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.

2) The following Summary page will result.

Summary for polysaccharide metabolism

<table>
<thead>
<tr>
<th>Term Accession</th>
<th>Term Name</th>
<th>Synonym</th>
<th>Definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>GO:0005976</td>
<td>polysaccharide metabolism</td>
<td>glycan metabolism</td>
<td>The chemical reactions and physical changes involving polysaccharides (synonym:glycans), a polymer of more than about 10 monosaccharide residues joined by glycosidic linkages.</td>
</tr>
<tr>
<td>GO:0008653</td>
<td>lipopolysaccharide metabolism</td>
<td>None</td>
<td>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.</td>
</tr>
<tr>
<td>GO:0046379</td>
<td>extracellular polysaccharide metabolism</td>
<td>None</td>
<td>The chemical reactions and physical changes involving polysaccharides used in extracellular structures.</td>
</tr>
</tbody>
</table>

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: polysaccharide metabolism (GO:0005976)

<table>
<thead>
<tr>
<th>Term Name</th>
<th>Synonym</th>
<th>Definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>polysaccharide metabolism</td>
<td>glycan metabolism.</td>
<td>The chemical reactions and physical changes involving polysaccharides (synonym: glycans), a polymer of more than about 10 monosaccharide residues joined by glycosidic linkages.</td>
</tr>
</tbody>
</table>

#### Derivation

- biological_process (GO:0008150) #19728
  - physiological_process (GO:0007582) #19354
    - metabolism (GO:0008152) #10584
      - macromolecule metabolism (GO:0043170) #4291
        - carbohydrate metabolism (GO:0005975) #747
          - polysaccharide metabolism (GO:0005976) #122
            - polysaccharide biosynthesis (GO:0006271) #53
            - polysaccharide catabolism (GO:0000272) #58
            - glucan metabolism (GO:0000273) #57
            - chitin metabolism (GO:0006030) #40
            - mannan metabolism (GO:0006080) #0
            - lipopolysaccharide metabolism (GO:0008653) #4
            - colanic acid metabolism (GO:0046377) #0
            - O antigen metabolism (GO:0046492) #0
            - enterobacterial common antigen metabolism (GO:0046378) #0
            - K antigen metabolism (GO:0046375) #0
            - fructan metabolism (GO:0010145) #0
            - GDP-alpha-D-mannosylchitosylphosphodolichol metabolism (GO:0046376) #0
            - poly-N-acetyllactosamine metabolism (GO:0030309) #0
            - alginic acid metabolism (GO:0042120) #0
            - extracellular polysaccharide metabolism (GO:0030309) #0
            - pectin metabolism (GO:0045458) #0
            - xylan metabolism (GO:0045491) #0
            - galactomannan metabolism (GO:0051069) #0
            - 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.
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.
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.

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

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

3) The following summary will result. Those terms with a [i] indicate a “instance of.”
4) Click on sporophyte to find various parts and instances of this plant structure.

Summary for PO Term: sporophyte (PO:0009003)

<table>
<thead>
<tr>
<th>Term Name</th>
<th>sporophyte</th>
</tr>
</thead>
<tbody>
<tr>
<td>Definition</td>
<td>A diploid plant, or phase of a life cycle, that bears spores formed by meiosis.</td>
</tr>
</tbody>
</table>

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)

<table>
<thead>
<tr>
<th>Term Name</th>
<th>sporophyte</th>
</tr>
</thead>
<tbody>
<tr>
<td>Definition</td>
<td>A diploid plant, or phase of a life cycle, that bears spores formed by meiosis.</td>
</tr>
</tbody>
</table>

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.
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.”

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.

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 agrivitropism-1 and report:
   a. What does the description say about this gene?
   b. Name the germplasm where it was identified.
   c. What are the associated traits?
   d. At what growth stages were the traits assayed?
   e. 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.
2) Select the term “agravitropism,” as shown below.

