Human Genome news

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NIH Launches New Genome Center To Unify Fruit Fly Mapping Efforts

Three-Year Grant Will Centralize Drosophila *Resources, Technologies*

A new multicampus research center based at the University of California, Berkeley (UCB), will spearhead a project to map the complete genome of the fruit fly *Drosophila melanogaster*. The center, directed by Gerald Rubin (UCB), will unify *Drosophila* mapping efforts and provide a centralized source of technologies and materials for the large number of scientists studying fruit fly genetics. The NIH National Center for Human Genome Research (NCHGR) awarded the 3-year grant that includes $1,651,562 for the first year.

Center Comprises Work at Four Laboratories

The center comprises the four investigators listed below with their laboratories.

- Rubin (UCB);
- Daniel Hartl (Washington University, St. Louis; Harvard University in January 1993);
- Allan Spradling (Carnegie Institution of Washington); and
- Michael Palazzolo [Lawrence Berkeley Laboratory (LBL)].

"The information gathered on the fruit fly thus far gives scientists the best opportunity to combine knowledge about DNA sequence and gene function in a complex organism," observed Rubin. "Maps constructed by center researchers will provide a natural stepping stone to sequencing the fly's DNA," he continued.

A Valuable Model

One reason for including *Drosophila* studies in the Human Genome Project is that extensive biological information on fly genes is already available or rapidly being acquired. Large numbers of genes of known function, timing, and tissue-specific expression or genes whose disruption is lethal to the organism will all be localized along the physical map. The map's very high biological content will be useful for *Drosophila* biologists and will provide the opportunity to study the genomic organization of many identified fly

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Drosophila's Multiple-stranded Chromosomes Aid Mapping

genes. Studying genomic organization on the human map lies several years in the future.

Functional information about fruit fly genes is also valuable in deciphering human gene function. Many fruit fly protein types, such as receptors, regulatory proteins, and enzymes, are already known to have direct counterparts in humans, indicating that the most significant portions of the two genomes have been preserved during evolution. To date, over 400 *Drosophila* genes with human counterparts have been described.

An additional reason for the fruit fly's value as a model organism is the giant polytene chromosomes found in cells of the insect's salivary glands. Each of these chromosomes is made up of more than 1000 identical strands of DNA instead of the usual 1 strand. Each gene is therefore present 1000 times, with the copies lined up adjacent to each other. This alignment makes the chromosomes so large that they can be seen under a simple light microscope, and their DNA sequences can be mapped by in situ hybridization with a resolution of 20,000 to 80,000 bp (about 100-fold better than that possible for human chromosomes). This technique can be used to correlate the cytogenetic positions of known genes and transposable element insertion sites with the physical map.

Representative Clone Set

To make more-detailed physical maps of the fruit fly genome, center investigators will use P1 bacterial virus vectors capable of holding a cloned piece of DNA about 100,000 bp long. By mapping the overlapping sections of the DNA pieces using a nonrandom sequence-tagged-site (STS) selection scheme and STS-content mapping procedure, the team will construct contiguous segments covering large portions of each of the four *Drosophila* chromosomes. This cloning system should provide to the research community a readily accessible, truly representative set of clones for sequencing the 165-Mb *Drosophila* genome.

Production-Level Automation

LBL, one of the subcontractors under the grant, is also the home of a DOE-sponsored human genome center, whose ongoing development of automated instrumentation and processes is contributing significantly to mapping both the *Drosophila* and human genomes.

A key to the center's approach is the use of large-scale automation to provide the throughput necessary for efficient experiments of this scale. Working closely with the Human Genome Center instrumentation group, biologists at LBL have achieved a high degree of automation in several areas of production-level physical mapping: robotic preparation for polymerase chain reactions, large-scale loading and running of gels using a robot-compatible format, and automatic image acquisition and interpretation. Efforts are well under way to integrate these and other essential biological protocols into an automated, robot-controlled system for large-scale map production.

Informatics Resources

A mapping project of this size and complexity requires software for (1) accurate and efficient tracking of clones, DNA preparations, and laboratory results (including imaged data); (2) directing the experimental strategy; (3) communicating

(see Drosophila, p. 3)

FlyBase: A *Drosophila* Relational Database

The NIH National Center for Human Genome Research (NCHGR) has awarded a 3-year grant for development of FlyBase, a relational database that will facilitate access to and handling of *Drosophila* information. The award is $610,390 for the first year.

Four project sites will help to establish and maintain the database, with each location undertaking specific curatorial functions. Sites, responsible investigators, and functions are listed below.

- Harvard University (William Gelbart) will serve as programming center and maintain the master database, major programs, and tables relating to mobile genetic elements and genes introduced by germline transformations. These data tables will allow representation of up-to-date genetic and molecular maps of the fruit fly genome.
- University of Cambridge (Michael Ashburner) will function as the European database server site for FlyBase and maintain genetic tables.
- Indiana University, Bloomington (Thomas Kaufman and Kathleen Matthews), will maintain tables of strains from the two funded U.S. *Drosophila* stock centers.
- University of California, Los Angeles (John Merriam), will maintain tables relating to the molecular properties of genes.

"In the past, dedicated volunteers from the *Drosophila* genetics and molecular biology research community have maintained and distributed essential data resources for *Drosophila* genetics," said David Benton, NCHGR Program Administrator. "The rapid increase in the amount of available information now requires that a public database be established. This database will incorporate the wealth of information collected by Dan Lindsley and Michael Ashburner and others over many years and will be continuously updated with new research findings," he added.

