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

Source: GO teaching resources
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 within a kingdom/sub-class/family even as knowledge of phenotypes and the associated gene and their roles in cells is accumulating and changing”

Source: GO teaching resources
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.

Source: GO teaching resources
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

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.
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

Molecular function

Enzyme activity

Ligase activity

Hydrolase activity

glutamate-ammonia ligase activity

Alpha-amylase activity

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

<table>
<thead>
<tr>
<th>Term Name</th>
<th>Definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>alpha-amylase activity</td>
<td>Catalysis of the endohydrolysis of 1,4-alpha-D-glucosidic linkages in polysaccharides containing three or more 1,4-alpha-linked D-glucose units.</td>
</tr>
</tbody>
</table>

- Gene_Ontology (GO:0003673) #46769
  - molecular_function (GO:0003674) #13432
    - catalytic_activity (GO:0003824) #5179
      - hydrolase_activity (GO:0016160) #1766
        - hydrolase_activity, acting on glycosyl bonds (GO:0016798) #231
        - hydrolase_activity, hydrolyzing O-glycosyl compounds (GO:0004553) #229
          - amylase activity (GO:0016160) #22
            - 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 OSA1 and SAP1 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
How to search or browse ontologies on the Gramene website at www.gramene.org?

Please follow the instructions / pointers in the following slides.
1. Click “Ontology” on the Gramene navigation bar

2. Click on “Current Ontologies”

3. Click on “BROWSE” to navigate through the desired ontology type.
Searching the Gene Ontology (GO) Database

Click “Ontology” on the Gramene navigation bar

Select “Gene Ontology”

Type your query e.g. search for function alpha-amylase
Gene Ontology (GO) search results

<table>
<thead>
<tr>
<th>#</th>
<th>TO ID</th>
<th>GO ID</th>
<th>Term Name</th>
<th>Synonym</th>
<th>Definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>GO:004556</td>
<td>alpha-amylase activity None</td>
<td>Catalysis of the endohydrolysis of 1,4-α-D-glucosidic linkages in polysaccharides containing three or more 1,4-α-linked D-glucose units.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>GO:0015066</td>
<td>alpha-amylase inhibitor activity None</td>
<td>No Definition Available</td>
<td></td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>GO:0004574</td>
<td>oligo-1,6-glucosidase activity sucrose-isomaltase</td>
<td>Catalysis of the hydrolysis of 1,6-α-D-glucosidic linkages in some oligosaccharides produced from starch and glycogen by alpha-amylase, and in isomaltose.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>GO:0030157</td>
<td>pancreatic juice secretion None</td>
<td>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.</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
### Features of a GO term

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

<table>
<thead>
<tr>
<th>Term Name</th>
<th>alpha-amylase activity</th>
</tr>
</thead>
<tbody>
<tr>
<td>Definition</td>
<td>Catalysis of the endohydrolysis of 1,4-alpha-D-glucosidic linkages in polysaccharides containing three or more 1,4-alpha-linked D-glucose units.</td>
</tr>
<tr>
<td>Derivation</td>
<td></td>
</tr>
</tbody>
</table>

- **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) #336
          - [i] amylase activity (GO:0016160) #34
            - [i] alpha-amylase activity (GO:0004556) #25

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

- **Definition of the term**

- **The lineage of alpha-amylase activity as a molecular function**

- **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)**

<table>
<thead>
<tr>
<th>Term Name</th>
<th>Definition</th>
<th>Derivation</th>
</tr>
</thead>
<tbody>
<tr>
<td>alpha-amylase activity</td>
<td>Catalysis of the endohydrolysis of 1,4-alpha-D-glucosidic linkages in polysaccharides containing three 1,4-alpha-linked D-glucose units.</td>
<td></td>
</tr>
</tbody>
</table>

- **Gene symbol (allows alphabetical sorting)**
- **Download the whole list**
- **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**

