + ▪ [p] photosynthetic phosphorylation (GO:0009777) #0 + ▪ [p] photosynthetic water oxidation (GO:0009781) #0 ▪ [p] primary charge separation (GO:0009766) #0 + ▪ [p] regulation of photosynthesis, light reaction (GO:0042548) #0 +

Gene Product Association (6 records found)

Download

#	Associated Term (sort)	Associated Gene Product Name (sort)	Gene Product Symbol (sort)	Evidence Codes
1	photosynthesis light harvesting	Putative low molecular mass early light-induced protein, chloroplast	OJ1361_E02.9	IEA
2	photosynthesis light harvesting	Putative low molecular mass early light-induced protein, chloroplast	OJ1361_E02.10	IEA
3	photosynthesis light harvesting	OSJNBa0036B21.6 protein	OSJNBa0036B21.6	IEA

How to search or browse ontologies on the Gramene website at www.gramene.org ?

Please follow the instructions / pointers in the following slides.

Browsing the Ontology Database

1. Click "Ontology" on the Gramene navigation bar

The screenshot shows the Gramene website interface. At the top, there is a search bar with the text "Search for:" and a dropdown menu for "Database:" set to "All". Below the search bar is a navigation bar with several links: "Genome Browser", "BLAST", "SSR Search", "CMap", "Markers", "Protein", "Ontology", "Mutant", "OTL", "Literature", "Resources", "About Gramene", and "Site Map". The "Ontology" link is circled in red. Below the navigation bar, there is a section for "Current Ontologies" with links to "Documentation", "Evidence code", "FTP", "Ontology suggestion", "Associations", "Publications", "Tutorial", and "FAQ". The "Current Ontologies" link is also circled in red. Below this is the "Ontology Database" search interface, which includes a search box, a "Search" button, a "Clear" button, and a "HELP" link. There are also checkboxes for "Gene (GO)", "Plant structure (PO)", "Growth stage (GRO)", "Trait (TO)", and "Environment (EO)".

2. Click on "Current Ontologies"


Current Ontologies	Browse option	Text dump
<p>Trait Ontology™ (TO)</p> <p>It represents a controlled vocabulary to describe each trait as a distinguishable feature, characteristic, quality or phenotypic feature of a developing or mature individual. Examples are glutinous endosperm, disease resistance, dwarf, photosensitivity, male sterility, etc. The present trait ontology is rice specific (modified from IRRI's Standard Evaluation System for Rice, 1996), though we aim to extend it for generic use of other cereal crops also.</p>	BROWSE	Ontology Definitions
<p>Gene Ontology™ (GO)</p> <p>Developed by the Gene Ontology Consortium to help annotate information on gene products (not the genes) using the following three organizing principles of molecular function, biological process and cellular component. Copyright © Gene Ontology Consortium.</p> <p>Molecular Function: The tasks performed by individual gene products; example is Rubisco</p> <p>Biological Process: Broad biological goals, such as photosynthesis or ripening, that are accomplished by ordered assemblies of molecular functions.</p> <p>Cellular Component: Subcellular structures, locations, and macromolecular complexes; examples include chloroplast, telomere, vacuole, nucleus, etc. .</p>	BROWSE	Definitions (combined) Ontology Ontology Ontology

3. Click on "BROWSE" to navigate through the desired ontology type.

Searching the Gene Ontology (GO) Database

Click "Ontology" on the Gramene navigation bar

A Comparative Mapping Resource



Search for: Database: All

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

[Current Ontologies](#) | [Documentation](#) | [Evidence code](#) | [FTP](#) | [Ontology suggestion](#) | [Associations](#) | [Publications](#) | [Tutorial](#) | [FAQ](#)

Ontology Database

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

select ontology (optional)

Gene (GO) Plant structure (PO) Growth stage (GRO)
 Trait (TO) Environmental (EO)

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

Select "Gene Ontology"

Type your query
e.g. search for function **alpha-amylase**

Gene Ontology (GO) search results

Accession for the Ontology term. Select to view detailed information.

