

IS-MPMI *Reporter*

Fall 1995

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Further Improvements to MPMI Planned

Stanton B. Gelvin, Editor-in-Chief, MPMI The Senior Editorial board of Molecular Plant-Microbe Interactions (MPMI) met this past July at APS Press headquarters in St. Paul, Minnesota. This was the first time that the board had held such a "board meeting," and these discussions promise to result in a number of improvements to the journal.

The current Senior Editorial board consists of Drs. Stanton Gelvin (Editor-in-Chief), David Baulcombe (virus-plant interactions), Jan Leach (bacterial pathogenesis), John Ryals (plant response), Gary Stacey (bacterial-plant symbioses), and Jonathan Walton (fungus-plant interactions). John Ryals' position is newly-established and reflects the increased emphasis MPMI will be placing upon manuscripts dealing with the plant's response to microbes. In addition, the Senior Editors discussed changes in the Associate Editorial board. Most of the current Associate Editors were appointed in 1988 when MPMI was first published, and only approximately 1/3 of the board has changed since that time. The expertise of the new Associate Editorial board will better reflect the range of manuscripts currently published, and will include editors representing the areas of nematode-plant interactions and biocontrol. The new board, whose members will serve a three-year term with approximately 1/3 of the board changing each year, will assume its duties in January, 1996.

Readers of MPMI and scientists submitting manuscripts to the journal will soon see a number of improvements. Most noticeable will be an increase from six to nine issues published per year. This jump in the frequency of issues has been made possible by a steady increase in the number of high-quality manuscripts submitted to the journal. Our ultimate goal is to publish 12 issues per year.

The increase in the number of annual issues will permit more rapid publication of manuscripts. In addition, the Senior Editorial board and the publications staff have made a number of changes in the manuscript routing procedures. Taken together, these changes will reduce the average time of publication (from submission to final

publication) by two to three months. As an additional incentive to encourage manuscript submissions, we have just lowered the price of publishing color plates in MPMI.

The new charges will be \$500 for each of the first two plates, and \$250 for each additional figure. These prices are equal to or lower than those of other leading journals publishing articles in the areas of plant-microbe interactions and plant molecular biology.

Readers will also soon see an increased number of "review-type" articles published in MPMI. These reviews will be of several types, including standard 4-6 page reviews of a particular field, short "current opinion" types of articles that cover important advances within a field during the past 12 months, "point/counter-point" discussions in the form of letters from scientists having differing views on currently-important topics, and summaries of important meetings. In addition, MPMI may soon publish issues devoted to a particular "theme." Authors should consult the appropriate Senior Editor before submitting these types of articles.

In only a few short years, MPMI has become a leading journal in the molecular plant sciences. To continue and build on this tradition, we need your help. We encourage you to submit your best manuscripts to MPMI. In addition, we encourage you to take out a personal subscription to the journal. Finally, to assure that articles published in MPMI receive maximum exposure within the scientific community, we request that you encourage your institutional library to subscribe to MPMI.

We encourage your suggestions regarding how MPMI can better serve your needs and the needs of the scientific community. Please address your comments to the appropriate Senior Editor or to the Editor-in-Chief.

IS-MPMI Needs a Logo!

IS-MPMI incorporated as a non profit association in 1990. To date, members have focused their efforts on building a database of members, organizing a biennial meeting and contributing to the ongoing promotion of the *Molecular Plant-Microbe Interactions* journal. Now that membership is approaching 400 and the meeting draws close to 800 people, the Board recognizes that there is a need for additional member services.

Increased services in 1996 will include publishing the *IS-MPMI Reporter* three times a year, the development of the IS-MPMI home page on the internet, and publication of the full proceedings of the 1996 Knoxville meeting.

With the growth and increased visibility of IS-MPMI, the Board wants to create an image for the society through the development of a logo. Members are invited to share their comments, suggestions and ideas. Please send your thoughts and concepts by January 15, 1996, to IS-MPMI headquarters, attention Corie Dacus. It is anticipated that this logo will be introduced at the Knoxville meeting.

Update on the Eighth International Molecular Plant-Microbe Interactions Congress

Registration materials were mailed the first week of November. If you have not received them by the end of November, contact: UT Conferences, The University of Tennessee, P.O. Box 2648, Knoxville, TN 37901 USA
Phone: 615/974-0250, Fax: 615/974-0264,

E-Mail: UTCconferences@gateway.ce.utk.edu

WWW: <http://www.ce.utk.edu/departments/conferences/confhome.html>

IS-MPMI *Reflector* Links Members Via E-Mail

IS-MPMI maintains an electronic mail reflector that can be used to announce positions available or discuss topics within molecular plant-microbe interactions. The *Reflector* is currently maintained by Kent Peters at the University of Tromsø, Norway.

To be added to the reflector simply send a message requesting to be added to: ISMPMI-request@ibg.uit.no. In your message, please include your institutional address and phone numbers for our database.

If you wish to have your name removed from the *Reflector*, send the appropriate message to the same address as above.

To post a message to all participants of the Reflector, send your message to ISMPMI@ibg.uit.no

If you receive a message from the *Reflector* and wish to send a response to the individual who posted the message, simply use the respond function within your electronic mail program. If you wish to send a response to everyone, then you must send a new message to the *Reflector* at ISMPMI@ibg.uit.no

Kent Peters

Department of Plant Physiology and Microbiology

Institute for Biology and Geology

University of Tromsø

N-9037 Tromsø, Norway

E-mail: kent@ibg.uit.no

Phone: +47 77 64 63 24

Fax: +47 77 65 00 00

IS-MPMI Is On The Internet !

