



# New Features and New Tools, Challenges and Opportunities

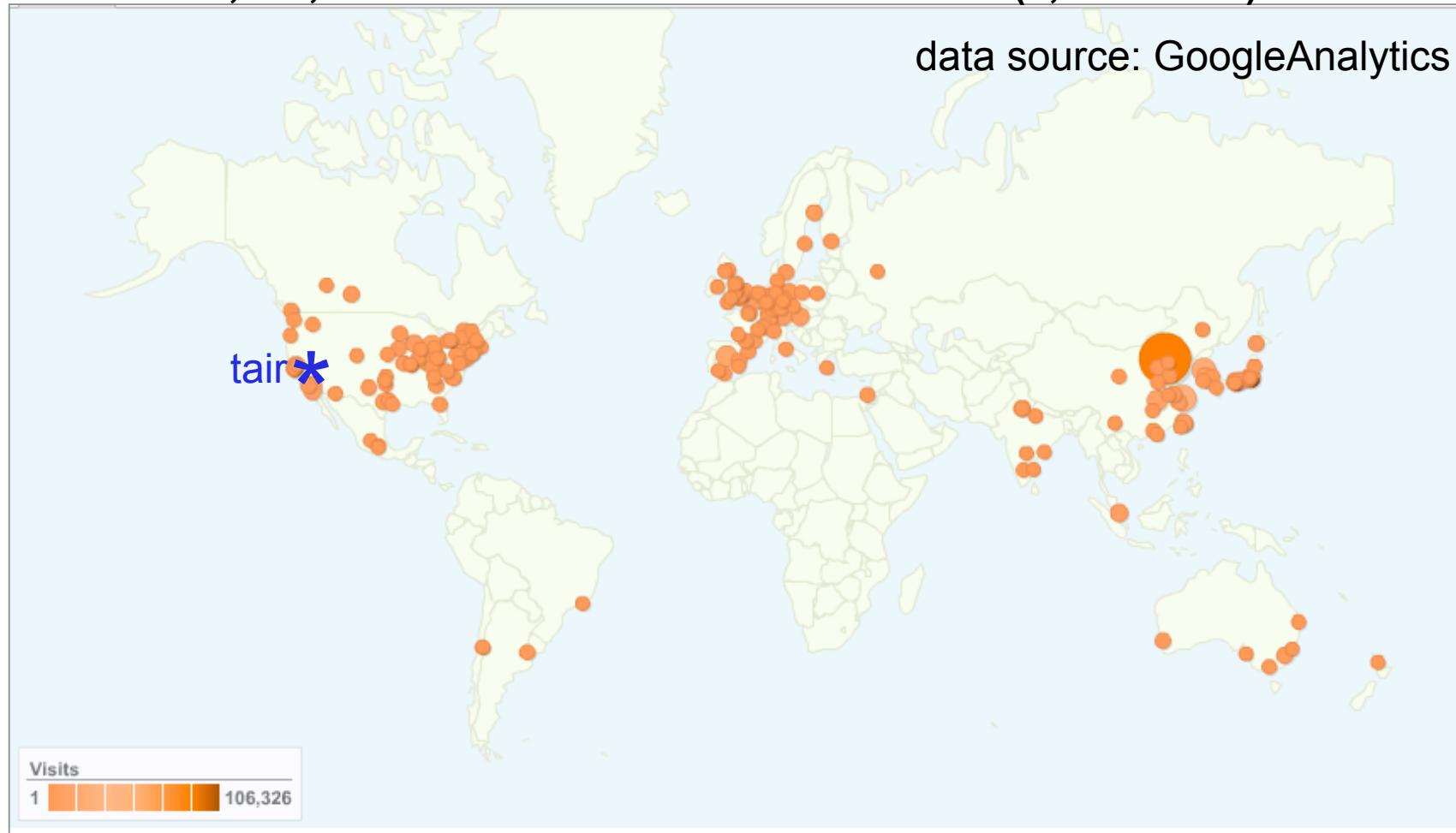
[www.arabidopsis.org](http://www.arabidopsis.org)

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Eva Huala (Director)  
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# TAIR is THE global information HUB for Arabidopsis and plant biology research

**1,710,900 visits came from 186 countries (9,593 cities)**



Source: GoogleAnalytics; date range: Oct 9, 2008 - Nov 8, 2009

# Access to information is key to success

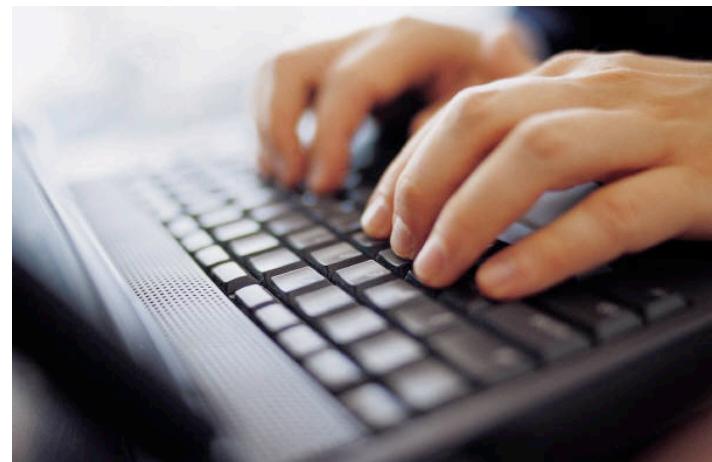
- Improve efficiency productivity
- Stimulate innovation

How do I find a paper?



北大 → 中科院图书馆

10 years ago



today

Access to information is the key to success

How can we create a win-win situation by fostering  
a closer tie between TAIR and the Chinese  
Arabidopsis / plant biology community?

1. Overview: Staff, usage, impact
2. Major roles of TAIR
3. New features, new tools
4. Collaboration opportunities

# Meet the TAIR team



Eva Huala (PI&Director)   Sue Rhee (co-PI)

## Genome Annotation



David Swarbreck  
Philippe Lamesch  
Raj Sasidharan

## Gene Function/GO



Tanya Berardini  
Donghui Li

## Metabolic Pathways



Peifen Zhang  
Kate Dreher  
**(PMN)**

## Technical Staff



Bob Muller



Shanker Singh  
Larry Ploetz



Cynthia Lee  
Chris Wilks



Raymond Chetty  
Tom Meyer

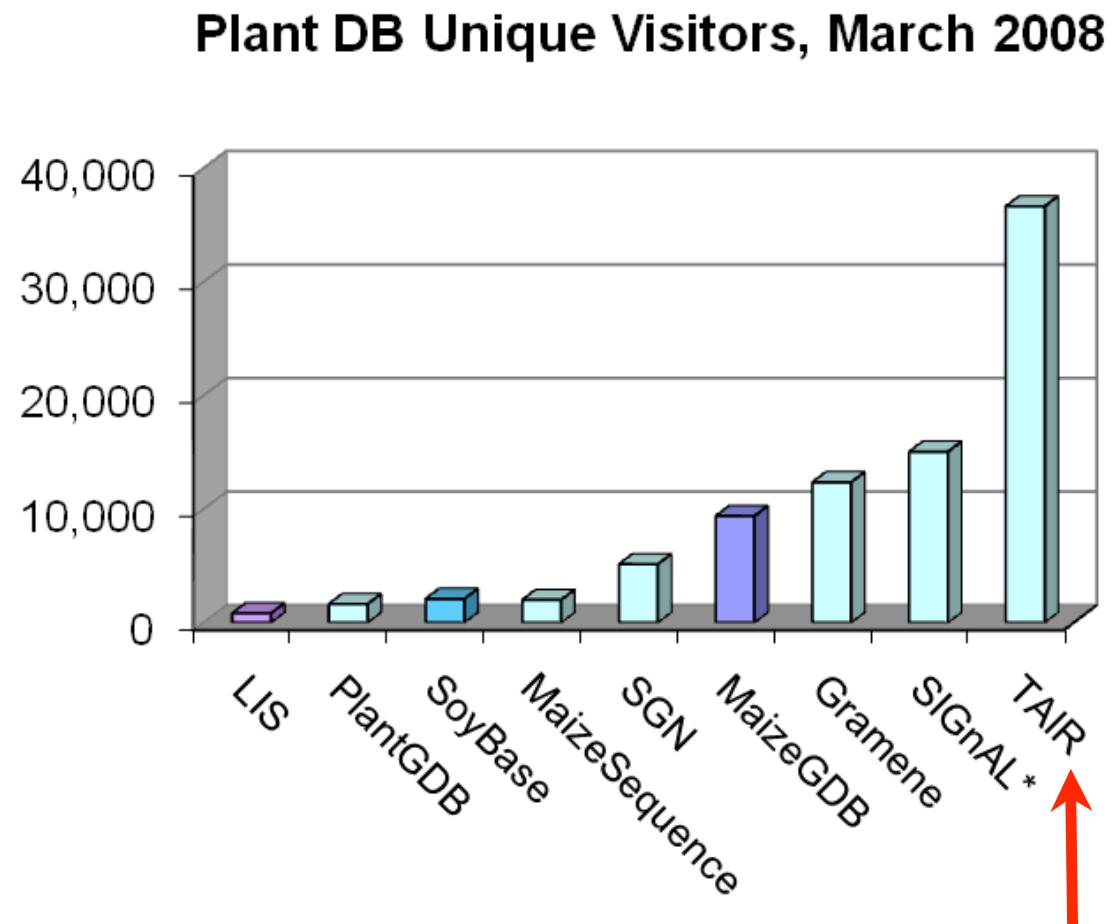


# 10 year anniversary

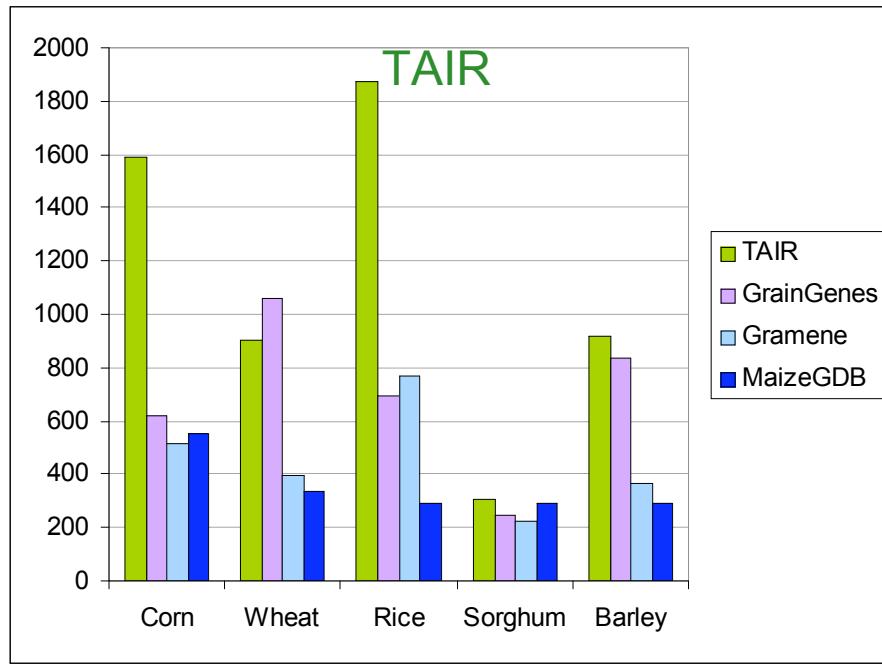
- The Arabidopsis Information Resource
- Started in 1999
- Located at Carnegie Institution for Science,  
Stanford University
- Funded by National Science Foundation (NSF)
- Free access