Exact ontology term

Synonyms (if any)

Definition of the term

Summary for *alpha-amylase*

Items 1 to 4 of 4.

#	TO ID GO ID	Term Name	Synonym	Definition
1	GO:0004556	alpha-amylase activity	None	Catalysis of the endohydrolysis of 1,4-a-D-glucosidic linkages in polysaccharides containing three or more 1,4-a-linked D-glucose units.
2	GO:0015066	alpha-amylase inhibitor activity	None	No Definition Available
3	GO:0004574	oligo-1,6-glucosidase activity	sucrose-isomaltase.	Catalysis of the hydrolysis of 1,6-alpha-D-glucosidic linkages in some oligosaccharides produced from starch and glycogen by alpha-amylase , and in isomaltose.
4	GO:0030157	pancreatic juice secretion	None	The regulated release of pancreatic juice by the exocrine pancreas into the upper part of the intestine. Pancreatic juice is slightly alkaline and contains numerous enzymes and inactive enzyme precursors including alpha-amylase , chymotrypsinogen, lipase, procarboxypeptidase, proelastase, prophospholipase A2, ribonuclease, and trypsinogen. Its high concentration of bicarbonate ions helps to neutralize the acid from the stomach.

Features of a GO term

Exact ontology term

Definition of the term

The lineage of alpha-amylase activity as a molecular function

Summary for GO Term: *alpha-amylase activity* (GO:0004556)

Term Name	alpha-amylase activity
Definition	Catalysis of the endohydrolysis of 1,4-alpha-D-glucosidic linkages in polysaccharides containing three or more 1,4-alpha-linked D-glucose units.
Derivation	

- [molecular function \(GO:0003674\)](#) #22805 +
 - [i] [catalytic activity \(GO:0003824\)](#) #10525 +
 - [i] [hydrolase activity \(GO:0016787\)](#) #2741 +
 - [i] [hydrolase activity, acting on glycosyl bonds \(GO:0016798\)](#) #380 +
 - [i] [hydrolase activity, hydrolyzing O-glycosyl compounds \(GO:0004553\)](#) #356 +
 - [i] [amylase activity \(GO:0016160\)](#) #34 +
 - [i] **alpha-amylase activity (GO:0004556) #25**

Term-term relationship
[i]: IS A (instance/type of)

Number of gene products listed in the database associated with this activity

Expandable tree
Click on term to expand.

GO Associations

Summary for GO Term: *alpha-amylase activity* (GO:0004556)

Term Name alpha-amylase activity
Definition Catalysis of the endohydrolysis of 1,4-alpha-D-glucosidic linkages in polysaccharides containing three 1,4-alpha-linked D-glucose units.
Derivation

- [molecular function \(GO:0003674\)](#) #22805
 - [\[i\] catalytic activity \(GO:0003824\)](#) #10525
 - [\[i\] hydrolase activity \(GO:0016787\)](#) #2741
 - [\[i\] hydrolase activity, acting on glycosyl bonds \(GO:0016798\)](#) #380
 - [\[i\] hydrolase activity, hydrolyzing O-glycosyl compounds \(GO:0004553\)](#) #35
 - [\[i\] amylase activity \(GO:0016160\)](#) #34
 - [\[i\] alpha-amylase activity \(GO:0004556\)](#) #25

Gene symbol (allows alphabetical sorting)

Download the whole list

Children terms in the tree following the Primary vocabulary term for which the protein function was annotated

Gene Product Association (25 records found)