The IS-MPMI*net* home page is up and running and can be reached at:

<http://www.scisoc.org/ismpmi>

IS-MPMI*net* currently contains updates on meetings, *MPMI* information (including titles of recently accepted articles) and the *IS-MPMI Reporter* newsletter. The on-line databases listed in this issue of *IS-MPMI Reporter* can be accessed via links on the Internet. Future plans call for more elaborate services like on-line discussion groups, full text of *MPMI*, electronic meeting abstract submissions, access to all previously published articles, job bulletin board and on-line membership renewal.

Plant Genome Databases

A new resource for your research on plant-microbe interactions

Thanks to the financial support of the United States Department of Agriculture and the Ministry of Agriculture, Forestry, and Fisheries of Japan, genome databases for many tree and plant species now exist. These databases are accessible through the internet or by CD-ROM and provide up to date information about genome organization (genetic maps, contig maps), mapping probes, QTL traits, genomic DNA and cDNA libraries, cloned genes and DNA sequences, metabolic pathways, proteins such as nodulins, germplasm and pedigrees, plant diseases, investigators' names and addresses, and literature references. The following pages review the currently available plant genome databases and how to find them on the internet. Similar databases are being planned and developed for microorganisms such as the rice blast fungus *Magnaporthe grisea*. These databases will be reviewed in an upcoming issue of the *Reporter*. If you know of such databases, please relay this information to Sally Leong.

- [Agricultural Genome Information Server \(AGIS\)](#)
 - [Arabidopsis thaliana Database \(AtDB\)](#)
 - [CottonDB](#)
 - [Dendrome Project Databases](#)
 - [GrainGenes](#)
 - [MaizeDB](#)
 - [RiceGenes](#)
 - [SolGenes](#)
 - [SorghumDB](#)
 - [Soybase](#)
-

Agricultural Genome Information Server (AGIS)

Description

The Agricultural Genome Information Server (AGIS) provides genome databases of agriculturally important plant and animal (Sept. 1995) species, and model organisms. The plant species include alfalfa, Arabidopsis, common bean and soybean, Chlamydomonas, cotton, small grains (wheat, barley, rye, etc.), maize, rice, tomato, potato, pepper, sorghum, and forest trees. Also included is Mendel, the database from the Commission on Plant Gene Nomenclature.

The WWW versions of the databases are provided in ACEDB format and are browsable via hypertext links. They are also searchable via WAIS, fuzzy searching (agrep), and querying through ACEDB (query by example, query builder, and ACEDB query language).

The databases are characterized by links to external databases, including EMBL, Enzyme Data Bank, Genbank, Genbase, GRIN (Germplasm Resources Information Network), Kyoto Ligand Database, Medline, PDB (Protein Database), PIR (Protein Information Resource), Prosite, Rebase, Selkov Enzyme and Metabolic Pathways, and SwissProt, and tools are provided to enhance and augment external connections.

Documentation on the server includes a full suite of ACEDB documentation, electronic newsletters, journals, and other publications including: Plant Genome meeting abstracts, *Weeds World*, the *Rice Genetics Newsletter*, *Report of the Tomato Genetic Cooperative*, and the announcement for the new peer-reviewed electronic

journal, *The Journal of Quantitative Trait Loci*.

As a novel extension of ACEDB for non-genome databases, several plant databases are provided, including PhytochemDB (plant phytochemicals), EthnobotDB (world wide plant uses), FoodplantDB (Native American food plants), MPNADB (Medicinal Plants of Native America), and PVP (Plant Variety Protection - soybean subset).

The AGIS is a service provided by the U.S. Department of Agriculture's National Agricultural Library in Beltsville, Maryland, USA. Funding is provided through the USDA, Agricultural Research Service, National Genetic Resources Program.

Access

The AGIS is located at WWW <http://probe.nalusda.gov/>

NOTE: If you do not have a WWW browser, but have telnet capability, use the lynx, text-based browser.

Telnet to probe.nalusda.gov and use the login "lynx" (no quotes). No password is necessary. You MUST use vt100 terminal emulation in order to use lynx. Also, lynx has been modified so you can only browse the AGIS along with a few related servers:Gopher: probe.nalusda.govAnonymous ftp: probe.nalusda.gov

For More Information

Send comments to: feedback@probe.nalusda.gov

Send requests for help to: help@probe.nalusda.gov

Genome Informatics Group

USDA, National Agricultural Library10301 Baltimore Blvd.Beltsville, MD 20705

Arabidopsis thaliana Database (AtDB)

The AtDB Project at Stanford

AAtDB (An Arabidopsis thaliana Database) and associated WWW, Gopher and ftp resources have recently been transferred from MGH/Harvard to Stanford.

With this move comes a change in title and its meaning. The AAtDB name, which in the past has represented the name of the formal database, will not be used. The Stanford effort will be known as the Arabidopsis thaliana Database Project or AtDB (one A). The name AtDB will be used for all aspects of the Stanford effort including a formal database, WWW and Gopher search facilities to Arabidopsis literature and electronic manuals, plus a variety of future analysis-resources. The AtDB name is thus not just a database, but a collection of information and analytical resources maintained by the Stanford project.

A small proportion of the NSF-funded project is to maintain and distribute the information previously collected by the AAtDB group in Boston. This includes the following.

Description of AAtDB

The latest version of AAtDB is available for UNIX and Macintosh operating systems. To get your own copy of the software, connect via either ftp or WWW to genome-ftp.stanford.edu. Other sites are listed below. The information is also available through the Internet using the Gopher and WAIS software clients.