Programs integrating FlyBase with DNA and protein sequence databases are being developed in collaboration with Carolyn Tolstoshev and James Ostell of the National Center for Biotechnology Information.◊

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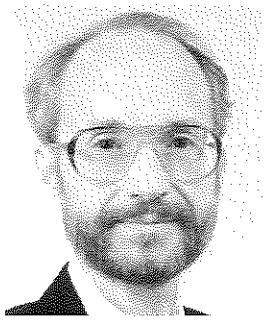
Wooley Named OHER Deputy Assoc. Director

John C. Wooley recently joined the staff of the DOE Office of Health and Environmental Research (OHER) as Deputy Associate Director. Wooley comes to OHER from the National Science Foundation (NSF), where he was Director of the Biological Instrumentation and Resources Division of the Directorate for Biological Sciences.

At NSF, Wooley was responsible for several new initiatives and programs that bear directly on OHER interests (e.g., bioinformatics and computational biology, instrument development, and structural biology). Previously, as Program Director for Biological Instrumentation, he managed awards relating to biochemical and biological instrumentation such as electron microscopes, computers, mass spectrometers, and cell sorters.

Wooley received his Ph.D. in biophysics from the University of Chicago in 1975 and was a biochemistry research fellow at Harvard University from 1976 to 1978. He held positions in the departments of biology and biochemical sciences at Princeton University from 1978 to 1983 and served at NSF from 1984 to 1992. Wooley's research interests have included the structure and function of nucleoprotein complexes (chromatin and ribonucleoproteins).

Associate Director of OHER David Galas said, "We are indeed fortunate to have Dr. Wooley join us at this critical and exciting time in the development of our programs. His experience in government service and academia will be invaluable in helping us forge and conduct the interactive and dynamic programs that OHER is building and that are so important to the future of DOE, the national laboratories, and the U.S. scientific community."◊



John C. Wooley
Deputy Associate Director
DOE Office of Health and Environmental Research

Drosophila (from p. 2)

among the different experimental sites; and (4) local assembly of a physical map consistent with all the data. The genome center informatics group at LBL is now constructing a system in which ACEDB (the *Caenorhabditis elegans* database) is being adapted for management, query, retrieval, and graphical display of *Drosophila* data. LBL has developed a new display that presents map information beside a digitized image of the polytene chromosome. Digitized images of actual microscopic in situ hybridization results are being added to the database.

Drosophila Maps Available

Fly genome maps will be contributed to and available for use by the very large and diverse research community, which includes biochemists, cell biologists, neurobiologists, geneticists, and molecular biologists. Supported by the sophisticated status of *Drosophila* genetics, this cooperation should lead to rapid exploitation of mapping and sequence information derived from the genome center.

The fruit fly has been intensely studied by geneticists for over 80 years. Examples of major genetic principles established by *Drosophila* researchers in the early 1900s are nondisjunction and its consequences, the genetic behavior of chromosome aberrations, the mutagenicity of ionizing radiation, and the discovery of chemical mutations. Modern investigators have used the organism to learn how combinations of genes control the head-to-tail and side-to-side development of the insect's body. More precise knowledge about rules governing body formation will help researchers understand human fetal development and errors resulting in birth defects.

In addition to the NCHGR center grant and DOE support through LBL, the fly project receives funds from the Howard Hughes Medical Institute for the work of Rubin and Spradling.◊

Reported by Leslie Fink, Chief
Office of Communications
NIH NCHGR

Over 400 *Drosophila* Genes Known To Have Human Counterparts

¶ Computational Workshop Proceedings Offered

Proceedings of the 1991 Workshop on Open Problems in Computational Molecular Biology, which was held in Telluride, Colorado, are contained in *Computers and Chemistry* **16**(2)(1992). Andrzej K. Konopka (National Cancer Institute), one of the conference organizers, was guest editor of the special issue devoted to the workshop proceedings. [For more information on the workshop, see *HGN* **3**(5), 11–12 (January 1992)].

Special issue, free to *Computers and Chemistry* subscribers. Others, $112. (Pergamon Press; 660 White Plains Road; Tarrytown, NY 10591-5153; 914/524-9200; or Jane Macmillan, Marketing Department; Headington Hill Hall; Oxford OX3 OBW, U.K.)◊

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Schloss Joins Research Centers Branch

Jeffery A. Schloss
Program Administrator
NIH NCHGR Research
Centers Branch

Jeffery A. Schloss recently joined the staff of the Research Centers Branch, National Center for Human Genome Research, in Bethesda, Maryland, as a program administrator. His responsibilities include administration of genome research centers involved in physical and genetic mapping, DNA sequencing, and development of software and technology related to human and model organism genomes.

Schloss graduated with honors and a B.A. degree in biology from Case Western Reserve University and worked as a research technician at Carnegie-Mellon University and Cold Spring Harbor Laboratory. He earned his Ph.D degree in cell biology from Carnegie-Mellon and held a postdoctoral position in the biology department at Yale University. As an assistant professor at the University of Kentucky in Lexington, Schloss taught introductory, cell, and developmental biology to undergraduate and graduate students and supervised their research projects. Among other activities, he helped to institute new training programs for graduate students in cell biology and genetics, participated actively in networking the biology department laboratories and offices to the university computing center, and assisted in the acquisition of DNA sequencing collection and analysis facilities.

Schloss has done research on mammalian cell movement, investigating the ultrastructure, biochemistry, and function of the microfilamentous component of the cytoskeleton. He also studied the unicellular green alga *Chlamydomonas reinhardtii*, cloning and characterizing the cDNAs of genes whose expression increases when the cells replace their flagella (organelles responsible for motility and cell-to-cell interaction during mating).◊

DOE Awards Human Genome Postdoctoral Fellowships

The DOE Office of Health and Environmental Research has announced the award of six Human Genome Distinguished Postdoctoral Fellowships. The winners, listed in the box below with their graduate departments and host institutions, were selected from 31 applicants.