#	Associated Term (sort)	Associated Gene Product Name (sort)	Gene Product Symbol (sort)	Evidence Codes
1	alpha-amylase activity	Alpha-amylase isozyme 3D	P0013B04.36	IEA
2	alpha-amylase activity	Alpha-amylase isozyme 3E	P0013B04.34	IEA
3	alpha-amylase activity	Isoamylase	Not available	IEA
4	alpha-amylase activity	Starch-branching enzyme 1	SBE1	IEA
5	alpha-amylase activity	Putative isoamylase-type starch debranching enzyme ISO2	OSJNBa0014C03.3	IEA
6	alpha-amylase activity	Branching enzyme-3	P0475F05.16	IEA
7	alpha-amylase activity	Isoamylase	Not available	ISS
8	alpha-amylase activity	OSJNBb0118P14.8 protein	OSJNBb0118P14.8	IEA
9	alpha-amylase activity	Putative isoamylase-type starch debranching enzyme	OJ1595_D08.13-1	IEA
10	alpha-amylase activity	Alpha-amylase isozyme 3C	B1045B05.11	IEA
11	alpha-amylase activity	Alpha-amylase isozyme 3B	B1045B05.10	IEA
12	alpha-amylase activity	Alpha-amylase isozyme 3A	B1045B05.8	IEA
13	alpha-amylase activity	Alpha-amylase isozyme 2A precursor	AMY1.5	IEP ISS
14	alpha-amylase activity	Alpha-amylase isozyme 3A precursor	AMY1.2	IEP ISS
15	alpha-amylase activity	Alpha-amylase isozyme 3B	AMY1.6	IEP ISS
16	alpha-amylase activity	Alpha-amylase isozyme 3C precursor	AMY1.7	IEP ISS
17	alpha-amylase activity	Alpha-amylase isozyme 3D precursor	AMY1.3	ISS
18	alpha-amylase activity	Alpha-amylase isozyme 3E precursor	AMY1.4	IEP ISS
19	alpha-amylase activity	Alpha-amylase isozyme C2 precursor	AMY1.8	IEP ISS
20	alpha-amylase activity	Alpha-amylase precursor	AMY1.1	ISS
21	alpha-amylase activity	Alpha-amylase	OJ1004_A11.13	IEA
22	alpha-amylase activity	Putative alpha-amylase	OJ1004_A11.11	IEA
23	alpha-amylase activity	BRANCHING ENZYME-I PRECURSOR	SBE1	IEA
24	alpha-amylase activity	OSJNBa0019G23.3 protein	OSJNBa0019G23.3	IEA
25	alpha-amylase activity	Starch debranching enzyme	Not available	IEA

Download

Suggests the type of experiments carried out to ascertain its function.

Protein/gene name. Links to the Gramene Protein Database.

Click here to find functional homologs from other model organisms. Links to source. The Gene ontology website

Information about this term can be found at the [GO browser of Gene Ontology Database](#).

Searching Plant Ontology (PO): Plant structure

[Current Ontologies](#) | [Documentation](#) | [Evidence code](#) | [FTP](#) | [Ontology suggestion](#) | [Associations](#) | [Publications](#) | [Tutorial](#) | [FAQ](#)

Ontology Database

Type ID or keyword to search

culm

Search

Clear

HELP

select ontology (optional)

Gene (GO) Plant structure (PO) Growth stage (GRO)
 Trait (TO) Environment (EO)

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

Type your query
e.g. search for the plant part
culm

Select "Plant structure (PO)"

Plant Ontology (PO) search results

Accession for the Ontology term. Select to view detailed information.

Exact ontology term

Synonyms (if any)

Definition of the term

Summary for *culm*

Items 1 to 2 of 2

#	Term Accession	Term Name	Synonym	Definition
1	PO:0000112	stem epidermis	culm epidermis.	Epidermal layer of the stem.
2	PO:0009047	stem	cane, culm , stalk.	An axial system which is usually above ground and more or less negatively geotropic, bears leaves and buds, is exogenous in origin, often indeterminate in growth and with secondary thickening

Culm is a synonym for **Stem**

Summary for PO Term: *stem* (PO:0009047)

Term Name	stem
Synonym	cane, culm, stalk.
Definition	An axial system which is usually above ground and more or less negatively geotropic, bears leaves and buds, is exogenous in origin, often indeterminate in growth and with secondary thickening
Derivation	