Special features of the latest release include:

- Updated Chromosome Maps with the new Recombinant Inbred Maps from Clare Lister and Caroline Dean.
- Updated Contact information from nearly 200 people on the Arabidopsis BioSci e-mail news list.
- yUP Hybridization data from the ATGC web server.
- CAPS markers from Drenkard and Ausubel are now included.
- Sequence updates from GenBank including over 4000 new EST entries.
- New bibliographic information from Agricola and Medline

Numbers of Objects in selected Classes for version 3-6:

Map 31
 Allele 1334
 Author 5981
 Clone 23168
 Contact 1447
 DNA-Resource 2869
 Gene-Class 244
 Gene-Product 830
 Germplasm-Resource 3520
 Image 819
 Journal 411
 Locus 1988
 Map-Population 26
 Motif 349
 Paper 4441
 Probe 528
 Sequence 41755
 Sequence-EST 18277
 Sequence-Homol 20780
 Sequence-Genomic+ 2665
 Source 61
 2-point-data 4877

AAtDB features a wide variety of public information that is presented using graphical, text, and tabular formats. The user interface, which was designed to invite browsing, allows users to explore information by pointing and clicking with the workstation mouse or by using a versatile query facility. This UNIX release of AAtDB runs using the ACEDB 3.0 software. ACEDB allows all parts of the database to be cross-referenced with each other. The large number of interconnections provides a dense navigable network in which information can be located from many different starting points.

All information contained within AAtDB was obtained directly from the original authors or from publicly available collections and databases. Updates to AAtDB are made periodically, the current version of the database is 3-6. The next update should be early this year (1996).

The database features:

- The Hauge/Goodman cosmid physical map including greater than 14,000 cosmid clones. The contigs of

the physical map are associated with the genetic maps.

- Genetic markers, including CAPS, RFLP, RAPD, and "classical" visible markers.
- Genetic maps, including an update to the RI map of Lister and Dean (1993) *The Plant Journal*, the Integrated map from Hauge et al. (1993) *The Plant Journal*. The "Classical" marker map from Koornneef (1994) in; Arabidopsis, Meyerowitz and Somerville editors, Cold Spring Harbor Labs, publisher.
- Primary F2 and RI population recombination data from the Goodman, Meyerowitz, Scolnik, and Dean laboratories.
- Primary 2-point data from M. Koornneef, D. Meinke, and others.
- Stock lists, maintained and entered for AAtDB by Mary Anderson at the Nottingham Arabidopsis Stock Centre.
- List of Arabidopsis researchers, including postal mail address, telephone and FAX numbers, electronic mail address, publications, research interests, and research associates.
- All Arabidopsis DNA sequences from GenBank and EMBL DNA sequence databases (GenBank version 89, June 1995) - NCBI BLASTX (six frame translations searched against the NCBI non-redundant peptide database) defined peptide sequence homologies for all DNA sequences included in AAtDB.
- Phenotype descriptions from the Green Book by Meyerowitz and Pruitt, updated with descriptions from the Nottingham and Ohio State stock centers.
- Scanned images of RFLP autoradiograms from the Goodman lab, photographs of mutant plants from G. Redei and M. Anderson, and ethidium bromide-stained restriction enzyme digests of RFLP probes distributed by the ABRC.
- Bibliographic citations, including references for all articles from the Arabidopsis Information Service.

AAtDB uses the ACEDB software developed by Richard Durbin (MRC-LMB, Cambridge, U.K.) and Jean Thierry-Mieg (CNRS, Montpellier, France). Precompiled executables of ACEDB are available for Sun SPARC (SunOS and Solaris), DEC Alpha, and Silicon Graphics workstations under the X-windows environment. Source code is available for compilation with other computer architectures.

All the AAtDB information in text form is available from AtDB the *Arabidopsis thaliana* Database, at Stanford. The images obtained from the ABRC at Ohio State University and the Nottingham Arabidopsis Stock Centre (NASC) are available as via Gopher and anonymous ftp from the hosts genome-ftp.stanford.edu and genome-gopher.stanford.edu.

Connecting via the Web

The AtDB is also connected to the World Wide Web. The URL is

<http://genome-www.stanford.edu/>.

If you are unfamiliar with ACEDB software, there is a revised version of the primer "An Introduction to ACEDB for AAtDB, which is available through the Web server (URL=<http://genome-www.stanford.edu/Arabidopsis/introaatdb/>). This manual is approximately 20 pages of text and graphics which briefly describes the data and how to use the database.

How to obtain the Unix version of AAtDB:

UNIX files are available via anonymous FTP from three sites. Note the new UK site at the European Bioinformatics Institute, the URLs are:

<ftp://ftp.ebi.ac.uk/pub/databases/ace/aatdb>

<ftp://ncbi.nlm.nih.gov/repository/aatdb/aatdb.3x>

<ftp://genome-ftp.stanford.edu/arabidopsis/aatdb/aatdb.3x>

Detailed information about how to retrieve the Unix update information is included in the file [AAtDB.Retrieval_Installation_ver_3-6](#) available via anonymous ftp on the AAtDB server (genome-ftp.stanford.edu, in the /arabidopsis/aatdb/aatdb.3x directory) . You will need to obtain the INSTALL script, the compressed binary for your machine and the update files. currently we have binaries for Sun Sparc running Sun OS or Solaris, DEC mips and alpha and SGI. You will need approximately 400 Mb of disk space to load and install, approximately 310 Mb final if you download all the image files.

How to obtain the Macintosh version:

Macintosh files are available from;

<ftp://ncbi.nlm.nih.gov/repository/aatdb/MacAAtDB>

<ftp://genome-ftp.stanford.edu/arabidopsis/aatdb/MacAAtDB>

To install the Macintosh version you need only retrieve the file MacAAtDB.sea.bin (using binary mode if you are retrieving with ftp). On the anonymous ftp server, the file is in /arabidopsis/aatdb/MacAAtDB. Double clicking on the file should launch the extraction process. Two version are available; one with EST sequences and homology data, and one without. The 'full' version requires 142,456 kb of disk space and the 'demo' version requires 52,587 kb of disk space. Neither version has the entire set of Stock Center images due to space limitations.

This is the first AtDB update from David Flanders and Mike Cherry, Dept. of Genetics, School of Medicine, Stanford University, Stanford, CA 94025.

Thanks to those that have submitted information, and especially to the previous keepers of AAtDB: John W. Morris and Howard M. Goodman, MGH/Harvard.

