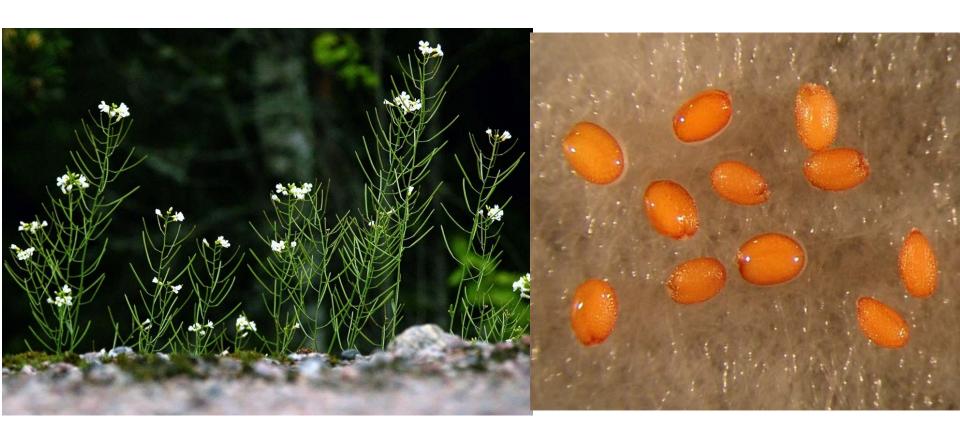
How a model genome can change your life?



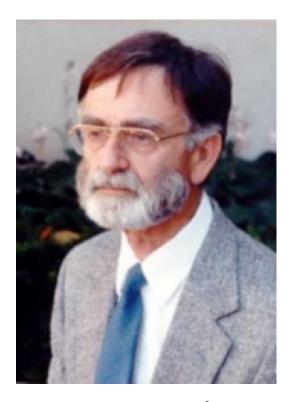
Dirk Inzé / Marnik Vuylsteke

VIB - Department of Plant Systems Biology Ghent University

Arabidopsis thaliana



Sequence since 2000, but already model plant since 1980



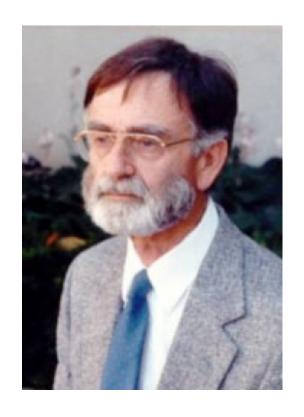
George Redei Missouri



George Redei Barbara McClintock

1957: He was the only person in the world to work with Arabidopsis.

2013: ~ 16,000 laboratories worldwide are pursuing research with Arabidopsis





George Redei

Patrick Sorgeloos

First International Symposium on Arabidopsis Research in Göttingen, April 21–24, 1965



Second International Symposium on Arabidopsis Research in Frankfurt am Main, September 13–15, 1976.

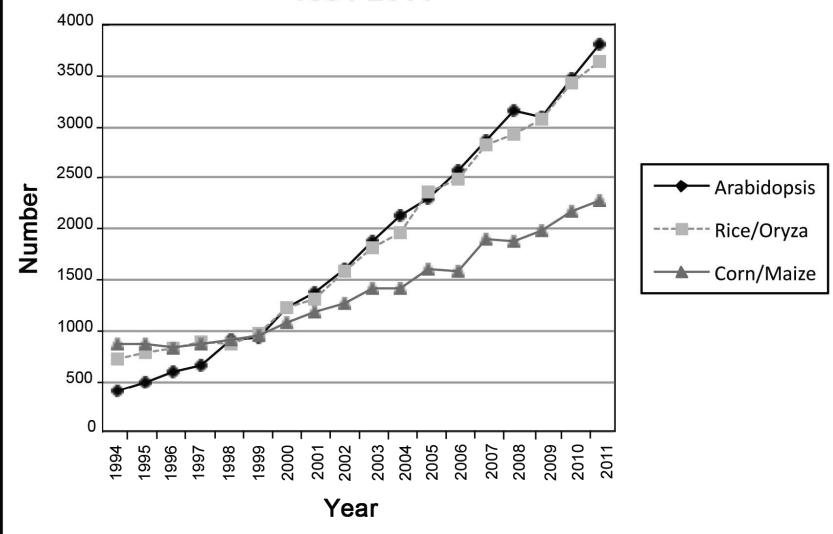


International Conference Arabidopsis Research

Yearly ICAR meeting







Model Organism Research Papers Published in Peer-reviewed Journals [Data source: NCBI-PubMed: Searches: Arabidopsis; Rice/Oryza; Corn/Maize]

Why is Arabidopsis so successful as a model organism?