# TAIR is the most popular plant database (by number of monthly unique visitors)

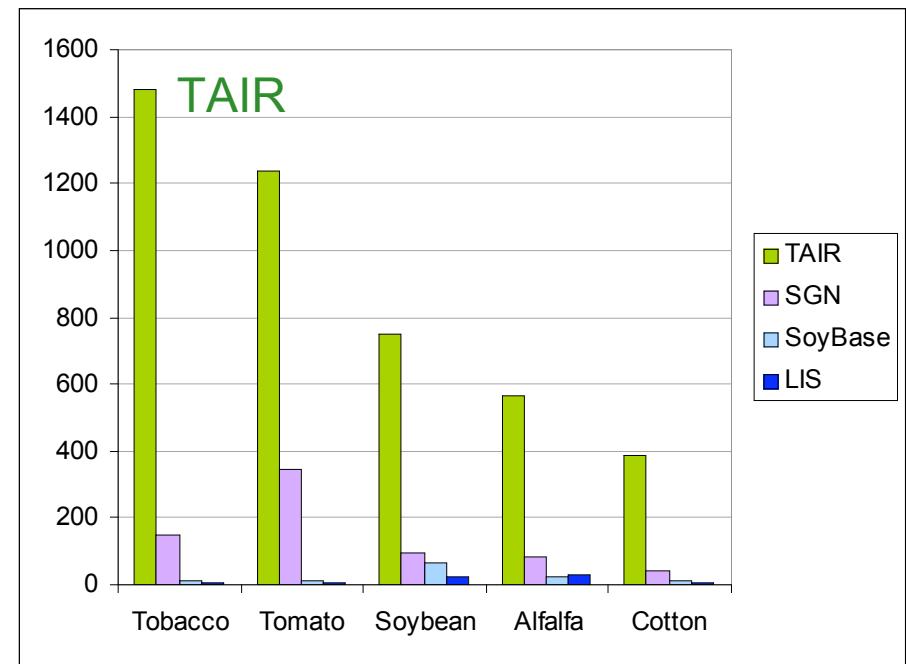
1. TAIR
2. SIGnAL
3. Gramene
4. MaizeGDB
5. SGN (Solanaceae)
6. MaizeSequenceDB
7. SoyBase
8. PlantGDB
9. LIS (Legume)



# TAIR is also valuable for non-Arabidopsis research



Monocots

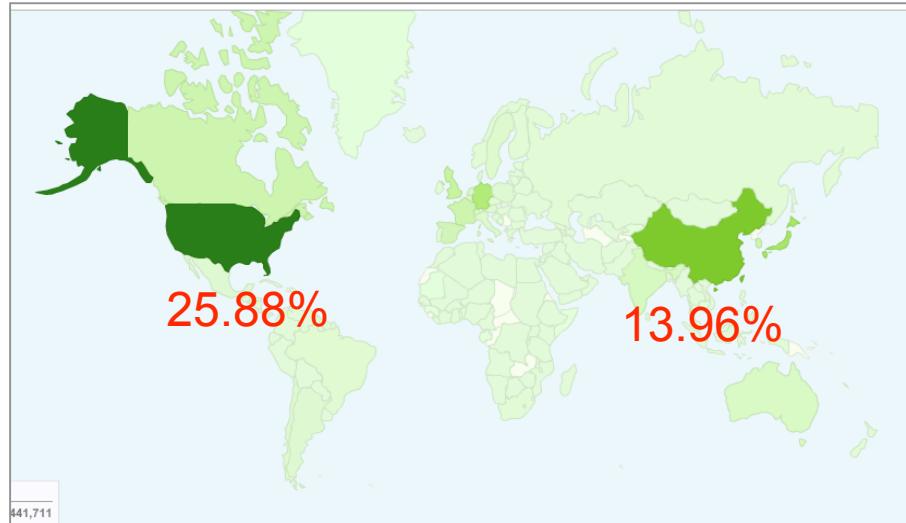


Dicots

Association of plant databases and crop names in articles

Source: Google Scholar

# China has become the second-largest user of TAIR (measured by site visits)

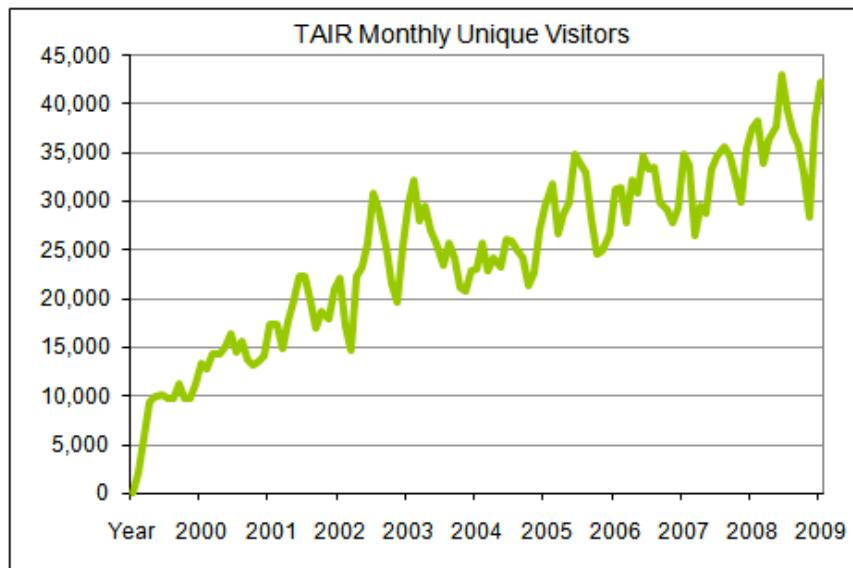


	Detail Level: Country/Territory	Visits	Visits
1.	■ United States	441,711	25.88%
2.	■ China	238,269	13.96%
3.	■ Japan	163,341	9.57%
4.	■ Germany	142,739	8.36%
5.	■ United Kingdom	81,604	4.78%
6.	■ Canada	65,875	3.86%
7.	■ South Korea	63,554	3.72%
8.	■ France	62,555	3.67%
9.	■ Spain	50,933	2.98%
10.	■ India	39,416	2.31%

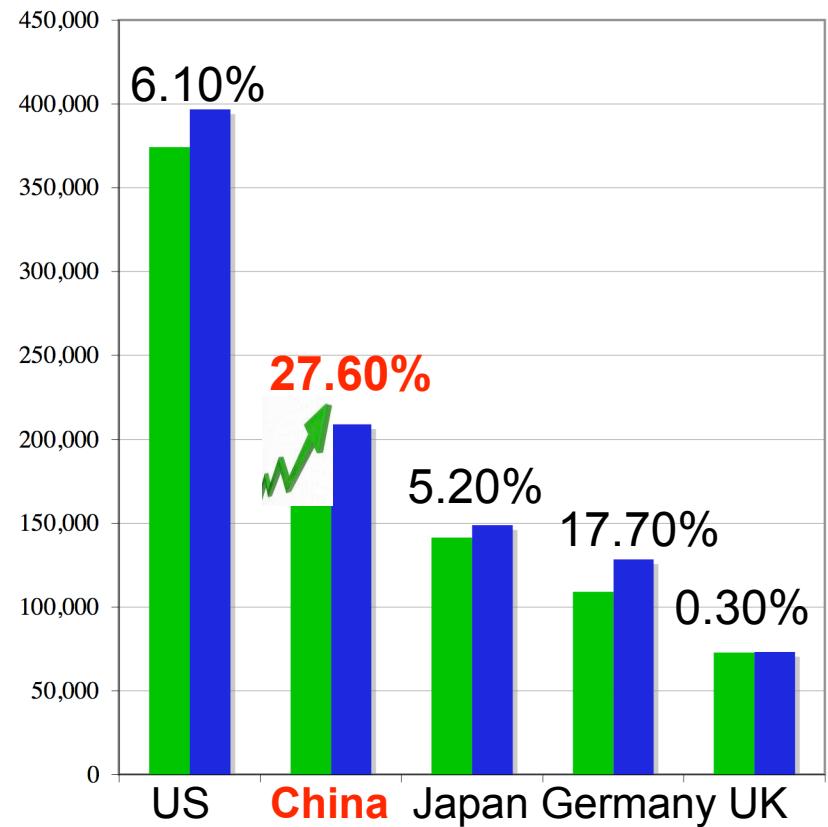
Source: GoogleAnalytics; date range: Oct 9, 2008 - Nov 8, 2009

# Demand for TAIR is increasing

Steady increase in worldwide usage  
(past 10 years)



Rapid increase in China usage



number of visits in Year 4 and Year 5

Year 4: 09/2007-08/2008

Year 5: 09/2008-08/2009

# TAIR is widely used inside China

238,629 visits came from 232 cities



1009 registered users  
582 registered labs

more unregistered users

	Detail Level: City	Visits	Individual City performance:
1.	Beijing	106,162	44.56%
2.	Shanghai	35,269	14.80%
3.	Wuhan	18,876	7.92%
4.	Hangzhou	7,515	3.15%
5.	Nanjing	6,880	2.89%

