



Valuable Internet Resources for Plant Molecular Biology Research

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Summary

Over the past few years TAIR (the *Arabidopsis* Information Resource) has developed into a supercenter of information on *Arabidopsis*. It describes molecular aspects of genetic research activities of important research institutes all over the globe via its website: www.arabidopsis.org. The review article gives a bird's eye view of some of the important features of this organization's website. It is intended to help those new to the science of molecular genetics to use this website in order to gain knowledge about all aspects of *Arabidopsis* genome, molecular identity of its various classes of genes, their functions; and how knowledge gained through the study of this website will enable them to organize their research in the crops of their interest. In addition, we have summarized the internet resources available on various crop genome research.

Introduction

The past ten years have witnessed phenomenal changes in the approaches of scientists towards sharing knowledge in research topics of mutual interest. Recent advances in information technology have broken many barriers in scientific information exchange. Prior to this time, scientists were hesitant to share pre-published results, fearing that the competing laboratories would rush to publish their results based on their preliminary findings. Now the tide has dramatically changed. Regardless of their political or academic affiliations, scientists all over the world have joined hands in handling certain areas of research, which are of vital interest to the world community. For instance, a team of Chinese, Japanese, Korean and American scientists collaborated to determine the DNA sequence of *indica* and *japonica* rice and published the results of rice genome projects in the World Wide Web (Table 1). Earlier, scientists from three continents worked together and sequenced the entire genome of the model plant, *Arabidopsis thaliana*: (http://www.arabidopsis.org/genome_release.html). The attitude of the funding agencies

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and private donors also changed radically. Funding was provided to establish organizations for deposition and recording of data relating to genomic structure of various species, DNA and protein sequence of individual genes, their functionality, promoters, enhancers, enzymes, primary, secondary and tertiary protein structure, biochemical pathways and many more. Scientists all over the world have free access to these web sites. Gone are the days when scientists had to spend hours after hours in the library, retrieving information relating to their topics of research. Now this information is only a click away from investigators, provided they have access to the World Wide Web. Notable among these publicly-funded organizations are the following : the *Arabidopsis* Information Resource (TAIR) <http://www.arabidopsis.org/>, The Institute of Genomic Research (TIGR) (<http://www.tigr.org/>), RIKEN Genomic Sciences Center (Japan) (<http://www.gsc.riken.go.jp/>), *Arabidopsis* Biological Resource Center (ABRC) <http://www.biosci.ohio-state.edu/~plantbio/Facilities/abrc/abrchome.htm>, Nottingham *Arabidopsis* Stock Center (NASC). Recently the American Society of Plant Biologists (ASPB) has published an electronic book, entitled, "The *Arabidopsis* Book (TAB)". The Society is providing funds for its maintenance and updating. The latest article posted on its website was on "The Secretory System of *Arabidopsis*" by Anton A. Sanderfoot and Natasha V. Raikhel (2003). The book is only available online (<http://www.aspb.org/publications/arabidopsis/index.cfm> and access is free. The Society is doing this as a public service in order to establish a new mode of communication between researchers. It is also an attempt to establish a new and unique model for scientific publishing in the sense that there will be continuous updating of the content of this book, as new information becomes available. This online publication is not only the most comprehensive and recent work on *Arabidopsis* but also a very useful reference to researchers in biology all over the world.

In addition to all the information available on *Arabidopsis*, plenty of genetic information is available on the agronomic crops such as rice, maize and cotton. See Table 1 for a list of such sites on the Internet. Many others will soon become available to the public as they are being developed.

Internet sources are not fully utilized in developing countries: While most of the students and researchers from the developed countries take full advantage of these extremely useful web sites and resources, those in most of the developing countries are not fully aware of these Internet resources. The situation is true even in the institutes where students have access to computers. Those who are not familiar with TAIR website will be astonished to find out the depth and variety of information covered in it. In this review, the authors

discuss these websites in general and TAIR in particular with the goal of providing newcomers with a starting point for using these websites. Thus, by

