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NIH-DOE Award Supports Genome Data Base at Hopkins

In a move to ensure easy worldwide access to accurate information for human genome research, NIH and DOE have awarded the Johns Hopkins University School of Medicine $5.3 million to support the Genome Data Base (GDB). Since it went online in September 1990, GDB has been the main repository for information about the location and description of genes, including disease genes, and other genetic markers on chromosomes.

The new award, said GDB Scientific Director Peter Pearson, "affirms the enormous need for a well-organized informatics component to the Human Genome Project. We see the GDB becoming the fulcrum around which all groups interested in the Human Genome Project can operate to their best advantage."

Announcement of the 3-year award came in a September 19 briefing by NIH and DOE officials and representatives of Hopkins. James D. Watson, Director of the NIH National Center for Human Genome Research, and David J. Galas, Associate Director of the DOE Office of Health and Environmental Research, announced that their agencies were making equal awards, which became effective September 1. Future funding will depend in part on support given by other countries with genome research interests.

Designed at Hopkins' Welch Medical Library Laboratory for Applied Research in Academic Information by a team of software engineers, database experts, and geneticists, GDB collects, organizes, stores, and distributes human gene mapping information. This material, generated and provided by investigators, includes data derived from Human Gene Mapping Workshops (HGMW) since their inception in 1973. An interface allows retrieval by general users, and specialized interfaces permit database editors to make and update entries at any time.

Galas said, "Some day soon scientists. . .will seek information about the functioning of living things from their computer terminals before they approach the laboratory bench. GDB is part of this revolutionary change that is catalyzed by the Human Genome Project."

Yale University supported the first gene mapping database in the mid-1970s, with some support from the NIH National Institute for General Medical Sciences. In 1985 the Gene Mapping Project of the Howard Hughes Medical Institute (HHMI) undertook the further development, management, and online support of the Human Genome

Peter Pearson
Scientific Director
Genome Data Base

Some International Support Sought for Future

In This Issue. . .

GDB Forum

GDB User Support, Services, Registration

Use of GDB is free. New registrants receive the following:

- login and password;
- name, address, and telephone numbers for verification;
- for U.S. users, WelComm software for PC or Macintosh (see SprintNet access, p. 4); and
- documentation (see box on documentation, p. 3).

To facilitate effective database access, GDB provides the following services without charge:

- account set-up,
- user online searching,
- training courses, and
- help-line support.

Registration

To become a registered GDB/OMIM user, contact one of the User Support offices listed below (a user may register to access both Baltimore and a remote site):

United States. GDB/OMIM User Support; William H. Welch Medical Library; 1830 E. Monument Street, Third Floor; Baltimore, MD 21205; 301/955-7058, Fax: 301/955-0054; Internet: "help@welch.jhu.edu". Office hours: 8 a.m. to 5 p.m. EST.

United Kingdom. Christine Bates; Human Gene Mapping Program Resource Center; Clinical Research Centre; Watford Road, Harrow; MIDDX HA1 3UJ, U.K.; (Int.) 44/81-869-3446; Fax: (Int.) 44/81-869-3807; E-mail: "cbates@uk.ac.crc".

Germany. Otto Ritter; Molecular Biophysics Group; German Cancer Research Center; Im Neuenheimer Feld 280; D-6900 Heidelberg 1, FRG; (Int.) 49/6221-42-2372; Fax: (Int.) 49/6221-40-1271; E-mail: "dok261@cvx12.dkfz-heidelberg.de".

Mapping Library at Yale. In 1989 HHMI, already supporting five genome-related databases, collaborated with Hopkins to create GDB. GDB is built on the Sybase relational database system and uses a powerful Sun hardware platform. (A relational database uses mathematical set theory concepts in data modeling.) The database is designed to work in a SprintNet or Internet environment with most personal computers or terminals.

GDB is expected to cost up to $15.9 million over 3 years. The new DOE-NIH award supports operational expenses, further development, and expansion. GDB staff plan to enhance and maintain interlocking database services, including:

- Connection with other major centers to provide a more integrated set of database services to the scientific community.
- Interaction with research laboratories to facilitate the flow of data to GDB.
- Research and development of new and more useful database operations.
- User services, including manuals and staff assistance for scientists.

Some 25 people work full-time on GDB at Hopkins, in addition to editors who review and standardize material to be entered in the information base. Another 12 work full- or part-time on GDB at other sites.

Arranged by cytogenetic band location, GDB entries are organized into the following categories:

- loci (genes, fragile sites, DNA segments, and breakpoints);
- associated symbol; disorder or syndrome name; chromosomal location; Victor McKusick's *Mendelian Inheritance in Man* (MIM) number; polymorphisms; alleles; allele population/frequency; and probes (cloned probes, polymerase chain reaction primers, and allele-specific oligonucleotides).
- sources (journals, books, theses, and personal communications);
- contacts [for probes and users of GDB and the Online Mendelian Inheritance in Man (OMIM™)]; and
- maps (genetic and physical).

Also online are known mouse genes that are homologous to human genes in function or DNA sequence.

Users can define searches for any category and move from one data type to another (see figure, p. 3). For example, moving from the cystic fibrosis gene (CFTR) locus to polymorphisms will display all polymorphisms related to the CFTR locus.

A direct searching link through MIM numbers corresponds to entries in OMIM. Additional cross references to related databases include relevant GenBank® and American *Type Culture* Collection numbers.

OMIM

Gene mapping and sequencing information in GDB will continue to be integrated with clinical genetics data already at Hopkins in OMIM, a catalog of all known human phenotypes, gene locations and functions, and disease effects. OMIM contains information on more than 5500 inherited traits and diseases. Updated daily by McKusick's staff, the database serves both the clinical and laboratory communities by providing data helpful in differential diagnosis, genetic counseling, biochemical defect identification, and linkage studies.

OMIM entries are arranged by clinical disorder or trait name (including MIM number) and may list clinical observations, inheritance patterns, linkage information, allelic variants, chromosomal location, defective gene products, and references.

Searchers can locate relevant information in OMIM and then use the MIM number or chromosomal location for cross-referencing with GDB. A direct searching link through MIM numbers leads to entries in OMIM, and a similar link to GDB is planned.

User Support

GDB/OMIM User Support (see box, p. 2) provides assistance, training, and documentation (see box below) to the scientific community in a number of general interest and technical areas, including registration, access, communication, and scientific/data issues. The staff encourages user feedback to correct errors and identify areas for future enhancement. Details on registration and requirements for accessing the databases are given in the boxes on pp. 2 and 4, respectively.

Training

To meet the needs of GDB users, two training courses will be offered without charge next year in Baltimore to provide comprehensive hands-on experience. A 2-day course for the general scientific user will provide a basic understanding of GDB and OMIM and the relationships among the different data. A 3-day course, to include directions on adding, modifying, and deleting GDB data, is designed for users who have editing privileges. Current and potential users interested in attending a course should contact GDB/OMIM User Support at the Baltimore address (in box on p. 2) as soon as possible so the course schedule can reflect user needs. (See related article in box, p. 6.)