Source: GoogleAnalytics; date range: Oct 9, 2008 - Nov 8, 2009

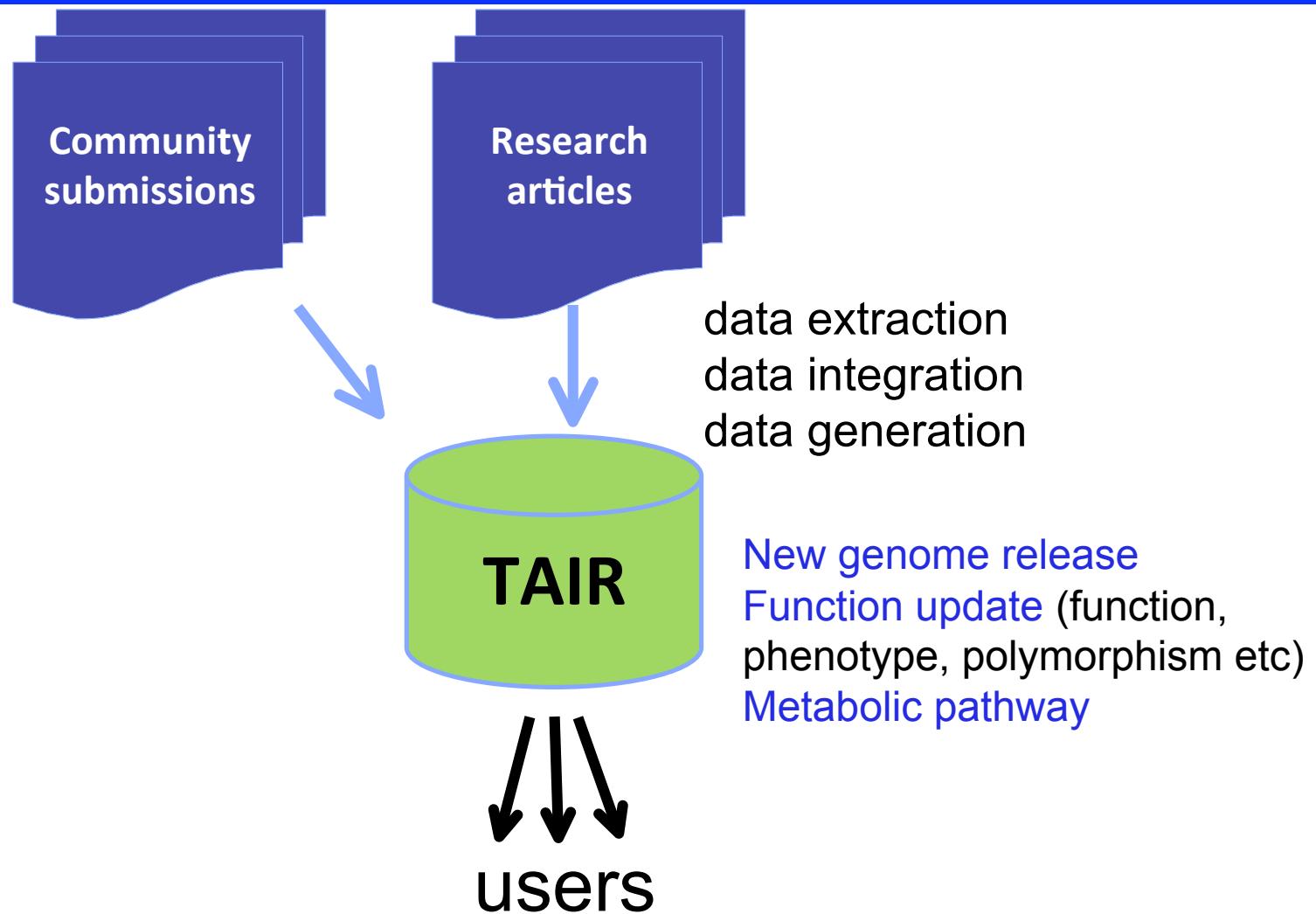
1. Overview: Staff, usage, impact

2. Major roles of TAIR

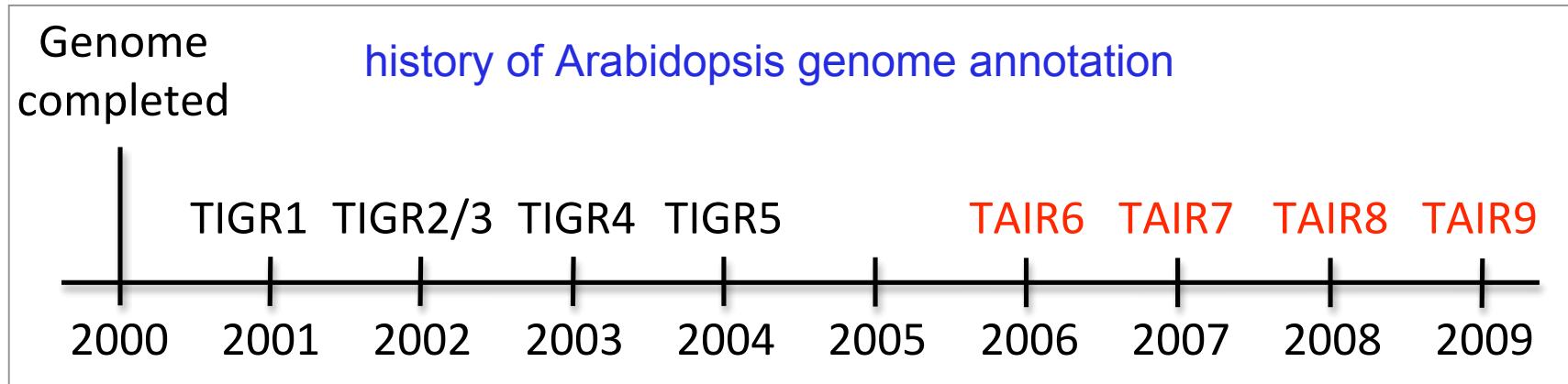
3. New features, new tools

4. Collaboration opportunities

## 1. TAIR as data producer:

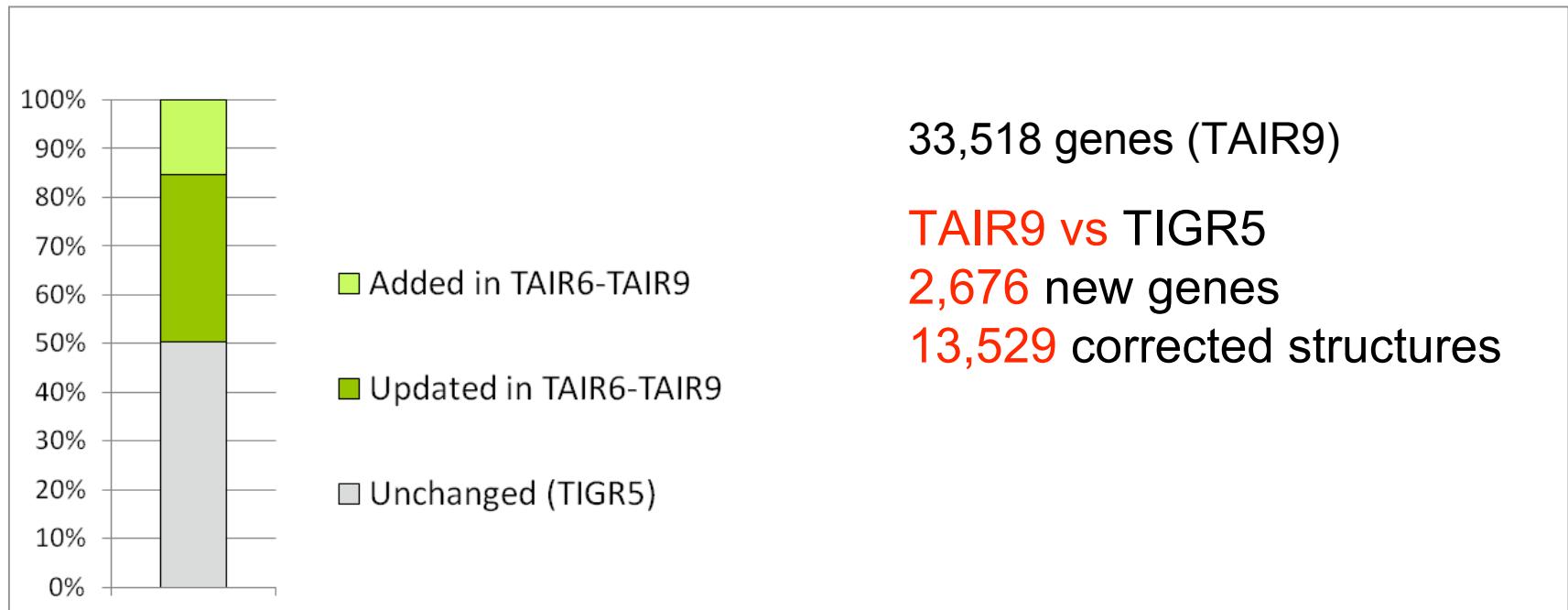


# 1. TAIR as data producer: major accomplishment in Arabidopsis genome annotation



# 1. TAIR as data producer: major accomplishment in Arabidopsis genome annotation

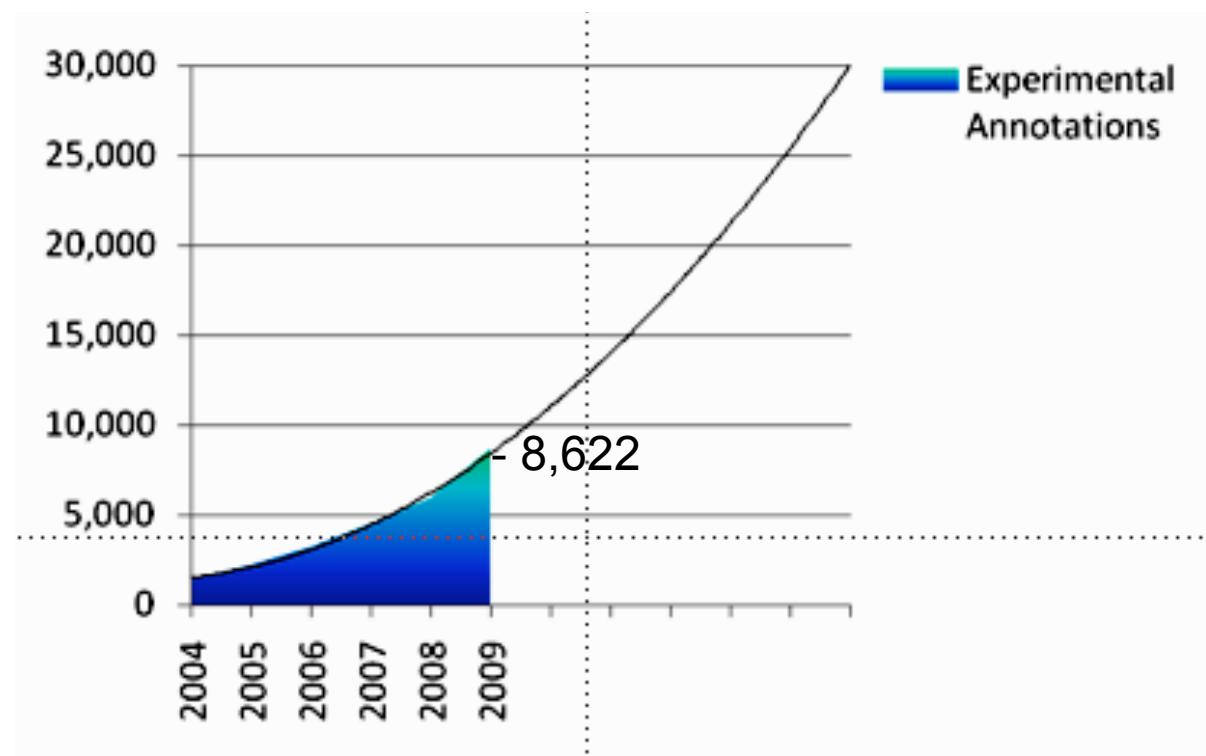
major accomplishment: half of the genes in the current release are updated/added by TAIR



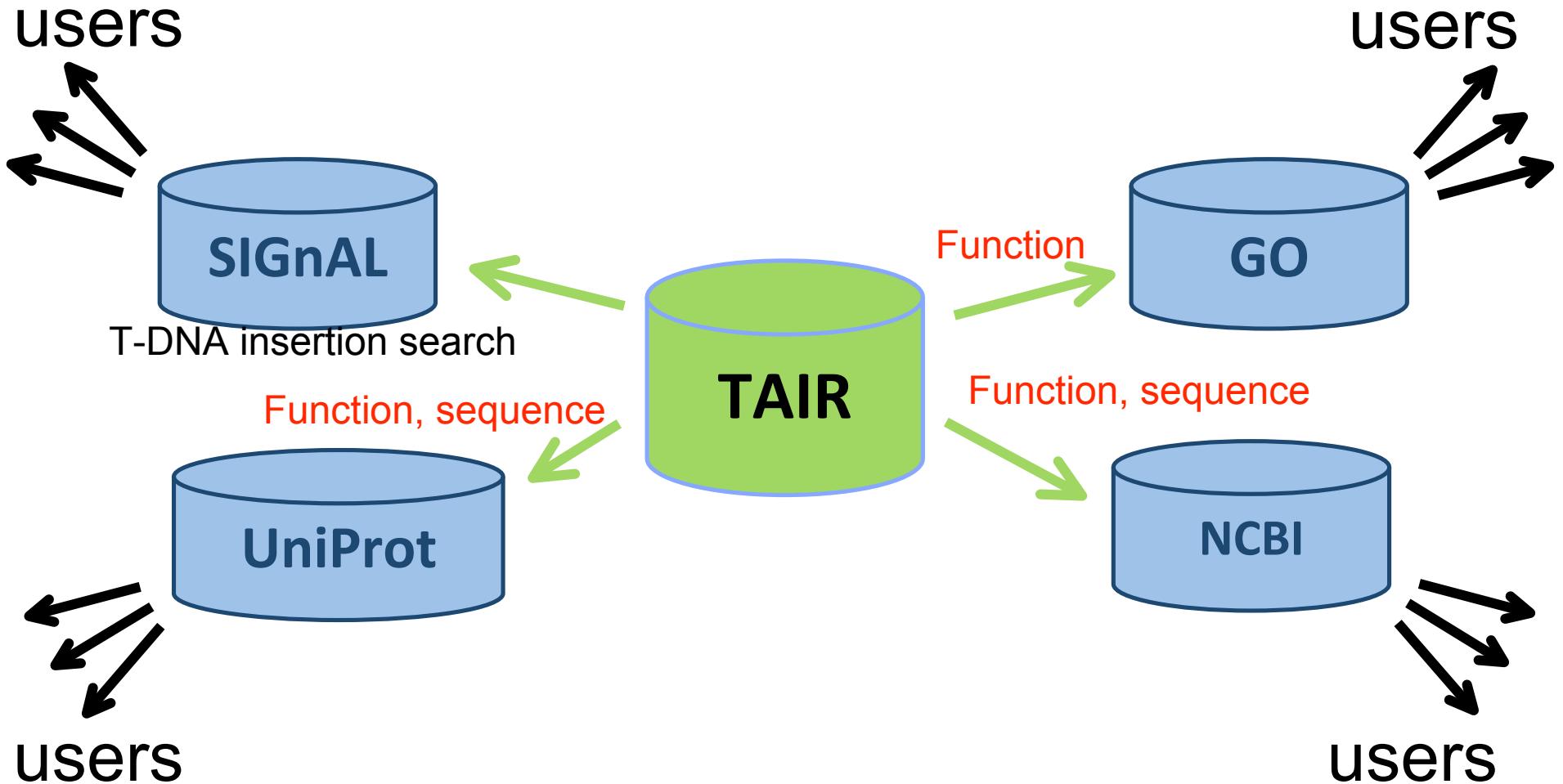
There are still lots of work to do, as new datasets come in

# 1. TAIR as data producer: Major accomplishment in extracting gene function information

- Experimental data (function, polymorphism, phenotype) extracted from **7,300** articles
- **8,622** genes annotated with experimental function data



## 1. TAIR as data producer: Feed data into other databases: the ‘hidden hero’



# 1. TAIR as data producer: Feed data into other databases: the ‘hidden hero’

★ Reviewed, UniProtKB/Swiss-Prot Q9SP32 (DICER\_ARATH)  
Last modified October 13, 2009. Version 70. [History...](#)

Clusters with 100%, 90%, 50% identity | [Documents \(2\)](#) | [Third-party data](#) | [Customize](#)

Gene Ontology (GO)  
Biological process

RNA interference, production of lsiRNA  
Inferred from mutant phenotype. Source: TAIR

