

TAIR Newsletter Spring 2008

TAIR8 release

TAIR is pleased to announce the release of the latest version of the Arabidopsis genome annotation (TAIR8) at TAIR and NCBI. The TAIR8 release contains 27,235 protein coding genes, 4759 pseudogenes or transposable elements and 1288 ncRNAs (33,282 genes in all, 38,963 gene models).



A total of 1291 new genes and 2009 new gene models were added. Overall 23% of all existing TAIR7 genes (7380 genes) were updated (includes split, merged and deleted genes as well as locus type changes, structural updates and sequence updates) for TAIR8. Changes to chromosome sequences include removal of vector/Ecoli contamination and 1425 single nucleotide substitutions. Additional details can be viewed at the TAIR website. http://www.arabidopsis.org/portals/genAnnotation/gene_structural_annotation/annotation_data.jsp.

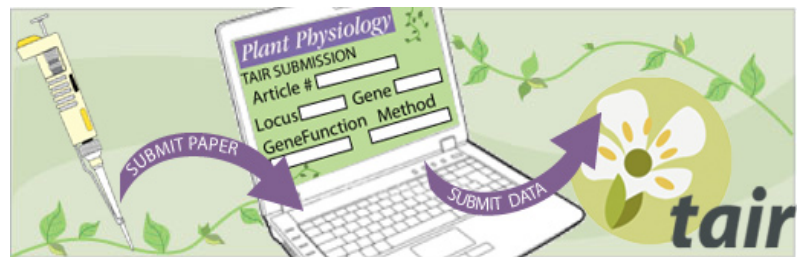
New GBrowse tracks

Our new Vista plugin from JGI displays nucleotide similarity between *A. thaliana* and 5 other plant species (poplar, rice, *Medicago truncatula*, *Physcomitrella patens* and *Selaginella moellendorffii*).

Other new tracks include transposable element genes, methylation profiles, community annotations, CATMA primers and expression data, MPSS expression data, Brassica sequences, Microarray ATH1-121501 probes and the JAtY Clone library. We would like to thank the AtIDB project, Shinhan Shiu, Alexandre Souvorov, the Aubourg Lab, the Quesneville Lab and the Dubchak Lab for allowing us to add these new tracks.

Collaboration with Plant Physiology

A unique partnership has been formed between Plant Physiology and TAIR to ensure that Arabidopsis data published in the Journal are reliably captured in TAIR's database. This collaboration --the first of its kind-- provides a mechanism for authors to submit Arabidopsis gene function information to TAIR as part of the publication process.



Textpresso

We've been working together with the Textpresso team at Wormbase to get an Arabidopsis version of Textpresso up and running. This version of Textpresso, which is currently in its beta stage, allows full-text mining of all papers available at TAIR. Go to www.textpresso.org/arabidopsis to try it out.

GO introduces new relationship types into the Biological Process Ontology

On March 25, 2008, the Gene Ontology Consortium introduced three new relationship types -- regulates, negatively_regulates and positively_regulates -- into the Biological Process ontology. Until now, regulatory processes have been represented as part_of the processes they regulate. These part_of relationships were replaced with the new 'regulates' relationship type. Positively_regulates and negatively_regulates relationships were also added for appropriate child terms. The improved and updated ontology can be accessed both through the GO (<http://amigo.geneontology.org/cgi-bin/amigo/search.cgi>) and TAIR (http://www.arabidopsis.org/servlets/Search?action=new_search&type=keyword) websites.

New Seed Stocks at ABRC

17,291 SALK-C (confirmed) lines are now stored in-house. ABRC is continually receiving new lines from the J. Ecker lab, Salk Institute. As soon as each line is received, its data is entered in TAIR and the stock can be ordered. Information on handling of SALK lines can be found at the SIGnAL Web site (<http://methylo.me.salk.edu/cgi-bin/homozygotes.cgi>). We expect to be receiving new homozygous lines on a regular basis until the full 50,000-line collection is completed.

For more information regarding our new Seed Stocks please go to <http://www.arabidopsis.org/news/news.jsp>

New clones received at ABRC

- a. 10,209 Gateway™ cDNA/ORF clones from J. Ecker (Salk)
- b. 15 vectors from various donors (D. Hegedus, S. P. Dinesh Kumar)
- c. 2,425 transcription factor expression clones from S. P. Dinesh Kumar
- d. 82 cloned genes and constructs (A. Nebenfuhr, J. Harper, H. Sze)

For more information regarding the new clones at ABRC go to <http://www.arabidopsis.org/news/news.jsp>

TAIR survey still open!

Please click on the survey button or banner at the top of our homepage to give us your comments and feedback on how well TAIR is serving your needs and what additional tools and data you would like to see. The survey will be open for only a short time, so please act now to be sure your input is included.