(continued)

GDB User Documentation

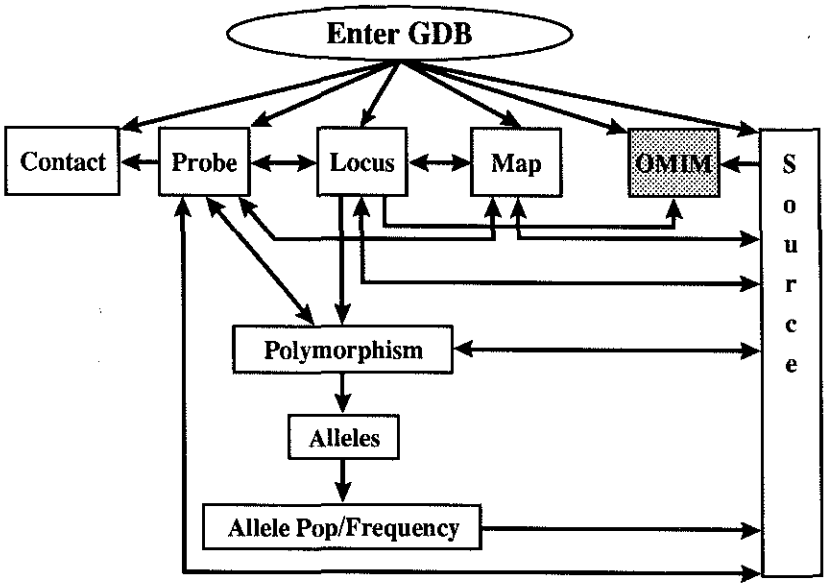
GDB and OMIM Quick Guide (for Version 4.0, July 1991) assists new users with simple searches.

User Guide to GDB and OMIM (September 1990) provides detailed coverage of methods for accessing the computer through SprintNet and Internet and different communications software (WelComm for PC or Macintosh and commercial software packages). GDB descriptions and examples reflect the September 1990 database, and new features are covered in a supplement. A comprehensive guide to searching OMIM is included.

Supplement for GDB Version 4.0 (July 1991) includes cross references to appropriate pages in the User Guide.

GDB and OMIM Quick Card (for Version 4.0, July 1991), a six-panel summary, serves as a quick reference for the novice user with some experience in searching the databases.

All documentation except the **User Guide to GDB and OMIM** is updated with each GDB version, providing new users with up-to-date information. Current users are informed online about new features and may request a set of the latest printed documentation materials from GDB/OMIM User Support in Baltimore. (See user registration box, p. 2.)



GDB data organization. Arrows indicate paths to move from one data type to another.

Submitting Data to GDB

Researchers wishing to submit their data to GDB and receive a D-number assignment for a new segment of anonymous DNA must include the following minimal information on a GDB Submission form:

- probe name;
- vector;
- insertion site;
- cytogenetic localization;
- mode of assignment;
- contact's name, address, and phone number; and
- additional information concerning the significance of the marker (e.g., polymorphism data, physical map, and evidence for expression).

D-segment numbers will be assigned according to the guidelines established in the "Report of the DNA Committee of Human Gene Mapping Workshop 11," (*Cytogenet. and Cell Genet.*, 1991, in press). A copy of the guidelines is available upon request from Michael Chipperfield at the address below.

If a D-segment is polymorphic, a GDB Polymorphism Submission form should be completed, as well as a GDB PCR Submission form if the polymorphism is formatted by polymerase chain reaction. These forms may also be used when submission to GDB is required for journal publication.

All GDB data submission forms are available in both hard-copy and electronic form. Direct inquiries to

- Michael A. Chipperfield; William H. Welch Medical Library; 1830 E. Monument Street, Third Floor; Baltimore, MD 21205; 301/955-0884, Fax: 301/955-0054; Internet: "chipper@welch.jhu.edu".

GDB Forum

GDB Establishes Remote Sites

Online Access to Databases

GDB and OMIM may be accessed online through (1) SprintNet (Telenet) from a modem at 1200, 2400, or 9600 baud or (2) the Internet computer network. Hardware and software requirements for accessing the Welch Library computer are detailed in the box below.

SprintNet Access

WelComm, a free, specially prepared communications program that allows database access to SprintNet via modem for U.S. users, is available on diskette for both the IBM-compatible PC and the Apple Macintosh systems. The WelComm software supports function keys for GDB. Other commercial communications software packages can also be used.

Internet

For database access through Internet, a Sun workstation or other hardware must have a program that allows emulation of a VT100, VT220, or VT320 series terminal. For Sun workstations such a program is crttool, the public-domain package available by anonymous file transfer protocol from general distribution sites such as "titan.rice.edu" or "uunet.uu.net".

Crttool has provided reliable access for some users, but because it is public-domain software, GDB/OMIM staff do not offer technical support and cannot guarantee how it will work with GDB on any specific workstation.

Any software supporting the TCP/IP protocol can also be used for Internet access [e.g., National Center for Supercomputing Applications (NCSA) Telnet].

Worldwide Distribution Sites

Although users worldwide can access the GDB and OMIM databases through either SprintNet (Telenet) or Internet, communication through networks is not always reliable.

To increase database accessibility outside the United States, a series of remote, self-supporting distribution sites (nodes) is being established, the first of which has been providing service to U.K. users since the fall of 1990. The remote site is run by the Medical Research Council, which set up the U.K. Human Gene Mapping Resource Center.

A second remote site, initiated by the European Community at the German Cancer Research Center in Heidelberg, Germany, began providing service to European users in the fall of this year. Other centers are planned in Japan, Australia, and Sweden. Names and addresses of contacts at existing remote sites are listed in the box on p. 2. ◇

Reported by GDB Staff

Accessing GDB and OMIM on the Welch Medical Library Computer

SprintNet Access

Hardware Options

- IBM-compatible PC (at least 512 K of RAM if using WelComm).
- Apple Macintosh (512, XL, 512e, Plus, SE, or II).
- Terminal (at least a VT100; to use GDB function keys, VT220 is required).

Communications Software Options

- WelComm for PC or Macintosh.
- Commercially available communications software.

Modem

- Hayes-compatible if using WelComm software.
- Local SprintNet phone number corresponding to modem speed is available from SprintNet customer service (800/336-0437).

The SprintNet address of the Welch Library computer is 30155030.

Internet Access

Hardware and Communications Options

- Terminal, PC, Macintosh computer, or Sun workstation with terminal emulation capabilities of VT100, VT220, or VT320 series.

Internet Connection Options

- Direct connection to Internet.
- Connection through host machine to Internet.

Telnet Software Options

- Direct connection through the public-domain software package: NCSA Telnet for PC or Macintosh.
- Connection through host machine using other Telnet version.

The Internet address of the Welch Library computer is "welch.jhu.edu" or 128.220.59.10.