Please send all correspondence regarding AtDB to: atdb-curator

CottonDB

Description

CottonDB was recently constructed under a project sponsored by the United States Department of Agriculture (USDA), Agricultural Research Service (ARS) and was released to the National Agricultural Library (NAL) Agricultural Genome WWW Information Site to serve as a resource on the developing knowledge base of Cotton Genetics.

The collection of information to be entered into CottonDB may also be carried out over the World-Wide-Web using form pages at the designated CottonDB Data Collection Site. Forms are available for inputting information about COLLEAGUES, LITERATURE, RESEARCH, and other COMMENTS by accessing the URL: <http://algodon.tamu.edu/>

The RESEARCH form is set-up to speed entry of information about cotton genetics, plant-microbe interactions, metabolic pathways, sequence information and other observations.

Presently, CottonDB (version 95.1) is based on ACeDB version 3.0 (Richard Durbin and Jean Thierry-Mieg, MRC LMB Cambridge, England and CNRS, Montpellier, France, respectively) with modifications to AGsDB

1.0 (Leland Ellis, Chris Floyd, Janis Bender and Jeff Kirk, IBT TAMU, Houston, TX). Other plant genome databases were used as models in setting up some of the data entries.

At present, CottonDB ver. 95.1 (10 January 1995) contains:

Colleagues: 1150 names and addresses of cotton- associated people
Papers: 7208 Cotton-related Agricola and direct-entry literature
Pathology: 284 Biotic and abiotic factors associated with cotton
Trait Scores: 22380 Germplasm yield, fiber, and seed data (detailed)
Collection: 613 Germplasm Resource Information Network (GRIN) entries
Authors: 8265 Authors associated with Paper entries
Loci: 962 Observed and molecular markers
Sequence: 73 Cotton-associated sequences from GenBank and others
Journal: 805 Journal headings
Trait Study: 1029 Traits associated with GRIN entries
Map: 98 Maps for observed and molecular markers

A revised version of CottonDB is planned using ACeDB version 4.0. This revised release will contain updated information about molecular markers, germplasm collections, species descriptions, nucleic acid sequences, and literature. It is hopeful that usage of the CottonDB Data Collection Site will speed access and availability of up-to-date research information. A short description of the CottonDB 95.1 database is available at:

<http://algodon.tamu.edu/homepage/lazo/docs/acedb95.html>

Access

CottonDB is accessible over the World-Wide-Web at the URL: <http://probe.nalusda.gov:8300/index.html>

For More Information

Contact, Gerard R. Lazo, Research Geneticist & Curator lazo@tamu.edu

Sridhar Madhavan, Graduate Research Assistant & Curator msridhar@tamu.edu

Russell J. Kohel, Director & Research Leader rjk0339@acs.tamu.edu

USDA ARS

Southern Crops Research Laboratory

2765 F&B Road, Building #11

College Station, TX 77845-9593

Phone: 409/260-9311

Fax: 409/260-9333

Dendrome Project Databases

Description

The Dendrome project is based at the Institute of Forest Genetics of the USDA Forest Service Pacific Southwest Research Station, in Placerville and Albany California. The project aims to provide a central electronic resource for the study of the molecular biology of forest trees. Funding for the project comes from the USDA Plant Genome Research Program and the USDA Forest Service.

TreeGenes is a repository of genetic maps and associated information about species, germplasm, laboratories, researchers, probes, protocols, loci, DNA sequences, publications and more. It employs the ACEDB database software. The entire database is available for anonymous ftp, and a variety of access mechanisms are available through the World-Wide Web.

Over 2000 images of autoradiograms, rangemaps, and species are included. The project maintains the ACEDB Frequently Asked Questions documentation.

The *Dendrome Forest Tree Research Updates* is published twice per year and includes short articles concerning tree molecular biology. All issues can be accessed via WWW or Gopher. Researchers can be included on the mailing list by sending e-mail or surface mail to the project.

A variety of detailed laboratory protocols related to tree molecular biology research are available. Expressed sequence data and gene family identities and information about commercially available 10-mers for PCR are included.

A Calendar of upcoming events is provided and a searchable bibliography is available on the Gopher server.

In coordination with F. Thomas Ledig, Dendrome has updated the IUFRO World Directory of Forest Geneticists and Tree Breeders. This directory can be searched via WWW. A paper edition is planned. About 2000 researchers have contributed biographical and research interest data to the collection.

The California Flora Database contains geographic and ecological distribution information for 6717 California vascular plant taxa, as well as additional habitat information for rare taxa and species of the Sierra Nevada. The entire database is available for anonymous ftp or can be searched via WWW.

Access

The project coordinates data with the Agricultural Genome Information Server at the National Agricultural Library, Beltsville Maryland. All services of the Dendrome project can be explored via the World-Wide Web at URL: <http://s27w007.pswfs.gov/>

We also maintain Gopher servers at s27w007.pswfs.gov port 70 and at probe.nalusda.gov port 7508

For More Information

Email can be sent to dendrome@s27w007.pswfs.gov Surface mail to Dendrome, Institute of Forest Genetics, PO Box 245, Berkeley, CA, 94701, USA.

GrainGenes

Description

GrainGenes is a central repository for information about wheat, barley, rye, triticale, oats, sugarcane and related wild grasses. GrainGenes includes genetic and cytogenetic maps; information on mapping probes (including nucleotide sequences and digitized images of mapping data); information on genes, alleles and gene products; genotypes and pedigrees of cultivars, genetic stocks, and other germplasms; information on phenotypes, quantitative traits and QTLs; images depicting plant morphology and pathology; addresses and research interests of colleagues; and relevant bibliographical citations.

Access

GrainGenes is currently available in two formats (ACEDB and Gopher) and a Web Server Home Page is under development.

