

MASC Phenomics- 2007 Subcommittee Report

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New Phenotyping Facility Approved in Australia

The Australian Government has recently awarded funding for a new Australian Plant Phenomics Facility (APPF) to be established. The APPF aims to be a state-of-the-art plant phenotyping facility with sophisticated plant growth facilities and cutting edge technologies for plant performance and function monitoring. Construction of the Facility is expected to begin in 2007. A primary objective is the analysis of model species such as *Arabidopsis* and rice for gene function discovery. The technologies used for screening will include various imaging approaches including morphological growth and colour analysis, chlorophyll fluorescence and hyperspectral reflectance. These will be coupled to robotic systems which will allow medium throughput screening of plant material grown under controlled environment conditions. See the Australia country report for further information.

Updates on Recent Phenomics Resources

- **Homozygous Mutant *Arabidopsis* Collection**
 1. This project at the Salk Institute aims to create a 'phenome-ready' genome through the identification of two T-DNA homozygous mutants for every *Arabidopsis* gene. As of March, 2007, the project has sent seeds from 9,198 plant lines representing 7,105 individual genes to the ABRC (US) for distribution. (URL: <http://methylo.me.salk.edu/cgi-bin/homozygotes.cgi>). Seeds of the Salk homozygous lines are being prepared at ABRC for forward screening. Pools of lines will be available, and the feasibility of distributing sets of individual lines is being investigated.
 2. The Homozygote Collection Gene Family Viewer is a new resource that groups genes by gene family, and lists the corresponding homozygous plant lines currently available, or that are being targeted, for each gene. Selecting a gene reveals a diagram of the sequence and the insertion location(s) and line(s) available for that gene. Genotyping primer sequences are included, and you can select lines to order. (URL: http://methylo.me.salk.edu/gene_fam/)
- **At the RIKEN Plant Science Center (Japan) two types of mutant resources are being developed for phenome analysis:**
 1. Ac/Ds type transposon lines containing single gene insertions. A recent publication describes phenomic analysis of 4000 Ds mutants. (RAPID: <http://range.gsc.riken.jp/phenome/> and Kuromori *et al*, Plant J. (2006) 47:640-651). Homozygous Ds mutant lines are also being generated.
 2. Full-length cDNA overexpression (FOX) lines: gain-of-function mutant resource overexpressing *Arabidopsis* full-length cDNAs in *Arabidopsis* plants. Over 10,000 FOX lines were made out of around 10,000 independent full-length cDNAs. A database including these mutant lines is under preparation. (Ichikawa *et al*, Plant J. (2006) 25:974-985)
- ***Artificial microRNAs: a complementary tool for gene silencing***

A new versatile tool for gene knockouts that complements T-DNA insertions and TILLING lines are artificial microRNAs (amiRNAs). AmiRNAs allow highly specific and predictable gene silencing, from constitutive, inducible or tissue-specific promoters. A particular advantage of amiRNAs is that they allow the simultaneous inactivation of several, sequence-related genes. An important application is the analysis of tandemly duplicated genes, which are difficult to knock out by conventional means, as well as knockout of genes in accessions other than the standard Columbia strain. A web-based platform for the design of amiRNAs has been developed by the Max Planck Institute for Developmental Biology

(<http://wmd.weigelworld.org>). The platform includes automated primer design for cloning into the pRS300 vector. In addition, Cold Spring Harbor Laboratory has obtained NSF Arabidopsis 2010 funding to generate multiple amiRNAs against all genes in the *A. thaliana* genome, including pairs of segmentally duplicated genes and tandemly duplicated genes (AT2010 award #0617983.) The corresponding ~80,000 amiRNAs were also designed by the Max Planck Institute for Developmental Biology. Preliminary user feedback indicates that amiRNAs are successful in about 75% of all cases.

New Phenotype data and tools at TAIR

In the last 12 months TAIR has separated phenotype data from other germplasm information and now stores phenotype descriptions for 1768 genes, including 417 genes identified as mutants but lacking sequence information and 1351 sequenced genes with AGI codes. TAIR has also added the capacity to search for genes, germplasms, and polymorphisms using associated phenotype information. The gene, locus, germplasm, polymorphism and stock detail pages were also updated to display phenotype data. When available, the reference that describes the phenotype is cited. TAIR curators will continue to extract phenotype descriptions along with other types of data from the current literature and add them to TAIR. It is expected that TAIR will transition to using the GO (Gene ontology), PO (Plant Ontology) and PATO (phenotypic quality) controlled vocabularies to describe phenotypes in the coming year.

NCBiO develops phenotype curation tool

A curation tool designed to annotate phenotypes using an EQ model (entities represented by Gene Ontology or Plant Ontology terms combined with qualities such as absent, abnormal, decreased length, etc. represented by the PATO ontology) has been developed by Mark Gibson for NCBiO. Genotypes and publications can also be associated with each phenotype annotation. The standalone tool, called Phenote, is available for download from <http://www.phenote.org/>. The PATO ontology is undergoing rapid development, see http://www.bioontology.org/wiki/index.php/PATO:Main_Page for more information and to submit new terms.

Publications / presentations / workshops relating to Arabidopsis PO/PATO and phenotyping

- The Plant Ontology Consortium (POC, <http://www.plantontology.org>), formed in 2003 and headed by Lincoln Stein, presented a summary "The Role Of Plant Ontology In Comparative Plant Genomics And Gene Discovery" at Plant & Animal Genome XV (available at http://www.intl-pag.org/15/abstracts/PAG15_P08a_841.html). For contact purposes, the coordination of PO has passed from Katica Ilic (ex-TAIR) to Chih-Wei Tung (Cornell University).
- A subset of the PO consortium published a definitive paper (Plant Structure Ontology. Unified Vocabulary of Anatomy and Morphology of a Flowering Plant. Ilic *et al* Plant Phys. Dec 2007); describing the rationale and development of the ontology for *Arabidopsis* by TAIR, and subsequent integration into a range of databases (including a description of the PATO implementation at NASC).

Open Workshops

- Ontologies, Standards and Best Practice, PSB, Gent (Belgium), May 21-23, 2007 - including a practical by NASC on the laboratory use of PO and PATO; talks on the integration of PO/PATO into NASC (since 2005 but now including web-services); and presentations on the development and applications of PO as a coordinated program by Katica Ilic and Chih-Wei Tung. See: <http://www.agron-omics.eu/>
- Growth Phenotyping and Imaging in Plants, LEPSE, Montpellier (France), July 17-19, 2007 - including presentations of automated phenotype analysis, growth imaging and modeling for leaves and roots. See: <http://www.agron-omics.eu/>