<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>embryo</td>
<td>agravitropism-1</td>
<td>agrf1</td>
<td>TAS</td>
</tr>
<tr>
<td>2</td>
<td>embryo</td>
<td>An</td>
<td>Anf</td>
<td>TAS</td>
</tr>
<tr>
<td>3</td>
<td>embryo</td>
<td>apical displacement-1</td>
<td>apd1</td>
<td>TAS</td>
</tr>
<tr>
<td>4</td>
<td>embryo</td>
<td>club-shaped embryo-1</td>
<td>ceb1</td>
<td>TAS</td>
</tr>
<tr>
<td>5</td>
<td>embryo</td>
<td>Dominant hybrid lethal-1</td>
<td>Enl1</td>
<td>TAS, IACP</td>
</tr>
<tr>
<td>6</td>
<td>embryo</td>
<td>Dominant hybrid lethal-2</td>
<td>Enl2</td>
<td>TAS, IACP</td>
</tr>
<tr>
<td>7</td>
<td>embryo</td>
<td>depressed glossy-1</td>
<td>dp1</td>
<td>TAS, IACP</td>
</tr>
</tbody>
</table>

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**
agrf1

**Phenotypic Description**
Abnormal germination, embryo with shrunken shoot and root. Seedlings have various morphological and histological abnormalities of leaves and roots, loss of gravitropism.

**Alleles**
agrf1

**Germplasm**
Odm24

**Associated Feature**

<table>
<thead>
<tr>
<th>Associated Feature</th>
<th>Trait</th>
<th>Developmental Stage</th>
<th>Anatomy Location</th>
<th>Evidence Code</th>
</tr>
</thead>
<tbody>
<tr>
<td>Leaf related trait</td>
<td>02-seeding</td>
<td>Leaf</td>
<td>Leaf</td>
<td>TAS</td>
</tr>
<tr>
<td>Root related trait</td>
<td>01-germination</td>
<td>Root</td>
<td>Root</td>
<td>TAS</td>
</tr>
<tr>
<td>Embryo related trait</td>
<td>01-germination</td>
<td>Embryo</td>
<td>Embryo</td>
<td>TAS</td>
</tr>
<tr>
<td>Embryo related trait</td>
<td>01-germination</td>
<td>Embryo</td>
<td>Embryo</td>
<td>TAS</td>
</tr>
</tbody>
</table>

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

Summary for plant growth stage ontology

<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:0007199</td>
<td>plant growth stage ontology</td>
<td>None</td>
<td>Ontology of the growth stages in various cereal crops.</td>
</tr>
</tbody>
</table>

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:00080001) #1332
  - [ ] plant growth stage ontology (GRO:0007199) #1332
    - [ ] maize growth stage (GRO:0007002) #0
    - [ ] rice growth stage (GRO:0007040) #1332
    - [ ] sorghum growth stage (GRO:0007124) #0
    - [ ] 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 08
Definition: One of the ripening stages when endosperm starts hardening.

Derivation:
- cereal plant ontology (GRO:00080001) #144
  - [ ] plant growth stage ontology (GRO:0007199) #1332
    - [ ] rice growth stage (GRO:0007040) #1332
    - [ ] C-embryo stage (GRO:0007141) #1332
    - [ ] 06 dough stage (GRO:0007042) #133
      - [ ] 1-hard dough stage (GRO:0007152) #0
      - [ ] 2-hard dough stage (GRO:0007164) #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.