ACEDB format:

Graphical user interface format; multi-windowed, mouse-controlled environment with both graphic and text displays. Connections are made between related pieces of information by clicking on data objects with a mouse. The ACEDB format allows users to perform sophisticated queries of the database and is available to users with direct TCP/IP Internet connections and X11 graphics capability (Unix workstations or most personal computers with inexpensive software).

Gopher format:

Text interface format; menu-driven, displays all information as text and contains tabular data and text documents not available in the ACEDB format, some of which can be searched, downloaded or browsed. This format allows for fast searching by any word in the text and can be accessed with a modem connection to an Internet host. There is enhanced capability to download and view images.

The GrainGenes Gopher at greengenes.cit.cornell.edu contains the latest version of the GrainGenes ACEDB dataset in searchable form as well as a variety of information about wheat, barley, oats, and sugarcane in simple text or tabulated formats. Many of the files can be browsed, searched or downloaded to your own computer.

A sampling of the data offered as of June 1994 follows:

Search the following files by any word in the text:

- The latest (often unreleased) version of the GrainGenes ACEDB dataset
- The Catalogue of Gene Symbols for Wheat
- Annual Wheat Newsletters from 1991, 1992, 1993 and 1994
- Quality evaluation data for many wheat cultivars including flour, dough, baking and milling characteristics
- HMW glutenin subunit composition data for 1800 wheat cultivars
- Compendium of 1,600 US commercial wheat cultivars, including growth habits, market classes, pedigrees, and registration information

Browse the following data files:

- Maps and mapping data from *T. tauschii*, barley (Steptoe x Morex, Harrington x TR306, Proctor x Nudinka, Vada x *H. spontaneum*), diploid oats, and sugarcane
- Barley QTL studies (Steptoe x Morex)
- Standard karyotype and nomenclature for chromosome bands in Chinese Spring wheat
- Nomenclature guidelines for wheat DNA markers and QTLs
- Descriptions of wheat aneuploid types
- Cereal Rust Bulletins

Download the following data to your own computer:

- Names, abbreviations, and origins for 8,700 wheat and triticale cultivars from CIMMYT
- The Catalogue of Gene Symbols for Wheat, 1993 edition

- Digitized images of hybridization patterns of more than 130 mapping probes
- Wheat quality evaluation data for many wheat cultivars
- More than 450 digitized images of disease symptoms
- Results of wheat variety trials from different locations

The GrainGenes ACEDB Database:

Version 1.4 of the GrainGenes ACEDB Database, a central repository for information on wheat, barley, oats, sugarcane, and other small grains, was released on October 28, 1994 and contains 22 maps and 163 mapped linkage groups; more than 3,300 loci and 600 genes; more than 2,400 probes with nucleotide sequences from the ends of 100 probes; information about 22,000 wheat, rye and triticales germplasms; information about 1400 plant, pathogen, and insect species; 14,000 trait scores from the International Spring Wheat Yield Nursery Trials; 450 pathology entries, many with digitized images of disease symptoms; names, addresses and research interests of more than 950 colleagues and more than 1,400 references.

For More Information

David E. Matthews (curator)

Dept. of Plant Breeding and Biometry

Cornell University

Ithaca, NY 14853

Phone: (607) 255-9951

E-mail: matthews@greengenes.cit.cornell.edu

Olin D. Anderson (coordinator)

USDA-ARS-WRRC

800 Buchanan Street

Albany, CA 94710

E-mail: oandersn@wheat.pw.usda.gov

MaizeDB

Description

The Maize Genome Database or MaizeDB provides free, up-to-the-minute information about the maize genome and is a component of the Plant Genome Database network of the National Agricultural Library. Over the past 1.5 years, use of the database has grown from 100-200 transactions/month to some 20,000. Information input and database design are a cooperative on-line effort of several persons, both on and off-site.

In June 1995, the database contained over 104,000 records describing 3059 mapped genes and gene candidates, 19821 genetic variations (including allozyme typing for 21 loci and 437 elite stocks), 2465 molecular probes, 240 genetic maps, 2966 raw map data entries, 33 QTL experiments (a new area this year), 1985 genetic/cytogenetic stocks, 4662 elite stock pedigrees, 2430 addresses of research workers, and 6700 bibliographic references which increase by over 800 annually and are connected with the other database objects, including agronomic traits such as pest and disease responses.

Individual MaizeDB records are hard-linked over the World Wide Web to 18 external databases, permitting seamless retrieval of nucleotide and protein sequences, motifs, germplasm, related genes and/or sequences of

other species and certain full journal articles.

Access

To connect, use any computer with a connection to the Internet, including by modem.

Telnet to: [teosinte.agron.missouri.edu](telnet://teosinte.agron.missouri.edu)

(For Web, gopher, or direct access to relational query forms.)

a. login: guest

b. password: corncob

If using your own Web or gopher software, connect to: <http://www.agron.missouri.edu> or [gopher.agron.missouri.edu](gopher://teosinte.agron.missouri.edu), respectively.

For More Information

For assistance or any comments, please contact the curator: Dr. Mary Polacco, aryp@teosinte.agron.missouri.edu Fax: 314/ 874-4063.

RiceGenes

Description

RiceGenes is an internationally accessible computer database containing a wide variety of information pertaining to rice genetics. It is organized around the basic concept of a genetic map, with markers on the map providing "hot links" to related pieces of information such as marker sequences, vectors, homology to known genes, and map locations in other species. The links allow the researcher to move seamlessly among related items of interest.

The database currently consists of information on over 3,000 DNA markers (including a contact person for acquiring probes or additional information); 5 genetic maps of rice (including the classical morphological linkage map and molecular maps developed at Cornell, in Tsukuba, Japan, and in Beijing, China); a genetic map of maize; relevant bibliographic citations; digitized images of autoradiograms; disease symptoms; and plant morphologies; and over 1,300 DNA sequences.