GDB Proves Itself at HGM 11

The Genome Data Base (GDB) underwent a fitness test at the Eleventh International Workshop on Human Gene Mapping (HGM 11) and came through as a solid and reliable tool for the scientific community. The database got a vigorous workout during the week of the workshop, held August 16–23 in London. "The word I kept hearing people use in relation to the database was 'robust'," said Robert Robbins, Director of the Welch Medical Library Laboratory for Applied Research in Academic Information. "There was essentially zero downtime."

The success of the database demonstration at HGM 11, in fact, can be measured by the small amount of attention given to it by the 28 committee chairpersons and their cochairs. "No one was talking much about GDB," commented Chris Brunn, the Welch Laboratory's Assistant Director for Technical Development. "The software let the committees do their work of entering and verifying data without hindrance. That's what software is supposed to do. You shouldn't have to think about it."

> *"The word I kept hearing people use in relation to the database was 'robust'."*
>
> *— Robbins*

Figures from the meeting also show how much the system was used; the database server logged more than 58,000 connections to GDB. During the peak hours of 8 a.m. to 8 p.m., an average of 50 people were using the system simultaneously; at one point, close to 100 users were noted.

Another indication of usage is the amount of data added to the database. More than 2000 new entries were made, including 504 mapped loci, 652 probes, and 196 polymorphisms.

Because the system performed well, GDB staff had time to gather information from the committee chairs about their needs in using the database. "We learned about new things they would like to do and things they would like to do more easily," Brunn stated.

Map Manager Module

"Mapping information represents the intellectual focus of the database," said Peter Pearson, GDB Scientific Director. He added that most of the database information, such as DNA marker descriptions and probe availability, primarily supports map construction and maintenance.

The DNA committee at HGM 11 urged that each chromosome committee construct at least one map giving the order of reference markers on its chromosome. To aid this construction at HGM 11, the GDB staff provided a working version of Map Manager, a new module.

GDB consultant Ken Fasman, whose job was to get Map Manager up and running, reports that this software is at a stage of growth comparable to that of GDB a year ago. Still in a preliminary form, Map Manager will be expanded over the next few months, according to Fasman, who expects module evolution to continue for quite some time. "New mapping methods are developed continuously," he said, "and Map Manager has to keep up with new developments."

HGM 11 started with only a few maps in GDB, but during the workshop over 100 maps were entered and fully approved by the chromosome committees. As with other GDB information, an approval process is required: committee members verify the map and associate it with at least one source (i.e., one reference). After this is done, the map can be viewed by general users.

Shortening the Publication Cycle

As Robbins described it, the experience of GDB at HGM 11 illustrates a new application for scientific databases. In the past, investigators built databases by extracting and reproducing the findings of other

Map Manager Module Speeds Data Entry, Approval

Workshop Users Add 2000 New Entries

ATCC Repository Catalogue

The fifth edition of the American *Type Culture* Collection (ATCC)/NIH *Repository Catalogue of Human and Mouse DNA Probes and Libraries* (1991) describes related materials from the ATCC molecular biology collection and Patent Culture Depository. [Catalog: 800/638-6597 or 301/881-2600, Fax: 301/321-5826; Repository information: Donna Maglott (301/231-5586, Fax: 301/770-1541).]

Expressed Sequence Tagged (EST) Clones

ATCC is in the early stages of establishing a cDNA clone resource and plans to receive clones in microtiter dishes, replicate and store them, and offer copies as either plates or individual clones (supplied as stabs), along with information sheets. Most EST clones described in *Science* **252:** 1651–56 (1991) are currently available.

investigators from the literature. Scientific databases that can themselves be a means of publication, and no longer merely derivative products, will be possible in the future, Robbins believes.

Many of the 700 HGM 11 participants presented posters, abstracts of which were published in the proceedings. After review by Human Gene Mapping Workshops committee members, information from these posters went into the database, with the abstract cited as the source. When the updated database tapes were installed at Hopkins shortly after HGM 11, the new findings were instantly made available to GDB users worldwide. In fact, students in Heidelberg used the updated data at a European Molecular Biology Laboratory practical course held the week following HGM 11 (see box at left).

Future of HGM Workshops

HGM 11 could be the last comprehensive human genome workshop, according to meeting organizers; the logistics and tremendous expense of mounting such large workshops, with the extensive support facilities they require, make their continuation doubtful, particularly when different sites are used for each meeting. The future may lie, the organizers believe, in single-chromosome workshops, which are playing an increasingly important role in the review and achievement of consensus maps. As worldwide access to GDB improves, so does the feasibility of small workshops spread throughout the international community of geneticists. ◊

Reported by GDB Staff

GDB Training Program Off to Ambitious Start

Kerryn Brandt, training coordinator for the Welch Medical Library Laboratory for Applied Research in Academic Information, and Robert Robbins, Laboratory Director, participated as instructors in the recent European Molecular Biology Laboratory (EMBL) practical course, "Exploring Genome Information," held August 26–30 in Heidelberg, Germany. The course offered 20 European and Israeli students hands-on training in genetic and molecular biology databases and software programs.

The course was challenging for instructors and rewarding for students, who came to Heidelberg from diverse educational and professional backgrounds. Database managers, graduate students active in gene mapping, and postdoctoral fellows pursuing improvements in gene-sequencing technologies were among those represented. While some students had years of laboratory experience in molecular biology, others were still grappling with the field's jargon. Course evaluations suggest that despite this challenge, the students left with a thorough knowledge of Genome Data Base (GDB) and Online Mendelian Inheritance in Man (OMIM), the role of these databases, and their practical applications to professional life.

Robbins, who lectured on the development, structure, administration, and future of GDB and OMIM, had discussed the role of the databases at the previous week's HGM 11 Workshop in London. In a series of sessions, Brandt provided over 7 hours of hands-on instruction in the use of the Welch databases, including opportunities for in-depth work on specific problems of interest to each student. Through the entire course, students had access from their own terminals to both GDB and the international network.

The EMBL copy of GDB, updated with the most current database brought directly from HGM 11, was the first in Europe and is intended for training, research, and collaborative projects. GDB is available at the German Cancer Research Center (DKFZ) under support from the European Commission's human genome program.

Course instructors were drawn mainly from EMBL, DKFZ, Centre d'Etude du Polymorphisme Humain, University of Utah Human Genome Center, Research Institute for Molecular Pathology (IMP) in Vienna, and the Medical Research Council Clinical and Population Cytogenetics Unit in Edinburgh. The course was organized by Howard Bilofsky and Patricia Kahn (EMBL), Richard Lucier (former Welch Laboratory Director), Andreas Weith (IMP), and Sandor Suhai (DKFZ). ◊

Human Genome Project Video Available

A new 23-minute video, loaned free, describes the international Human Genome Project and discusses genetic linkage mapping, physical mapping, DNA sequencing, and the social and ethical problems that may arise from data produced by the application of these new tools. Produced by the National Center for Human Genome Research (NCHGR) and intended for high school age and older, the video features James Watson (NCHGR), C. Thomas Caskey (Baylor University College of Medicine), David Housman (Massachusetts Institute of Technology), Nancy Wexler (Hereditary Disease Foundation), and Robert F. Murray, Jr. (Howard University College of Medicine).