RNA interference, production of ta-siRNAs  
Inferred from mutant phenotype. Source: TAIR

cytokinesis [Ref.1](#)  
Inferred from mutant phenotype. Source: TAIR

embryonic pattern specification  
Inferred from mutant phenotype. Source: TAIR

flower development  
Traceable author statement. Source: TAIR

gene silencing by miRNA, mRNA cleavage  
Inferred from mutant phenotype. Source: TAIR

NCBI Entrez Gene

All Databases PubMed Nucleotide Protein Genome Structure OMIM PMC Journals

Search Gene for Go Clear

Limits Preview/Index History Clipboard Details

Display Full Report Show 20 Sort by Relevance Send to

All: 1 Current Only: 1 Genes Genomes: 1 SNP GeneView: 0

1: DCL1 DCL1 (DICER-LIKE 1); ATP-dependent helicase/ double-stranded RNA binding / protein binding / ribonuclease III [Arabidopsis thaliana]

GeneID: 839574 updated 04-Oct-2009

Summary

Gene name DCL1  
Primary source [TAIR:AT1G01040](#)  
Locus tag AT1G01040  
Gene type protein coding  
RefSeq status REVIEWED  
Organism [Arabidopsis thaliana \(ecotype: Columbia\)](#)  
Lineage Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis  
Also known as ABNORMAL SUSPENSOR 1; ASU1; ATDCL1; CAF; CARPEL FACTORY; DCL1; DICER-LIKE 1; EMB60; EMB76; EMBRYO DEFECTIVE 60; EMBRYO DEFECTIVE 76; SHORT INTEGUMENTS 1; SIN1; SUS1; SUSPENSOR 1; T25K16.4; T25K16\_4

Data from TAIR

## 2. TAIR is portal for data access: navigate to other useful sites

### External Link



[AtGDB View](#)

[MPSS](#)

[NASCArrays Digital Northern](#)

[NASCArrays Spot History](#)

[Genevestigator Gene Atlas](#)

[Genevestigator Gene Chronologer](#)

[Genevestigator Response Viewer](#)

[e-FP Browser](#)

[AtGenExpress Visualization Tool](#)

[MIPS View](#)

[NCBI-Entrez Gene](#)

[InParanoid Ortholog Groups](#)

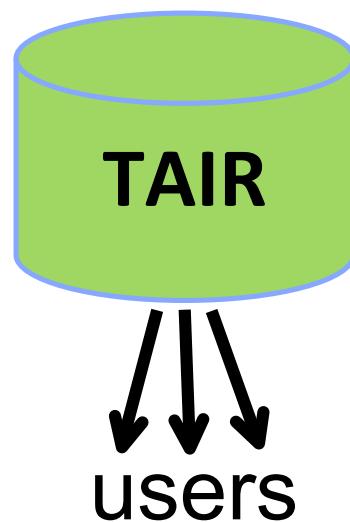
[Plant Proteome Database](#)

### 3. TAIR is home to valuable data sets

About NSF 2010:

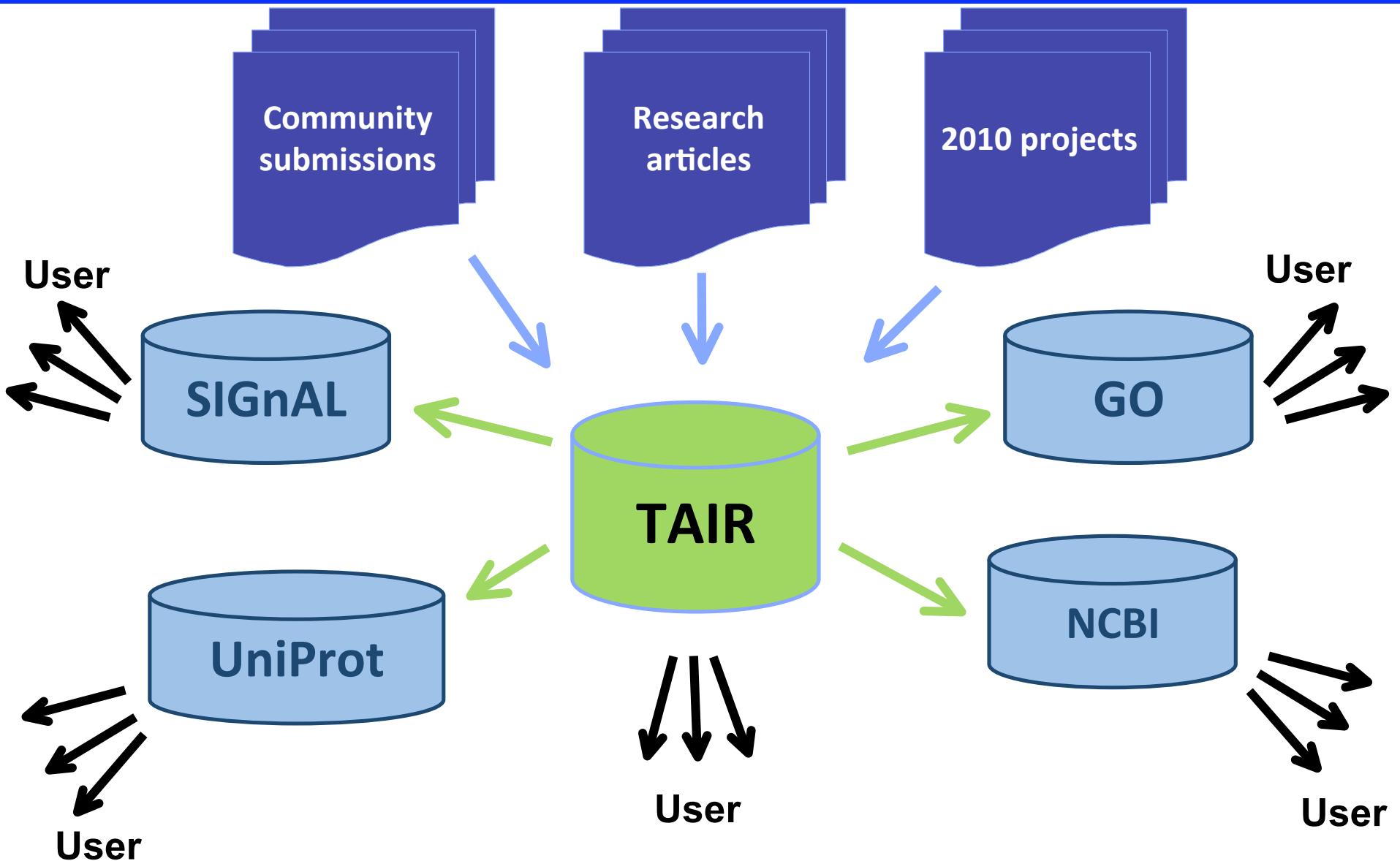
goal: understand the function of each *Arabidopsis* gene by year 2010

USD 200 million awarded so far (2001-2008)