The database also includes RFLP profiles of rice germplasm, information about genetic stocks, and sequence information related to markers or known genes of rice. Detailed comparisons between the maize and rice maps have also been included. In collaboration with other groups we hope to develop interrelated genome databases for important pests and pathogens of rice, such as blast and bacterial blight.

Access

RiceGenes is accessible via the Internet in 4 forms. The easiest form is at a Gopher server. The Gopher interface is menu-driven and can be used with only a modem connection to an Internet host. The first 9 volumes of the Rice Genetics Newsletter are currently available as text documents on the Gopher server. Preindexed for fast searching on any word in the text, the Gopher versions of such documents are expected to be more useful to a wider group of people than printed versions.

The second format is a graphical user interface based on the ACEDB software, available to users with direct TCP/IP network connections and X11 graphics capability (most UNIX workstations, or personal computers

with inexpensive software). The ACEDB format provides live graphics, photographic images, and text displays, with hot links between data objects that can be activated by clicking with the mouse.

The third format is a World Wide Web server, maintained by the USDA/NAL. This is also a graphical inter-face and provides the capability of hot links between, in addition to within, databases.

The final format is an electronic mail query capability, for users who do not have full Internet access, but do have Internet mail service.

For non-Internet sites, the U.S. National Agricultural Library has made available a CD-ROM which contains all the USDA-funded genome databases (rice, maize, wheat and other small grains, arabidopsis, and many more).

Access points:

ACEDB version - UNIX version available via anonymous ftp from: probe.nalusda.gov directory /pub/rice

WWW version - URL <http://probe.nalusda.gov:8000>

Gopher version - gopher nightshade.cit.cornell.edu port 70

WAISmail - send mail to waismai@probe.nalusda.gov with just the word help in the body.

For More Information

Eddie Paul (curator)

Dept. of Plant Pathology & Biochemistry

Cornell University

Ithaca, NY 14853

Phone: 607/255-9951

E-mail: epaul@nightshade.cit.cornell.edu

Susan McCouch (PI)

Dept. of Plant Pathology & Biochemistry

Cornell University

Ithaca, NY 14853

Phone: 607/255-0420

E-mail: srm4@cornell.edu

SolGenes

Description

SolGenes is one of three plant genome databases, based on the ACeDB software and funded by the USDA's Plant Genome Project, that are maintained at Cornell University. The scope of SolGenes is the solanaceous crop species - presently including tomato (*Lycopersicon* spp.) potato (*Solanum* spp.), and pepper (*Capsicum* spp.) - and their wild relatives.

Genomic research data from other *Solanum* species (such as *S. melongena*, eggplant) and other genera in the family (*Datura*, *Petunia*, and *Nicotiana* for example) are also invited. The core of SolGenes consists of genetic maps, displayed in ways that allow ready cross-referencing. Presently available are various tomato, potato, and pepper RFLP maps constructed at Cornell and elsewhere; others are being added.

Users may search a catalog of more than 3000 tomato genetic stocks (mutants, chromosome testers, sources of named resistance genes, etc.), maintained at the Tomato Genetic Resources Center (TGRC) in Davis, CA by R. Chetelat. A recently developed set of 50 *L. pennellii* single-segment introgressions into a *L. esculentum* background, characterized with some 350 RFLP and isozyme markers and available from the TGRC, is shown graphically on the genome maps. There is ample scope for developing SolGenes as a tool for research into plant-microbe interactions; we haven't pursued this prospect yet but invite discussion.

Entries are cross-referenced against a background of literature citations (130), a colleague directory (541), and catalogs of probes (1000), loci (2000), and restriction enzymes (340).

Access

The entire database may be obtained via anonymous ftp from [probe.nalusda.gov/pub/solgenes](ftp://probe.nalusda.gov/pub/solgenes), if you wish to set it up on a local (typically Unix-based) computer. There is also a Macintosh version of ACeDB called MacAce, but the SolGenes data are not yet available on this platform. You can access SolGenes via a text interface through either of these Gopher servers: [nightshade.cit.cornell.edu](gopher://nightshade.cit.cornell.edu) port 71 or [probe.nalusda.gov](gopher://probe.nalusda.gov) port 7006

The text-based ways of accessing the database don't offer the graphical displays available with a version running locally, although data and images are retrievable. An X-window emulator program running on your local PC or Macintosh (MacX for example) will provide, via remote logon, the full range of graphical displays built into ACeDB databases. Another route is via Netscape or the World Wide Web URL: <http://probe.nalusda.gov:8300>

For More Information

Messages may be sent to other SolGenes users at solfolk@nightshade.cit.cornell.edu To be placed on this mailing list or to obtain further information about SolGenes, write the curator (Clare Nelson) at jcn5@cornell.edu or cnelson@nightshade.cit.cornell.edu

Several scientists in the U. S. and Europe have agreed to serve on an informal steering committee for SolGenes and can assist as liaisons with Solanaceae workers. They are: for potato, Herman van Eck, Wageningen, Netherlands Herman.vanEck@users.pv.wau.nl for pepper, Molly Kyle, Cornell mmk9@cornell.edu and Paul Bosland, New Mexico State pbosland@nmsu.edu for tomato, Pim Lindhout, Wageningen Pim.Lindhout@users.pv.wau.nl, Roger Chetelat, UC Davis chetelat@vegmail.ucdavis.edu and Martin Ganai, Inst. f=FCr Pflanzengenetik, Gatersleben, Germany, Fax: 49-39482-280.

SorghumDB

Description

SorghumDB is a joint project of USDA National Agricultural Library and Texas A&M University. This is a part of the Genome Database Project of NAL. It is curated by Najeeb Siddiqui under the supervision of Dr. Keith Schertz at Texas A&M University and supported by a whole group of scientists with interests in sorghum breeding, pathology, physiology, genetics, etc. Sorghum Genome Database Project was started June 1994. Since then, an experimental version of SorghumDB was released in January, 1995 and a complete version 1.0 was released in May, 1995. Version 1.1 is expected to be released by the end of August, 1995.