**Gene Product Association (25 records found)**

<table>
<thead>
<tr>
<th>#</th>
<th>Associated Term (sort)</th>
<th>Associated Gene Product Name (sort)</th>
<th>Gene Product Symbol (sort)</th>
<th>Evidence Codes</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>alpha-amylase activity</td>
<td>Alpha-amylase isozyme 3D</td>
<td>P0013B04.36</td>
<td>IEA</td>
</tr>
<tr>
<td>2</td>
<td>alpha-amylase activity</td>
<td>Alpha-amylase isozyme 3E</td>
<td>P0013B04.34</td>
<td>IEA</td>
</tr>
<tr>
<td>3</td>
<td>alpha-amylase activity</td>
<td>Isoamylase</td>
<td>Not available</td>
<td>IEA</td>
</tr>
<tr>
<td>4</td>
<td>alpha-amylase activity</td>
<td>Starch-branching enzyme 1</td>
<td>SBE1</td>
<td>IEA</td>
</tr>
<tr>
<td>5</td>
<td>alpha-amylase activity</td>
<td>Putative isomaltase-type starch debranching enzyme ISO2</td>
<td>OSJNBa0014C03.3</td>
<td>IEA</td>
</tr>
<tr>
<td>6</td>
<td>alpha-amylase activity</td>
<td>Branching enzyme-3</td>
<td>P047F05.15</td>
<td>IEA</td>
</tr>
<tr>
<td>7</td>
<td>alpha-amylase activity</td>
<td>Isoamylase</td>
<td>Not available</td>
<td>IEA</td>
</tr>
<tr>
<td>8</td>
<td>alpha-amylase activity</td>
<td>OSJNBa0118P14.8 protein</td>
<td>OSJNBa0014C03.3</td>
<td>IEA</td>
</tr>
<tr>
<td>9</td>
<td>alpha-amylase activity</td>
<td>Putative isomaltase-type starch debranching enzyme ISO2</td>
<td>OSJNBa0014C03.3</td>
<td>IEA</td>
</tr>
<tr>
<td>10</td>
<td>alpha-amylase activity</td>
<td>Alpha-amylase isozyme 3C</td>
<td>B1045B05.11</td>
<td>IEA</td>
</tr>
<tr>
<td>11</td>
<td>alpha-amylase activity</td>
<td>Alpha-amylase isozyme 3B</td>
<td>B1045B05.10</td>
<td>IEA</td>
</tr>
<tr>
<td>12</td>
<td>alpha-amylase activity</td>
<td>Alpha-amylase isozyme 3A</td>
<td>B1045B05.8</td>
<td>IEA</td>
</tr>
<tr>
<td>13</td>
<td>alpha-amylase activity</td>
<td>Alpha-amylase isozyme 2A precursor</td>
<td>AMY1.5</td>
<td>IEP ISS</td>
</tr>
<tr>
<td>14</td>
<td>alpha-amylase activity</td>
<td>Alpha-amylase isozyme 3A precursor</td>
<td>AMY1.2</td>
<td>IEP ISS</td>
</tr>
<tr>
<td>15</td>
<td>alpha-amylase activity</td>
<td>Alpha-amylase isozyme 3B</td>
<td>AMY1.6</td>
<td>IEP ISS</td>
</tr>
<tr>
<td>16</td>
<td>alpha-amylase activity</td>
<td>Alpha-amylase isozyme 3C precursor</td>
<td>AMY1.7</td>
<td>IEP ISS</td>
</tr>
<tr>
<td>17</td>
<td>alpha-amylase activity</td>
<td>Alpha-amylase isozyme 3D precursor</td>
<td>AMY1.3</td>
<td>ISS</td>
</tr>
<tr>
<td>18</td>
<td>alpha-amylase activity</td>
<td>Alpha-amylase isozyme 3E precursor</td>
<td>AMY1.4</td>
<td>IEA</td>
</tr>
<tr>
<td>19</td>
<td>alpha-amylase activity</td>
<td>Alpha-amylase isozyme C2 precursor</td>
<td>AMY1.8</td>
<td>IEP ISS</td>
</tr>
<tr>
<td>20</td>
<td>alpha-amylase activity</td>
<td>Alpha-amylase isozyme C3 precursor</td>
<td>AMY1.1</td>
<td>ISS</td>
</tr>
<tr>
<td>21</td>
<td>Alpha-amylase activity</td>
<td>Alpha-amylase</td>
<td>C1104_1A11.13</td>
<td>IEA</td>
</tr>
<tr>
<td>22</td>
<td>Alpha-amylase activity</td>
<td>Putative alpha-amylase</td>
<td>C1104_1A11.11</td>
<td>IEA</td>
</tr>
<tr>
<td>23</td>
<td>Alpha-amylase activity</td>
<td>BRANCHING ENZYME-I PRECURSOR</td>
<td>SBE1</td>
<td>IEP ISS</td>
</tr>
<tr>
<td>24</td>
<td>Alpha-amylase activity</td>
<td>OSJNBa0118P14.8 protein</td>
<td>OSJNBa0014C03.3</td>
<td>IEA</td>
</tr>
<tr>
<td>25</td>
<td>Alpha-amylase activity</td>
<td>Starch debranching enzyme</td>
<td>Not available</td>
<td>IEA</td>
</tr>
</tbody>
</table>

