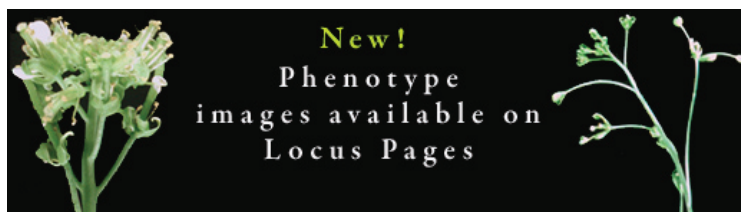


TAIR Newsletter Fall 2008

New *A. thaliana* phenotype pictures available

Phenotype images are now available for a subset of Arabidopsis mutants. Images are shown on the Locus pages in the Germplasm section. All available phenotype images can be downloaded from our ftp server: ftp://ftp.arabidopsis.org/home/tair/germplasm_images. If you would like to submit phenotype data/images to TAIR, please visit our data submission site at http://www.arabidopsis.org/submit/phenotype_submission.jsp

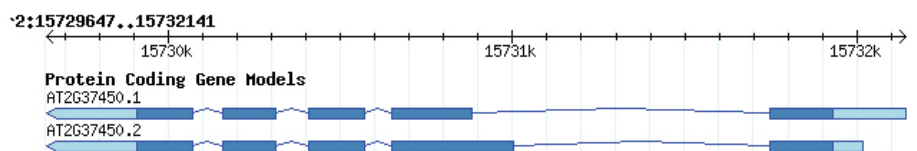


New GBrowse tracks

Over the summer we added new tracks to GBrowse, the TAIR genome browser. Data represented in these tracks include Orthologs (Inparanoid), Plant Gene Families (Phytozome), Proteomics data (Baerenfaller et al. 2008), Polymorphic Regions (Zeller et al., 2008), Promoter Elements (PlantPromoterDB, Yamamoto et al., 2008), mRNAs (Col-0) and smRNAs (Col-0) (Lister et al., 2008; Gregory et al., 2008), Gaps, Phosphorylation data (PhosPhAt database) and polymorphisms for ecotypes Bur-0 and Tsu-1 (Ossowski et al. 2008). These datasets can be selected from the tracks menu in GBrowse (<http://www.arabidopsis.org/cgi-bin/gbrowse/arabidopsis/>). For additional information and references regarding the data displayed in GBrowse, please click on the title of the track of interest.

Gene detail page update

Gene and Locus Detail pages now display an image showing a snapshot of the exon-intron structure of all isoforms related to the gene model or locus. By clicking on the image, the user is redirected to GBrowse. Please allow a few seconds for the image to load.



Update on our collaboration with Plant Physiology

Since the launch of the collaboration this spring, we have received gene information from 34 authors whose papers appeared in recent issues of Plant Physiology (from May to September 08). Based on the information provided, we added 136 Gene Ontology and 92 Plant Ontology annotations to TAIR. In total, annotations for 75 Arabidopsis genes were updated. All annotations are attributed to the contributing author. We would like to thank all authors who have generously contributed their time and data. If you would like us to include information from your own publication (from any journal), please visit:

http://www.arabidopsis.org/submit/functional_annotation_submission.jsp



TAIR survey results now available

TAIR conducted a survey of Arabidopsis users aimed at measuring the level of satisfaction with various aspects of TAIR's performance and learning what new data and tools the community is interested in having TAIR provide. The survey, which ran from April 23 - May 8, 2008, was ad-

ministered in two ways: by email to a random sample of 300 abstract submitters to the 18th ICAR conference (95 responses) and by posting a link to the survey within the header for all TAIR pages (293 responses). The survey results are now available at TAIR: <http://www.arabidopsis.org/about/survey.jsp>

AraCyc 4.5 release and PMN 1.0 debut

In June 2008, a new version of AraCyc was released containing 11 new metabolic pathways. Data from the literature and the TAIR 8 genome release led to changes in the assignment of over 300 genes in this metabolic pathway database. For more details on the AraCyc updates please visit <http://www.arabidopsis.org/biocyc/releasenotes.jsp>. Going beyond Arabidopsis, the Plant Metabolic Network (PMN) has launched its official web site and released the first version of PlantCyc, a comprehensive biochemical pathway database for the entire plant kingdom. PlantCyc 1.0 has over 500 pathways containing enzymes from over 250 plant species. Please visit **www.plantcyc.org** to learn more about this database and to use it to investigate metabolism in Arabidopsis and many other plants.



New Polymorphisms & Markers submitted to TAIR

New Bur-0 and Tsu-1 SNPs and indels

823,325 SNPs and 79,961 indels for Bur-0 and Tsu-1 are now available on TAIR's GBrowse and FTP site ftp://ftp.arabidopsis.org/home/tair/Sequences/Ossowski_Resequencing_Data_2008 and at 1001 Genomes (Ossowski et al. 2008, Genome Research).

Polymorphisms and markers submitted by individual labs

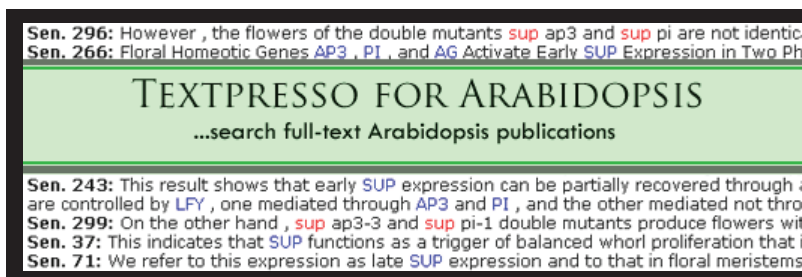
This year, we received more than 250 markers and polymorphisms from individual labs. We would like to thank the Juenger, Dobritsa, Nandi and Shigeru labs as well as Laura Gilliland.

If you would like to submit your marker/polymorphism data to TAIR please go to:

http://www.arabidopsis.org/submit/marker_submission.jsp

Textpresso for Arabidopsis

Textpresso is an information extracting and processing package for biological literature. Textpresso for Arabidopsis allows users to search all abstracts and over 15,700 full-text publications in TAIR. It is now available at www.textpresso.org/arabidopsis and can be linked to from the TAIR tools menu. Key-word searches can be narrowed by searching in specific categories. Textpresso was initially developed by Hans-Michael Muller, Eimear Kenny and Paul W. Sternberg, with contributions from Juancarlos Chan and David Chen. This new version, Textpresso 2.0, was developed by Hans-Michael Muller with contributions from Arun Rangarajan and Tracy K. Teal.



TAIR curation booth

TAIR and PMN curators took to the road this past summer to attend several meetings. They also had the opportunity to host a curation booth at the 19th annual International Conference on Arabidopsis Research in Montreal from July 23- July 27. Thanks to the generous support of Joanna Friesner (MASC Coordinator) and the conference organizers, TAIR curators were able to answer questions on gene structure, gene function, and metabolic pathway annotation throughout the meeting from a booth with internet access. Many people were treated to a helpful demonstration of GBrowse's newest features, got tips about finding valuable Annotation Details, or had the chance to learn more about the OMICS viewer. But, the curators also benefited when users gave helpful feedback or provided new data and experimental references to load into the databases. TAIR and the PMN hope to provide this type of direct outreach again in summer 2009.