The fellowship program was created to offer challenging training opportunities for recent doctoral degree recipients to conduct research in support of the DOE Human Genome Program. Up to 2 years are served at university and DOE laboratories having substantial DOE-sponsored genome research. Stipends are $35,000 for the first year and $37,000 for the second.

The fellowship program is administered by the Oak Ridge Institute for Science and Education (ORISE). The next application deadline is February 1, 1993. For more information, contact ORISE at 615/576-9975.

ORISE is managed by Oak Ridge Associated Universities, a nonprofit association of colleges and universities and a management and operating contractor for DOE. ORISE also administers three other DOE fellowship programs: the Alexander Hollaender Distinguished Postdoctoral Fellowship Program for research in the life, biomedical, and environmental sciences; the Global Change Distinguished Postdoctoral Fellowships for research related to global climate change; and the DOE Distinguished Postdoctoral Fellowships for research in the physical sciences, computer sciences, and engineering.◊

1992 DOE Human Genome Distinguished Postdoctoral Fellows

RHETT AFFLECK (*University of California, Berkeley*) – Chemical Engineering
Host: Los Alamos National Laboratory

WILLIAM BRUNO (*University of California, Berkeley*) – Physics
Host: Los Alamos National Laboratory

DAVID LEVER (*University of Utah*) – Chemistry
Host: Duke University

JULIE PARRISH (*University of Houston*) – Biology/Molecular Genetics
Host: Baylor University

MICHAEL W. SMITH (*Johns Hopkins University*) – Biology/Genetics
Host: Salk Institute of Biological Studies

JANET WARRINGTON (*University of California, Irvine*) – Biochemistry
Host: University of California, San Francisco

Task Force on Genetics and Insurance Sets New Focus on Principles and Policy Options

The Task Force on Genetics and Insurance of the NIH-DOE Joint Working Group on Ethical, Legal, and Social Issues met May 31–June 1 in Chevy Chase, Maryland. The meeting marked the 1-year anniversary of the task force and served as a transition from its first-year goal of gathering information to its second-year focus on principles and policy options.

Areas for Further Investigation

Task force members identified three remaining gaps in their factual knowledge and took steps to fill them.

- Adverse selection. A subcommittee chaired by Ray Moseley (University of Florida) was established to investigate the number of insurance applicants who know they will become ill from a genetic disorder, conceal this information from the insurance company, and purchase large amounts of insurance at a low premium. [See *HGN* **4**(2), 3 (July 1992).]
- Management of genetic information. A subcommittee chaired by Betsy Anderson (Federation for Children with Special Needs) was formed to look into medical record ownership, whether research records are kept with regular medical records, and potential abuses of information in the records. It will also examine how genetic information is handled by researchers, clinicians, registries, and the insurance industry, as well as legal rights of access to the data.
- Self-insured employers [see *HGN* **4**(1), 6–7 (May 1992)]. The task force will look closely at the practices of these employers, who are exempt from state regulations governing insurance companies.

Significance of Genetic Information

As a transition step from fact gathering to principle development, the task force worked to define problems presented by genetic information in the areas of underwriting, reimbursement, and records management. Members examined the consequences of genetic knowledge that distinguish it from other types of information, including family stigma, psychological and emotional import, the authoritarian shadow of eugenics, reproductive impact, and prognostic uncertainty. The group also considered the improving quality of genetic data, its potential application to increased numbers of people, the lack of clear clinical protocols for its use, and potential overinterpretation and misinterpretation of such information by the insurance industry and the public.

Defining the Scope

To clarify discussions, future reports, and recommendations, task force members defined "genetic information" as it relates to insurance policies to mean "alterations of the genome that one is born with or that one acquires." This definition includes alterations discovered through methods cited by Anderson, Jonathan Beckwith (Harvard Medical School), and Rob Bier (American Council of Life Insurance). These methods are molecular genetic techniques; examination of chromosomes by microscopy; chemical, immunochemical, or biochemical analysis; medical or physical examination; and family history.

Principles and Report

The task force established a subcommittee to define principles and circulate them to the full group. Members also drafted an outline for the final report, which is to be completed in May 1993.◊

Reported by Jane Loewenson
NIH NCHGR

HUGO Gathering Mouse Information

The Human Genome Organization (HUGO) Mouse Genome Committee is compiling mouse mapping resource and project information not generally available from regular sources. HUGO plans to sponsor a database of such material and will distribute hard copies to HUGO members and other interested people. This database is seen as an important opportunity to highlight the usefulness of mouse resources to both the mouse and human genome communities and to foster many new contacts between the two groups.

To gather information for the database, the HUGO Mouse Genome Committee is circulating a questionnaire to mouse genetics laboratories and investigators. The form, only one of which is needed from each laboratory or center, asks for areas of expertise, genetic mapping facilities, clone library facilities, and somatic cell and irradiation hybrids. To obtain a questionnaire, contact Steve Brown; Department of Biochemistry and Molecular Genetics; St. Mary's Hospital Medical School; Norfolk Place, London W2 1PG; (Int.) 44-71/723-1252, ext. 5484; Fax: (Int.) 44-71/706-3272.◊

HUGO

HUGO EUROPE Change of Address

Beginning October 12, the address for HUGO Europe will be
One Park Square West,
London NW1 4LJ, U.K.
(Int.) 44/71- 935-8085
Fax: -8341

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Topics:

- **Technology**
- **Physical Mapping**
- **Automation and Robotics**
- **CEPH YAC Library**
- **Outreach and Education**

NIH, DOE Evaluate Progress at Retreat

Administrators from the NIH and DOE genome programs held their annual meeting with genome research center directors and others on June 22–23 in Bethesda, Maryland, to evaluate progress toward the 5-year goals of the U.S. Human Genome Project. (See goals in box below.) The meeting focused on the implications of rapidly changing technology and several recent developments in physical mapping.