Table 1. Internet resources to aid plant molecular biology research

Internet Resource	Website	Location
The Arabidopsis Information Resource	http://www.arabidopsis.org/ (TAIR)	U.S.A.
The Institute of Genomic Research	http://www.tigr.org/ (TIGR)	U.S.A.
Arabidopsis Biological Resource Center (ABRC)	http://www.biosci.ohio-state.edu/~plantbio/Facilities/abrc/abrchome.htm	U.S.A.
The Arabidopsis Book (TAB)	http://www.aspb.org/publications/arabidopsis/	U.S.A.
Rice genome Projects	http://rgp.dna.affrc.go.jp/	Japan
	http://genome.sinica.edu.tw/	Taiwan
	http://www.rice-research.org/	U.S.A.
	http://bioserver.myongji.ac.kr/ricemac.html	Korea
Wheat and barley genome projects	http://wheat.pw.usda.gov/index.shtml	U.S.A.
Plant Genome Entries in NCBI	http://www.ncbi.nlm.nih.gov/PMGifs/Genomes/PlantList.html	U.S.A.
Plant Genome Exptl. Concepts	http://www.nal.usda.gov/pgdic/pgexpcon.html	U.S.A.
Plant Genome Information Resource	http://www.nal.usda.gov/pgdic/ http://www.nal.usda.gov/pgdic/Map_proj/	U.S.A.
Plant genome Grant Information	http://www.nal.usda.gov/pgdic/pggrantinfo/	U.S.A.
Maize Mapping Project	http://www.maizemap.org/	U.S.A.
Genomic <i>Arabidopsis</i> Resource Network (Garnet)	http://www-2.cs.cmu.edu/afs/cs.cmu.edu/project/garnet/www/garnet-home.html	U.K.
European Molecular Biology Lab	http://www.embl-heidelberg.de/	Germany
Munich Information Center for Protein Sequences (MIPS)	http://mips.gsf.de/	Germany
RIKEN Genomic Sciences Center	http://www.gsc.riken.go.jp/	Japan

highlighting a few important features of TAIR, this review is intended to present a general overview to researchers unfamiliar with this website. In addition, a list of other interesting and useful websites is given to illustrate the wealth of scientific resources available, just a click away. This is by no means a comprehensive catalog of TAIR or any other resources in the Internet. Readers are recommended to refer to the “help” menu in the TAIR website in order to

clear up their understanding of any section described in this article. Another relevant publication in this context is "Bioinformatics: Sequence and Genome Analysis" available from Cold Spring Harbor Laboratory Press.

Gene symbols : For a scientist new to this discipline, the easiest way to begin the search in the TAIR website is to go to the "Gene Symbols" section. (http://www.arabidopsis.org/info/Gene_Symbols.html). Gene symbols are mnemonic names that reflect some aspect of what is known about a gene or class of genes (<http://www.arabidopsis.org/links/nomenclature.html>). This section lists 1420 symbols, reflecting a variety of gene classes. Types of symbols that reflect gene function/localization include transcription factors, clock-, transmembrane-, while photoperiodic, phytochrome-, trichome- and seed coat gene symbols reflect traits associated with wild type genes and their mutants. Thus, this section gives a very general overview of what is known about *Arabidopsis* genes, including the functionality and traits associated with mutant genes under study. By far the majority of symbols consist of three letters, only a few of two such as *YI* (yellow inflorescence), and a few of four, such as *SERK* (somatic embryogenesis receptor kinase), or more such as *STARIK* (chlorotic dwarf).

TAIR gene search : The next step for the beginner is to go to section, "TAIR Gene Search". Suppose the researcher chooses the gene symbol *PHYC* (phytochrome C) and wants to know what traits this gene controls and whether this gene has been isolated. Using this page, the user can search for a specific gene by typing in the gene name (*PHYC*) in the "name" input box and check the features, such as whether the gene is sequenced and has a full length cDNA. To view all of the information about this gene, the investigator needs to click the "Gene Model" which is shown in the second column. After clicking on the submit button, the results of the search are displayed, in this case *PHYC* along with a brief description of the gene and key words that describe the gene. It also shows that it has been sequenced and has full length cDNA. The other information include : the specific chromosome in which it resides, its accession number, the length of the protein it encodes, the genes associated with it, polymorphisms available and many other details. Also displayed are key words, which are controlled vocabularies, used by databases to describe a gene. Because names convey only a part of what is known about a gene (e.g. mutant phenotype or enzymatic activity), the key words are important as they function as multiple descriptors. So a gene is associated through these key words to its molecular function, subcellular localization and role within the organism. Once the accession number of this gene is retrieved, one can use this number to dig out more information about this gene, searching sequence

similarity for the DNA or amino acid sequence. The page ends with a list of papers published about this gene.