Natural features

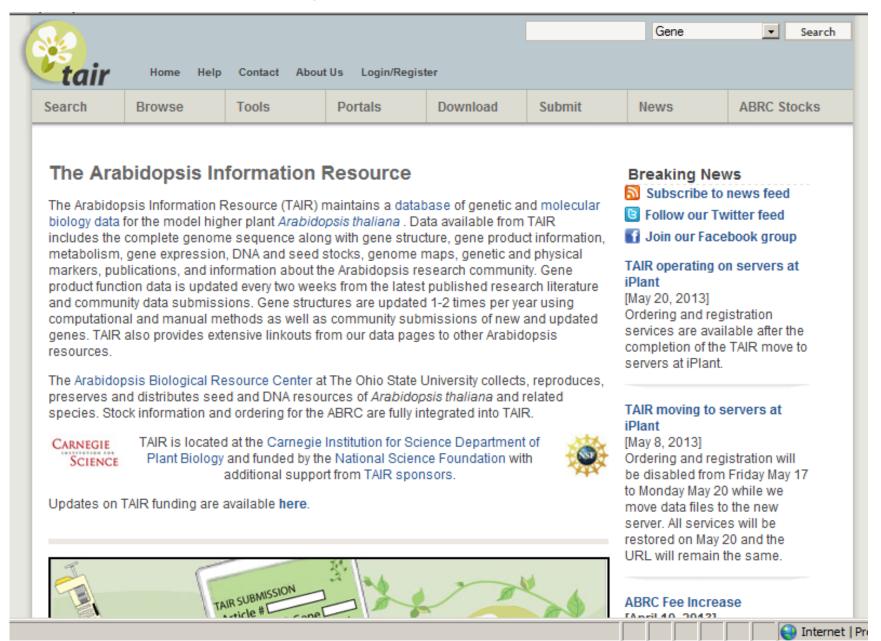
- Small sized plant
- short generation cycle ~ 3 months
- natural inbreds
- Very amenable to genetic engineering
- small size genome ~120 Mb
- Only 5 chromosomes