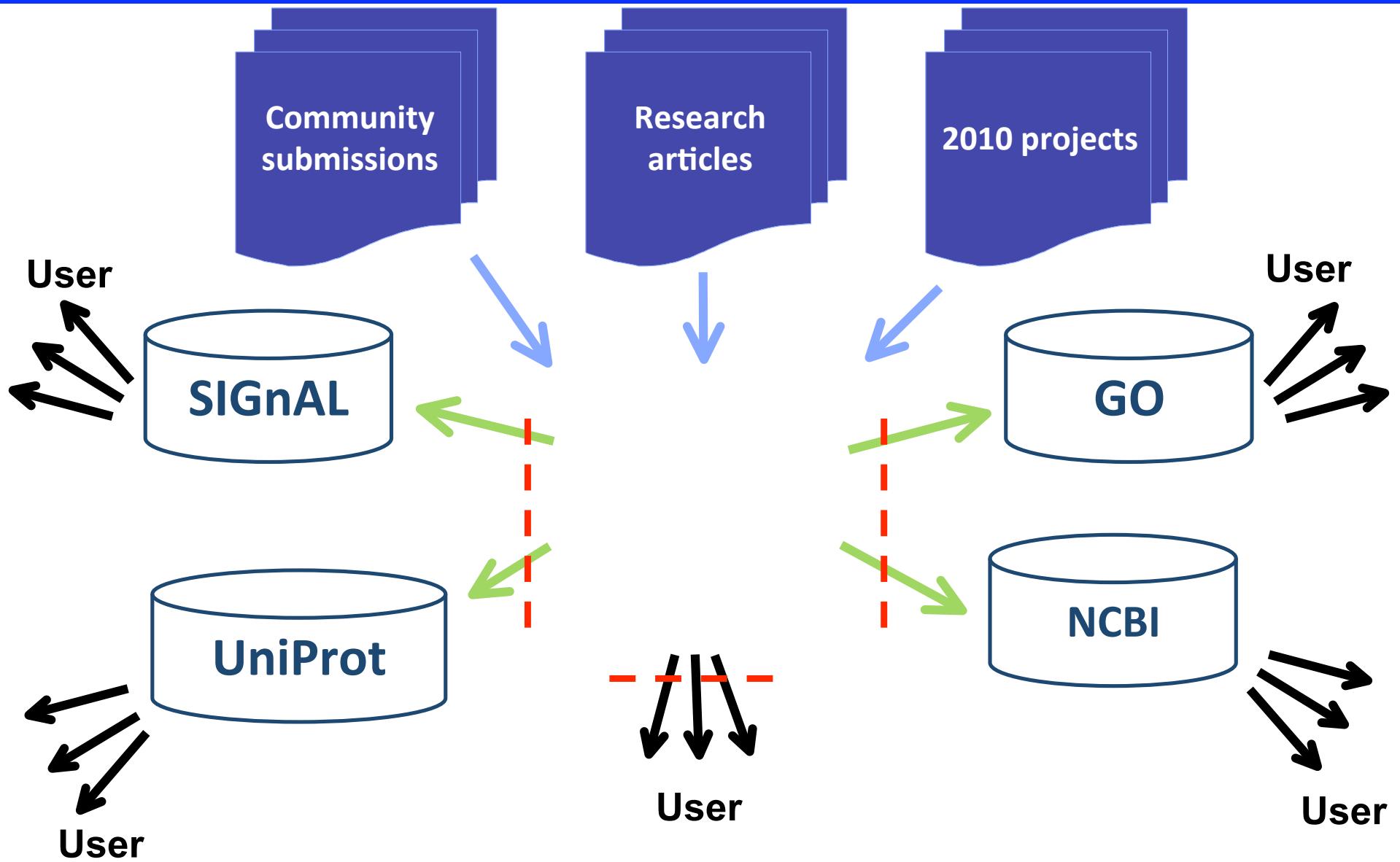


DNA microarray  
Protein interaction  
'Omics' data

# TAIR is information hub



# TAIR is information hub



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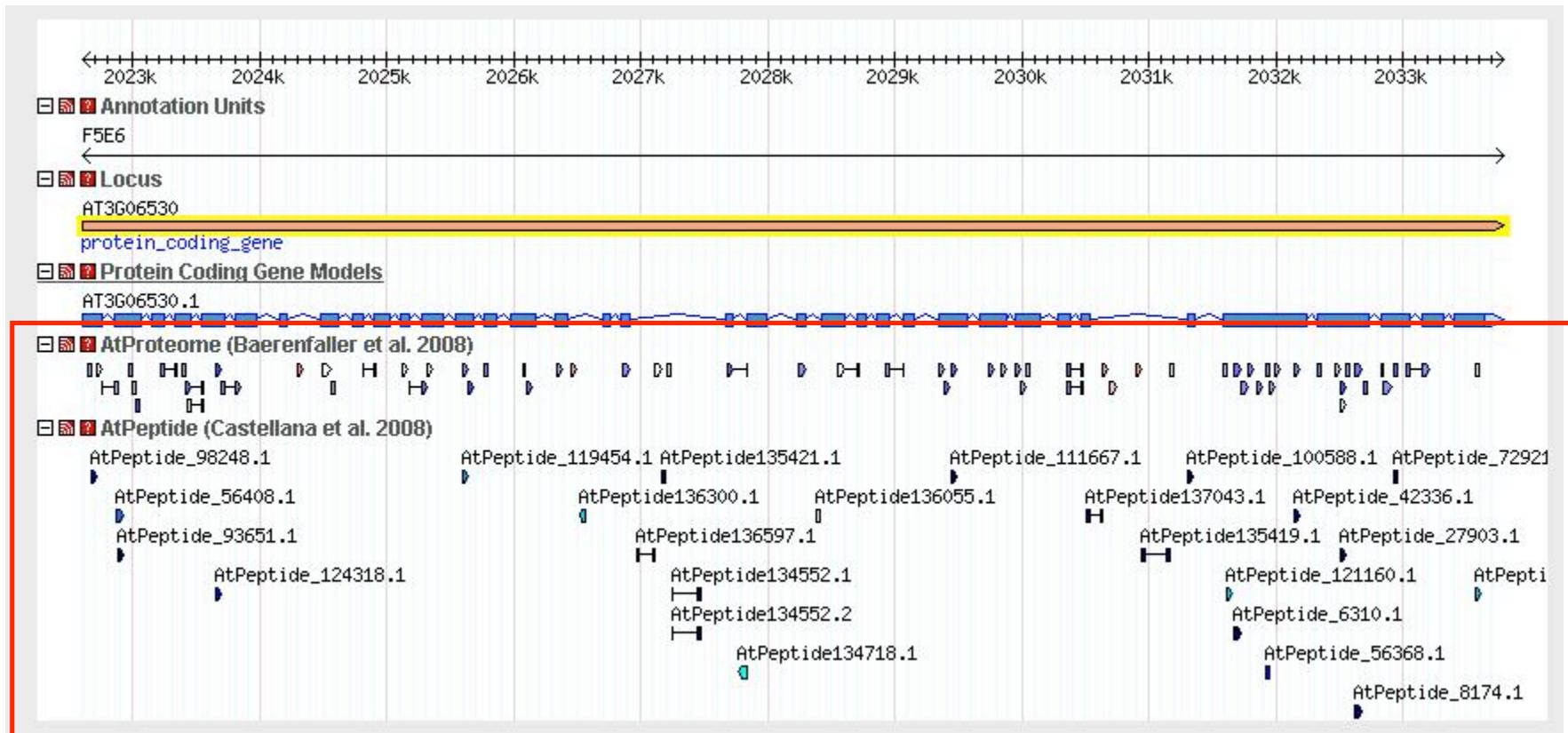
4. Collaboration opportunities

Tools	Stocks
Tools Overview	
GBrowse	
Synteny Viewer	
Seqviewer	
Mapviewer	
AraCyc Metabolic Pathways	
BLAST	
WU-BLAST	
FASTA	
Patmatch	
Motif Analysis	
VxInsight	
Java Tree View	
Bulk Data Retrieval	
Chromosome Map Tool	
Restriction Analysis	
Gene Symbol Registry	
Textpresso Full Text	

# New data sets in TAIR Genome Browser

## Proteomics data track

Data source: Baerenfaller 2008; Castellana et al. 2008



# New data sets in TAIR Genome Browser

## Promoter elements track

Data source: PlantPromoterDB

Genomic Features  All on  All off  
 Natural transposons  PlantPromoterDB

plantpromoterdb 2.0

Arabidopsis thaliana Go

Top About Promoter Comparison Index of Genes

PlantPromoterDB PlantPromoterDB promoter information of AT1G05240.1

Locus Summary of Gene (AT1G05240.1)

Organism	Arabidopsis thaliana
Chromosome	1
Locus	AT1G05240
Gene model	AT1G05240.1
Description	peroxidase, putative, similar to peroxidase; peroxidase ATP11a (Arabidopsis thaliana); gil1546688 emb CAA67334

Overview

chromosome 1 1519500 1520000 1520500 1521000 1521500 1522000 1522500 1523000

AT1G05240.1 Not reliable + Not reliable -

focused region TSS peak TSS clone TATA box Y patch REG CDS UTR

Focused view (chromosome 1: 1520201-1521400)

Genome position from initiation codon 1521101 -100 AT

TSS from cDNA TSS information AT1G05240.1 Promoter sequence 5'→3' (+) CTATTCAAAGCCGCTGGGTGATCTATAAAAGGCCCTGAGAATGTCCTCCTACITTOATCTCCAAGCTCGTTCTCACCTTACTTGGCAAT

AtTATA252: ATCTATAAAAG TCTCCCTC

AtTATA245: TCTATAAA AtY019: TCTCCCTC

AtTATA247: CTATAAAA

AtTATA216: TATAAAG

TSS from cDNA TSS information 3'→5' (-) GATAAAGTTTCCGGCACCCACTAGATATTTCCGACTCTTACAGAGGAAGTAGAGGTTTCGAGCAAGAGTGGAAATGAAACGTT

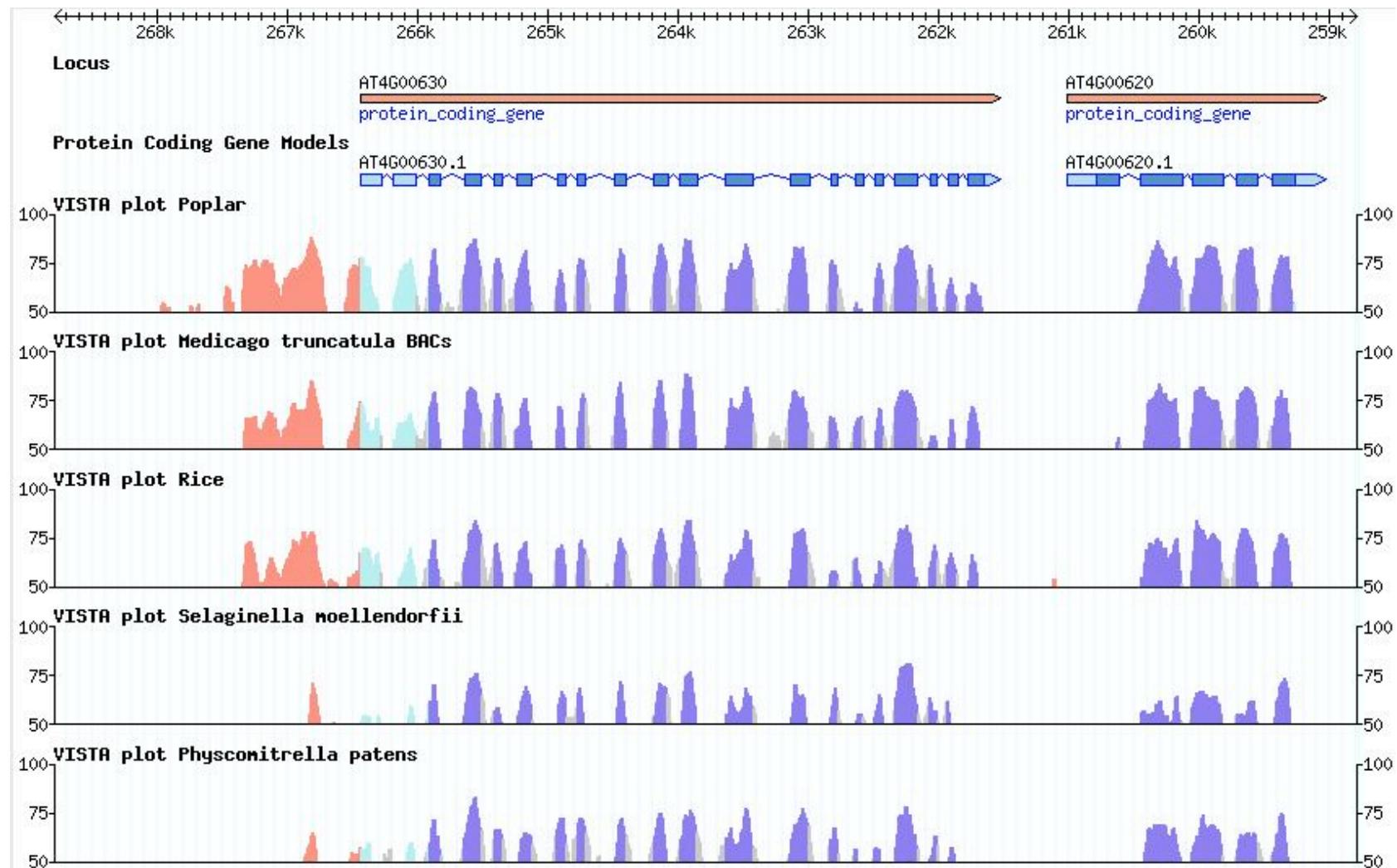
Promoter Summary of AT1G05240.1

TSS information

Type	Sequence	TPM score	Genome position	Position from initiation codon
------	----------	-----------	-----------------	--------------------------------

## New data sets in TAIR Genome Browser

# Vista plots for cross species comparison



VISTA is a comprehensive suite of programs and databases for comparative analysis of genomic sequences. Data source: Berkeley National Lab (LBNL)

# New data sets in TAIR Genome Browser

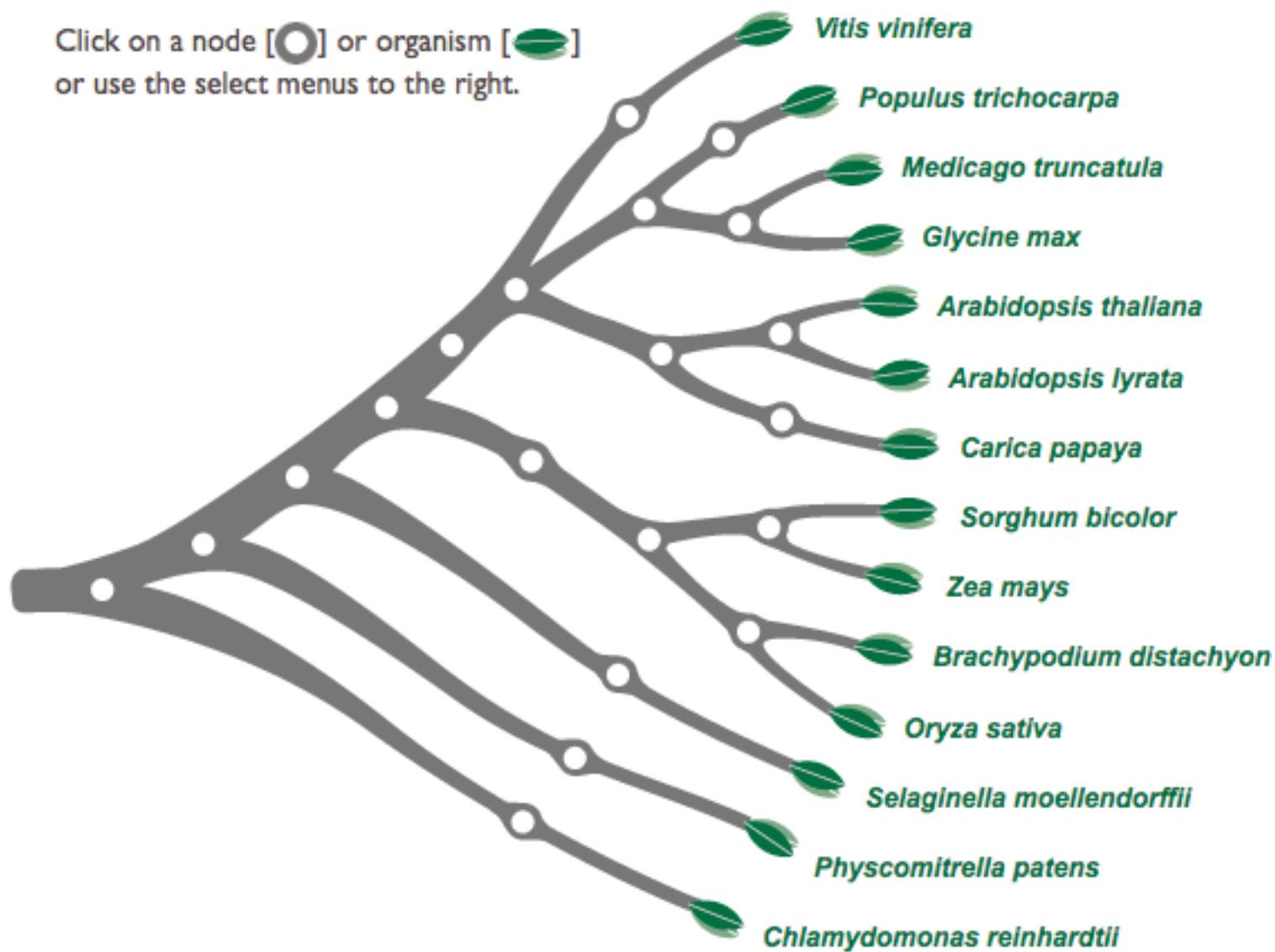
## Plant gene family track (provided by Phytozome)



see next slide for species included

## Phytozome: a tool for green plant comparative genomics

Click on a node [ ] or organism [ ]  
or use the select menus to the right.