Directors of NIH- and DOE-supported centers reported that physical mapping of large chromosomal regions, the development of new tools, and increased automation are progressing well.

The group discussed the large-insert yeast artificial chromosome (YAC) library recently developed by Daniel Cohen and colleagues at Genethon and the Centre d'Etude du Polymorphisme Humain (CEPH). Because the particularly large clones in this YAC set represent the entire human genome, the library promises to aid completion of the map of overlapping human clones. U.S. and French investigators are eager to collaborate in using the YAC technology to build chromosome maps.

The availability of such YACs and other improvements in physical mapping techniques encouraged discussion about genome-wide versus single-chromosome–based approaches to completing the physical map; participants concluded that both avenues are valuable at this time and cited the continued need for better cloning methodology to close single-chromosome gaps smaller than 200 kb. Attendees suggested holding a workshop to assess YAC-associated technical problems related mainly to chimeras (YACs containing DNA from two different locations) and other large-fragment cloning systems.

Other topics included the experiences of different centers in using automation and robotics for mapping projects. Attendees agreed on the need for (1) improved communication among centers to optimize rapid information exchange and (2) increased outreach and education about the accumulation of mapping data and materials and the usefulness of such resources to other researchers.◊

Reported by Leslie Fink, NIH NCHGR
and
Daniel Drell, DOE OHER

U.S. Human Genome Project 5-Year Goals* *(Implemented October 1, 1990)*

GENETIC MAPPING

- Complete a fully connected human genetic map with markers spaced an average of 2 to 5 cM apart and identified by a sequence tagged site (STS).

PHYSICAL MAPPING

- Assemble STS maps of all human chromosomes, with markers spaced at intervals of approximately 100,000 bp.
- Generate overlapping sets of cloned DNA or closely spaced, unambiguously ordered markers with continuity over lengths of 2 Mb for large parts of the human genome.

SEQUENCING

- Improve current and develop new methods for large-scale DNA sequencing at a target cost of $0.50 per base pair.
- Determine the sequence of an aggregate of 10 Mb of human DNA in large continuous stretches in the course of technology development and validation.

MODEL ORGANISMS

- Prepare a mouse genome genetic map based on DNA markers. Start physical mapping on one or two chromosomes.
- Sequence an aggregate of about 20 Mb of DNA from a variety of model organisms, focusing on stretches that are 1 Mb long, in the course of developing and validating new and improved DNA sequencing technology.

INFORMATICS

- Develop effective software and database designs to support large-scale mapping and sequencing projects.
- Create database tools that provide easy access to up-to-date mapping and sequencing information and allow ready comparison of the data in these data sets.
- Develop algorithms and analytical tools that can be used in the interpretation of genomic information.

ETHICAL, LEGAL, AND SOCIAL ISSUES

- Develop programs directed toward understanding the ethical, legal, and social implications of Human Genome Project data. Identify and define the major issues and develop initial policy options to address them.

TRAINING

- Support research training of pre- and postdoctoral fellows starting in FY 1990. Increase the number of trainees supported until a steady state of about 600 per year is reached by the fifth year.
- Examine the need for other types of research training in FY 1991.

TECHNOLOGY DEVELOPMENT, TRANSFER

- Support automated instrumentation and innovative and high-risk technological developments as well as improvements in current technology to meet the needs of the genome project as a whole.
- Encourage and facilitate the transfer of technologies and of medically important information to the medical community. Enhance the already close working relationships with industry.◊

*From *Understanding Our Genetic Inheritance; The U.S. Human Genome Project: The First Five Years, FY 1991–1995*, DOE/ER-0452P, U.S. Department of Health and Human Services and U.S. Department of Energy, April 1990.

Upcoming GDB Release: An Improved User Interface

GDB will soon release version 5.0 of its database and its text-based interface software. New features will include (1) an interface that does not use control-K and number keys, (2) access to specific menu choices through "hot key" letters (such as R for Retrieve) consistent across all screens and managers, (3) more efficient screen repainting to eliminate delays, and (4) full point-and-click mouse control for those who access GDB via X-Windows and a network connection. Expanded graphics support will be provided in future releases of GDB.

Accessing GDB via X-Windows can be done easily, provided (1) a single copy of the GDB front-end software is installed on some host on the user's local network and (2) the user's own computer is capable of using generic X-windows software (available for most systems) to access hosts on the local network. [For information on installing X-Windows GDB when it becomes available, contact GDB User Support in Baltimore.]◊

GDB BIOSCI Newsgroup*

A recently established BIOSCI newsgroup dedicated to GDB will allow rapid dissemination of information and provide a forum for GDB users to communicate among themselves. The newsgroup will be monitored regularly by GDB staff but will not replace the support lines for direct user aid. It is listed as GDB (bionet.molbio.gdb) in the USENET newsgroup hierarchy.

The BIOSCI newsgroup network was developed to facilitate worldwide communication among biological scientists working on a variety of computer networks. Distribution sites or nodes on each major network allow users to communicate without needing to learn a variety of computer-addressing protocols. Messages posted to the regional BIOSCI node are distributed automatically to subscribers on all participating networks, including Internet, USENET, BITNET, EARN, NETWORTH, HEANET, and JANET.