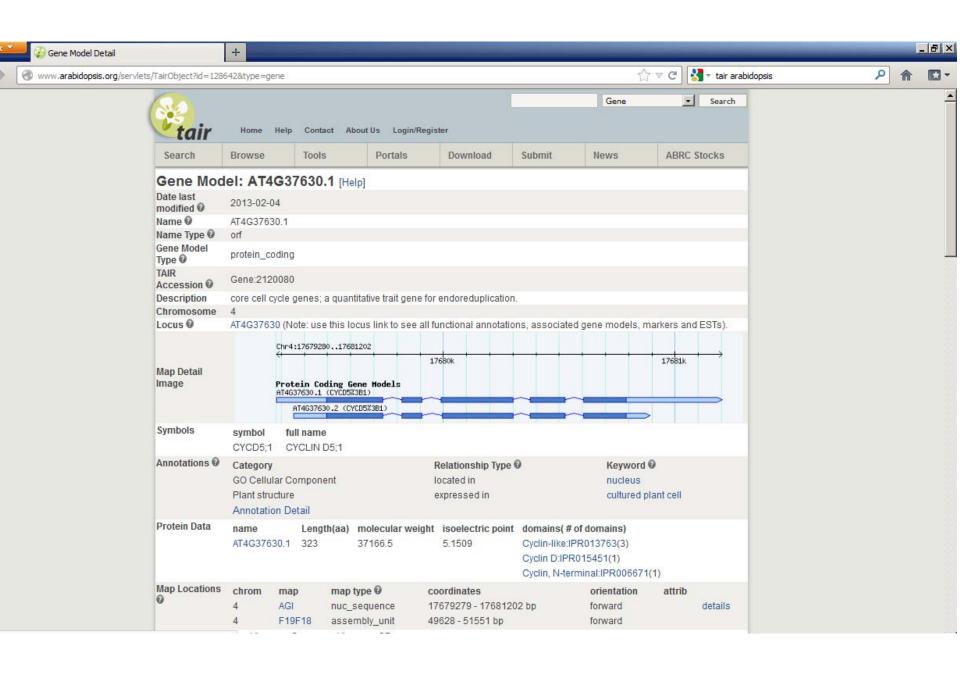


Natural features

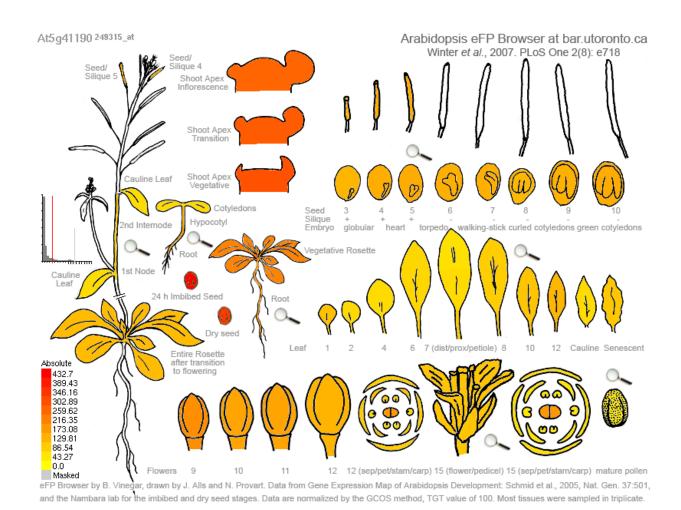
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The Arabidopsis Information Resource



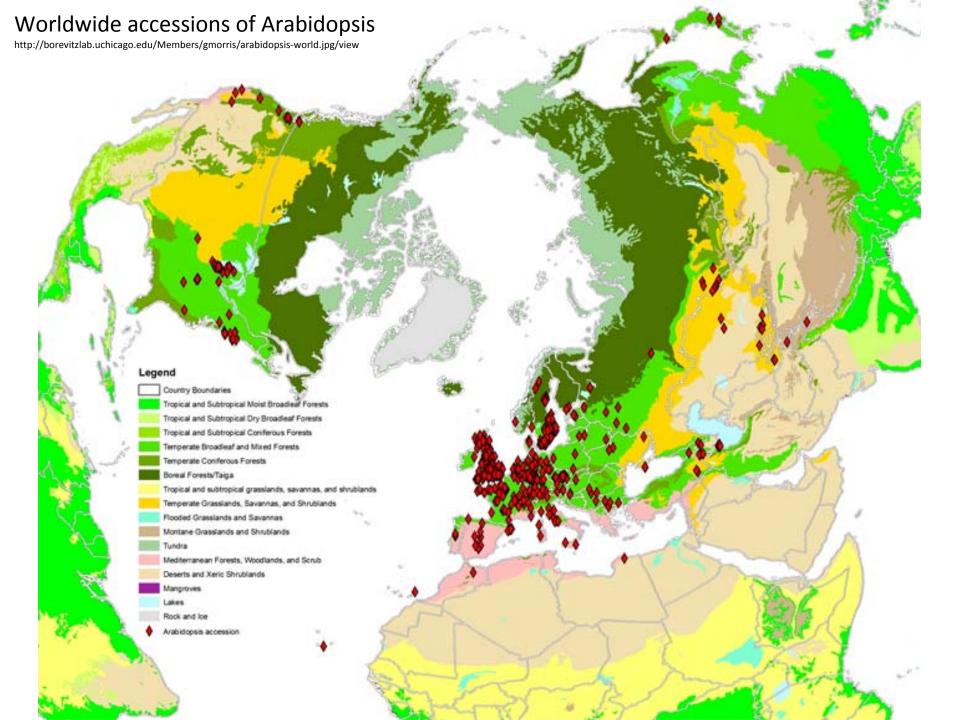


Bio-Analytic Resource for Arabidopsis



Arabidopsis stock centers

- Arabidopsis Biological Resource Center (ABRC)
- Nottingham Arabidopsis Stock Center (NASC)
- •RIKEN Bioresource Center (BRC)/ SENDAI Arabidopsis Seed Stock Center (SASSC)
 - ➤ 300,000 stocks (mutants, insertion/deletion lines, accessions, mapping populations...)
 - Minimal handling fee
 - Requirement for publication (some journals)



