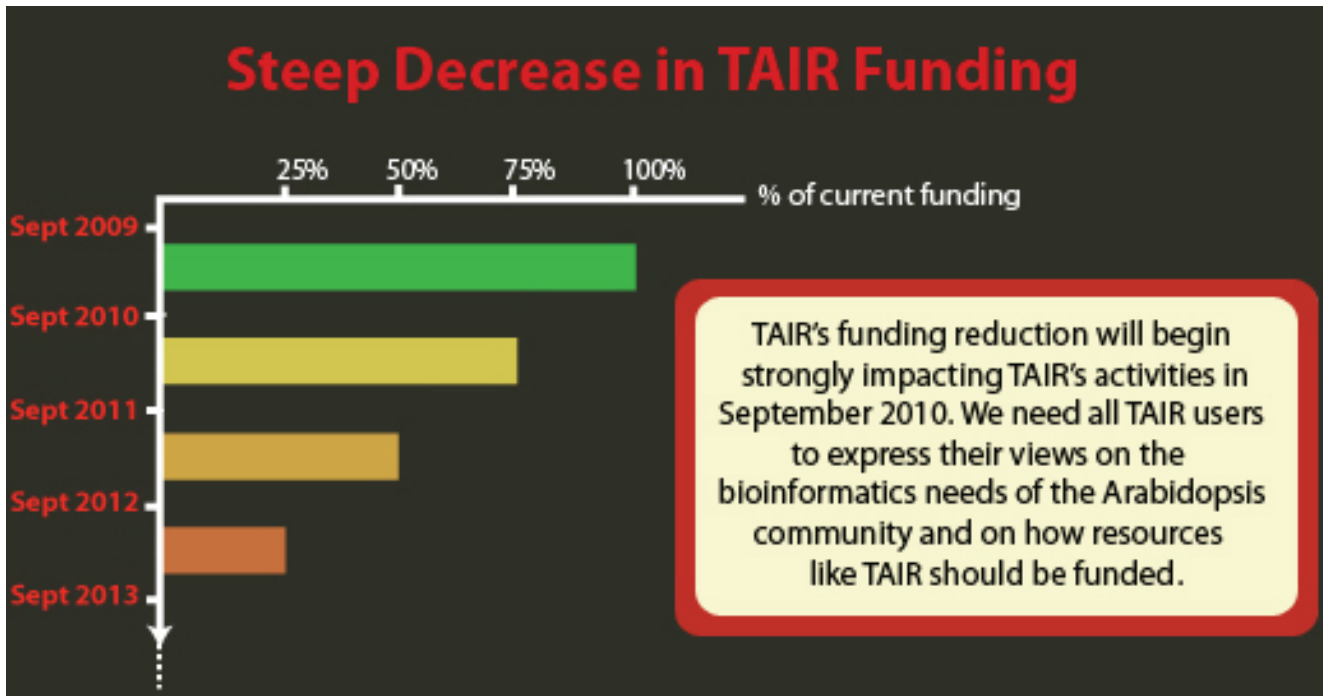# TAIR Newsletter Fall 2009

Steep Decrease in TAIR Funding

Our previous five year NSF grant supporting TAIR ended on August 31 2009. The TAIR project did obtain a renewal from NSF that provides level funding for the current year (September 2009 - August 2010) followed by steeply decreasing budgets (75%, 50% and 25% of the current year) for the remaining three years. There is currently no funding mechanism in place at NSF for ongoing operational costs of long term data resources like TAIR. NSF has strongly encouraged TAIR to seek funding from other sources, including subscription fees for companies and/or academic labs and funding from other US agencies or other countries. A change in our funding model could have wide-ranging effects on how we operate (including our ability to export gene structure and function data to other resources such as NCBI, SIGnAL, UniProt, etc.); therefore it is essential that the impact is carefully considered before a new funding strategy is implemented. The steep reduction in funding for TAIR requires that we either scale back our work to a corresponding degree or obtain funding from other sources. **The funding reduction will begin strongly impacting TAIR's activities in September 2010**. A public discussion is urgently needed on community bioinformatics needs, TAIR's role in fulfilling these needs and viable funding strategies for this type of resource. It is essential that this discussion include the viewpoints of plant biology researchers, educators and students from around the world.

