

The Plant Ontology
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Plants to be Studied:

- Principal: All flowering plant species (Angiosperms) having/upcoming whole genome sequences and/or large genomics datasets on expression and phenotypes.
Secondary: Bryophytes (mosses and liverworts), Pteridophytes (ferns) and Gymnosperms.

Project Objectives:

1. Develop and enrich the Plant Ontology (PO) to describe plant anatomy and developmental stages of all green plants.
2. Develop PO as reference ontology of plant structures and growth stages by doing mappings to similar vocabularies that are in use by plant databases.
3. Outreach and education activities to extend the PO usage in gene expression and phenotype annotations and awareness on Plant Biology research.

Experimental Approaches:

1. Develop the ontology (controlled vocabulary) for all flowering and major non-flowering plant representatives to describe all plant structures and the growth and development stages.
2. Test the newly developed ontologies and encourage their application in annotation by organizing annual jamborees at important plant biology meetings. A specific number of targeted participants (under represented and young investigators) and a select number of open invitees will be invited to these meetings to learn how to do functional annotation of genes, phenotypes and germplasms using Plant Ontology and other related ontologies, such as the Gene Ontology (GO) and Phenotype Attribute and Trait Ontology (PATO). They will be encouraged to do annotations at the meetings as well as offsite. We will host web accessible tools for allowing researchers to contribute functional, expression and phenotype annotations of genes, QTLs, mutants, germplasms and natural variants.
3. Collaborate with known plant genomics and germplasms repository databases to map their existing annotation and species specific vocabularies to the PO, by using both text mining and manual curation
4. Organize teachers' training workshops for area schools at Cornell University and organize exhibits for students and general public at New York Botanical Garden. The focus of these workshops/exhibits will be Plant Biology awareness.

Information/Materials to be Generated:

- A set of ontologies describing plant anatomy and developmental stages
- Annotations submitted to the PO database by collaborative project and individual researchers.
- An image library for use as reference material with links established from the Plant Ontology terms.
- Project database, website content, image libraries, a modest number of software tools, and shared annotations from contributors.

Contact Information for Outcomes:

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Internet Addresses (Web or Email) for Project Information:

1. **Plant Ontology™ Consortium** www.plantontology.org
2. po-internal@plantontology.org

Informatics Contact Person(s):

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Practical Applications of Research:

The Plant Ontology is a uniquely effective tool to bridge the genetics, molecular biology, cell biology, taxonomy, botany, and the genomics research communities. Its development will contribute to resolution of divergences both in the numerous terminologies used by different genomics projects and in the nomenclatures used for various plant parts and developing stages as described classically by taxonomists, botanists and developmental biologists. Therefore, the project is developing a common set of controlled vocabulary terms describing anatomical structures and developmental stages of both the flowering and non-flowering plants. These terminologies will be applied to the task of annotating the spatial and temporal aspects of gene expression and observed phenotypes of mutants, natural variants and associated quantitative trait loci. The annotations will be carried out in collaboration with the participating plant genomics databases and large repositories of sequence datasets and seed stocks. We will map the ontology terms developed in this project to similar vocabularies developed and used in annotation by various national and international projects working on plant genomics and phenotyping of germplasm seed stocks. In this way the Plant Ontology (PO) developed in this project will serve as a common reference point, allowing comparative analysis of these datasets. This may also help us to answer questions such as: 'Are the expression patterns and phenotypes of homologous genes from rice that are co-expressed during rice inflorescence development the same as those expressed in the developing inflorescence of maize, barley, *Sorghum* and *Arabidopsis*?'

Project Participants:

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