Natural variation in rosette size and architecture



Plant genomes may help next generation respond to climate change



1001 Genomes

A Catalog of Arabidopsis thaliana Genetic Variation

Home

Data Providers

Accessions

Tools

Software

Data Center

About

Help desk

Welcome to the 1001 Genomes Project

Check

Track the progress of genome sequencing and availability of *A. thaliana* accessions

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Browse

Select, query and visualize polymorphisms of your favorit loci using POLYMORPH and GBrowse

Download

Use the Data Center to download project related SNPs, indels, SVs and genome sequences

Gn s

The 1001 Genomes Vision

The 1001 Genomes Project, launched at the beginning of 2008, has as a goal to discover the whole-genome sequence variation in 1001 strains (accessions) of the reference plant Arabidopsis thaliana. The resulting information is paving the way for a new era of genetics that identifies alleles underpinning phenotypic diversity across the entire genome and the entire species. Each of the accessions in the 1001 Genomes project is an inbred line with seeds that are freely available from the stock centre to all our colleagues. Unlimited numbers of plants with identical genotype can be grown and phenotyped for each accession, in as many environments as desired, and so the sequence information we collect can be used directly in association studies at biochemical, metabolic, physiological, morphological, and whole plant-fitness levels. The analyses enabled by this project will have broad implications for areas as diverse as evolutionary sciences, plant breeding and human genetics.

The complete genome sequences of over 80 accessions were released in early 2010 by the Max Planck Institute, and many more have been added since by the Salk Institute, the Gregor Mendel Institute and Monsanto. We are on track and for completion of the 1001 Genomes project by the end of 2013. As of June 2013, over 1001 lines have been sequenced and the final set is being analyzed.

Below are the main papers that should be cited for the different datasets:

Ossowski, S., Schneeberger, K., Clark, R.M., Lanz, C., Warthmann, N., and Weigel, D. (2008).

Links

- > GBrowse
- > WGS of 80 strains
- > Assemblies project
- > POLYMORPH
- > NCBI SRA Genomes Project
- > Map resource for 1001 Genomes

News

August 1, 2013

SHOREmap v2.1 released.

August 6, 2012

Nd-1, sequenced by Center for Biotechnology of the University of Bielefeld (CeBiTec), is now available in the Data Center. See the project page for more information.

November 29, 2011

JGI strains Bay-0 and Sha (both TAIR10) are now available in the Data Center. See the project page for more information.

November 15, 2011

JGI strains (Alc-0, Blh-1, Jea, Oy -0, Ri-0 and Sakata) are now available in the **Data Center**.

August 28, 2011

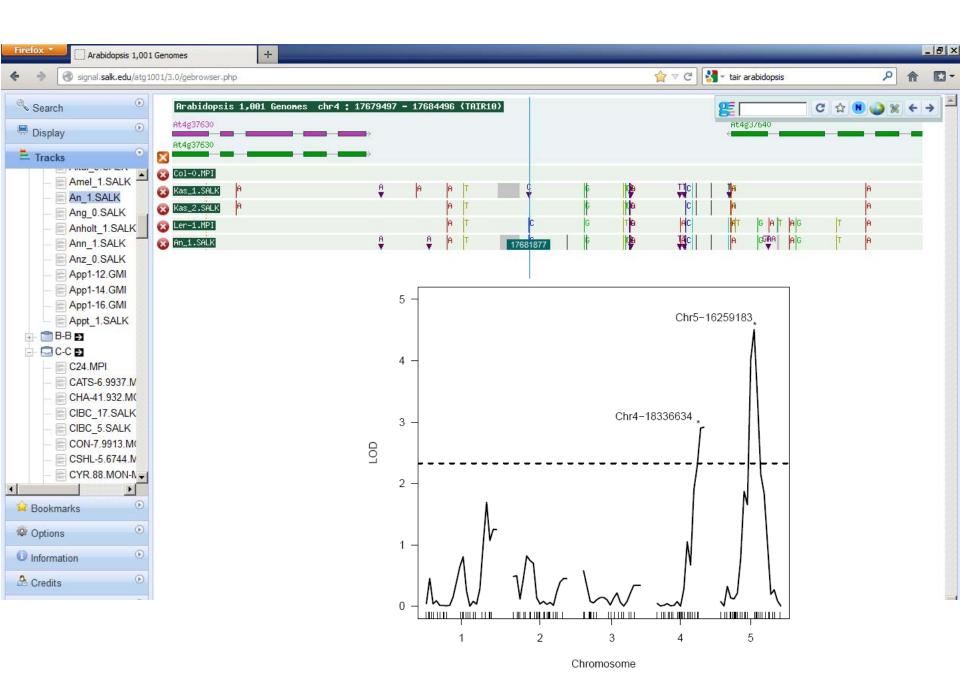
Cao et al. Whole-genome sequencing of multiple Arabidopsis thaliana populations published in Nature Genetics.