To make your voice heard, please add a comment by following this link:
http://www.arabidopsis.org/doc/about/tair_funding/410#comment_anchor
in order to express your views on (1) the bioinformatics needs of the Arabidopsis and wider plant biology communities and (2) how resources like TAIR should be funded. It is important that we hear from a variety of people in the USA and from other countries including wet lab researchers, computational biologists, researchers working on crop plants or basic biological questions, students and teachers, and those working within a company as well as those in academic institutions.

In addition, if you use TAIR for your research, please do one or more of the following in your publications:
- Cite the most recent TAIR publication: http://www.arabidopsis.org/about/citingtair.jsp
- Acknowledge TAIR (http://arabidopsis.org) as a source of data in your methods section
- Include TAIR (http://arabidopsis.org) in your acknowledgement section.

AraCyc 6.0, PlantCyc 3.0 & PoplarCyc 1.0 released

A new version of the AraCyc database (6.0) was released on October 15, 2009 by the Plant Metabolic Network (PMN). This PMN release includes many updates to AraCyc enzyme/reaction assignments based on a new PMN enzyme annotation pipeline. In addition, 34 pathways have been newly added to the database. Several of these pathways focus on glucosinolate metabolism and hormone modification. For more information, please see the AraCyc release notes:
http://www.plantcyc.org/release_notes/aracyc/aracyc_release_notes.faces

The PMN also released the first version of the PoplarCyc (1.0) database (321 pathways) and an updated version of the PlantCyc (3.0) database (714 pathways, 300+ species). Users can compare metabolism in Arabidopsis, poplar, and other plant species using tools available at the PMN, including the Comparative Analysis page: http://www.plantcyc.org:1555/comp-genomics??

PoplarCyc now available!
321 pathways , 3434 enzymes, 1363 compounds
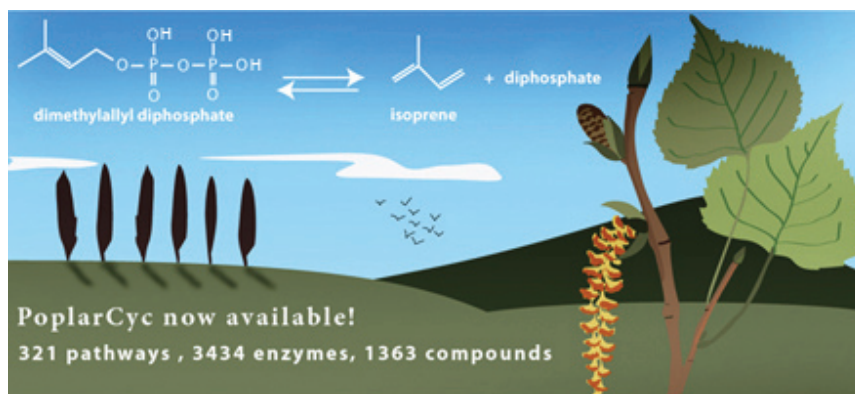
The PMN also now provides a BLAST tool and two customized BLAST enzyme data sets:
http://www.plantcyc.org/tools/Blast/blast.faces
More information about the new data and new tools can be found at the PMN website: www.plantcyc.org.

TAIR and the GO Reference Genome project

With more and more genomes being sequenced, we are in the middle of an explosion of genomic information. The limited resources to manually annotate the growing number of sequenced genomes imply that automatic annotation will be the method of choice for many groups. The GO Consortium coordinates an effort to maximize and optimize the GO annotation of a large and representative set of key genomes known as reference genomes. The goal of the Gene Ontology Consortium Reference Genome Annotation Project (http://www.geneontology.org/GO.refgenome) is to completely annotate twelve reference genomes so that those annotations may be used to effectively seed the automatic annotation efforts of other genomes (http://www.ncbi.nlm.nih.gov/sites/entrez?db=pubmed&cmd=search&term=19578431). TAIR participates in this ongoing project with the responsibility of comprehensively annotating a selected set of Arabidopsis genes.

TAIR & PMN at IPMB

TAIR and the PMN will present a joint workshop at the International Plant Molecular Biology (IPMB) conference in St. Louis on Tuesday, October 27 at 6 - 9 PM entitled:
TAIR and the PMN: Making Effective Use of an Arabidopsis Genome Resource and Plant Metabolic Pathway Databases. Information provided about search strategies and tools can help both beginning and advanced users gain access to the data they need. The director of TAIR and a PMN curator will be available to answer questions and give one-on-one help for the last hour of the workshop. For more details, please see:
http://www.ipmb2009.org/WorkshopTitles/Tuesday1.html.
If you would like to schedule a meeting with a TAIR or PMN representative during this conference to ask questions, share data, etc., please send an e-mail to curator@arabidopsis.org.