Sequence viewer (SeqViewer): The next step for the investigator will be to visit one of TAIR's chief features, namely, Sequence Viewer (SeqViewer: <http://www.arabidopsis.org/servlets/sv>). It displays the whole genome view consisting of five *Arabidopsis* chromosomes. The chromosomes are numbered and colored in green solid thick line. Each chromosome shows the position of its centromere indicated by a small blue segment. Besides, a small set of markers are displayed for orientation (Fig. 1). It includes masses of data arranged at several levels. Clicking anywhere on the chromosome bars allows the user to browse and see close-up view of the region of the chromosome. A text input box below the chromosome bars allows the user to search for a specific gene. Let us find out the details about two genes: *PHYB* and *PHYC*.

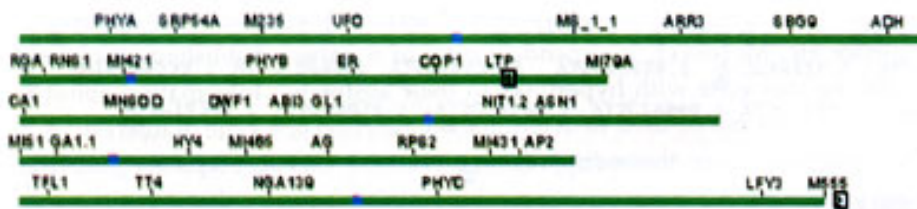


Fig 1. An idiogram of the five chromosomes in the model plant, *Arabidopsis thaliana*. Loci for different traits have been shown distributed on five chromosomes. Note the position of the *PHYB* gene in the middle of chromosome 2 and the *PHYC* gene right to the centromere (indicated in blue) on chromosome 5. (Courtesy TAIR)

Typing in the name of *PHYB* and selecting gene will open a close-up view of the chromosome highlighting the matching gene. The accession number of the marker gene *PHYB* (*Phytochrome B*) is given and it is *At2G18790*. The symbol *At* stands for *Arabidopsis thaliana*. The number 2 between *t* and *G* refers to the chromosome number in which the gene is located. Besides its exact location on chromosome 2, SeqViewer pulls up several relevant subsections giving information on : polymorphisms (e.g., deletion, insertion, substitution), T-DNA flanks, gene structure, UTRs (untranslated regions), number of introns (non-coding regions; indicated by blank space), exons (coding regions), cDNA version of the gene (the gene without the introns). In addition, are shown ESTs (expressed sequence tags), or short cDNA sequences obtained from cDNA libraries. An EST represents a small segment of an entire gene, capable of expressing the trait partially. Because ESTs are obtained from a variety of

RNA samples from different tissues, they provide information about where the individual genes are expressed (and presumably where they act) and the degree of their expression. Suitable diagrams back all of this body of information. One can view as little as 10,000 (=10KB) base pairs at a time. From the search the investigator will retrieve the following piece of information: the expressed protein encoded by *PHYB* belongs to the nucleus and functions in signal transduction.

The investigator may like to know about another marker gene of this category, say, *PHYC* (*Phytochrome C*). A quick look at the abridged map will indicate that it is located on chromosome 5. A click on this annotation will present the viewer the details about this gene, its function and other relevant information such as that it encodes a phytochrome C apoprotein, constituted of 1111 amino acids. It also describes the function of this protein in that it is a member of a family of photoreceptors that modulates plant growth and development. It also provides the same pieces of information given for the marker gene *PHYB*, namely, T-DNA insertion sites and their nucleotide sequence etc. Moreover, it appends a total of 6 papers published since 1994, describing this gene with hyperlinks to their abstracts. Information about T-DNA insertions can be used to determine the function of a gene of interest. A T-DNA insertion within the coding region of the gene usually stops the gene from being expressed. An investigator can pinpoint the sequence that constitutes the gene under investigation by using the T-DNA to locate the gene associated with the trait of interest. Sequencing of both the wild type gene and the mutated (with T-DNA insertion) is one way to confirm the association between the gene and the trait it controls.