More information about this term can be found at the GO browser of Gene Ontology Database.
Searching Plant Ontology (PO): Plant structure

Type ID or keyword to search

- culm

Select ontology (optional)
- Plant structure (PO)

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

Select “Plant structure (PO)”
### Plant Ontology (PO) search results

**Summary for culm**

<table>
<thead>
<tr>
<th>#</th>
<th>Term Accession</th>
<th>Term Name</th>
<th>Synonym</th>
<th>Definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>PO:0000112</td>
<td>stem, epidermis</td>
<td>culm epidermis</td>
<td>Epidermal layer of the stem.</td>
</tr>
<tr>
<td>2</td>
<td>PO:00009047</td>
<td>stem, cane, stalk</td>
<td>culm, stalk</td>
<td>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</td>
</tr>
</tbody>
</table>

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

**Exact ontology term**

**Synonyms (if any)**

**Definition of the term**

**Culm is a synonym for Stem**
Features of a PO term

Summary for PO Term: stem (PO:0009047)

<table>
<thead>
<tr>
<th>Term Name</th>
<th>stem</th>
</tr>
</thead>
<tbody>
<tr>
<td>Synonym</td>
<td>cane, culm, stalk.</td>
</tr>
<tr>
<td>Definition</td>
<td>An axial system which is usually above ground and more or less negatively geotropically, bears leaves and buds, is exogenous in origin, often indeterminate in growth and with secondary thickening</td>
</tr>
<tr>
<td>Derivation</td>
<td><img src="image" alt="Diagram of plant structure and stem intercalary meristem" /></td>
</tr>
</tbody>
</table>

- **stem** (PO:0009047) #115
  - **stem intercalary meristem** (PO:0006347) #0
  - **stem cortex** (PO:0000223) #0
  - **stem endodermis** (PO:0005058) #0
  - **stem hypodermis** (PO:0005057) #0
  - **stem epidermis** (PO:0000112) #0
  - **stem periderm** (PO:0005048) #0
  - **stem pith** (PO:0005041) #0

**Stem is a PART OF “Shoot”**

# Number of mutants associated with this plant part

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

<table>
<thead>
<tr>
<th>#</th>
<th>Associated Term</th>
<th>Associated Gene Name</th>
<th>Gene Symbol</th>
<th>Evidence Codes</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>internode</td>
<td>accelerated overgrowth of internode</td>
<td>ao</td>
<td>TAS</td>
</tr>
<tr>
<td>2</td>
<td>internode</td>
<td>Big uppermost culm</td>
<td>Buc</td>
<td>TAS, IAGP</td>
</tr>
<tr>
<td>3</td>
<td>internode</td>
<td>dwarf-1</td>
<td>dwf1</td>
<td>TAS, IAGP</td>
</tr>
<tr>
<td>4</td>
<td>internode</td>
<td>dwarf-9</td>
<td>dwf9</td>
<td>TAS</td>
</tr>
<tr>
<td>5</td>
<td>internode</td>
<td>elongated uppermost internode-1</td>
<td>eui1</td>
<td>TAS, IAGP</td>
</tr>
<tr>
<td>6</td>
<td>internode</td>
<td>gold hull and internode-1</td>
<td>gh1</td>
<td>TAS, IAGP</td>
</tr>
<tr>
<td>7</td>
<td>internode</td>
<td>gold hull and internode-3</td>
<td>gh3</td>
<td>TAS, IAGP</td>
</tr>
<tr>
<td>8</td>
<td>internode</td>
<td>Inhibitor for purple leaf-2</td>
<td>IPI2</td>
<td>TAS, IAGP</td>
</tr>
</tbody>
</table>