USENET News users do not need an e-mail subscription to BIOSCI. Subscription requests, cancellations, and questions about using BIOSCI should be sent to the Internet address (biosci@genbank.bio.net).

*This information on BIOSCI is taken from the "BIOSCI Electronic Newsgroup Network Information Sheet" by Dave Kristofferson of IntelliGenetics, Mountain View, California.◊

GDB User Support, Registration

To become a registered user of GDB and OMIM, contact one of the User Support offices listed at right below (a user may register to access both Baltimore and a remote node). Questions, problems, or user-registration requests may be sent by telephone, fax, or e-mail. User-registration requests should include name, institutional affiliation, and title (if applicable), street address (no P.O. box numbers), telephone and fax numbers, and e-mail address.

GDB and OMIM Training Course Schedule

Comprehensive hands-on training courses on the use of GDB and OMIM will have at least one computer workstation for two participants. Registrants will receive at least 3 weeks notice if insufficient registration causes class cancellation.

- The general course for scientific users provides a basic understanding of the databases and relationships among different types of data.
- The course for users with editing privileges includes instructions on adding, modifying, and deleting GDB data.

Class frequency and location will be determined by demand (schedule below). Courses are free, but attendees must pay their own travel and lodging expenses. Hotel information and directions will be mailed with registration materials.

As interest in GDB continues to grow, organizations around the world will offer training that requires access to GDB in Baltimore. Notifying GDB User Support about planned training activities will enable the staff to ensure database availability by scheduling maintenance and repairs at other times.

COURSE REGISTRATION INFORMATION: contact U.S. GDB User Support Office (at right).

PLANNED EXHIBITIONS (acronym list, p. 16)

- NSGC, San Francisco, Nov. 6–8.
- ASHG, San Francisco, Nov. 10–12.
- AAAS, Boston, Feb. 11–16, 1993.
- Experimental Biology '93, New Orleans, March 28–April 1, 1993.
- AAP/AFCR/ASCI, Washington, D.C., April 30–May 3, 1993.

Course	Dates
BALTIMORE	
General User	Nov. 23–24
General User	February 22–23, 1993
General User	April 26–27, 1993
Editing	May 9–11, 1993
General User	June 21–22, 1993
PITTSBURGH	
General User	October 25
(1-day, primarily for ASIS meeting attendees)	
SAN FRANCISCO	
Editing	Nov. 6–7
General User	Nov. 8
(1-day, for ASHG meeting attendees)	

USER SUPPORT OFFICES

United States

GDB User Support
Welch Medical Library
1830 E. Monument Street,
Third Floor
Baltimore, MD 21205
410/955-7058
Fax: 410/614-0434
Internet:
help@welch.jhu.edu

The Help Line is staffed from 9 a.m. to 5 p.m. EST for information on accounts and training courses, technical support, and data questions. Calls received after hours will be forwarded to the appropriate voice mail and returned as soon as possible. To obtain a user's local SprintNet (Telenet) number for locations within the United States: 800/736-1130.

United Kingdom

Christine Bates
Human Gene Mapping
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CRC, Watford Road
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GDB Forum

Software Designed To Run on Sun Workstation with Internet Connection

GDB Software Offers Quicker Display, Other Features

The Genome Data Base (GDB) offers front-end software that enables quicker screen displays, supports use of the mouse, and provides a local copy of the Online *Mendelian Inheritance in Man* (OMIM) database. The software is designed to run on a Sun workstation with an Internet connection to the GDB host machine. Recommended for use of this software are Sun OS 4.1.1 or 4.1.2, Sunview or Open Windows 3.0, at least 16 MB of ram, 100 MB of disk space, and a tape drive for Sun 150-MB or Exabyte 8-mm cartridge.

The front-end software includes two packages: (1) IRX software from the National Library of Medicine for accessing OMIM and (2) Sybase software libraries for accessing GDB. GDB can provide a free licensing agreement for the use of IRX software, and a Sybase license can be purchased through Johns Hopkins University (JHU). Sybase requires an individual license for each machine on which their Application Productivity Tool (APT) library and Open Client/C software are installed.

Users of GDB front-end software will pay an annual fee to cover initial distribution handling costs, software updates, and the Sybase license, if required. This front-end software must be updated for each new version of GDB released.

Prices as of August:

- Institutions that already have the Sybase license pay $100 annually.
- Institutions that wish to purchase the Sybase license through JHU must pay a first-year charge and then an annual charge thereafter, as follows: United States, $325, $150; Canada, $450, $150; and all others, $375, $150.

Front-end software may be ordered from GDB User Support. Users should indicate whether they have the appropriate Sybase license or wish to purchase it through JHU.◊

Chromosome Editors Ensure Database Integrity

To ensure database integrity, all information submitted for inclusion in GDB is reviewed by the chromosome editors, an international panel of scientists recommended by members of the mapping community and appointed by the Human Genome Organization's Human Genome Mapping Committee (formerly known as the Human Gene Mapping Workshop group).

Assisted by periodic Medline searches, these editors transfer to GDB relevant data gathered from the literature, as well as mapping data and consensus maps derived from single-chromosome workshops, Human Genome Mapping meetings, and Chromosome Coordinating Meetings.

The senior editor for each chromosome (listed in boldface capitals in the following table) coordinates the activities of coeditors and makes sure that information is entered promptly into GDB.