Catalog No. 24754. Contact: Modern Talking Picture Service; Film Scheduling Center; 5000 Park Street North; St. Petersburg, FL 33709; 800/243-6877. ◊

Congress Hears Testimony on ELSI Issues

The House Committee on Government Operations, in keeping with its decade-long interest in protecting the privacy of medical information, held the second in a series of hearings on October 17 to address the question of privacy of genetic information emerging from the Human Genome Project. Committee members cited insurance problems and forensic uses of genetic data, as well as the potential for redefining the doctor-patient relationship, the risk of creating a genetic underclass, and the use of genetic information in marketing strategies. Two four-member panels of distinguished witnesses testified before the committee.

Panel 1

On the first panel James Watson (Director, NIH National Center for Human Genome Research) briefly described the science of the Human Genome Project. Bernadine Healy (Director, NIH), noted that the NIH mission is to improve human health through research. She pointed out that the power of the new science has great potential for good; the discovery of genes can lead to prevention, treatment, and cure of many genetic illnesses. "I believe future historians will point to the last decades of the 20th century as the time when America helped the life sciences come of age," she said.

Healy stated that NIH is committed to studying the social consequences of the genome program and announced the formation of a new Center for Science Policy Studies within the NIH Director's office to integrate studies of ethical, legal, and social issues (ELSI) with other NIH research.

David Galas (Associate Director, DOE Office of Health and Environmental Research) noted the close cooperation of DOE and NIH in the Human Genome Project and predicted a shift from patient treatment to illness prevention. He said many ELSI considerations are not novel; they have existed for a long time, but the genome project provides urgent motivation for addressing them anew.

Galas described the separate but cooperative nature of the NIH and DOE ELSI programs. Both are coordinated by the Joint ELSI Working Group (appointed by the DOE-NIH Joint Subcommittee on the Human Genome), with DOE emphasizing science education. The Human Genome Project raises questions for study, he said, including the kind of health care system needed, balancing of privacy rights with public rights, the state of current privacy protection, and the possible usefulness of other countries' experiences in this area.

Watson and Galas both stressed the importance of allowing time for the Joint ELSI Working Group and its Privacy and Insurance task forces to discuss these issues and submit their findings to the joint subcommittee before legislative action is taken. "About 1 to 2 years will be needed," Watson predicted.

W. French Anderson (NIH Heart, Lung, and Blood Institute), a pioneer in gene therapy, advocated privacy and confidentiality of genetic information. He also stressed that the predictive power of genetic knowledge is incomplete; most traits are multigenic and are expressed differently in individuals, depending on environmental influences.

Panel 2

Nancy Wexler (Hereditary Disease Foundation and Columbia University), Joint ELSI Working Group Chair, began the second panel by sharing her experience of having a 50% chance of carrying the gene for Huntington's disease. She described the fear of stigmatization, stressing that genetic privacy must be protected. One problem is the time lapse between presymptomatic test availability and the ability to provide treatment or cure. Wexler concluded on a positive note, describing the genome project as a great source of hope for affected people and their families.

Paul Billings (Pacific Presbyterian Medical Center, San Francisco) discussed the history of genetic abuses in the United States and the potential role of genetics in modern society. Genetics and eugenics played a significant part in social policymaking in the early 20th century and led to sterilization of the mentally impaired, criminals, and others deemed genetically unfit. Marked improvement in genetic technologies since World War II has sparked a resurgence of genetics applications. In this country, entire families, including adopted children not genetically related to the family, are losing insurance because of genetic test results. Billings concluded by warning that many potential benefits of the Human Genome Project would be lessened by lack of privacy protection.

(continued)

Panels Address Genetic Data Privacy

ELSI Working Group Findings Expected in 1 to 2 Years

Genome News

Human Genome news

National Center for Human Genome Research

This newsletter is intended to facilitate communication among genome researchers and to inform persons interested in genome research. Suggestions are invited.

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Jeremy Rifkin (Foundation on Economic Trends) testified that Congress had requested a coordinated social study of genetic research 14 years ago. He called the current ELSI program a good beginning but was dismayed at the prospect of waiting another 1 to 2 years for results. He stressed the need for legislation to ensure that a eugenics movement could not gain momentum.

Philip Reilly (Eunice Kennedy Shriver Center for the Mentally Retarded) testified on behalf of the American Society of Human Genetics and as a private citizen with an academic interest in genetic databases and DNA banks. According to Reilly, state-based mandatory screening programs have helped in the treatment of metabolic disorders and other diseases, but such genetic information may be misused without proper protection. Also, health care providers are in a quandary when a patient tests positive for a genetic disease; unauthorized disclosure of genetic information is a violation of the physician-patient relationship, yet the doctor has an interest in warning family members at risk. Reilly recommended (1) devising and implementing guidelines for the use and collection of genetic data, (2) limiting access to genetic information by insurers and employers, (3) mandating strict research protocols, (4) treating violations of confidentiality regulations as a criminal act with potential for civil remedies, and (5) undertaking innovative efforts to educate relevant parties. Reilly noted the especially sensitive question of testing children.

Three common points emerged from the remarks of the eight panelists:

- genetic information has been misused in the past,
- current laws and regulations may be inadequate to protect people from discrimination in the present, and
- work must be done to ensure that genetic information is protected in the future.

These important issues are being addressed by the NIH-DOE Joint ELSI Working Group and its task force on privacy. ◊

Reported by Elinor Langfelder
NIH NCHGR
and
Daniel W. Drell
DOE

NIH-DOE ELSI Working Group Hears Panel on Genetic Privacy

A diverse panel of experts led spirited discussions in an open workshop on "Protecting the Privacy of Genetic Information," held September 11–12 in Bethesda, Maryland. The meeting was hosted by the NIH-DOE Joint Working Group on Ethical, Legal, and Social Issues (ELSI) related to data generated by the Human Genome Project.

Anita Allen (Georgetown University Law Center) defined genetic privacy as (1) the inaccessibility of personal information and (2) the right of individuals to make decisions about themselves. Allen stated that privacy is valued in modern society as an element of personhood and may also protect people from embarrassment or stigmatization. However, some believe that warning family members about impending disease may sometimes justify overriding individual privacy interests.

Harold Edgar (Columbia University Law School) noted that groups are not recognized as having privacy rights under the law; in some circumstances, however, an aggregate of people can be regarded legally as an individual and an implicit privacy right conceded. These contradictions have led to mixed case law; for example, the Amish in Pennsylvania gained the right to teach their children according to their cultural beliefs, while the U.S. Supreme Court held in another case that a group could not be defamed as an individual can be. According to Edgar, biological "leavings" such as hair and urine are probably not subject to current privacy protections under the doctrine of "abandonment"; anything thrown out or deliberately discarded is no longer protected.

Paul Mendelsohn (Neurofibromatosis Inc.) gave a forceful description of real-life concerns of afflicted individuals, particularly in the areas of employment and insurance. Mendelsohn asserted that antidiscrimination laws do not work; furthermore, filing a discrimination suit is a sure way to announce one's disability to the world. Affected people also have difficulty in dealing with familial and societal responses to

a genetic disability, especially a clearly visible one; these responses often include guilt, denial, and ostracism.