# TAIR GBrowser: new data tracks added regularly

**Tracks**

<input type="checkbox"/> <b>Analysis</b> <input type="checkbox"/> All on <input type="checkbox"/> All off			
<input type="checkbox"/> VISTA Plot			
<input type="checkbox"/> <b>Assembly</b> <input type="checkbox"/> All on <input type="checkbox"/> All off			
<input checked="" type="checkbox"/> Annotation Units	<input type="checkbox"/> Assembly Updates	<input type="checkbox"/> Gaps	
<input type="checkbox"/> <b>Community Annotation</b> <input type="checkbox"/> All on <input type="checkbox"/> All off			
<input type="checkbox"/> Aceview Gene Models	<input checked="" type="checkbox"/> Gnomon Predictions	<input type="checkbox"/> Polyadenylation sites (AtPolyA-DB)	
<input type="checkbox"/> Eugene Predictions	<input type="checkbox"/> Hanada et al. 2007 Gene Models	<input type="checkbox"/> Quesneville et al. Natural transposons	
<input type="checkbox"/> <b>DNA</b> <input type="checkbox"/> All on <input type="checkbox"/> All off			
<input type="checkbox"/> 6 Frame Translation	<input type="checkbox"/> DNA/GC		
<input type="checkbox"/> <b>Expression</b> <input type="checkbox"/> All on <input type="checkbox"/> All off			
<input checked="" type="checkbox"/> AtPeptide (Castellana et al. 2008) (Aubourg et al. 2007)	<input type="checkbox"/> CATMA transcriptome data (analysis) (Aubourg et al. 2007)	<input type="checkbox"/> MPSS seed 1	<input type="checkbox"/> Small RNAs (ASRP)
<input checked="" type="checkbox"/> AtProteome (Baerenfaller et al. 2008)	<input type="checkbox"/> Microarray ATH1-121501 probes	<input type="checkbox"/> MPSS seed 2	<input type="checkbox"/> smRNA col-0 (Gregory et al. 2008)
<input type="checkbox"/> CATMA primers	<input type="checkbox"/> MPSS flower (Lu et al. 2005)	<input type="checkbox"/> mRNA col-0 (Lister et al. 2008)	<input type="checkbox"/> smRNA col-0 (Lister et al. 2008)
<input type="checkbox"/> <b>Gene</b> <input type="checkbox"/> All on <input type="checkbox"/> All off			
<input type="checkbox"/> CDS	<input type="checkbox"/> Noncoding RNAs	<input checked="" type="checkbox"/> Protein Coding Gene Models	<input type="checkbox"/> Transposable element genes
<input checked="" type="checkbox"/> Locus	<input type="checkbox"/> Obsoleted Genes	<input type="checkbox"/> Pseudogenes	
<input type="checkbox"/> <b>Genomic Features</b> <input type="checkbox"/> All on <input type="checkbox"/> All off			
<input type="checkbox"/> Natural transposons	<input type="checkbox"/> PlantPromoterDB		
<input type="checkbox"/> <b>Methylation and Phosphorylation</b> <input type="checkbox"/> All on <input type="checkbox"/> All off			
<input type="checkbox"/> HMBD col BU/UB	<input type="checkbox"/> mCIP col/met1 BU	<input type="checkbox"/> mCIP met1 BU/UB	
<input type="checkbox"/> mCIP col BU/UB	<input type="checkbox"/> mCIP ddc BU/UB	<input type="checkbox"/> mCIP met1/col BU	
<input type="checkbox"/> mCIP col/ddc BU	<input type="checkbox"/> mCIP ddc/col BU	<input type="checkbox"/> Phosphorylation (PhosPhAt)	
<input type="checkbox"/> <b>Orthologs and Gene Families</b> <input type="checkbox"/> All on <input type="checkbox"/> All off			
<input type="checkbox"/> Fish Orthologs (Inparanoid)	<input type="checkbox"/> Model Organism Orthologs (Inparanoid)	<input type="checkbox"/> Other Orthologs (Inparanoid)	<input type="checkbox"/> Vertebrate Orthologs (Inparanoid)
<input type="checkbox"/> Insect Orthologs (Inparanoid)	<input type="checkbox"/> Nematode Orthologs (Inparanoid)	<input type="checkbox"/> Plant Gene Families (Phytozome)	<input type="checkbox"/> Yeast and Fungi Orthologs (Inparanoid)
<input type="checkbox"/> <b>Sequence Similarity</b> <input type="checkbox"/> All on <input type="checkbox"/> All off			
<input checked="" type="checkbox"/> Arabidopsis cDNAs	<input type="checkbox"/> Brassica cDNAs	<input checked="" type="checkbox"/> Dicot Transcript Assemblies (selected)	<input type="checkbox"/> Radish Clones
<input type="checkbox"/> Arabidopsis ESTs	<input type="checkbox"/> Brassica ESTs	<input type="checkbox"/> JAtY Clone Library	
<input type="checkbox"/> Brassica BAC clones	<input type="checkbox"/> Brassica GSSs	<input type="checkbox"/> Monocot Transcript Assemblies (selected)	
<input type="checkbox"/> <b>Variation</b> <input type="checkbox"/> All on <input type="checkbox"/> All off			
<input type="checkbox"/> Bay-0 and Shakdara polymorphisms (JGI)	<input type="checkbox"/> Marker	<input type="checkbox"/> Polymorphisms	
<input type="checkbox"/> Bur-0 and Tsu-1 polymorphisms (Ossowski et al. 2008)	<input type="checkbox"/> Polymorphic Region Predictions (Zeller et al. 2008)	<input type="checkbox"/> T-DNAs/Transposons	

[Configure tracks...](#) [Update Image](#)

## New pathway releases

Arabidopsis metabolic pathway: AraCyc6.0  
Poplar metabolic pathway PoplarCyc1.0  
other species PlantCyc3.0

# New tools: Textpresso for Arabidopsis

## Search full text (Arabidopsis literature)

***Textpresso for Arabidopsis***

[About Textpresso](#) [Categories/Ontology](#) [Copyright](#) [Document Finder](#) [Downloads](#) [Feedback](#) [Home](#) [Query Language](#) [Search](#) [User Guide](#)

**Search for keywords or categories or both**

**Keywords ?**  
SALK\_012745  
 Exact match  Case sensitive

**Categories ?**  
[List >](#)  
Select category 1 from list above   
Select category 2 from list above   
Select category 3 from list above   
Select category 4 from list above

**Advanced Search Options :** [on](#) | [off](#) [location (abstract, full text), sorting (year, score,...), filtering (author, journal,...)]

**Database Description**  
Currently, this site contains information about the following literatures and data types (data count in parenthesis):  
Arabidopsis: abstract (34635), body (21918), title (36056)  
Summary: abstract : 34635, body : 21918, title : 36056, total : 92609  
Bibliography last updated: 21 September 2009.

**News & Messages**

Welcome to Textpresso for Arabidopsis!  
This site was developed in collaboration with [TAIR](#).  
Bibliography last updated: 21 September 2009.  
Please note that case-sensitivity functionality only applies to the first character of a word and not the whole string; special names such as AT1G03457 will not be correctly translated into lower cases. AT1G03457 would be transformed into aT1G03457 and not at1g03457. This limitation prevents the search engine from generating exponentially growing lists of variations. If you want to search for variations you are interested in, please type them in by hand, separated by a comma.

In collaboration with WormBase

**PubMed.gov**  
U.S. National Library of Medicine  
National Institutes of Health

Search: PubMed

SALK\_012745 

 The following term was not found in PubMed: SALK\_012745.

 See [Details](#).

 No items found. 

## *Textpresso for Arabidopsis*

2 matches found in 1 documents. Search time: 0.025 seconds.

Global links/files: [all results in endnote](#) [all results in print version](#) [all results in xml](#)

**Title:** A genome-wide functional investigation into the roles of receptor-like proteins in Arabidopsis .  
**Authors:** Wang G Ellendorff U Kemp B Mansfield JW Forsyth A Mitchell K Bastas K Liu CM Woods-Tr A Zipfel  
**Journal:** Plant Physiol  
**Year:** 2008

 matches highlighted in full text

 [Bibliographic Information](#)  
 [Abstract](#)  
 [Matching Sentences](#)

**Match:** For two T-DNA insertion lines , FLAG\_524A03 and SALK\_012745 with an insertion in AtRLP19 and insertion lines were obtained , suggesting that homozygosity of these T-DNA mutations caused embryonic

**Match:** [Sentence(s) appears to be scrambled. Click to see (opens new window)] [Field: body, subscore: ]

Supplemental links/files: [reference in endnote](#) [reference in xml](#) [online text](#) [related articles](#) [Pubmed citation](#)

## New stocks from ABRC (Arabidopsis Biological Resource Center)

### DNA

- 10,209 Gateway cDNA/ORF clones from J. Ecker (Salk) ORF clones
- genome wide artificial microRNAs constructs for RNAi interference in Arabidopsis by Greg Hannon et al
- 2,425 transcription factor expression clones from S. P. Dinesh Kumar

### Seeds

- 17,291 SALK-C (confirmed) lines

Coming soon: Protein interaction viewer

TAIR continues to grow as a community resource:  
we respond to community needs by developing  
new tools and bringing in latest data sets

1. Overview: Staff, usage, impact
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4. Challenges&Collaboration opportunities

TAIR:

How to keep up with the pace of data increase with limited resources?

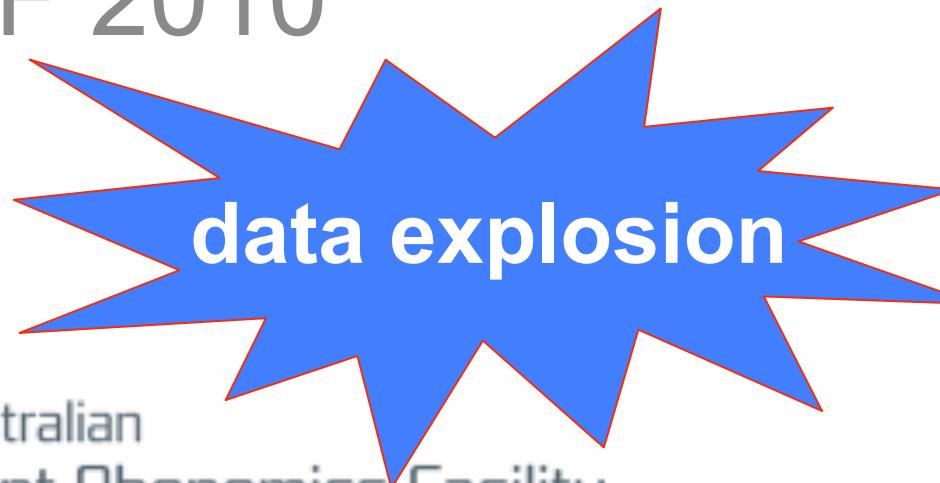
**1001 Genomes**  
A Catalog of *Arabidopsis thaliana* Genetic Variation



NSF 2010



Australian  
Plant Phenomics Facility



**NIBS**

北京生命科学研究所

National Institute of Biological Sciences, Beijing

TAIR:

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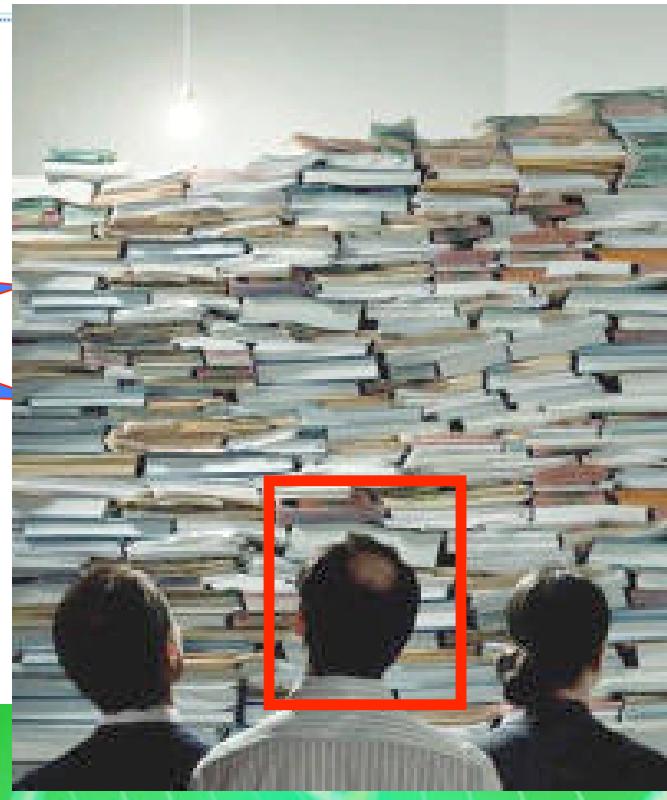
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NSF 2010



Australian  
Plant Phenomics Facility



**NIBS**

北京生命科学研究所

National Institute of Biological Sciences, Beijing

# Challenges

TAIR:

How to keep up with the pace of data increase with limited resources?