- **Mutant gene symbol** (allows alphabetical sorting)
- **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**

- **Type ID or keyword to search**: germination
- **Select ontology (optional)**: 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

B. Select “Trait (TO)”
## Summary for plant height

Items 1 to 5 of 5

<table>
<thead>
<tr>
<th>#</th>
<th>Term Accession</th>
<th>Term Name</th>
<th>Synonym</th>
<th>Definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>GRO:0007012</td>
<td>03-rapid stem elongation</td>
<td>maize growth stage-3, mid-whorl stage, stem elongation, telescoping.</td>
<td>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.</td>
</tr>
<tr>
<td>2</td>
<td>GRO:0007048</td>
<td>04-stem elongation stage</td>
<td>internode elongation, jointing stage, rice growth stage-4.</td>
<td>Begins about the same time panicle initiation is occurring. It continues until full plant height is reached.</td>
</tr>
<tr>
<td>3</td>
<td>TO:0000207</td>
<td>plant height</td>
<td>Ht, PTHT.</td>
<td>Actual measurement of plant height from soil surface to the highest point in plant as identified in the study.</td>
</tr>
<tr>
<td>4</td>
<td>TO:0000368</td>
<td>shoot elongation rate</td>
<td>elongation of plant height, SHELRATE.</td>
<td>No Definition Available</td>
</tr>
<tr>
<td>5</td>
<td>TO:0000296</td>
<td>vegetative vigor</td>
<td>vegetative growth vigor, Vg, VGVIG.</td>
<td>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).</td>
</tr>
</tbody>
</table>
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.
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)

Phenotypes
- Mutants
- QTL

Published report
- PubMed
- BIOSIS
- Others

Gene products
- Protein
- Sequences

Electronic Curation information
- Sequence similarity
  - ClustalW / BLAST
- Traceable author statement
- Predictions/identification
  - Gen Ontology mapping
    - Gramene & Interpro (EBI)
- Pfam
- PROSITE
- PROTOMAP
- Transmembrane helices
- Cellular localization
- Predictions based on HMM
- Physiochemical properties
- ProDom
- 3D-Structural alignments
- DBXref / References

Trait Ontology

Plant Ontology
- Anatomy &
  - growth stages

Gene Ontology
- Molecular function
- Biological process
- Cellular localization

Computed

Manual
**Annotations were modified based on further reading**

<table>
<thead>
<tr>
<th>From abstract (manual/computed)</th>
<th>From manual curation and further reading</th>
</tr>
</thead>
<tbody>
<tr>
<td>Oxidase enzyme</td>
<td>Oxidoreductase activity GO:0016491</td>
</tr>
<tr>
<td>Biosynthesis of gibberellin</td>
<td>Gibberellin 20-oxidase activity** GO:0045544</td>
</tr>
<tr>
<td>Reduced height</td>
<td>Plant height TO:0000207</td>
</tr>
<tr>
<td>Reduced height</td>
<td>Culm length** TO:0000309</td>
</tr>
</tbody>
</table>

** Function **

** Process **

** Trait **

_Green revolution: a mutant gibberellin-synthesis gene in rice._


Bioscience Center, Nagoya University, Nagoya 464-8601, Japan. makoto@nuagrl.aer.nagoya-u.ac.jp

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]
Ontology Exercise
TRY ON YOUR OWN!

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 our 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.

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

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<th>Code</th>
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<td>Inferred from Direct Assay</td>
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<td>IPI</td>
<td>Inferred from Physical Interaction</td>
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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.

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

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