Phillip Reilly (Eunice Kennedy Shriver Center for the Mentally Retarded) discussed storage of biological materials in DNA banks and genetic information in databanks. The largest collections of medical samples are in academia (well over 50,000 specimens, with the number growing slowly) and in state forensic laboratories (over 50,000 samples, growing rapidly). State health departments, which collect and store blood spots from all newborn babies, have accumulated the largest numbers of samples, and 11 states are following Virginia's lead in establishing state DNA banks for convicted felons. The military, also studying the use of stored DNA for identification purposes, could begin the accumulation of millions of samples.

Lance Hoffman (George Washington University) discussed computer databanks, which are often designed for utility rather than security. In a world of networked computers, however, common sense must play a role; too simple computer passwords are easily bypassed. Solutions range from good locks to very sophisticated computer security systems.

Jan-Lori Goldman (American Civil Liberties Union) emphasized the need for individuals' control over their own identifying information and personal data. She differentiated between the banking of identifiable data and the public health interest in accumulating statistical information. The Supreme Court has held that a reasonable expectation of privacy associated with certain activities or personal conduct can be protected by the Fourth Amendment. In Goldman's view, this reasonable expectation is decreasing.

Bartha Knoppers (University of Montreal) cited three widespread myths: (1) genes determine what people are; (2) people are defined by their genetic diseases; and (3) genetic disease is abnormal. She also gave an overview of genetic privacy perspectives among different countries, many of which have recommended or passed legislation prohibiting access to such information by insurers and employers; in the Netherlands, insurance companies have a self-imposed ban on genetic testing. Knoppers described a French study in which physicians have been prevented from aggressively treating individuals at risk for glaucoma who were identified through a genetic-marker study of another illness [*Science* (April 19, 1991)].

Current Laws on Genetic Privacy Often Apply Only to Physicians

Lori Andrews (American Bar Foundation) described the legal patchwork of state regulations governing confidentiality of medical records, including genetic records. Existing laws often apply to physicians only, rather than to the entire field of health professionals, researchers, and other interested third parties. Andrews stressed the importance of developing a model for consistent state legislation to protect genetic information, because medical care historically has been managed at the state level.

John Fanning (U.S. Department of Health and Human Services) discussed the limitations of federal laws governing privacy. These laws often cover only those receiving federal research dollars, and regulations are difficult to enforce for secondary and tertiary recipients of information.

A concern that arose several times was the question of consent when data are collected for one purpose but unexpectedly become valuable for another. Consent agreements may not be clearly understood, participants noted, or they may not be written specifically enough. The availability and cost savings of using an already assembled sample set may prove very attractive, and the voluntary nature of true consent may be subtly compromised.

ELSI Working Group Committed to Educating Professionals and Public on Genetic Privacy

Diane Hinton (Human Genome Organization and Howard Hughes Medical Institute) described the evolution of strict confidentiality rules for handling identifiable genetic data contributed by members of the Mormon Church in Utah. Hinton recommended that the ELSI working group produce an educational document explaining minimum standards for confidentiality practices.

The full ELSI working group considered a plan of action and chartered a task force on privacy issues; the task force will commission papers for continued discussions, recommend research guidelines, and analyze state and federal legislative agendas on privacy regulations. In addition, the group reaffirmed its commitment to educating professionals and the public on privacy and other concerns pertinent to the Human Genome Project.

Reported by Daniel W. Drell
DOE
and
Elinor Langfelder
NIH NCHGR

Genome News

Faculty Discuss Participation of Minorities in NCHGR Research

JHU Meets With Minority University Faculty

Scientists from Johns Hopkins University (JHU) School of Medicine and three predominantly minority institutions in the greater Baltimore area met on August 23 at JHU. The purpose of the meeting was to discuss minority student and faculty participation in the Human Genome Project through research at JHU supported by the NIH National Center for Human Genome Research (NCHGR). (See box for a list of meeting participants).

Randall Reed (JHU) described a newly established summer research program for minority students. The number of U.S. students applying to graduate school is dwindling, according to Reed, and minority students should be aggressively recruited; a summer research experience is one way to stimulate interest. At the beginning of 1991, Reed polled the JHU faculty about the possible program, in which faculty members might use their research funds to support students; of the 50 faculty members polled, 49 favored such a project. Five students took part in the 1991 program, and JHU plans to enlarge it next year.

Cecil Payton (Morgan State University) stated that his students participated in similar activities at other institutions. He said a JHU program would be very beneficial because of proximity to the students' home institutions and the possibility that research projects could be continued during the school year. At present, only students participating in Minority Access to Research Careers programs have opportunities to conduct research in laboratories outside their home universities.

Neba Ngwa-Suh (Bowie State University) expressed concern that students, especially freshmen or sophomores, might not be properly prepared for research. Participants agreed that students without research experience should not be excluded from the program, because its main purpose is to introduce them to an intense research environment. JHU faculty members indicated that every effort would be made to match each student's experience with the appropriate research situation; motivation was seen as more important than grades. The group also believed that the application process should be simple, consisting of a transcript, two letters of recommendation, and a one-page questionnaire to assess the student's motivation.

Coordinators at each institution will act as liaisons with JHU faculty and be responsible for identifying promising students. Recruitment for the JHU 1992 summer program began this fall, and Roger Reeves (JHU) developed a recruitment package containing information about faculty and various research projects at JHU.

(continued)

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NIH NCHGR
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Bettie J. Graham
Chief, Research Grants Branch

*Coordinators.

Speaking about program financing and coordination, Bettie Graham (NCHGR) described the minority supplement available to all NIH grantees. She stated that each NIH component has its own policy and that grantees seeking a minority supplement should contact their respective NIH program directors.

Graham emphasized that the minority supplement should not be used instead of the National Research Service Award (NRSA) to support minority graduate students. Graham stated that NCHGR would be receptive to a request for a minority-supplement in addition to the NRSA if the student slots on this grant are already filled with an adequate number of minorities and if the investigator wishes to recruit additional minority students.

JHU representatives suggested many possible opportunities for minority-institution faculty, including sabbatical leaves. Short-term research could be full-time in summer and extend to part-time during the academic year. Minority-institution representatives were very enthusiastic about updating faculty research expertise. Graham stated that the minority supplement and the NRSA senior fellowship program could support these activities.

Payton reported on other activities at his institution, such as providing public school students and teachers with greater science exposure. JHU faculty encouraged this effort and expressed interest in giving seminars as part of the program.

The meeting stimulated institutions in the greater Baltimore area to discuss how students and faculty from predominantly minority institutions could participate in research at JHU. It also provided the opportunity for JHU faculty to use input from minority scientists to expand their summer program for minority students. An additional benefit was that JHU faculty agreed to participate in activities sponsored by minority institutions.