Loss-of-function and gain-of-function mutants : One general strategy currently being used to learn more about a plant gene's function is to obtain a loss-of-function mutant for the gene of interest. One type of loss-of-function mutants, that plant scientists use currently, is generated by T-DNA insertion in the gene under investigation. T-DNA is a large segment of plasmid DNA from a bacterium, called *Agrobacterium tumefaciens*. It causes tumor into the plant it infects. However, the T-DNA element can also be utilized to disrupt a gene. In the course of infection, the bacterium transfers some of its DNA into the host species and in the process knocks out its function. Historically, this approach was experimentally difficult because it involved an enormous effort of screening T-DNA libraries for an insertion in the particular gene. However, in recent years sequencing of entire insertion libraries from the T-DNA border has become a common practice. This procedure allows an investigator to do a sequence search for insertions in the gene. There are now many T-DNA insertion libraries

available and TAIR is an excellent resource to begin a search. (<http://www.arabidopsis.org/links/insertion.html>). The sequence of the putative gene of interest can be used to search for insertions using the Wu- BLAST sequence

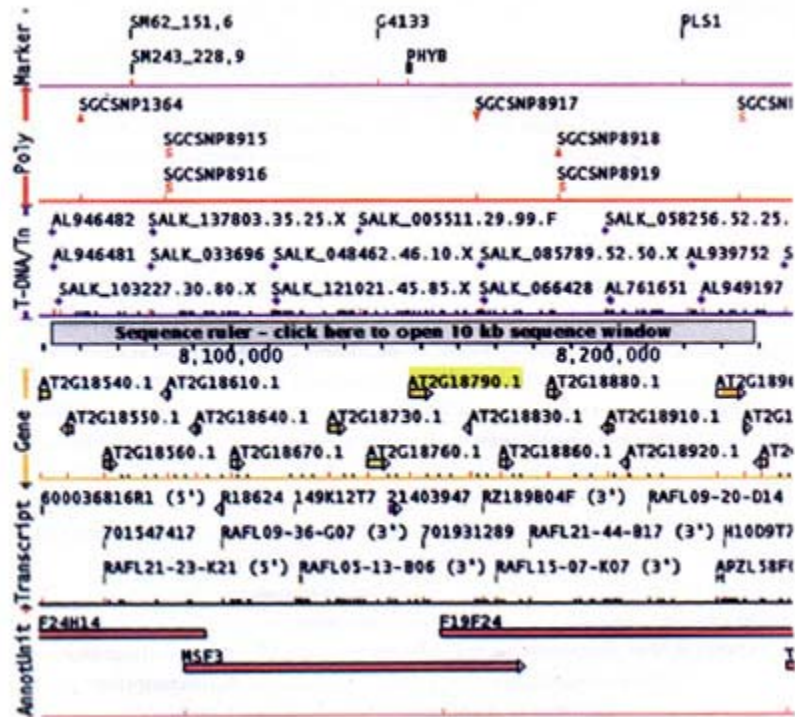


Fig 2. All information about the gene *PHYB* (AT2G18790) on chromosome 2 can be viewed in this figure. These include: gene structure, T-DNA insertion sites, transcripts etc as well as research centers where T-insertion lines are available etc. The cursor on the gene of interest will release a drop down menu. Clicking on the last item i.e., nucleotide sequence will open the entire DNA base sequence, constituting the AT2G18790 gene. (Courtesy TAIR)

similarity search against the T-DNA insertion flank sequences (<http://www.arabidopsis.org/wublast/index2.html>). If the query sequence matches the plant genomic sequence flanking a T-DNA insertion, chances are that particular line has been sequenced by the SALK. If the query sequence search is positive, the investigator can then order such seeds by visiting the appropriate section of the TAIR website: (http://www.arabidopsis.org/servlets/Search?action=new_search&type=germplasm).