Community:

Data accessibility? New tools to analyze/maximize the value of data?

# Challenges

TAIR:

How to keep up with the pace of data increase with limited resources?



**increased demand for TAIR**

Community:

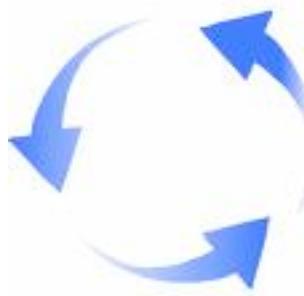
Data accessibility? New tools to analyze/maximize the value of data?

# Challenges

TAIR:

How to keep up with the pace of data increase with limited resources?

**enhanced productivity**

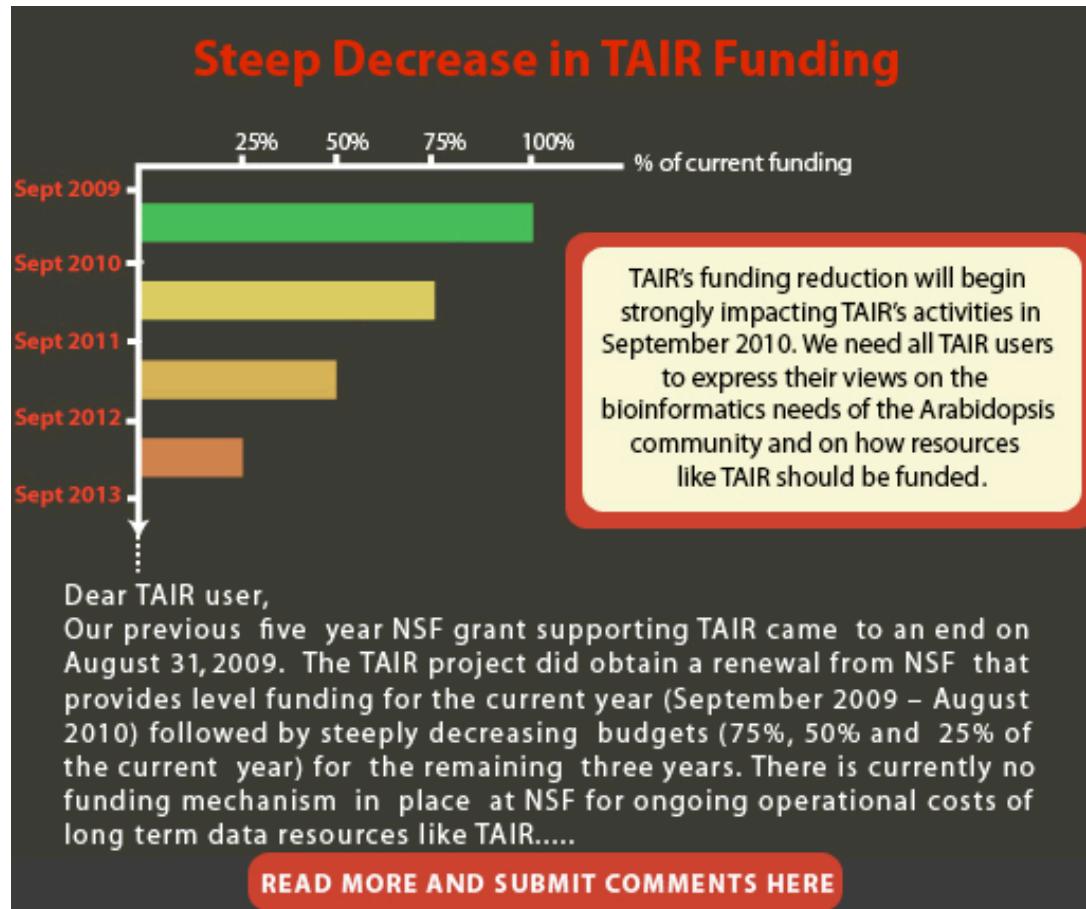


**increased demand for TAIR**

Community:

Data accessibility? New tools to analyze/maximize the value of data?

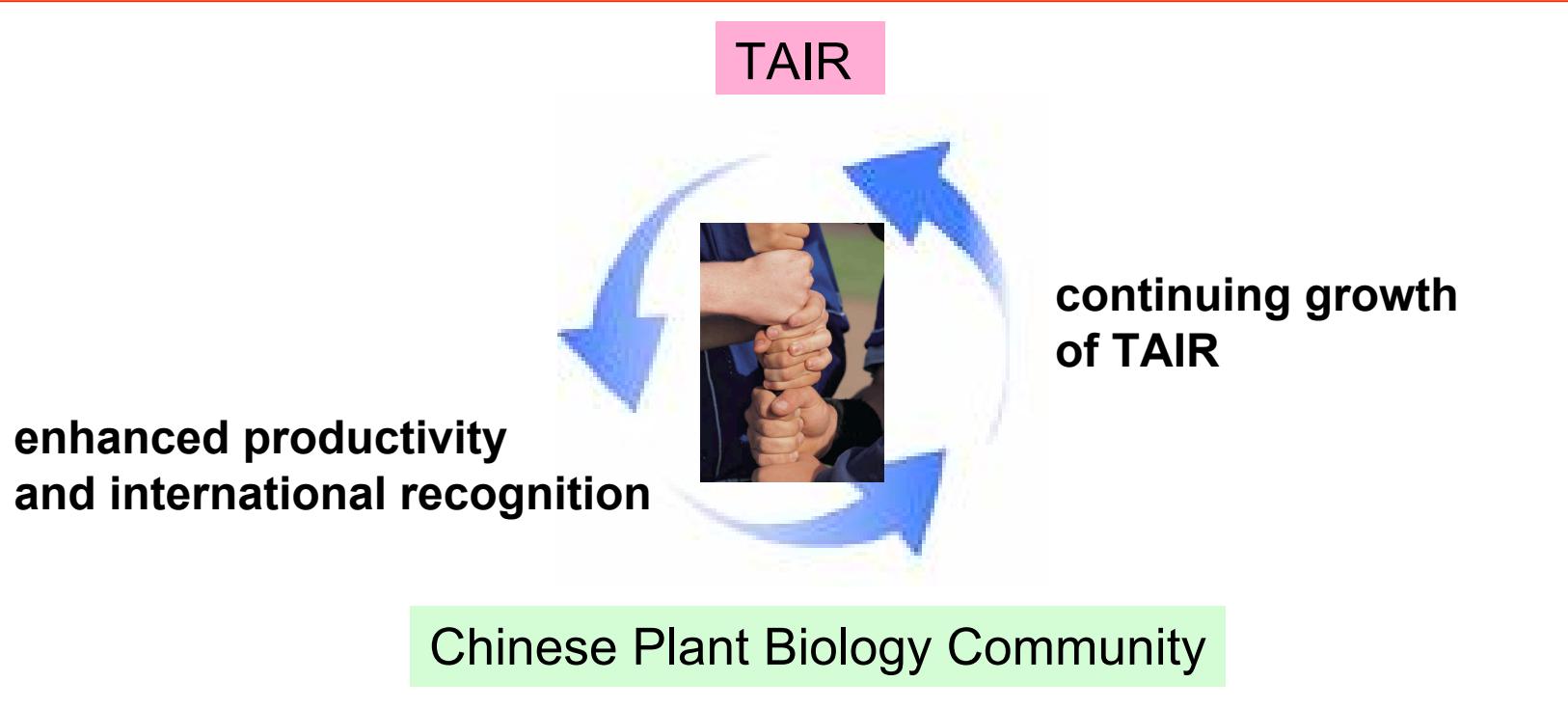
# Challenges



Please add your comments by click here

# Opportunities

How can we create a win-win situation through increased collaboration?



**COMMENTARY**

## **Plant Biology Research Comes of Age in China**

**Haodong Chen,<sup>a,b,c</sup> Valerie J. Karplus,<sup>b</sup> Hong Ma,<sup>d</sup> and Xing Wang Deng<sup>a,b,c</sup>**

<sup>a</sup> Peking-Yale Joint Center of Plant Molecular Genetics and Agrobiotechnology, College of Life Sciences, Peking University, Beijing 100871, China

<sup>b</sup> National Institute of Biological Sciences, Zhongguancun Life Science Park, Beijing 102206, China

<sup>c</sup> Department of Molecular, Cellular, and Developmental Biology, Yale University, New Haven, Connecticut 06520-8104

<sup>d</sup> Department of Biology and the Huck Institutes of the Life Sciences, Pennsylvania State University, University Park, Pennsylvania 16802

A modern plant biology research enterprise is developing rapidly in mainland China. The cohort of well-trained young scientists

over the past two decades. China's broad-based reform program in the late 1970s focused on revitalizing the nation's science

(Tang and Loo, 1940). He was the first to reveal inducible activity of a nitrate reductase in rice seedlings (Tang and Wu,

## Key points

### Major accomplishments

#### 1) Rapid growth of Arabidopsis research

“before 1995, no Chinese scientists were doing internationally acknowledged research using the model plant Arabidopsis. Today, almost every major institute or university with a plant biology research program has multiple Arabidopsis groups, an indication that Chinese plant biologists now value both basic and applied research in crop plants.”

## Key points

### **Major accomplishments**

- 1) Rapid growth of Arabidopsis research
- 2) Breakthrough in rice research, new discoveries in other plant systems

### **Future trends and challenges**

- 3) Towards a world-class research environment / infrastructure
- 4) International excellence and recognition

# How TAIR can help

## Promote Arabidopsis research in China

- Continue to provide vital data, tools
  - Enhanced data accessibility
  - Training workshops
  - Simplified stock ordering/payment
- 
- enhanced productivity

On Oct 28, 2009, at 6:45 AM, 刘小强 wrote:

李博士：

你好，今天我已收到ABRC给我发来的我所订购的拟南芥突变体种子，但我这不方便用信用卡付款，请问有其他方式吗？有没有收款发票啊？

-----  
刘小强

2009-10-28

# TAIR HelpDesk helps Chinese users

## TAIR help desk issue tracker

T	Key	Summary	Assignee	Reporter	Pr	Status	Res	Created	Updated	Due
	<a href="#">HLP-3959</a>	Fwd: About the TDNA-insertion sequence	Kate Dreher	Liang Zhang	↑	Closed	Completed	12/Jul/09	14/Jul/09	
	<a href="#">HLP-3519</a>	Payment Error	Cynthia Lee	shlei1025@sina.com	↓	Closed	Fixed	30/Mar/09	10/Apr/09	
	<a href="#">HLP-3598</a>	a question about arabidopsis	Donghui Li	李肖	↓	Closed	Fixed	14/Apr/09	22/Apr/09	
	<a href="#">HLP-3349</a>	Sorry to disturb you! I need your help to transform gi number into AGI number.	David Swarbreck	陈同	↑	Closed	Completed	02/Mar/09	09/Mar/09	
	<a href="#">HLP-4205</a>	Hello	Donghui Li	Liguangyue	↑	Resolved	Fixed	21/Sep/09	23/Sep/09	
	<a href="#">HLP-2697</a>	I have a question about TAIR	Donghui Li	chunying liu	➡	Closed	Fixed	12/Nov/08	14/Nov/08	

# TAIR is already helping the *next generation* Chinese scientists

Chinese high school student with many questions!

## Description

[« Hide](#)

Hi,I am a high school student from a university of China.I wonder why I can't see all Phenotypes of different mutant seeds.Such as the web address: <http://arabidopsis.org/servlets/TairObject?type=locus&name=AtCg00150>

Whether I have got a

Thank you very muc

Best wishes!

Xiao Li

李肖 - 17/Apr/09 09:16 PM

Dear Professor Li,

It is very glad to receive your reply.Recently I have another question.There are some germplasms have more than one insert sites.For example, WiscDsLox433C8,(<http://arabidopsis.org/servlets/TairObject?type=gene&id=328608>)

some of whose associated genes are located on Chromosome 2,others located on mitochondrial genome.Those on Chromosome 2 get germplasm only one of whose associated genes is substituted.That is to say,the associated genes located on Chromosome 2 are substituted but the associated genes located on mitochondrial genome are not substituted.Those on mitochondrial genome are substituted but the associated genes located on Chromosome 2 are not substituted.