SorghumDB contains a wide variety of information on topics such as genetic maps, germplasm, gene loci, alleles, pathology/pathogens, taxonomy, multi-maps (sorghum vs. maize), etc. It is also a good source of reference

information for papers published in any research area of sorghum, and for the most updated information on colleagues working in sorghum research.

We have tried our best to include as much text information as possible on topics like germplasm, traits, pathology, and taxonomy with complete references to the source of the data. Included are all 108 RFLP maps of sorghum linkage groups and 12 multi-maps between sorghum and maize; a description of maturity alleles; a detailed description of all sorghum cultivar, germplasm, parental lines, genetic stocks, and converted lines; information on gene loci and RFLP probes; a description of sorghum diseases and sorghum pathogens; hierarchical description of sorghum taxonomy; reference information on approximately 11,000 authors and more than 10,000 published papers in various areas of sorghum reasearch, representing about 1,400 different journals and books.

We have more information on the existing classes of the database that will be incorporated and we also have some new classes in our plans which will be included in the future versions of the database.

Access

SorghumDB can be accessed from the ACEDB Moulon Server at NAL by connecting to <http://probe.nalusda.gov:8300/>

ACEDB 3.0 format of SorghumDB is available by anonymous ftp from the National Agricultural Library at probe.nalusda.gov in the pub/sorghumdb directory. It requires a UNIX machine.

To download the database, type at the prompt:

- a. ftp probe.nalusda.gov
 - b. anonymous
 - c. your e-mail address
 - d. binary
 - e. cd pub/sorghumdb
 - f. get sorghum-june-95.tar.Z
- (Login ID is anonymous and Password is your e-mail address)

After the transfer is complete, type bye to quit the session.

For More Information

Contact:Najeeb Siddiqui
Sorghum Genome Database Curator
Crop Biotechnology Center
Texas A&M University
College Station, TX 77843-2123
Phone: (409) 862-1523
Fax: (409) 862-4790
E-mail: najeeb@genome.tamu.edu or nus6389@tam2000.tamu.edu

Soybase

Description

Soybase is an ACe-type genetic database with hypertext links between topics. It currently contains approximately 100 megabytes of data including, but not limited to:

- the classical genetic map of soybean and four molecular marker maps,
- QTL studies on more than 30 traits,
- pedigree and phenotypic data for germplasm isolates,
- diagrams of selected metabolic pathways,
- information on approximately 15 diseases of soybean,
- data on 37 nodulins, and
- pertinent literature references.

Genetic Maps

The classical gene map contains 29 linkage groups and the underlying 2 point linkage data is in the database. The four molecular maps represent independent mapping populations with significant overlap between the markers used. Images of autoradiograms are available which indicate the exact DNA fragment that was used to place an RFLP marker on a map. Related information about genes, alleles, and molecular probes is available via hypertext links from the map diagrams.

QTL Studies

For each QTL study there are data on the trait evaluated, the population used and the associations between the phenotypic traits and the molecular markers. A hypertext link is available between these linked loci and the genetic map diagrams.

Metabolic Pathways

There are diagrams covering forty-one pathways for nitrogen and fatty acid synthesis and degradation. For each pathway, information is available for the enzymes, reactants, products, and cofactors involved along with the data on the kinetics, inhibition, activation, and regulation of the enzymatic steps. More than 200 individual enzymes are detailed.

Pathology and Diseases

Fifteen soybean diseases are covered in Soybase, including data on the causative organism, differentials and phenotypic scores, and the genetics of resistance.

Nodulins

Soybase currently includes information on 37 nodulins. Examples of the data available are the nature of the gene product encoded by the nodulin gene and its function, the host and inducing species, and information on the genetics and genome organization of the gene.

References

All references in AGRICOLA that are related to soybean genetics are incorporated into the database. In addition, other peripherally related references such as those for heterologous probes or metabolic data from other species are included.

Access

You can access Soybase in several ways. If you use a Macintosh or PC, options 1 and 3 require that you run an X-windows program on your local computer, as well as a WWW browser or Telnet client.

1. Remote login to our server.
Telnet to [mendel.agron.iastate.edu](telnet://mendel.agron.iastate.edu)
 - a. Login as guest, password soybean.
 - b. Type 'setenv DISPLAY and your IP# and :0' (e.g. setenv DISPLAY 129.142.80.121:0)
 - c. Type 'soybase' to launch the database. The additional command 'xhost +129.186.20.43' may be necessary from some terminals before launching Soybase
 - d. Logout when finished
2. Via the WWW to the National Agriculture Library URL: <http://probe.nalusda.gov:8300>
3. Via our own WWW connection URL: <http://mendel.agron.iastate.edu:8000/main.html> This access is currently only available when using Mosaic.
4. Through a Gopher Server at the National Agriculture Library [gopher probe.nalusda.gov](gopher://probe.nalusda.gov)

For More Information

Contact:David Grant

USDA-ARS

G 304 Agronomy Hall

Iowa State University

Ames, IA 50011-1010

Phone: 515/294-1205

E-mail: dgrant@mendel.agron.iastate.edu

Randy Shoemaker

USDA-ARS

G 401 Agronomy Hall

Iowa State University

Ames, IA 50011-1010

Phone: 515/294-6233

E-mail: rcsshoe@iastate.edu

Marcia Imsande

G 302 Agronomy Hall

Iowa State University

Ames, IA 50011-1010

Phone: 515/294-1297

E-mail: mimsande@mendel.agron.iastate.edu

Dave Schrader

G 316 Agronomy Hall

Iowa State University

Ames, IA 50011-1010

Phone: 515/294-0421

E-mail: schrader@mendel.agron.iastate.edu

Upcoming Meetings

December 4-6, 1995

The 7th Industrial Biotechnology Conference, Montreal, Quebec, Canada. Contact: Doris Ruest, Phone: 613/993-9228 Fax: 613/957-9828