The next step is to confirm that the putative T-DNA insertion is indeed in the reported location within the gene. Once the seeds have been obtained, the F₂ generation plants are grown and used as a source for genomic DNA. Using polymerase chain (PCR) reaction, this genomic DNA can serve as template and one can experimentally confirm the T-DNA insertion site following the standard procedure. Once a plant that is homozygous for the T-DNA insertion is obtained, the researcher must determine that there is only a single copy of the T-DNA insertion in that line. At this point, confirmation that the T-DNA insertion truly “knockouts” the corresponding message (prevents production of mRNA) for the gene can be achieved using RT (reverse transcription)-PCR and the search can begin for a phenotype caused by this knockout.

In addition to T-DNA insertion lines, resulting from loss-of-function mutants, there is another class of T-DNA insertion lines available through TAIR. This class is called gain-of-function mutants because such individuals show dominant phenotype (Rate et al. 1999). A mutant database and additional gain-of-function mutant lines are expected to be available soon from RIKEN in Japan via a link through TAIR. A newcomer may also be interested to know how these gain-of-function mutants are generated. Here also insertion of a T-DNA element takes place but the inserted DNA contains four copies of a transcription enhancer derived from the cauliflower mosaic virus (CaMV) 35S promoter *at the right border of the T-DNA element*. This process is called activation tagging and typically results in overexpression of the neighboring gene that is directly downstream of the 35S promoters. There are several advantages to obtaining a gain-of-function mutant. One of the important advantages is that it overcomes the problem in which loss of function mutants are lethal. Another advantage is that some genes may be redundant (about 60% of the *Arabidopsis* genome is duplicated), so a similar functional gene may mask a mutation in another gene. Activation of the gene usually results in a dominant mutant phenotype. However, if the T-DNA inserts into the CODING region of a gene, then a loss-of-function for that particular gene may result.

Typically, to check if the phenotype was due to loss-of-function, the investigator needs to take the mutant line and introduce the wild type version of the gene that has the T-DNA inserted into it and see if it can rescue the mutant, a phenomenon called complementation. To check if the phenotype was due to gain-of-function, one would simply overexpress the downstream gene.

Functional genomics (functional characterization of Arabidopsis genes): This section in TAIR symbolizes the concerted efforts launched recently all over the world to determine and understand the function of every gene of the

Arabidopsis genome by the year 2010 (http://www.arabidopsis.org/info/2010_projects/index.html). The DNA sequence of approximately 29,000 genes that constitute its genome were determined towards the turn of the century. This extraordinary feat, accomplished jointly by a number of institutes, inspired the *Arabidopsis* community to associate each and every gene/gene family with the function it executes. Of relevance in this connection is that only 35% in the genome are represented by one gene, while 37% belong to gene families with five or more different members in a family. The classification of functions of the remaining 28% is yet to be determined. The plant biology community realized that determining the genomic sequence is only a means to an end; and accomplishment of the ultimate goal, would entail unraveling the function of the remaining uncharacterized genes, some of which act singly and others as a team to condition the expression of both qualitative and quantitative traits.

MASC: A Multinational *Arabidopsis* Steering Committee (MASC) was formed to coordinate and overview the functional genomics work that institutions all over the world are carrying out. The countries represented in this committee are: Argentina, Australia and New Zealand, Canada, China, European Union, France, Germany, Italy, Japan, Nordic *Arabidopsis* Network, United Kingdom and United States. MASC not only coordinates the activities of the concerned institutions but posts latest information about their progress via TAIR website: (http://www.arabidopsis.org/info/2010_projects/MASC_Info.html). Interested persons can search the 2010 projects database to find out what genes are being analyzed and the title of the project dealing with such analysis of individual genes or gene families. (http://www.arabidopsis.org/info/2010_projects/index.html). The TAIR website gives a list of 43 National Science Foundation (NSF)-funded research projects along with a short description of each. All the projects are dedicated and focused on functional analysis of gene families including those involved in transcription network, disease and insect resistance, signaling elements, small RNAs. A survey of the titles of the project reveals that the NSF decision to complete the functional analysis of the complete set of about 29,000 *Arabidopsis* genes within the present decade is backed by financial commitment. Liberal grants were made available to various research groups to make this dream of finding function of each and every gene a reality. Geneticists are positive about the outcome of functional analyses of *Arabidopsis* genes. Already rice geneticists have discovered that in spite of the wide phylogenetic differences between rice (a monocot) and *Arabidopsis* (a dicot), most of the flowering genes in the two taxa are orthologous (Izawa et al. 2003). Such functional similarity between