Thank you very much!

Best wishes!

Xiao Li

## How TAIR can help

Promote Arabidopsis research in China

### Promote translational research

- More cross-species comparison tools and data
- Broaden TAIR's scope to include more species (data on rice, brassicas?)

# How TAIR can help

Promote Arabidopsis research in China

Promote translational research:

- More cross-species comparison tools and data
- Broaden TAIR's scope to include more species (data on rice, brassicas?)

**Improve research environment / infrastructure**

- Expertise sharing in bioinformatics platform, data curation, bio-resource management

# How TAIR can help

Promote Arabidopsis research in China

Promote translational research:

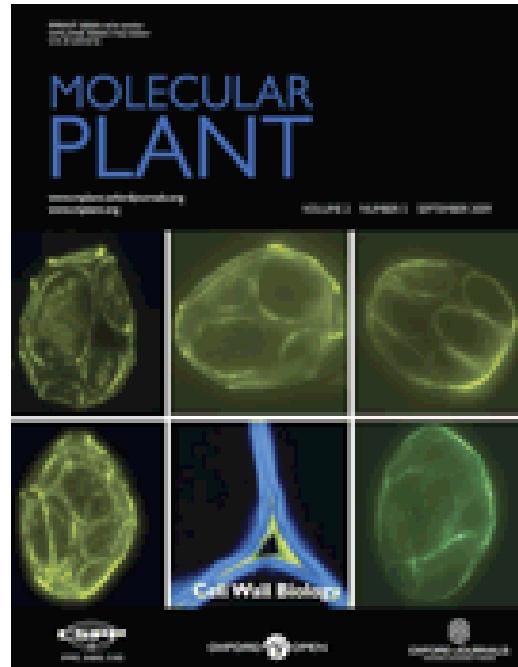
- More cross-species comparison tools and data
- Broaden TAIR's scope to include more species (data on rice, brassicas?)
- Collaborative projects

Improve research environment / infrastructure

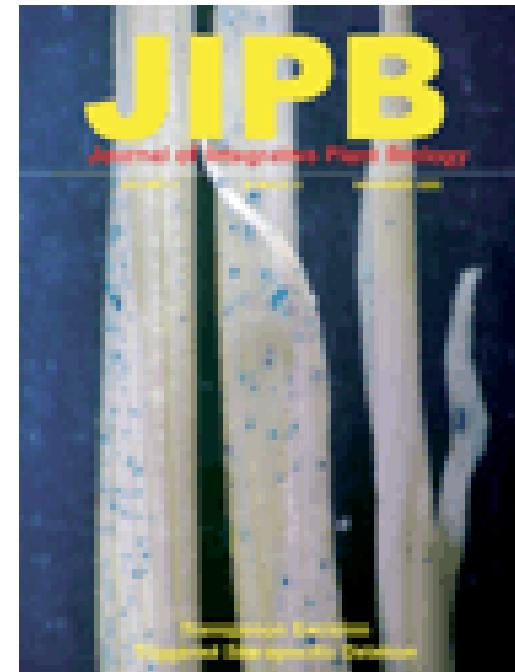
- Expertise sharing in bioinformatics platform, data curation, bio-resource management

International recognition:

- TAIR is a great platform to raise the **VISIBILITY** and **CREDIBILITY** of Chinese scientists



Chinese Academy of Sciences



Institute of Botany, CAS  
Botanical Society of China

# TAIR partners with leading journals to collect data

Author submit data to TAIR when manuscript accepted

Ensure most up-to-date information is in TAIR

**Plant Physiology®**

with the Illumina Ge

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Institution: Stanford University [Sign In as Member](#)

Perform your original search, **plant physiology tair**, in *Plant Physiol.* [Search](#)

*Plant Physiology* 146:1022-1023 (2008)  
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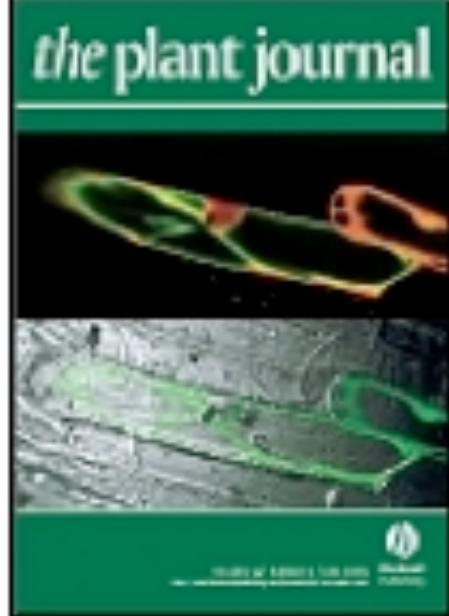
**EDITORIAL**

## **Plant Physiology and TAIR Partnership**

We are pleased to announce a unique partnership between **Plant Physiology** and The Arabidopsis Information Resource (**TAIR**) that we anticipate will increase the annotation of **Plant Physiology** in the **TAIR** database to nearly 100%. This partnership is the first of its kind, and, if successful, we hope this model can be extended to other journals, organisms, and databases.

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**the plant journal**



# How TAIR can help

Promote Arabidopsis research in China

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**International recognition:**

- TAIR is a great platform to raise the VISIBILITY and CREDIBILITY of the Chinese scientists
- TAIR is a great medium for stimulating innovation



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## The Arabidopsis Information Resource

The Arabidopsis Information Resource (TAIR) maintains a database of genetic and molecular biology data for the model higher plant *Arabidopsis thaliana*. Data available from TAIR includes the complete genome sequence along with gene structure, gene product information, metabolism, gene expression, DNA and seed stocks, genome maps, genetic and physical markers, publications, and information about the Arabidopsis research community. Gene product function data is updated every two weeks from the latest published research literature and community data submissions. Gene structures are updated 1-2 times per year using computational and manual methods as well as community submissions of new and updated genes. TAIR also provides extensive linkouts from our data pages to other Arabidopsis resources.

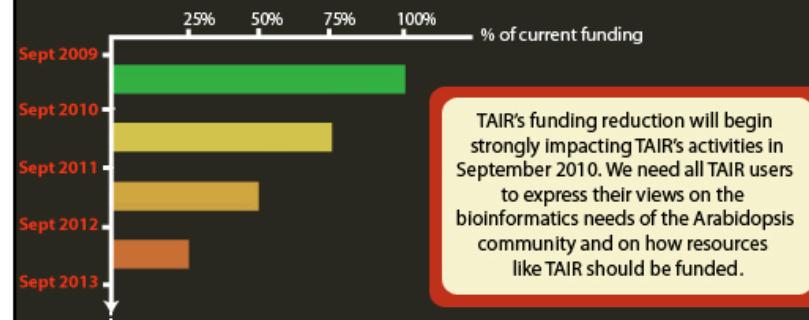
The Arabidopsis Biological Resource Center at The Ohio State University collects, reproduces, preserves and distributes seed and DNA resources of *Arabidopsis thaliana* and related species. Stock information and ordering for the ABRC are fully integrated into TAIR.



TAIR is located at the Carnegie Institution for Science Department of Plant Biology and funded by the National Science Foundation.



### Steep Decrease in TAIR Funding



TAIR's funding reduction will begin strongly impacting TAIR's activities in September 2010. We need all TAIR users to express their views on the bioinformatics needs of the Arabidopsis community and on how resources like TAIR should be funded.

Dear TAIR user,  
Our previous five year NSF grant supporting TAIR came to an end 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.....

[READ MORE AND SUBMIT COMMENTS HERE](#)

Oct 23, 2009

TAIR is the single most important data resource for researchers of *Arabidopsis* and other plants, and it cannot be that an established public resource, on which so many depend, will be reduced so dramatically. In addition, TAIR is very important for the wider research and database community. TAIR is at the forefront of Gene Ontology development and represents the plant aspect there. TAIR also is a leader in scientific journal / database cooperation, to streamline the annotation process and make published results available to all in a more efficient way - Petra Fey

Oct 23, 2009

I am also disheartened and appalled by these news. TAIR has been the #1 tool I've used since I began my research career as an undergraduate in 2002. The website greatly facilitates day to day tasks by providing plant scientist with a hub of information that otherwise would take great effort to acquire. I use TAIR tools such as seqviewer and tair blast on the daily basis. Additionally, materials such as cDNA plasmids and T-DNA seeds are readily available through the website making ordering simple. The bioinformatics tools provided by TAIR have helped me find gene homologues that were previously unidentified. The people at TAIR are also great resources. They not only keep the site running but they also are there to help us scientist with any questions and technical difficulties we may have. TAIR should continue being funded by the NSF, by other government agencies in the US and or perhaps Worldwide. I believe adding user fees is not going to help the situation. Instead, it will create a disadvantage for smaller plant labs that do not have resources that labs at "big" research institutions or in the industry posses. This will in turn increase the gap in research quality done at "smaller" schools. Thus, TAIR should remain a free source for everyone in the plant community. Brunie Burgos Doctoral Candidate Department of Genetics The University of Georgia

Oct 23, 2009

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Boon Leong Lim Oct 24, 2009

TAIR is the most useful website in plant researches. Without TAIR, the progress of plant biology will be greatly delayed, in terms of decades!!

Add your comment here!

[Add Comment](#) [Cancel](#)

AMINNA CLONES [May 20, 2009]

Are you searching for clones and vectors available from ABRC? Here are some tips for

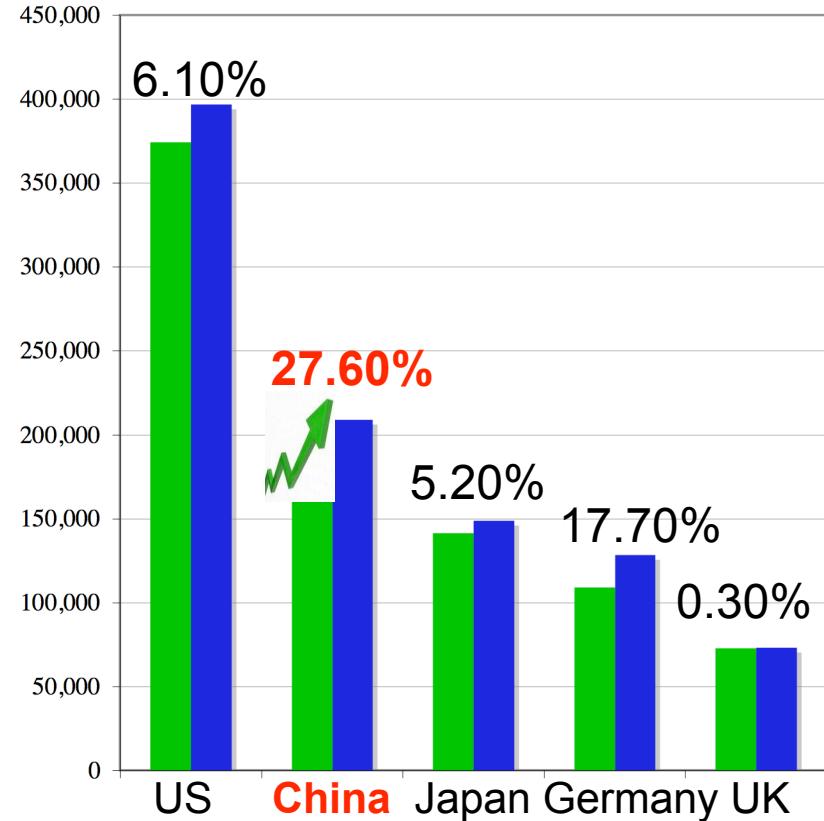
COMMENTARY

## Plant Biology Research Comes of Age in China

Haodong Chen,<sup>a,b,c</sup> Valerie J. Karplus,<sup>b</sup> Hong Ma,<sup>d</sup> and Xing Wang Deng<sup>a,b,c</sup>

*"Increased reform and openness in China have enabled Chinese scientists to take advantage of a broader trend toward the **globalization** of scientific research."*

### Demand for TAIR growing fast in China



number of visits in **Year 4** and **Year 5**

Year 4: 09/2007-08/2008

Year 5: 09/2008-08/2009

Download this talk from [drop.io/tair1234](https://drop.io/tair1234)  
TAIR Help Desk: [curator@arabidopsis.org](mailto:curator@arabidopsis.org)  
My email: [donghui@stanford.edu](mailto:donghui@stanford.edu)

How can we improve TAIR to better serve the Chinese Arabidopsis/plant biology research community?