E-mail to GDB Editors Available

A set of e-mail aliases has been established for the chromosome committees shown in the Chromosome Editors list. These aliases allow current committee members with e-mail addresses to be contacted by people who may not know the names of individual editors. The alias names are identical to the committee abbreviations used to retrieve editors in the GDB Contact Manager: cc1 through cc22, ccx, ccy, dna, nc, mim, ldg (or linkage), comap (or mapping), cld (or clinical), mdna (or mito).

The format for sending e-mail to a specific committee is

- name@library.welch.jhu.edu

For example, mail for Chromosome 22 committee members should be addressed to

- cc22@library.welch.jhu.edu

Note that this address is different from the "help" address and includes the additional component "library."◊

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.◊

Chromosome Editors*

Committee	Editors	Location	Fax	E-Mail
Chromosome 1	**GAIL A.P. BRUNS**	Children's Hospital Medical Center	617/735-7588	brun@rascal.bwh.harvard.edu
	Nicholas C. Dracopoli	Mass. Institute of Technology	617/258-8728	dracopol@eagle.mit.edu
Chromosome 2	**NIGEL K. SPURR**	Imperial Cancer Research Fund	(Int.) 44/707-49527	ns@clh.icnet.uk
	Andrew J. Pakstis	Yale University School of Medicine	203/785-6568	pakstis@yalemed.bitnet
Chromosome 3	**BENJAMIN CARRITT**	University College London	(Int.) 44/71-387-3496	b.carritt@crc.ac.uk
	Yusuke Nakamura	Cancer Institute, Tokyo	(Int.) 81/3-3918-0342	—
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Second National Conference on Genetics, Religion, and Ethics

The Institute of Religion (IOR) of the Texas Medical Center and Baylor College of Medicine (BCM) sponsored with DOE and NIH the Second National Conference on Genetics, Religion, and Ethics in Houston on March 13–15. "Implications of the Human Genome Project for Medicine, Theology, Ethics, and Policy" was part of a 3-year project by the same title that began in March 1990. About 160 participants from 8 countries included clinicians, researchers, ethicists, theologians, health policy analysts, and representatives of the news media and of genetics organizations. C. Thomas Caskey (BCM) and J. Robert Nelson and Hessel Bouma, III (both at IOR) organized the conference.

W. French Anderson (NIH) opened the conference with an update on the encouraging progress of patients undergoing human gene therapy for adenosine deaminase deficiency and suggested that genetic engineering would be limited to the quantifiable elements of body and not involve the nonquantifiable elements of spirit or "soul." Abby Lippman (McGill University), Paul Billings (California Pacific Medical Center), and Kenneth Vaux (University of Illinois College of Medicine) responded with alternative perspectives.

Archbishop of York John S. Habgood, author of Religion and Science, analyzed the effects of genetic knowledge on those to whom it applies, its possible misuse by others, and its therapeutic use. Aubrey Milunsky (Boston University School of Medicine), Ronald Cole-Turner (Memphis Theological Seminary), and Thomas F. Lee (St. Anselm College) responded.

Caskey presented an update on the Human Genome Project and the unique implications of recent developments for genetic counseling. Mark Hughes (BCM) described initial efforts to use polymerase chain reaction amplification and DNA probes to diagnose lethal genetic diseases in preimplantation blastocysts. Paul Simmons (Southern Baptist Theological Seminary) addressed the moral and religious implications of these recent developments.

Ruth Bulger (Institute of Medicine, National Academy of Sciences) pointed out that this is the beginning of a difficult era in which many genetic conditions can be diagnosed but not altered. She discussed appropriate behavior and how society might use genetic information constructively, citing particularly the need to listen to the voices and perspectives of women. Dorothy Wertz (Shriver Center), Robert Baumiller (University of Detroit), and Dianna Milewicz (University of Texas Medical School) responded.

James Gustafson (Emory University) addressed the thinking and action points at which theologians and geneticists might meet: the shared concern about the morality of certain genetic research and therapy, and the significance and use of genetic knowledge for interpreting the nature, meaning, and value of human life. LeRoy Walters (Kennedy Institute of Ethics), Kevin O'Connor (Office of Technology Assessment), and Richard Gatti (University of California, Los Angeles, School of Medicine) presented additional viewpoints.

Representatives from four interdisciplinary groups in Boston, Chicago, Houston, and Washington, D.C., gave reports, and seven persons representing a wide spectrum of different religious traditions addressed the relationship of genetics and religion in each tradition (see box below).

A draft Summary Reflection Statement, discussed at the conference and refined through correspondence, identifies medical, theological, ethical, and policy issues on which consensus could be reached as well as some unresolved, ongoing issues.◊

Reported by Hessel Bouma, III
IOR

Two edited volumes on this project are expected to be published in 1993: one on the overall project and conferences and the second featuring a series of genetic counseling case study interviews from the patients' perspective. (Information on books is available from Nelson at the address below.)

Copies of the draft summary statement are available postpaid and without charge from

- **J. Robert Nelson**
  Institute of Religion
  P.O. Box 20569
  Houston, TX 77225
  713/797-0600
  Fax: 713/797-9199

INTERDISCIPLINARY GROUPS

BOSTON – THOMAS SHANNON
(Worcester Polytechnic Institute)
"The Human Genome Project and Prenatal Diagnosis"

CHICAGO – JAMES BACHMAN
(Valparaiso University)
"The Human Genome Project: Issues for the Religious Communities"

HOUSTON – ANDREW LUSTIG
(IOR)
"Genetics, Religion and Ethics: The Clinical Connections"

WASHINGTON, D.C. – FRANK SEYDEL
(Georgetown University)
"Religious and Theological Attitudes Toward Genetic Intervention and Alteration of Life Forms"

RELIGIOUS GROUPS

ISLAM – HASSAN HATHOUT
(The Genetics Institute)