Positive interactions among participants emphasized the importance of face-to-face meetings. Written information from the federal government is overwhelming to the scientific community; a personal visit allows for an immediate exchange of information, ideas, and opinions. ◊

Submitted by Bettie J. Graham, Chief
Research Grants Branch
NIH NCHGR

Note: DOE Phone Changes

The telephone prefix for the DOE offices in Germantown, Maryland, changed from 353 to 903 on November 15. The Human Genome Program office numbers are now 301/903-5037, Fax: 301/903-5051. The FTS numbers are unchanged.

Genome-Related Tutorials Offered

Course on Genomic Information and Ethical Implications

"Ethics and the Human Genome Project" is the topic of an intensive advanced-level course to be offered June 15–19, 1992, at the University of Washington in Seattle.

The course, which will emphasize principles and methods for studying ethical and social issues relevant to mapping and sequencing the human genome, will include an introduction to ethics for genetic scientists and to genetics for medical ethicists. Joint sessions will allow for dialogue between the two groups.

Applications are due March 15, 1992. Minorities and women are especially encouraged to apply.

- Contact: Barbara Brownfield; Department of Medical History and Ethics, SB-20; University of Washington School of Medicine; Seattle, WA 98195 (206/543-5447).

Introductory Linkage Course

A course for researchers who have a basic understanding of linkage analysis but little or no experience in using linkage programs will be held at Columbia Presbyterian Medical Center in New York City on May 19–22, 1992. Attendance is limited to 25. An advanced linkage course will be held in the fall of 1992.

Topics will include an introduction to linkage analysis; practical aspects of data collection; strategies and methods of linkage analysis; incomplete penetrance; inbreeding loops; simple risk calculations; and an introduction to computer simulation. A major part of the course will consist of exercises using LINKAGE software programs.

- Contact: Katherine Montague (212/960-2507; Fax: 212/568-2750; BITNET: "ott@nyspi").

This newsletter is prepared at the request of the DOE Office of Health and Environmental Research and the NIH National Center for Human Genome Research by the Biomedical and Environmental Information Analysis Section of the Health and Safety Research Division at Oak Ridge National Laboratory, which is managed by Martin Marietta Energy Systems, Inc., for the U.S. Department of Energy, under Contract DE-AC05-84OR21400.

Genome News

HUGO Helps with cDNA Coordination

At many locations cDNA studies form an important part of Human Genome Project research. During the Human Gene Mapping 11 Workshop in London on August 18–22, about 25 people met to discuss a possible role for the Human Genome Organization (HUGO) in coordinating cDNA studies. Participants included representatives of many leading cDNA research groups and most funding agencies supporting cDNA programs.

The meeting, chaired by Charles Cantor, HUGO Vice-President, North America (Lawrence Berkeley Laboratory), and Edwin Southern (University of Oxford), heard brief summaries of current cDNA projects. The presentations indicated that the entire community would benefit if HUGO collated and provided information about the nature and scope of cDNA work worldwide. A small group of scientists, chaired by Chris Fields (NIH National Institute of Neurological Disorders and Stroke) and Ross Sibson (U.K. Human Genome Resource Center), agreed to hold further discussions to consider how best to accomplish this goal.

During the meeting several ways were identified in which HUGO can help the cDNA community avoid duplication of research efforts. These included (1) making arrangements for researchers to screen existing cDNA sequence databases to determine which sequences are already present and (2) establishing procedures for the exchange of characterized cDNAs so research groups can remove corresponding sequences from existing libraries. Both possibilities will be explored further within the community.

Major differences were discussed regarding the proprietary value of partial or complete cDNA sequences as viewed by U.S. and European research groups; other divergences were thought to exist in Japan and other nations. Issues raised by these contrasting views are complex and have the potential to influence the course of human genome research. ◇

Reported by Liz Evans
HUGO, London

Contacts:

- **Chris Fields**
  Fax: 301/480-8588
- **Ross Sibson**
  Fax: (Int.) 44/81-869-3807

U.S., European YAC Handling Practices Differ

HGM Group To Facilitate Work on Human YACs

At the Eleventh International Workshop on Human Gene Mapping (HGM 11) in London on August 18–22, a group of about 20 people, chaired by Charles Cantor, HUGO Vice-President (Lawrence Berkeley Laboratory) and Anthony Monaco [Imperial Cancer Research Fund (ICRF), London], met to discuss the availability and use of human yeast artificial chromosome (YAC) libraries within the genome community.

Several libraries have been distributed to a number of laboratories or are available through the human genome resource centers associated with the U.K. and European Community genome programs. These libraries include those made originally in the laboratories of Anthony Monaco, Maynard Olson (Washington University School of Medicine), Daniel Cohen (Centre d'Etude du Polymorphisme Humain, Paris), Rakesh Anand (ICI Pharmaceuticals), and Hans Lehrach (ICRF).

Discussions revealed that practices for handling YACs in the United States and Europe are quite different. In the United States, entire libraries are often available to many individual laboratories, while distribution in Europe usually has been limited to YAC arrays on filters or to pools of YACs. Laboratories screening these filters or pools then report their results to a center to receive the individual clones corresponding to the screening probe. While the U.S. system is much less restrictive because individual laboratories are free to handle the libraries and individual clones as they wish, the European approach has the advantage of accumulating a considerable amount of useful information by combining the results of many separate screening efforts.

Discussions indicated that most YAC users were not aware of the full range of libraries available and the various constraints on their use. To consider how information about YAC libraries might be spread within the community, a small group was established under the chairmanship of Gert-Jan van Ommen (Leiden University, Netherlands).

(see YACs, p. 13)

Contact:

- **Gert-Jan van Ommen**
  Leiden University
  Netherlands
  Fax: (Int.) 31/71-27-60-75

Funding Announcements

The National Center for Human Genome Research (NCHGR) invites applications:

■ PA-91-88
Development of short, advanced-level genomic analysis courses, particularly those that emphasize (1) new genetic and physical mapping laboratory techniques; (2) DNA sequencing technology applicable to large-scale projects; (3) genome-related informatics; (4) interdisciplinary training in principles of genomic analysis for nonbiologists; and (5) the study of ethical, legal, and social issues relevant to the Human Genome Project.

■ PA-91-89
Special Emphasis Research Career Awards for eligible institutions to offer biological science training to scientists highly qualified in disciplines having the potential to further technological developments critical to the Human Genome Project. These disciplines include mathematics, engineering, computer science, chemistry, and physics.

Applications for both PA awards are accepted February 1, June 1, and October 1. To expedite application review, consult program staff before developing the application. Contact:

- Bettie Graham (301/496-7531, Fax: 301/480-2770); NIH NCHGR; Building 38, Room 610; Bethesda, MD 20892. ◊

YACs *(from p. 12)*

Topics to be discussed by this group over the next few months:

- compiling a periodically updated, easily accessed inventory of YAC libraries;
- recording (in a public database) information about YAC screening with DNA probes to minimize unnecessary duplication; and
- developing accceptable mechanisms for exchanging characterized YACs among many screening centers to promote the worldwide integration of screening efforts. ◊

Reported by Liz Evans
HUGO, London

U.S. Genome Research Funding Guidelines

Note: Investigators wishing to apply for NIH funding are urged to discuss their projects with agency staff before submitting formal proposals. DOE requires no prior discussion on preproposals.