January 14-18, 1996

Plant Genome IV Conference, San Diego, California, Contact: Darrin Scherago, Scherago Int'l. Inc., 11 Penn Plaza, Suite 1003, New York, NY 10001, Phone: 212/643-1750 Fax: 212/643-1758 e-mail: scherago@biotechnet.com

March 15-21, 1996

Keystone Symposium on "The Extracellular Matrix of Plants: Molecular, Cellular and Developmental Biology", Tamarron, Colorado, US. Contact: Keystone Sympsia, Phone: 303/262-1230 Fax: 303/262-1525

April 18-20, 1996

Mosbach Colloquim: Pathogen defense in animals and plants, Mosbach, Germany. Contact: K. Hahlbroch, MPI f. Zuchtungsforchung, Carl-von-Linne Weg 10, 50829 KOLN, Germany. Fax: 49.221.5062.313

June 11-14, 1996

Agricultural Biotechnology International Conference (ABIC), Saskatoon, Saskatchewan, Canada. Contact: Ag-West Biotech Inc., 230-111 Research Drive, Saskatoon, SK S7N 3R2, Canada. Phone: 306/975-1939 Fax: 306/975-1966
E-mail: agwest@innovplace.saskatoon.sk.ca

June 16-21, 1996

Gordon Research Conference on Cellular and Molecular Mycology, Holderness School, Plymouth, New Hampshire, US. Contact: Dr. Anne Desjardins, Phone: 309/681-6378 Fax: 309/681-6686 e-mail: adesjardins@asrr.arsusda.gov

June 23-28, 1996

11th International Botrytis Symposium, Wageningen, Netherlands. Contact: Dr. Jan van Kan, Wageningen Agricultural Univ., Phone: 31 8370 83126 Fax: 31 8370 83412 e-mail: jan.vankan@medew.fyto.wau.nl

July 14-19, 1996

Eighth International Molecular Plant-Microbe Interactions Congress, Knoxville, Contact: UT Conferences, The University of Tennessee, P.O. Box 2648, Knoxville, TN 37901 USA Phone: 615/974-0250, Fax: 615/974-0264, E-Mail: UTConferences@gateway.ce.utk.edu
WWW: <http://www.ce.utk.edu/departments/conferences/confhome.html>

July 27-31, 1996

American Phytopathological Society Annual Meeting, Indianapolis, Indiana, US. Contact: Deb Merritt, Phone: (651) 454-7250 Fax: (651) 454-0766 E-mail: aps@scisoc.org
WWW: <http://www.scisoc.org>

July 30-August 8, 1996

5th International Oat Conference and 7th International Barley Genetics, Univ. of Saskatchewan, Saskatoon, Saskatchewan, Canada. Contact: C. Ouellet, Univ. of Saskatchewan, Fax: 306/966-5015

September 12-15, 1996

Fallen Leaf Lake Conference on Horizontal Gene Transfer: Implications and Consequences, Leaf Lake, South Lake Tahoe, California, US. Contact: Michael Syvanen, Dept. of Microbiology & Immunology, Univ. of California, Davis, CA 95616. E-mail: msyvanen@ucdavis.edu

If you have a meeting you would like to list here, please send the information to:

Corie Dacus
IS-MPMI
3340 Pilot Knob Road
St. Paul, MN 55121-2097
Phone: (651) 454-7250
Fax: (651) 454-0766
E-Mail: corie@scisoc.org

A Note From The Editors

Story Idea?

What would you like to see included in the *IS-MPMI Reporter*? We invite you to submit ideas for articles and stories for the *Reporter*. Below is the 1996 editorial calendar for IS-MPMI indicating the deadline for article submissions to each issue.

You can forward your article to either one of us or to Corie Dacus at IS-MPMI headquarters.

Spring Issue
Articles due: March 1
Mail date: March 29

Summer Issue (includes member directory and post meeting highlights)
Articles due: August 1
Mail date: August 30

Fall/Winter Issue
Articles due: December 1
Mail due: December 30

Sincerely,

Sally Leong
Co-Editor
USDA ARS
Plant Disease Unit
Madison, Wisconsin
USA
Phone: 608/262-5309

Fax: 608/262-1541

E-Mail: sal@plantpath.wisc.edu

Ulla Bonas

Co-Editor

CNRS Institut de Sciences Vegetales

Gif-sur-Yvette

FRANCE

Phone: 33-169-823-612

Fax: 33-169-823-695

E-Mail: bonas@trefle.isv.cnrs-gif.fr

IS-MPMI Officers

President

Eugene W. Nester

Dept. of Microbiology, SC-42

University of Washington

Seattle, WA 98195 USA

Phone: 206-543-0255

Fax: 206-543-8297

E-mail: jhalsey@u.washington.edu

President Elect

Barry G. Rolfe

Australian National University

Biological Sciences

GPO Box 475

Canberra ACT 2601

Australia

Phone: 61-6-249-4054

Fax: 61-6-249-0754

E-mail: rolfe@rsbs-central.anu.edu.au

Treasurer

Linda Thomashow

U.S. Dept. of Agriculture - ARS

Washington State University

Pullman, WA 99164-6430 USA

Phone: 509-335-0930

Fax: 509-335-7674

E-mail: thomasho@wsuvm1.csc.wsu.edu

Secretary

Sally Leong
U.S. Dept. of Agriculture - ARS
University of Wisconsin
Madison, WI 53706 USA
Phone: 608-262-5309
Fax: 608-262-1541
E-mail: sal@plantpath.wisc.edu

Business Executive

Steven C. Nelson
3340 Pilot Knob Road
St. Paul, MN 55121 USA
Phone: 612-454-7250
Fax: 612-454-0766
E-mail: snelson@scisoc.org