Accessions

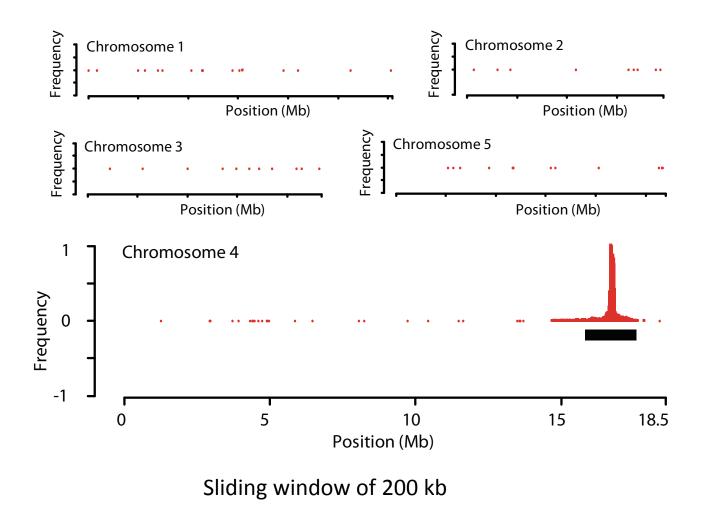
1049 accessions committed as of 4/17/2013.

Regarding the availability of not yet released genomes, please contact the individual data provider.