<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>003-dough stage</td>
<td>Activator for anthocyanin pigmentation</td>
<td>Ap</td>
<td>TAS, IAGP</td>
</tr>
<tr>
<td>2</td>
<td>003-dough stage</td>
<td>stick-like leaf-1</td>
<td>bdl1</td>
<td>TAS</td>
</tr>
<tr>
<td>3</td>
<td>003-dough stage</td>
<td>stick-like leaf-2</td>
<td>bdl2</td>
<td>TAS</td>
</tr>
<tr>
<td>4</td>
<td>003-dough stage</td>
<td>Ave-1</td>
<td>Ave1</td>
<td>TAS</td>
</tr>
<tr>
<td>5</td>
<td>003-dough stage</td>
<td>Ave-2</td>
<td>Ave2</td>
<td>TAS, IAGP</td>
</tr>
<tr>
<td>6</td>
<td>003-dough stage</td>
<td>Ave-3</td>
<td>Ave3</td>
<td>TAS, IAGP</td>
</tr>
<tr>
<td>7</td>
<td>003-dough stage</td>
<td>Ave-4</td>
<td>Ave4</td>
<td>TAS, IAGP</td>
</tr>
<tr>
<td>8</td>
<td>003-dough stage</td>
<td>ave-5</td>
<td>ave5</td>
<td>TAS, IAGP</td>
</tr>
<tr>
<td>9</td>
<td>003-dough stage</td>
<td>Ave-6</td>
<td>Ave6</td>
<td>TAS</td>
</tr>
<tr>
<td>10</td>
<td>003-dough stage</td>
<td>Ave-7</td>
<td>Ave7</td>
<td>TAS</td>
</tr>
<tr>
<td>11</td>
<td>003-dough stage</td>
<td>brittle culm-1</td>
<td>bcl1</td>
<td>TAS, IAGP</td>
</tr>
<tr>
<td>12</td>
<td>003-dough stage</td>
<td>brittle culm-2</td>
<td>bcl2</td>
<td>TAS, IAGP</td>
</tr>
<tr>
<td>13</td>
<td>003-dough stage</td>
<td>brittle culm-4</td>
<td>bcl4</td>
<td>TAS, IAGP</td>
</tr>
<tr>
<td>14</td>
<td>003-dough stage</td>
<td>brittle culm-5</td>
<td>bcl5</td>
<td>TAS, IAGP</td>
</tr>
</tbody>
</table>

Answer: There are four brittle culm genes associated with growth stage “dough stage.” They are brittle culm-1, brittle culm-2, brittle culm-4, and brittle culm-6.
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.

<table>
<thead>
<tr>
<th>Type ID or keyword to search</th>
<th>trait ontology</th>
</tr>
</thead>
<tbody>
<tr>
<td>select ontology (optional)</td>
<td>Gene (GO)</td>
</tr>
<tr>
<td></td>
<td>Plant structure (PO)</td>
</tr>
<tr>
<td></td>
<td>Growth stage (GRO)</td>
</tr>
<tr>
<td></td>
<td>Trait (TO)</td>
</tr>
<tr>
<td></td>
<td>Environment (EO)</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th>Term Name</th>
<th>trait ontology</th>
</tr>
</thead>
<tbody>
<tr>
<td>Synonym</td>
<td>TO.</td>
</tr>
<tr>
<td>Derivation</td>
<td></td>
</tr>
</tbody>
</table>

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.
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.

<table>
<thead>
<tr>
<th>Gene Name</th>
<th>Gene Symbol</th>
<th>Phenotypic Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Rice R gene (Anthocyanin biosynthesis)-a</td>
<td>Ra</td>
<td>One rice R gene. An active homologous 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.</td>
</tr>
</tbody>
</table>

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 amyllopectin ratio” belongs.

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

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:000017), 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.

<table>
<thead>
<tr>
<th>#</th>
<th>Term Accession</th>
<th>Term Name</th>
<th>Synonym</th>
<th>Definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>37</td>
<td>ctm length</td>
<td>reduced culm number-6</td>
<td>icw6</td>
<td>TAS</td>
</tr>
<tr>
<td>38</td>
<td>ctm length</td>
<td>semidwarf-1</td>
<td>ic61</td>
<td>TAS, IAGP</td>
</tr>
<tr>
<td>39</td>
<td>ctm length</td>
<td>Dwarf-44</td>
<td>Dwrl4</td>
<td>TAS, IAGP</td>
</tr>
<tr>
<td>40</td>
<td>internode length</td>
<td>apical meristem of internode</td>
<td>ipl</td>
<td>TAS</td>
</tr>
<tr>
<td>41</td>
<td>internode length</td>
<td>Dwarf-1</td>
<td>dwrl1</td>
<td>TAS, IAGP</td>
</tr>
<tr>
<td>42</td>
<td>internode length</td>
<td>dwarf-9</td>
<td>dwrl9</td>
<td>TAS</td>
</tr>
<tr>
<td>43</td>
<td>internode length</td>
<td>dwarf-10</td>
<td>dwrl10</td>
<td>TAS, IAGP</td>
</tr>
<tr>
<td>44</td>
<td>internode length</td>
<td>dwarf-24</td>
<td>dwrl24</td>
<td>TAS, IAGP</td>
</tr>
<tr>
<td>45</td>
<td>internode length</td>
<td>dwarf-25</td>
<td>dwrl25</td>
<td>TAS, IAGP</td>
</tr>
</tbody>
</table>

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.