NIH National Center for Human Genome Research (NCHGR)

Application receipt dates:

- R01, P01, R21, R29, P30, P50, and R13 grants – February 1, June 1, and October 1.
- Individual postdoctoral fellowships and institutional training grants – January 10, May 10, and September 10.
- Small Business Innovation Research Grants (SBIR: firms with 500 or fewer employees) – April 15, August 15, and December 15.
- Research supplements for underrepresented minorities – applications are accepted on a continuing basis.
- Requests for Applications (RFAs) – receipt dates are independent of the above dates. Notices will appear in *HGN* and other publications.

Program announcements are listed in the weekly *NIH Guide for Grants and Contracts*, which is available by

- Hard-copy subscription – call 301/496-7441.
- Remote log in via modem to NIH Grant Line – call John James, 301/496-7554.
- Listserver computer network subscription – call Dottie Baker, 919/966-5625; BITNET: "pjones@uncvx1.bitnet" or Internet: "jones@samba.acs.unc.edu".

Expanded statements of RFAs listed in the NIH grants guide may be obtained from either of the two electronic sources or from NIH NCHGR in Bethesda, MD (301/496-0844).

DOE Human Genome Program

Solicitations for proposals will be published in the February 1992 issues of the *Federal Register* and *Science* and in other publications. Formal proposals are due in August 1992.

For further information, contact the program office via

- 301/903-5037 or FTS 233-5037; Fax: 301/903-5051 or FTS 233-5051; or Internet: "genome@oerv01.er.doe.gov".

SBIR Grants. DOE also invites small business firms to submit grant applications addressing the human genome topic of SBIR programs, which are designed to strengthen innovative firms in areas of research and development and to contribute to the growth and strength of the nation's economy. The human genome topic emphasizes instrumentation development for automated clone processing, improvements in DNA sequencing technologies, and enhanced sequence data storage and processing capabilities. Next submission date: spring 1992. For more information, contact

- Samuel Barish; SBIR Program Manager, ER-16; DOE; Washington, DC 20585; 301/903-5707.

Human Genome Distinguished Postdoctoral Fellowships
Next deadline: February 1, 1992. For further information, see *HGN* **2**(3), 11 (September 1990) or contact

- Oak Ridge Associated Universities: 615/576-4805. ◊

Calendar of Genome Events*

December	4–6	**Human Gene Therapy Conference**; Bethesda, MD [*G. Wolfle, 301/496-9899, Fax: 301/402-1056*]
	8–11	**Human Genetics and Genome Analysis: A Practical Workshop for the Nonscientist**; Cold Spring Harbor, NY [*J. Witkowski, 516/549-0507*]
	9–10	**Genome Informatics Workshop II**; Tokyo, Japan [*S. Mitaku, (Int.) 81/423-81-4221, ext. 317, Fax:(Int.) 81/423-87-6591*]
	19	**NCHGR Lecture Series: Genetic Mapping of Human Breast Cancer**; Bethesda, MD [*C. Dahl, 301/402-0838*]
January 1992	3–4	**DOE/NIH Joint Subcommittee on the Human Genome; NIH Program Advisory Committee on the Human Genome**; Irvine, CA [*J. Ades, 301/402-2205, Fax: 301/402-2218*]
	4	***DOE Human Genome Coordinating Committee**; Irvine, CA
	7–10	**"Biotechnology Computing Minitrack"** at the **Hawaii International Conference on System Sciences-25**; Kailua-Kona, HI [*L. Hunter, 301/496-9300, Fax: 301/496-0673, E-mail: "hunter@nlm.nih.gov"*]
	16	**NCHGR Lecture Series: Mapping and Sequencing the *Caenorhabditis elegans* Genome**; Bethesda, MD [*see contact: Dec. 19*]
	19–21	**Advances in Genetic Technology: Feeding the World in the 21st Century**; Miami, FL [*The Miami Bio/Technology Winter Symposia, 800/642-4363, Fax: 305/324-5665*]
	25–Feb. 1	**Keystone Symposia Meeting: Molecular Mechanisms in DNA Replication & Recombination**; Taos, NM [*Keystone Symposia, 303/262-1230, Fax: 303/262-1525*]
February 1992	7	***National Advisory Council for Human Genome Research**; Bethesda, MD
	9–13	**Annual Meeting of the American Society for Biochemistry & Molecular Biology & Biophysical Society**; ASBMB/BS, Houston, TX [*G. Goodenough, 301/530-7010, Fax: 301/530-7014*]
	20	**NCHGR Lecture Series: High-Speed DNA Sequencing in Ultrathin Gels**; Bethesda, MD [*see contact: Dec. 19*]
	26–28	**Chromosome 16 Workshop**; Adelaide, Australia [*E. Hildebrand, 505/667-2746, Fax: 505/665-3024 or G. Sutherland, (Int.) 61/8-267-7284, Fax: (Int.) 61/8-267-7342*]
March 1992	13–15	***Second Invitational Conference on Genetics, Religion, and Ethics**; Houston, TX [*R. Nelson, 713/797-0600, Fax: 713/797-9199*]
	15–18	**30th Annual Meeting of the American Cytogenetics Conference**; Virginia Beach, VA [*A. Brothman, 804/446-5670, Fax: 804/624-2255 or P. Jacky, 503/652-2880, Fax: 503/652-5783*]
	19	**NCHGR Lecture Series: Social Implications: Genetics and Popular Culture**; Bethesda, MD [*see contact: Dec. 19*]
April 1992	3–10	**Keystone Symposia Meeting: Molecular Biology of Human Genetic Disease**; Copper Mountain, CO; (abstract deadline: Dec. 4) [*Keystone Symposia, 303/262-1230, Fax: 303/262-1525*]
	16	**NCHGR Lecture Series: Genome Mapping and Functional Organization of the Interphase Nucleus**; Bethesda, MD [*see contact: Dec. 19*]
	27–28	**Annual Biotechnology Patent Conference**; ATCC, Washington, DC [*ATCC Workshop Manager, 301/231-5566, Fax: 301/770-1805*]
	27–29	**Third European Workshop on Cytogenetics and Molecular Genetics of Human Solid Tumors**; Porto, Portugal [*S. Castedo, (Int.) 351/2-497-833, Fax: (Int.) 351/2-410-3940*]
May 1992	6–8	**6th Annual Seminar on Analytical Biotechnology**; Barr Enterprises, Cambridge, MA (Deadline for poster abstracts: April 24) [*J. Cunningham, 301/898-3772, Fax: 301/898-5596*]
	6–10	***Genome Mapping and Sequencing**; Cold Spring Harbor, NY
	14–16	**Second Nordic Genome Workshop**; Biotechology Center of Oslo, Oslo, Norway [*H. Prydz, (Int.) 47/2-958-754, Fax:(Int.) 47/2-694-130*]
	21	**NCHGR Lecture Series: The Human Genome Project and the Future of Medicine**; Bethesda, MD [*see contact: Dec. 19*]
	22	***National Advisory Council for Human Genome Research**; Bethesda, MD

*Attendance at meetings listed with asterisk is either limited or restricted. Dates may change; check with contact person.

