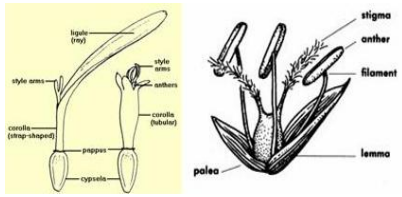
Phylogenetic diversity can result in inconsistency in nomenclature:

Instances of leaf: (PO:0025034)

maple leaf pine needle palm frond

Different names are used for the same structure



Asteraceae Poaceae

Different structures can have the same name e.g. 'floret'

The PO provides consistent terminology for annotation of plant structures and growth and developmental stages.

Contact us:

Visit http://plantontology.org and click on the **Feedback Tab** to send a message

Goals of the Plant Ontology:

Encompass **all** plants: include terms and annotations for flowering and non-flowering plants (angiosperms, gymnosperms, lycopods, ferns, and bryophytes)

Facilitate comparative genomics across diverse plant species

Create mappings (links) to other ontologies such as the Gene Ontology

Create logical *(genus-differentia)* definitions and follow OBO Foundry principles

Participants and Collaborators:

plantcode, GRAMENE, tair, MaizeGDB Maize Genetics and Genomics Database, IRRI, IRIS, COSMOSS.org, sol genomics network, SoyBase, Arabidopsis.info, Flora of North America, GrainGenes, Oryzabase Integrated Rice Science Database, mips, PLEXdb, PIONEER A DUPONT COMPANY, MONSANTO imagine, Missouri Botanical Garden, Oregon State University OSU, The New York Botanical Garden, Cornell University

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The Plant Ontology

What is the Plant Ontology?

A structured vocabulary for all plants that covers:

- plant anatomy and morphology
- plant growth and development

A source for:

- standard definitions reviewed by experts
- links to annotations from plant genome databases

A web-based interface that allows users to:

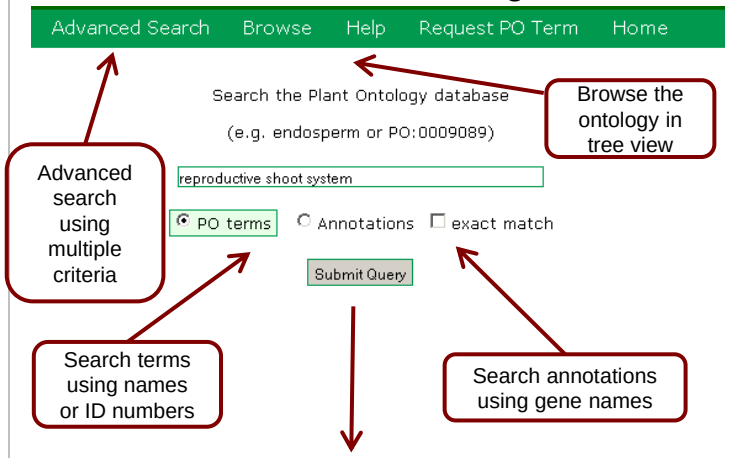
- browse the ontology
- search for terms and annotations
- summarize annotations

A teaching tool for plant anatomy and genomics

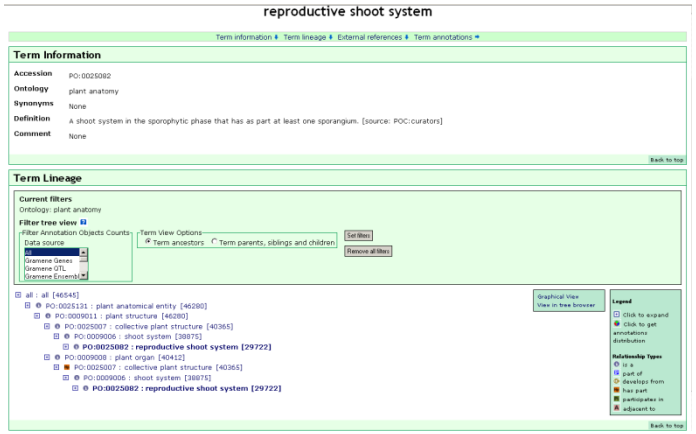
Find us on the web at: http://plantontology.org

Navigating the Plant Ontology website:

Basic Search Page:



The **Term page** shows the definition, synonyms and relationships to other terms.