genes that control flowering time in the two widely divergent taxa implies that sequence data from the *Arabidopsis* genome may be extrapolated to improve agronomic characters of crops and other plants of economic importance. The vast amount of genetic resources on *Arabidopsis* will help in discovering new genes in other agronomic crop plants such as rice, wheat, sugarcane and maize. The websites that store the results from the molecular analysis of agriculturally important crops are listed in Table 1. In addition, there are several other Internet resources that are helpful to researchers in plant molecular biology to widen their horizon of knowledge in this ever-expanding scientific discipline. These websites are constantly being enriched and updated through mutual collaboration of different research groups, enabling them to share their new exciting findings with others. The websites that have organized an extensive list of useful websites in molecular biology and biochemistry are listed in Table 2.

Table 2. List of websites that provide links to useful sites on molecular biology and biochemistry.

Website	Links to	Location in U.S.A.
http://www.ncbi.nlm.nih.gov/	Vast Genetic and Literature Source	National Institute of Health
http://www.mcb.harvard.edu/BioLinks.html	Biochemistry, Molecular, Educational sites	Harvard University
http://biotech.icmb.utexas.edu/	Biology Dictionary Cyberbotanica Professional sites	The University of Texas at Austin
http://core.biotech.hawaii.edu/b-htmrsc.htm	Bioinformatics Genomics Proteomics	Pacific Biomedical Research Center, Hawaii
http://www.public.iastate.edu/~pedro/rt_all.html	Molecular tools, literature search and protocols	Iowa State University
http://psyche.uthct.edu/ous/BiolRes.html	Online Molecular Biology Courses and other sites	University of Texas Health Center
http://www.esb.utexas.edu/sata/molbiolinks	All the sites referred in this paper are listed	University of Texas at Austin

Conclusion

The transition from an introductory genetics course to the advanced techniques at various levels of molecular biology is so drastic that many students and beginner scientists in molecular biology get lost. They feel the transitional gap more acutely. There are several factors that make it difficult for students from tropical countries to carry out research on the molecular aspects of *Arabidopsis thaliana*. Firstly, this plant does not grow well in temperatures above 22°C; secondly, lack of growth-room facility in a tropical country makes its almost

impossible to grow this model plant under controlled environment. In addition, unavailability of suitable chemicals, radioisotopes at short notice multiplies the problem to handle *Arabidopsis* as an experimental material. Thus, to carry out research on *Arabidopsis*, in laboratories of developing countries at a pace comparable to their counterparts in the developed world is out of question. And yet to keep abreast of the forefront of knowledge, molecular biology students at developing countries must learn about the advancements being constantly achieved in this model plant. The necessity has become all the more crucial in view of the fact that more than 60 percent of the plant-related molecular biology articles published in the world's prestigious journals are in molecular, biochemical and physiological aspects of *Arabidopsis*. To become top class researchers, students from developing countries need to know the current trends in molecular biology research in *Arabidopsis*, not so much to know about this plant species *per se* but to apply the newly reported novel findings to their own crop improvement programs. The molecular biology resources available on the Internet will go a long way in filling in the knowledge gap between the biologists of the two worlds.

This review article about TAIR is intended to open the gateway to a newcomer to equip himself with the multitude of information on the genetics and molecular aspects of *Arabidopsis*. Once the readers develop skill in consulting various sections of the TAIR website, they will find it extremely useful to discover a fascinating new world of molecular genetics, allowing them to apply such a wealth of information to the study of the crop of their interest. In spite of the vast amount of free information available in the Internet, one has to be critical in evaluating the reliability and effectiveness before applying this vast body of information to fit in their data and arrive at a dependable conclusion. Biologists like any other group of scientists are witnessing a phenomenal explosion of new information and the best thing that has happened to the world community is that the galloping progress that is being made everyday in all frontiers of science is accessible to all researchers through the World Wide Web.