Calendar of Genome Events*

June 1992	4–6	**Second International Conference on Bioinformatics, Supercomputing, and Complex Genome Analysis**; St. Petersburg Beach, FL [*H. Lim, 904/644-7046, Fax: 904/644-0098; Internet: "genome@scri.fsu.edu"*]
	20–25	**1992 World Congress on Cell and Tissue Culture**; Arlington, VA [*P. Reinsfelder, 301/992-0948, Fax: 301/992-0949*]
	22–24	**Annual Meeting of the Electrophoresis Society**; Barr Enterprises, Research Triangle Park, NC (deadline for paper abstracts: Jan. 27) [*see contact: May 6–8*]
	22	DOE/NIH Joint Subcommittee on the Human Genome; **NIH Program Advisory Committee on the Human Genome**; Bethesda, MD [*see contact: Jan. 3–4, 1992*]
	23	***DOE Human Genome Coordinating Committee**; Bethesda, MD
September 1992	18	***National Advisory Council for Human Genome Research**; Bethesda, MD
October 1992	11–15	**Sixth International Workshop on Mouse Genome Mapping**; Buffalo, NY [*V. Chapman, 716/845-5840, Fax: 716/845-8169*]

*Attendance at meetings listed with asterisk is either limited or restricted. Dates may change; check with contact person.

Training Calendar: Workshops and Coursework**

December	3–5	**Cytogenetics: Techniques & Applications**; ATCC, Rockville, MD [*ATCC Workshop Manager, 301/231-5566, Fax: 301/770-1805*]
	16–21	**Recombinant DNA Techniques II**; LTI, Germantown, MD (also offered Feb. 10–15) [*L. Kerwin, 301/921-2250, Fax: 301/258-8212*]
	17–20	**Basic Cloning Techniques**; BTP, Miami, FL [*S. Chance, 515/232-8306 (1:00–5:00 p.m. CST)*]
	18–21	**IBI Recombinant DNA Workshop**; Middletown, CT [*L. Salen, 800/243-2555 or 203/786-5600*]
January 1992	3–5	**PCR Techniques**; CUA, Washington, DC [*M. Miller, 202/319-5276, Fax: 202/319-5721*]
	6–10	**Recombinant DNA Methodology**; CUA, Washington, DC (also offered Mar. 2–6) [*see contact: Jan. 3–5*]
	6–10	**Recombinant DNA Methodology**; Exon-Intron, Inc., Columbia, MD (also offered Mar. 16–20) [*Workshop Coordinator, 410/730-3984, Fax: 410/730-3983*]
	13–17	**Recombinant DNA Techniques I**; LTI, Germantown, MD (also offered Mar. 23–27) [*see contact: Dec. 16–21*]
	27–31	**Biomedical Initiative Supercomputing Techniques Workshop**; Pittsburgh, PA (Deadline for application: Dec. 6) [*N. Blankenstein, 412/268-5206, Internet: "blankens@a.psc.edu, BITNET: "blankens@cpwpsca"*]
	27–Feb. 1	**cDNA Library Techniques**; LTI, Germantown, MD (also offered April 6–11) [*see contact: Dec. 16–21*]
February 1992	3–6	**PCR Methodology**; Exon-Intron, Inc., Columbia, MD (also offered April 6–9 and Sept. 14–17) [*see contact: Jan. 6–10*]
	20–21	**Molecular Cytogenetics: Chromosome In Situ**; Oncor, Inc., Gaithersburg, MD (also offered April 23–24) [*M. Williams, 301/963-3500, Fax: 301/926-6129*]
March 1992	2–6	**Recombinant DNA Methodology**; CUA, Washington, DC [*see contact: Jan. 3–5*]
	2–17	**Carolina Workshop on Yeast Molecular Genetics**; Chapel Hill, NC (application deadline: Feb. 1) [*W. Litaker, 919/966-1730, Fax: 919/966-6821*]
	9–13	**DNA-Protein Interactions**; LTI, Germantown, MD [*see contact: Dec. 16–21*]
	11–12	**Advanced Data Banks**; IntelliGenetics, Mountain View, CA [*N. Robinson, 415/962-7300, Fax: 415/962-7302*]
May	19–22	**Introductory Linkage Course**; New York, NY [*K. Montague, 212/960-2507, Fax: 212/568-2750*]
June	22–26	**Advanced Topics in Recombinant DNA**; Exon-Intron, Inc., Columbia, MD (also offered July 20–24) [*see contact: Jan. 6–10*]

**Dates and course status may change, and courses may be offered at other times and places; check with contact person.

Acronym List

Acronyms listed were chosen because they were either used in the text or are relevant to the human genome research community. Listed in parentheses after an organization is the branch of government or the organization to which it is responsible.

*Denotes U.S. Department of Energy organizations.
†Denotes U.S. Department of Health and Human Services organizations.

ASBMB/BS	American Society for Biochemistry & Molecular Biology & Biophysical Society
ASO	allele-specific nucleotide
ATCC	American **Type Culture** Collection
BTP	Biotechnology Training Programs
cDNA	complementary DNA
CFTR	cystic fibrosis gene locus
CSHL	Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.
CUA	Catholic University of America
DKFZ	German Cancer Research Center
DOE	Department of Energy (U.S.)
ELSI	Ethical, Legal, and Social Issues
EMBL	European Molecular Biology Laboratory
GDB*†	Genome Data Base
HGCC*	Human Genome Coordinating Committee
HGM 11	Human Gene Mapping Workshop 11
HGMIS*	Human Genome Management Information System (ORNL)
HGMW	Human Gene Mapping Workshops
HGN*†	**Human Genome News**
HHMI	Howard Hughes Medical Institute
HUGO	Human Genome Organization [International]
IBI	International Biotechnologies Inc.
ICRF	Imperial Cancer Research Fund
IMP	Institute for Molecular Pathology
JHU	Johns Hopkins University
JITF*†	Joint Informatics Task Force
LANL*	Los Alamos National Laboratory, Los Alamos, N.M.
LBL*	Lawrence Berkeley Laboratory, Berkeley, Calif.
LLNL*	Lawrence Livermore National Laboratory, Livermore, Calif.
LTI	Life Technologies, Inc.
MIM	**Mendelian Inheritance in Man**
NCHGR†	National Center for Human Genome Research (NIH)
NCSA	National Center for Supercomputing Applications
NIH†	National Institutes of Health
NRSA	National Research Service Award
OER*	Office of Energy Research
OHER*	Office of Health and Environmental Research (OER)
OMIM™	Online Mendelian Inheritance in Man
ORNL*	Oak Ridge National Laboratory, Oak Ridge, TN
PACHG†	Program Advisory Committee on the Human Genome (NIH)
PCR	polymerase chain reaction
SBIR	Small Business Innovation Research
TCP/IP	Transmission control protocol/Internet protocol
YAC	yeast artificial chromosome

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