- [plant ontology \(PO:0009075\)](#) #812 🗳
 - [i] [plant structure \(PO:0009011\)](#) #812 🗳
 - [i] [sporophyte \(PO:0009003\)](#) #788 🗳
 - [p] [shoot \(PO:0009006\)](#) #627 🗳
 - [p] **stem (PO:0009047)** #115
 - [p] [stem intercalary meristem \(PO:0006347\)](#) #0
 - [p] [interfascicular region \(PO:0006202\)](#) #0
 - [p] [internode \(PO:0020142\)](#) #23
 - [p] [node \(PO:0020141\)](#) #17
 - [p] [stem aerenchyma \(PO:0006214\)](#) #0
 - [p] [stem cortex \(PO:0000223\)](#) #0 🗳
 - [p] [stem endodermis \(PO:0005058\)](#) #0
 - [p] [stem hypodermis \(PO:0005057\)](#) #0
 - [p] [stem epidermis \(PO:0000112\)](#) #0
 - [p] [stem periderm \(PO:0005048\)](#) #0 🗳
 - [p] [stem pith \(PO:0005041\)](#) #0

Number of mutants associated with this plant part

Stem is a PART OF "Shoot"

Download/Display all the phenotypes associated with "stem"

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

Phenotype Association (115 records found)

Download

Display All

PO Associations

Mutant gene symbol
(allows alphabetical sorting)

Phenotype Association (115 records found)				Download
#	Associated Term (sort)	Associated Gene Name (sort)	Gene Symbol (sort)	Evidence Codes
1	internode	accelerated overgrowth of internode	ao	TAS
2	internode	Big uppermost culm	Buc	TAS, IAGP
3	internode	dwarf-1	dwf1	TAS, IAGP
4	internode	dwarf-9	dwf9	TAS
5	internode	elongated uppermost internode-1	eui1	TAS, IAGP
6	internode	gold hull and internode-1	gh1	TAS, IAGP
7	internode	gold hull and internode-3	gh3	TAS, IAGP
8	internode	Inhibitor for purple leaf-2	IPI2	TAS, IAGP

Children terms in the tree following the Primary vocabulary term for which the mutant gene was annotated

Mutant gene name. Links to the Gramene Mutant Database.

Searching Plant Ontology: Growth stages

Ontology Database

Type ID or keyword to search

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

Type your query
e.g. search for plant growth
stage **germination**

Select "Growth stage (GRO)"

Follow the search results by selecting the term e.g. "**germination**" in rice ([GRO:0007051](#)). Display / download all associations to view associated phenotypes.

Searching the Trait Ontology (TO) Database

A. Type your query
e.g. search for plant
trait **plant height**

Ontology Database

Type ID or keyword to search

select ontology (optional) Gene (GO) Plant structure (PO) Growth stage (GRO)
 Trait (TO) Environment (EO)

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

B. Select "Trait (TO)"

Accession for the Ontology term. Select to view detailed information.

Summary for *plant height*

Items 1 to 5 of 5

#	Term Accession	Term Name	Synonym	Definition
1	GRO:0007012	03-rapid stem elongation	maize growth stage-3, mid-whorl stage, stem elongation, telescoping.	After tassel initiation, stem length begins to increase rapidly, through elongation of cells formed by the intercalary meristem at the base of above-ground internodes. The rate of elongation decreases prior to anthesis, but plant height may continue to increase until after flowering
2	GRO:0007048	04-stem elongation stage	internode elongation, jointing stage, rice growth stage-4.	Begins about the same time panicle initiation is occurring. It continues until full plant height is reached.
3	TO:0000207	plant height	Ht, PTHT.	actual measurement of plant height from soil surface to the the highest point in plant as identified in the study.
4	TO:0000368	shoot elongation rate	elongation of plant height , SHELRATE.	No Definition Available
5	TO:0000296	vegetative vigor	vegetative growth vigor, Vg, VGVIG.	Represents the growth of plant. Used to evaluate genetic material under stress and non-stress conditions, several factors may interact, influencing the seedling vigor (e.g. tillering ability, plant height , etc),

TO Features and Associations

The ontology tree suggests the higher class of trait/category e.g. **stature or vigor**

Number of mutants associated with this trait.