Request New Terms:

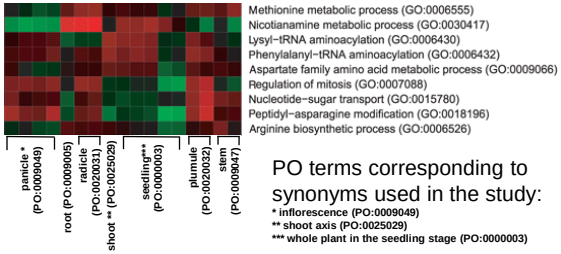
The **"Request PO Terms"** tab takes you to our Source Forge tracker.

Be sure to register and sign in before submitting requests.

Annotations:

Annotations may be created based on microarray, EST, QTL, protein, germplasm, phenotype or other data sets, or whole genome sequencing projects.

Example microarray data set with PO and GO annotations:

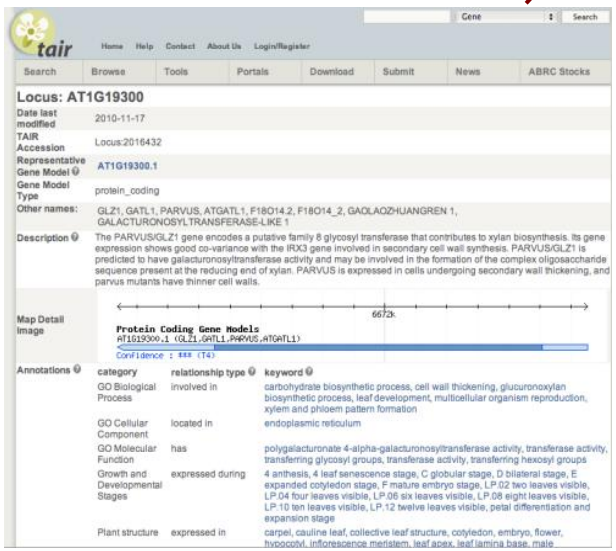


PO terms corresponding to synonyms used in the study:

* inflorescence (PO:0009049)
** shoot axis (PO:0025029)
*** whole plant in the seedling stage (PO:0000003)

Data Image From: Wang, et al. (2010). *The Plant Journal*, 61.

Contact us if you are interested in providing and maintaining annotations files for your project



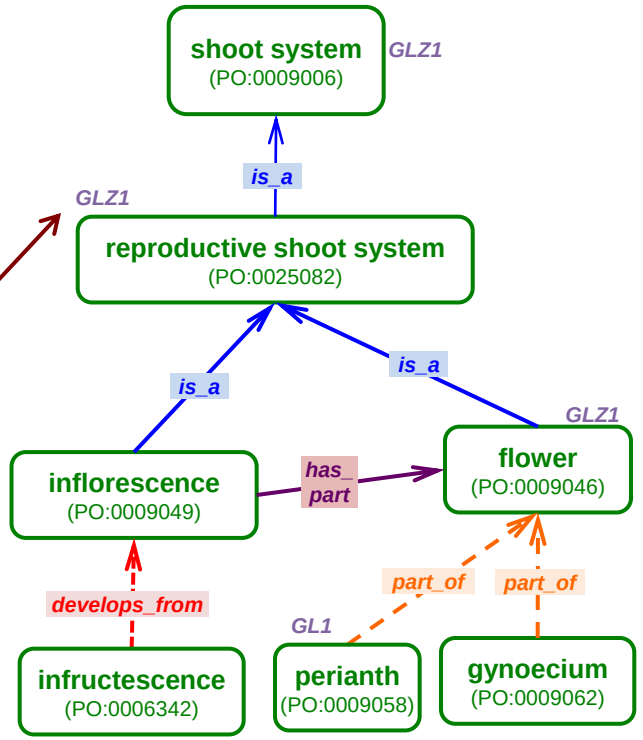
Links from the term page take you to gene annotation data

Using the Plant Ontology:

Hierarchical structure allows for taxon-specific annotation and comparisons across taxa.

You can ask questions such as:

- What genes are expressed in the reproductive shoot system of various plants?
- In *Arabidopsis thaliana,* is the gene ***GLZ1*** expressed in other structures?
- Are there ***GLZ1*** mutants available?



Relations in the Plant Ontology :

- ***is_a*** and ***part_of*** are the backbone of all anatomy onotologies
- ***develops_from*** describes shared developmental pathways across all taxa
- ***has_part*** allows the PO to describe structural variation among taxa
- Annotations are carried up to parents through ***is_a*** and ***part_of*** but not ***develops_from*** relations