PROTESTANT – ROBERT HERRMANN
(American Scientific Affiliation)

JUDAISM – FRED LEDLEY
(BCM)

PROTESTANT – GERALD MCKENNY
(Rice University)

CATHOLIC – KEVIN O'ROURKE
(St. Louis University Medical Center)

ORTHODOX CHRISTIAN – GEORGE PAZIN
(University of Pittsburgh School of Medicine)

HINDU – GEORGE SUDARSHAN
(University of Texas, Austin)

Meeting Reports

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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The Genie in the Genome: A *Choices and Challenges* Forum

On April 9 more than 500 people attended The Genie in the Genome, a 1-day forum held at Virginia Polytechnic Institute and State University in Blacksburg. The meeting was designed to enable a highly diverse audience to learn about the Human Genome Project and to examine social, ethical, and public policy issues raised by this scientific effort. The conference was sponsored by the NIH National Center for Human Genome Research and the Virginia Foundation for the Humanities and Public Policy.

The April conference was part of the *Choices and Challenges* project, directed by Doris T. Zallen, which was initiated in 1985 at Virginia Tech to identify and address humanistic aspects of rapidly growing scientific and technological areas. Thirteen previous forums each focused on one of a wide variety of subjects, ranging from medical and psychological topics to advances in physics and engineering.

Program sessions:

- Morning tutorial sessions providing basic scientific background, information on potential medical applications, and an overview of ethical and religious aspects.
- Plenary session featuring a panel of speakers who explored the scientific and humanistic aspects of the genome project.
- Postplenary discussion groups on international issues, healthcare effects, and strategies for bringing the Human Genome Project into the classroom.

The plenary session, moderated by Zallen, allowed many opportunities for audience questions and comments. The interactive video teleconference session was broadcast via satellite to more than 30 educational institutions and healthcare facilities throughout the United States.

Invited panelists were Robert Cook-Deegan (National Academy of Sciences), Daniel Kevles (California Institute of Technology), Abbey Meyers (National Organization for Rare Disorders), J. Robert Nelson (Institute of Religion, Texas Medical Center), Martin Rechsteiner (University of Utah School of Medicine), and Norton Zinder (Rockefeller University). These panelists provided historical context, debated the scientific goals, and probed likely personal and societal effects.

A transcript and video tape of the plenary session are available from the Choices and Challenges Project; 351 Lane Hall, Virginia Tech; Blacksburg, VA 24061-0227; 703/231-4216. The transcript is free, and the video (2 hours and 20 minutes long) can be provided for the cost of duplication and shipping.

In reviewing the success of the conference, Zallen stated that a vigorous and multifaceted publicity campaign attracted people from varied disciplines, professions, and stages of life. Many of these groups are generally not reached, she said, and may have been underrepresented at other conferences. Attendees included homemakers, healthcare professionals, scientists, lawyers, retirees, teachers and other educators, local pastors, business representatives, and people concerned about inherited illness in their families.

Zallen also stated that this conference brought prominent participants in the Human Genome Project into contact with individuals whose ideas they seldom hear. Physicians, potential patients, scientists, clergy, ethicists, lawyers, and the general public exchanged points of view.

The lively interactions fostered by the conference program, Zallen continued, have stimulated analysis of the Human Genome Project by the regional press and local groups and have demonstrated the value of making educational programs accessible to the wider community.◊

Reported by Doris Zallen
Virginia Tech

¶Genome-Related Publication

The report of a meeting held May 21 at the National Academy of Sciences in Washington, D.C., is available without charge. *Federally Funded Genome Research: Science and Technology Transfer Issues—Proceedings of a Public Meeting* was produced by the Genome Patent Working Group of the Committee on Life Sciences and Health, Federal Coordinating Council for Science, Engineering, and Technology. (Contact: Sandra Beaulieu; Oak Ridge Institute for Science and Education; 200 Badger Avenue; P.O. Box 117; Oak Ridge, TN 37831; Fax: 615/576-0202.)◊

Russian-American Human Genome Meeting

Some 55 Russian and 15 U.S. scientists attended the first Russian-American Human Genome Symposium, which was held July 27–29 in St. Petersburg, Russia. The meeting, sponsored by the Human Genome Council of Russia and the NIH National Center for Human Genome Research, was organized by the Russian Academy of Sciences Institute of Cytology and Engelhardt Institute of Molecular Biology.

Participants found the symposium timely and interesting as they discussed their countries' human genome research and assessed possibilities for communication, cooperation, and collaboration. In 32 presentations and 25 posters, investigators explored progress in genetic and physical mapping, DNA sequencing, medical genetics, chromosome structure and function, and bioinformatics.

Presentations and discussions showed that effective human genome research has continued in Russia despite recent economic and political difficulties. Russian-American cooperation was strongly encouraged by attendees, who agreed that collaborations should be based on complementary scientific interests and built on one-to-one interactions between individuals.

To facilitate the numerous possible collaborations identified at the meeting, genome programs in the two countries will exchange investigators' e-mail addresses for quick and effective electronic communication. Also, U.S. researchers who are interested in providing Russian institutes with urgently needed scientific and genome-related journals should contact A. V. Zelenin at the Engelhardt Institute of Molecular Biology (Internet: azel@imb.msk.su).◊

Reported by Jane Peterson
NIH NCHGR

Contact for additional information about the meeting or possible support for U.S.-Russian collaborations:

- **Jane Peterson**
  or Bettie Graham
  Bldg. 38A, Rm. 610
  9000 Rockville Pike
  Bethesda, MD
  20892
  301/496-7531

¶Genome-Related Databases, Publications

University of Delaware Databases

Important information accumulated worldwide in the 30-year history of clinical cytogenetics is accessible through two online databases maintained at the University of Delaware by Digamber Borgaonkar and his colleagues. These databases, organized by chromosomal abnormality according to structural and numerical aberrations, briefly describe the reported anomaly; the catalog database also gives bibliographic citations. Both databases are available in print form, as noted below.