Download the list of phenotypes associated with trait **plant height**

Summary for TO Term: *plant height* (TO:0000207)

Term Name	plant height
Synonym	Ht, PTHT.
Definition	actual measurement of plant height from soil surface to the the highest point in plant identified in the study.
Derivation	<ul style="list-style-type: none"> • trait ontology (TO:0000387) #789 <ul style="list-style-type: none"> ◦ [i] stature or vigor related trait (TO:0000133) #58 <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] culm length (sensu Poaceae) (TO:0000309) #53
Parent Term (1)	height related trait (TO:0000171)
Child Term (1)	culm length (sensu Poaceae) (TO:0000309)

Phenotype Association (56 records found)

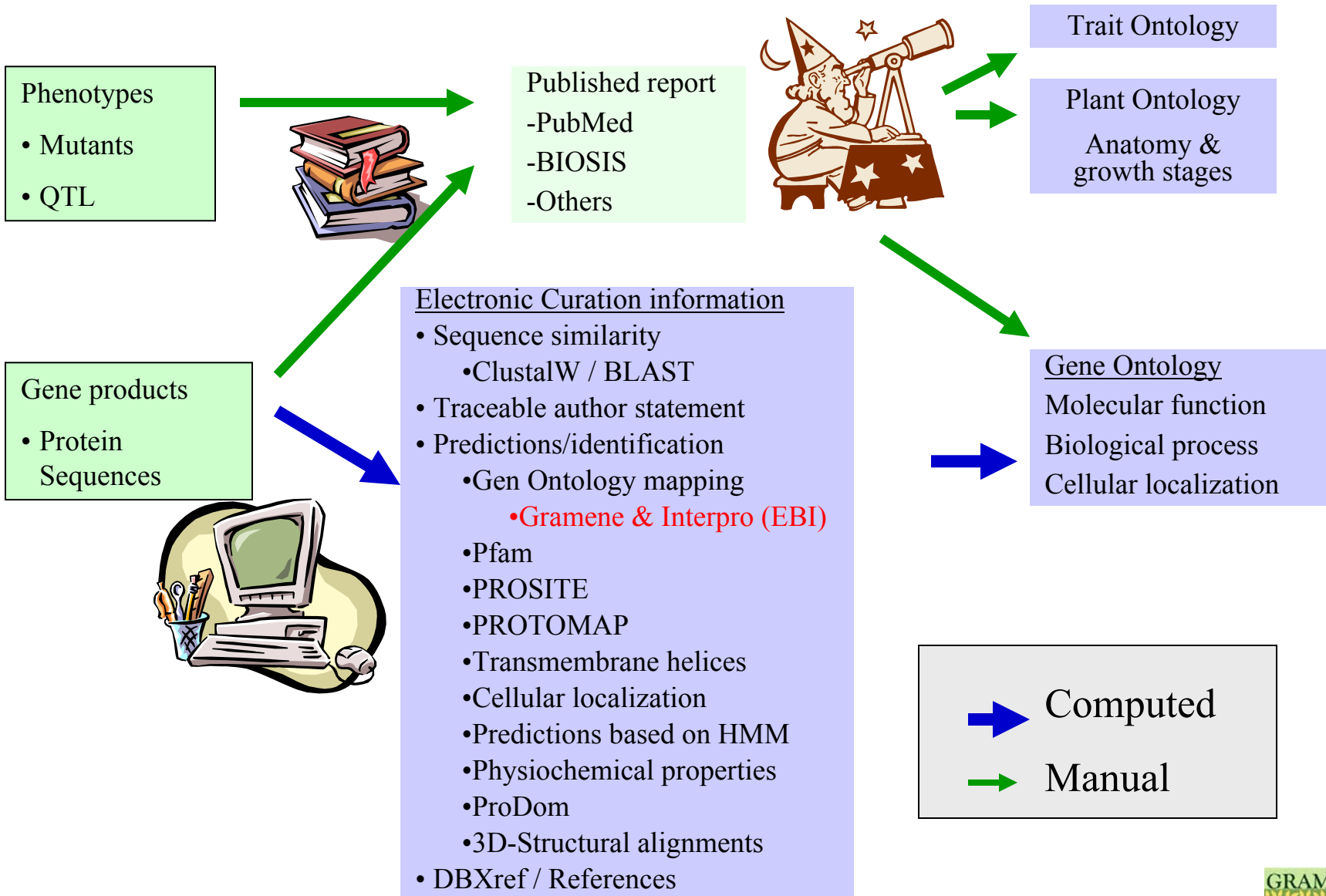
#	Associated Term (sort)	Associated Gene Name (sort)	Gene Symbol (sort)	Evidence Codes
1	culm length (sensu Poaceae)	adaxialized leaf-1	adl1	TAS
2	culm length (sensu Poaceae)	adaxialized leaf-2	adl2	TAS
3	culm length (sensu Poaceae)	apical displacement-1	apd1	TAS
4	culm length (sensu Poaceae)	cigar shaped panicle	cg	TAS
5	culm length (sensu Poaceae)	dwarf-1	dwf1	TAS, IAGP
6	culm length (sensu Poaceae)	dwarf-2	dwf2	TAS, IAGP
7	culm length (sensu Poaceae)	dwarf-3	dwf3	TAS, IAGP
8	culm length (sensu Poaceae)	dwarf-4	dwf4	TAS, IAGP
9	culm length (sensu Poaceae)	dwarf-5	dwf5	TAS, IAGP