GBrowse_syn added at TAIR

GBrowse_syn is a GBrowse-based synteny browser designed to display multiple genomes, with a central reference species compared to several additional species. It is included with the standard GBrowse package (version 1.69 and later). GBrowse_syn uses a central 'joining' database that contains information about the multiple sequence alignments as well as additional databases for each species represented in the alignments.
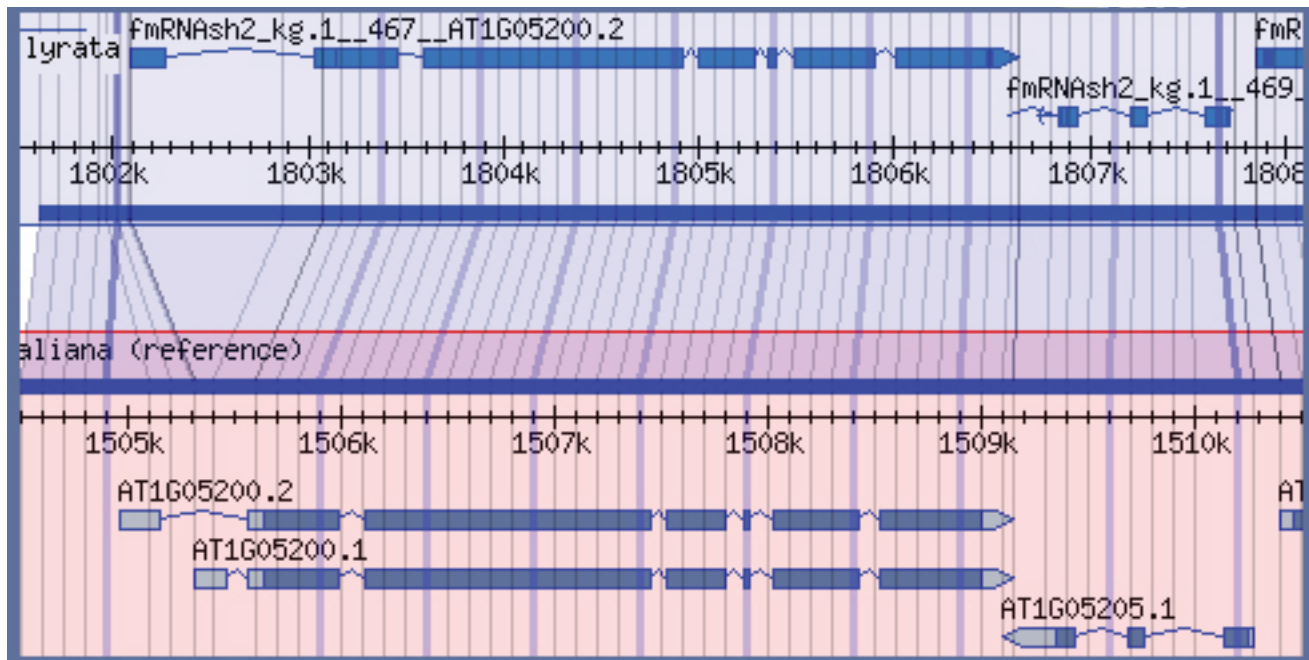
GBrowse_syn was built to help researchers study and analyze syntenic regions, homologous genes and other conserved elements between sequences. It can also be used to study genome duplication and evolution. By comparing newly sequenced or less studied genomes to the well annotated Arabidopsis genome in Gbrowse_syn, scientists can identify novel genes and putative regulatory elements.

The first version of the Gbrowse_syn tool at TAIR includes the genomes of *A. thaliana* and *A. lyrata*. The poplar genome will be added to this synteny viewer in a few weeks, followed by other plant genomes in the near future. This synteny browser can be accessed from the 'Tools' menu on any TAIR page.

For documentation on installing and configuring this tool, please refer to the official Gbrowse_syn Wiki page: http://gmod.org/wiki/GBrowse_syn
For the Gbrowse_syn Help page, go to: http://gmod.org/wiki/GBrowse_syn_Help

The *A. lyrata* and poplar alignment datasets were provided to us by Pedro Pattyn at the University of Ghent, a Ph.D student in the Bioinformatics & Evolutionary Genomics group headed by Yves Van de Peer. We would like to thank Sheldon McKay from CSHL for developing this valuable tool.