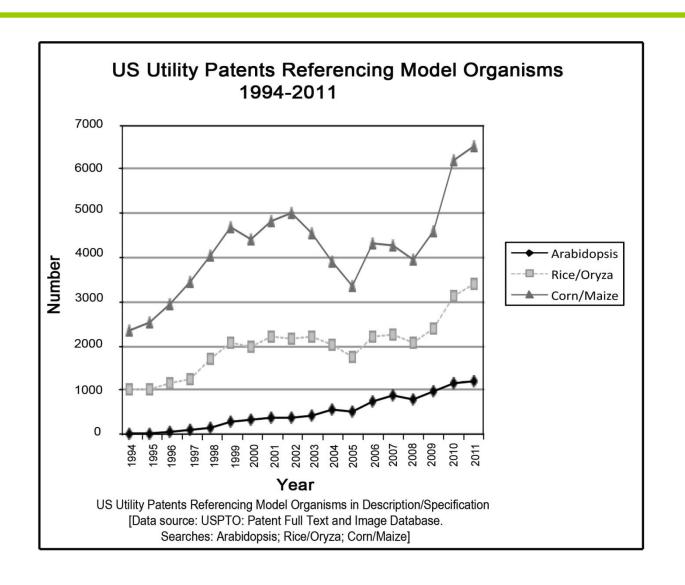
Accession 😕	Alternative ID	Sequenced by	Platform	Actions	Status
11C1	9503	Monsanto/MPI	Illumina	Download data ▼ Go!	Released
Aa-0	CS6600	Salk	Illumina	Download data • Go!	Released
Abd-0	CS932	Salk	Illumina	Download data ▼ Go!	 Released
Adam-1	9609	Monsanto/MPI	Illumina	Download data ▼ Go!	Released
Aedal-1	9321,Ådal-1	GMI	Illumina	Download data ▼ Go!	Released
Aedal-3	932,Ådal-3	GMI	Illumina	Download data ▼ Go!	Released
Ag-0	CS22630	Salk	Illumina	Download data ▼ Go!	 Released
Agu-1	CS76409	MPI	Illumina	Download data ▼ Go!	Released
Aiell-1	9646	Monsanto/MPI	Illumina	Download data ▼ Go!	Released
Aitba-1	9606	Monsanto/MPI	Illumina	Download data Go!	Released
Ak-1	CS6602	Salk	Illumina	Download data ▼ Go!	Released
Alc-0	INRA Versailles 178AV	JGI	Illumina	Download data ▼ Go!	Released
Ale-Stenar-44-4	992	GMI	Illumina	Download data ▼ Go!	Released
Ale-Stenar-56-14	997	GMI	Illumina	Download data ▼ Go!	Released
Ale-Stenar-64-24	1002	GMI	Illumina	Download data ▼ Go!	Released
Algutsrum	8230	GMI	Illumina	Download data ▼ Go!	Released
Alst-1	CS22550	Salk	Illumina	Download data Go!	Released
Alt-1	9774	Monsanto/MPI	Illumina	Download data ▼ Go!	Released
Altai-5	548AV	Salk	Illumina	Download data ▼ Go!	Released
Amel-1	CS22526	Salk	Illumina	Download data ▼ Go!	Released
An-1	CS22626	Salk	Illumina	Download data ▼ Go!	Released
Ang-0	CS6605	Salk	Illumina	Download data ▼ Go!	Released
Anholt-1	CS22313	Salk	Illumina	Download data ▼ Go!	Released
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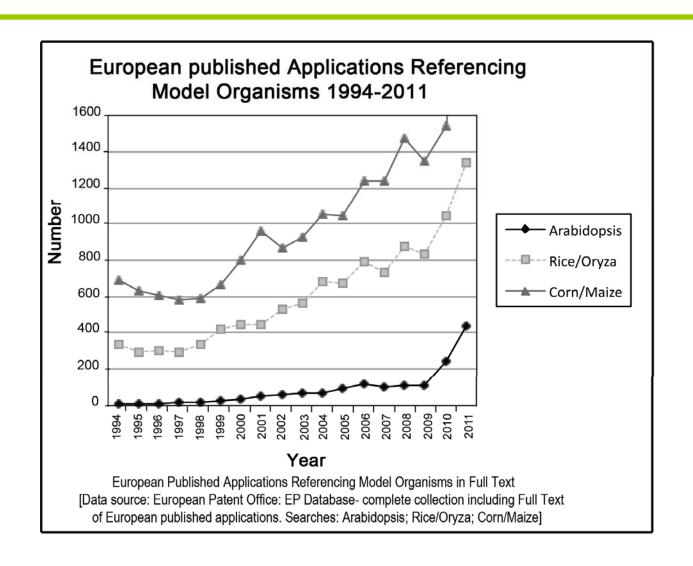
Mapping induced mutations in ~ 1 week



Translational research



Translational research





- Build a predictive model of an Arabidopsis plant from its molecular parts.
- Build the international Arabidopsis Informatics consortium, an international informatics and data infrastructure
- Exploit the wealth of natural variation that exists in Arabidopsis to further our understanding of Adaptation and evolution
- Establish an effective knowledge exchange pipeline from the laboratory to the field and vice versa

Artemia salina





Small, short generation cycle, but a large genome (1.6Gb),...

- Build a predictive model of an Arabidopsis plant from its molecular parts.
- Build the international Arabidopsis Informatics consortium, an international informatics and data infrastructure

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- Exploit the wealth of natural variation that exists in Arabidopsis to further our understanding of Adaptation and Evolution

 Build a predictive model of an Arabidopsis plant from its molecular parts

Importance of Model Systems

By focusing on one model system many novel finding for Plant Biology were made:

- -Plant hormone receptors and MOA
- -Flower induction mechanism (florigen)
- -Small RNAs

Multinational Arabidopsis Steering Committee

MASC

Yearly reporting

Continental subcommittees