How are associations built in an annotation process?

- The following slides will guide you through the methodologies used by Gramene on associating
 - Gene products to Gene Ontology terms for molecular function, biological process and localization (expression) in a cellular component.
 - Phenotypes to the plant ontology terms where (plant part) and when (growth stage) the phenotype is expressed.

Annotation-I: How are associations built in an annotation process?

Manual Vs Electronic (computed)



How are associations built as part of annotation exercise?

Nature. 2002 Apr 18;416(6882):701-2.

[Related Articles, Links](#)

nature

Green revolution: a mutant gibberellin-synthesis gene in rice.

Sasaki A, Ashikari M, Ueguchi-Tanaka M, Itoh H, Nishimura A, Swapan D, Ishiyama K, Saito T, Kobayashi M, Khush GS, Kitano H, Matsuoka M.

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The chronic food shortage that was feared after the rapid expansion of the world population in the 1960s was averted largely by the development of a high-yielding semi-dwarf variety of rice known as IR8, the so-called rice 'green revolution'. The short stature of IR8 is due to a mutation in the plant's sd1 gene, and here we identify this gene as encoding an oxidase enzyme involved in the biosynthesis of gibberellin, a plant growth hormone. Gibberellin is also implicated in green-revolution varieties of wheat, but the reduced height of those crops is conferred by defects in the hormone's signalling pathway.

PMID: 11961544 [PubMed - indexed for MEDLINE]

From abstract (manual/computed)

Oxidase enzyme	oxidoreductase activity	GO:0016491
Biosynthesis of gibberellin	gibberellic acid biosynthesis	GO:0009686
Reduced height	Plant height	TO:0000207

From manual curation and further reading

Oxidase enzyme	<i>gibberellin 20-oxidase activity**</i>	GO:0045544	-Function
Biosynthesis of gibberellin	gibberellic acid biosynthesis	GO:0009686	-Process
Reduced height	Culm length**	TO:0000309	-Trait

** Annotations were modified based on further reading

Ontology Exercise

TRY ON YOUR OWN !

□ 1: Proc Natl Acad Sci U S A. 2004 Jan 7 [Epub ahead of print].

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Full text article at
www.pnas.org

PLASTOCHRON1, a timekeeper of leaf initiation in rice, encodes cytochrome P450.

Miyoshi K, Ahn BO, Kawakatsu T, Ito Y, Itoh JI, Nagato Y, Kurata N.