<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>TO:0000424</td>
<td>brown planthopper resistance</td>
<td>BPH, BPHRS</td>
<td>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. Infected areas in the field may be patchy.</td>
</tr>
<tr>
<td>2</td>
<td>TO:0000205</td>
<td>white-backed planthopper resistance</td>
<td>WBP, WBPBPH</td>
<td>Causal agent: Sogatella 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)</td>
</tr>
</tbody>
</table>

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)

<table>
<thead>
<tr>
<th>Term Name</th>
<th>brown planthopper resistance</th>
</tr>
</thead>
<tbody>
<tr>
<td>Synonym</td>
<td>BPH, BPHRS</td>
</tr>
<tr>
<td>Definition</td>
<td>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.</td>
</tr>
<tr>
<td>Derivation</td>
<td></td>
</tr>
<tr>
<td></td>
<td>• trait ontology (TO:0000387) #73</td>
</tr>
<tr>
<td></td>
<td>• stress related trait (TO:0000134) #21</td>
</tr>
<tr>
<td></td>
<td>• biotic stress related trait (TO:0000479) #43</td>
</tr>
<tr>
<td></td>
<td>• crop damage resistance trait (TO:0000236) #95</td>
</tr>
<tr>
<td></td>
<td>• animal damage resistance (TO:000054) #23</td>
</tr>
<tr>
<td></td>
<td>• insect damage resistance (TO:0000261) #73</td>
</tr>
<tr>
<td></td>
<td>• brown planthopper resistance (TO:0000424) #13</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th>Term Name</th>
<th>white-backed planthopper resistance</th>
</tr>
</thead>
<tbody>
<tr>
<td>Synonym</td>
<td>WBPH, WBPHRS</td>
</tr>
<tr>
<td>Definition</td>
<td>Causal agent: Sogatella 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 white-backed planthopper).</td>
</tr>
<tr>
<td>Derivation</td>
<td></td>
</tr>
<tr>
<td></td>
<td>• trait ontology (TO:0000387) #73</td>
</tr>
<tr>
<td></td>
<td>• stress related trait (TO:0000134) #21</td>
</tr>
<tr>
<td></td>
<td>• biotic stress related trait (TO:0000479) #43</td>
</tr>
<tr>
<td></td>
<td>• crop damage resistance trait (TO:0000236) #95</td>
</tr>
<tr>
<td></td>
<td>• animal damage resistance (TO:000054) #23</td>
</tr>
<tr>
<td></td>
<td>• insect damage resistance (TO:0000261) #73</td>
</tr>
<tr>
<td></td>
<td>• white-backed planthopper resistance (TO:0000205) #9</td>
</tr>
</tbody>
</table>

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.


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.

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.

<table>
<thead>
<tr>
<th>Phrase from abstract</th>
<th>Trait Ontology term</th>
<th>Trait Ontology id</th>
</tr>
</thead>
<tbody>
<tr>
<td>heading date (HD)</td>
<td>Days to Heading</td>
<td>TO:0000137</td>
</tr>
<tr>
<td>plant height (PH)</td>
<td>Plant Height</td>
<td>TO:0000207</td>
</tr>
<tr>
<td>term</td>
<td>definition</td>
<td>code</td>
</tr>
<tr>
<td>-----------------------------------</td>
<td>---------------------</td>
<td>---------</td>
</tr>
<tr>
<td>flag leaf length (FLL)</td>
<td>Leaf length</td>
<td>TO:0000135</td>
</tr>
<tr>
<td>flag leaf width (FLW)</td>
<td>Leaf width</td>
<td>TO:0000370</td>
</tr>
<tr>
<td>panicle length (PL)</td>
<td>Panicle length</td>
<td>TO:0000040</td>
</tr>
<tr>
<td>spikelet number per panicle (SN)</td>
<td>spikelet number</td>
<td>TO:0000456</td>
</tr>
<tr>
<td>spikelet fertility (SF)</td>
<td>spikelet fertility</td>
<td>TO:0000180</td>
</tr>
</tbody>
</table>
Annotation exercise on Expression libraries

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.

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.
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