Appendix

A list of projects funded by National Science Foundation in the past two years:

1. Identification in the Photoperiod and Circadian Network of Flowering Control
2. Determining genome-wide transcription networks of TGA factors
3. In vivo genomics: Visualizing G protein interactions in *Arabidopsis*
4. Genomics approaches to finding transcriptional networks
5. Function of the *Arabidopsis* Small RNAs

6. Functional Analysis of the WRKY Transcription Factor Gene Family from *Arabidopsis*
7. Large-scale fluorescent tagging of full-length genes to characterize native patterns and subcellular targeting of *Arabidopsis* proteins of unknown function
8. Nitrogen Networks in Plants
9. The *Arabidopsis* RPM1 Disease Resistance Signaling Network Disease resistance is a significant problem in agriculture. We will add to the body of knowledge that will eventually lead to more effective control of plant disease. This is vital because we currently lose up to 30% of crop yield to pathogens and pests
10. Expression Profiling of Plant Disease Resistance Pathways
11. A Sequence-Indexed Library of Insertion Mutations in the *Arabidopsis* Genome
12. Identifying clients of 14-3-3 phosphoregulation
13. Identification, Modeling, and Prediction of *Arabidopsis thaliana* mRNA-3'-processing Sites
14. Assigning Gene Function in the *Arabidopsis* One-carbon Metabolism Network
15. Developing paradigms for functional genomics of protein kinases and phosphoproteins using the CDPK Superfamily
16. Discovering transporters for essential minerals and toxic ions in plants
17. Functional Genomics of Alpha-Helical Scaffold Proteins in *Arabidopsis thaliana*
18. Analysis of two-component signaling elements from *Arabidopsis*
19. Comprehensive Functional Analysis of the *Arabidopsis* RCD Gene Family
20. Phenylpropanoid Pathway Networks: An Integrated Approach to Establishing Protein/Enzyme Function in *Arabidopsis* and their Associated Networks
21. Determination of Biological Functions of the NPH3/RPT2 Family
22. Genomics and Proteomics Approaches to the Function of Tyrosine Phosphatases in *Arabidopsis*
23. A systematic approach to automated production of Recombinant Inbred Lines
24. Using Functional Genomics to Determine How and Why Plants Synthesize Diverse Triterpenoids
25. Investigating coiled-coil proteins in the *Arabidopsis* ORFeome
26. Essential Gene Functions in *Arabidopsis* Seed Development
27. Pre-mRNA splicing signals in *Arabidopsis*
28. Functional genomics of *Arabidopsis* starch granule metabolism
29. Development of Laser-Capture Microdissection for Plant Tissues
30. The genealogy of *Arabidopsis thaliana*
31. A Transposon-Based System for Site-Specific Recombination in *Arabidopsis*
32. Functional Genomics of *Arabidopsis* beta-Glucosidase and beta-Galactosidase Gene Families
33. From Seed to Seed: Genome-wide Expression Analysis of *Arabidopsis* throughout Its Life Cycle
34. Functional Genomics of *Arabidopsis* P450s
35. Identification of the function of a family of putative glycosyltransferases
36. Functional Genomics of Quantitative Traits: Expression Level Polymorphisms of QTLs Affecting Disease Resistance Pathways in *Arabidopsis*

37. The endgame for reverse genetics: isolation and distribution of a knockout mutant for every gene in *Arabidopsis*
38. Plant Peroxisomal Biogenesis: Sorting/Function of Membrane Proteins and Peroxins
39. Functional Analysis Of The Ubiquitin-Protein Ligase (E3) Families In *Arabidopsis*
40. Bioluminescence Resonance Energy Transfer (BRET): A tool to explore protein-protein interactions in *Arabidopsis*
41. Functional analysis of the *Arabidopsis* Yellow Stripe-Like (YSL) family: heavy metal transport and partitioning via metal-nicotianamine complexes
42. Visual Informatics Tools to Interactively Link *Arabidopsis* Metabolic and Regulatory Network Maps with Genome-Wide Expression Data
43. Genetic and Physiological Characterization of *Arabidopsis* Plasma Membrane H⁺-ATPase Mutants

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*Since the review article is based on a number of websites including that of TAIR, the number of references cited in the text are few. The readers are referred to the URLs mentioned in the body of the text to obtain detailed information.