*Plant Genetics Laboratory, National Institute of Genetics, Yata 1111, Mishima, Shizuoka 411-8540, Japan.

During postembryonic development of higher plants, the shoot apical meristem produces lateral organs in a regular spacing (phyllotaxy) and a regular timing (plastochron). Molecular analysis of mutants associated with phyllotaxy and plastochron would greatly increase understanding of the developmental mechanism of plant architecture because phyllotaxy and plastochron are fundamental regulators of plant architecture. *pla1* of rice is not only a plastochron mutant showing rapid leaf initiation without affecting phyllotaxy, but also a heterochronic mutant showing ectopic shoot formation in the reproductive phase. Thus, *pla1* provides a tool for analyzing the molecular basis of temporal regulation in leaf development. In this work, we isolated the *PLA1* gene by map-based cloning. The identified *PLA1* gene encodes a cytochrome P450, CYP78A11, which potentially catalyzes substances controlling plant development. *PLA1* is expressed in developing leaf primordia, bracts of the panicle, and elongating internodes, but not in the shoot apical meristem. The expression pattern and mutant phenotype suggest that the *PLA1* gene acting in developing leaf primordia affects the timing of successive leaf initiation and the termination of vegetative growth.

PMID: 14711998 [PubMed - as supplied by publisher]

Make your own assertions on which of the ontology terms from either the GO, PO or TO vocabularies appropriately match to the function and phenotype traits associated to *PLASTOCHRON1* gene.

Ontology Exercise

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For clues, please see the underlined portions of the text, to make your own assertions on the use of either the GO, PO or TO vocabularies.

Ontology Annotation includes various experimental evidence codes suggesting how the ontology term to gene/phenotype association was made.

ISS Inferred from Sequence/Structural Similarity

BLAST

IDA Inferred from Direct Assay

IPI Inferred from Physical Interaction

TAS Traceable Author Statement

NAS Non-traceable Author Statement

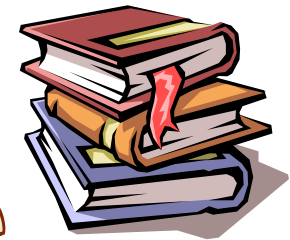
IMP Inferred from Mutant Phenotype

IGI Inferred from Genetic Interaction

IEP Inferred from Expression Pattern

IC Inferred by Curator

ND No Data available



IEA Inferred from electronic annotation



What else can YOU do?

- Send us your review of the terms, definitions and relationships to ensure accuracy.
- Suggest new terms, definitions, or improvements to the structures.
- Use the terms in describing data in publications and databases.
- If your project on cereal plants is generating data sets that may require these kinds of annotations and associations, please feel free to reach us at gramene@gramene.org. We will be happy to help guide you through the annotation process and if necessary in setting up an Ontology database.

Thank you for using this tutorial.

We appreciate your comments or suggestions.

Please click here to send your feedback.

The screenshot shows the GRAMENE website interface. At the top left is the GRAMENE logo. To the right is a search bar with a 'Search' button and a 'Feedback' button, both of which are circled in red. Below the search bar is a navigation menu with links: Genome Browser, BLAST, SSR Search, CMap, Markers, Protein, Ontology, Mutant, QTL, Literature, Resources, About Gramene, and Site Map. Below the navigation menu is another set of links: Current Ontologies, Documentation, Evidence code, FTP, Ontology suggestion, Associations, Publications, Tutorial, and FAQ, with the FAQ link also circled in red. Below the links is the 'Ontology Database' section, which includes a search input field, a 'Search' button, a 'Clear' button, and a 'HELP' link. Below the search input field are several checkboxes for selecting an ontology: Gene (GO), Plant structure (PO), Growth stage (GRO), Trait (TO), and Environment (EO). Below the checkboxes is a text input field with the example text '[e.g. flower or TO:0000303]'. A callout bubble points to the 'Feedback' button, and another callout bubble points to the 'FAQ' link.

If you have questions? Please browse the Frequently Asked Questions (FAQ)

You can also reach us by sending e-mail at gramene@gramene.org