Chromosomal Variation in Man: A Catalog of Chromosomal Variants and Abnormalities is a bibliographic database of previously karyotyped cases collected from published literature. Data are entered or updated daily. Because it identifies the chromosome breakpoint and quotes the Mendelian disorder, this catalog is particularly useful to gene mappers. The print version (sixth edition, 1991) is available through book stores or from Wiley/Liss; 605 Third Avenue; New York, NY 10158-0012; 800/225-5945 or 908/469-4400; Fax: 908/302-2300; Telex: 833434.

Repository of Human Chromosomal Variants and Anomalies/International Registry of Abnormal Karyotypes contains personally communicated, unpublished case histories from over 300 contributors in 33 countries. Data are entered at systematic intervals as needed. Clinical cytogenetics laboratories find this repository useful for studies of karyotype-phenotype relationships, rare anomaly searches, and accumulation of a large number of cases or families for a study. The print version (13th Listing, 1990) is available for $25 from the author at the address below. The 14th Listing is expected before the end of 1992.

For information, or to request a database printout, contact Digamber Borgaonkar; Medical Center of Delaware; Cytogenetics Laboratory; 4755 Ogletown-Stanton Road; P.O. Box 6001; Newark, DE 19718; 302/733-3350; Fax: -3773; Internet: fag22015@udelvm.udel.edu.◊

OMIM

The tenth edition of the book *Mendelian Inheritance in Man: Catalogs of Autosomal Dominant, Autosomal Recessive, and X-Linked Phenotypes*, by Victor McKusick, Clair Francomano, and Sylianos Antonarakis [all at Johns Hopkins University (JHU) School of Medicine], was published this year. Incorporating information through March 1, the two volumes contain 5710 entries (869 more than the ninth edition in 1990). The genetic code is presented in two alternative formats, and many more entries now list allelic variants. 2320 pp., $150. (JHU Press; 701 West 40th Street, Suite 275; Baltimore, MD 21211-2190; 800/537-5487 or 410/516-6960, Fax: 410/516-6998.)

Mendelian Inheritance in Man (MIM) is also available as OMIM—a full-text online database located at JHU. OMIM entries, which are arranged by clinical disorder or trait name, may include clinical observations, inheritance patterns, references, allelic variants, chromosomal location, defective gene products, and linkage information. Updated daily, the database serves both the clinical and laboratory communities by providing information helpful in differential diagnosis, genetic counseling, biochemical defect identification, and linkage studies. Searchers can locate relevant material in OMIM and then use the MIM number or chromosomal location for cross-referencing with Genome Data Base (GDB). Revision bars (" | ") in OMIM reflect material added to the database after the book was printed. [For more information on GDB and OMIM, see *HGN* **3**(4), 1–6, (November 1991).]

To become a registered GDB/OMIM user, contact one of the User Support offices listed in the GDB Forum on p. 7.◊

Calendar of Genome Events*

October

5–6. *Protecting Human Subjects in Research Involving Families: Points to Consider; Bethesda, MD [E. Langfelder, 301/402-0911, Fax: /480-2770]

7–9. "The Impact of Molecular Medicine on Clinical Practice" at the Anglo-American Conference; London, England [W. O'Reilly, 212/371-1150, Fax: -1151]

11–15. Sixth International Mouse Genome Conference; Buffalo, NY [V. Chapman, 716/845-5840, Fax: -8169]

14–17. Human Genome '92: The Human Genome Project International Conference; Nice, France [Am. Assoc. for the Advancement of Science (AAAS), 202/326-6461, Fax: /289-4021]

15. NCHGR Lecture Series. Mitchell Eggers: Genosensors—Microfabricated Devices for Automated DNA Sequence Analysis; Bethesda, MD [C. Dahl, 301/402-0838]

17–21. First International Conference on Mathematical and Computational Analysis of the Human Genome and Its Mutation Load; Szeged, Hungary [Human Genome Research Ltd., (Int.) 36/62-23855, Fax: -23844]

November

4–6. Third Meeting of Mammalian Genetics and Development Workshop; London [S. Rastan, (Int.) 44/81-869-3266, Fax: -3270]

4–8. Genetics of Cancer; Hilton Head, SC [Am. Assoc. for Cancer Research (AACR), 215/440-9300, Fax: -9313]

6–8. Chromosome 2 Workshop; Half Moon Bay, CA [S. Naylor, 512/567-3842, Fax: -6781]

6–8. Human Genome Project: Impact, Implications, and Issues; San Francisco, CA [B. Leopold, 215/872-7608, Fax: -1192]

9–10. ELSI Insurance Task Force; San Francisco, CA [see contact: Oct. 5–6]

9–11. Plant Genome I; San Diego, CA (abstract deadline: Oct. 1) [D. Scherago, 212/643-1750, Fax: -1758]

9–13. 42nd Annual Meeting of the American Society of Human Genetics (ASHG); San Francisco, CA [M. Ryan, 301/571-1825, Fax: /530-7079]

11. Planning meeting at ASHG for the First International Chromosome 8 Workshop ; San Francisco, CA [D. Drayna, 415/266-1413, Fax: -2739]

12–13. Impact of Molecular Genetics on the Treatment of Genetic Diseases; Bethesda, MD [R. Abizaid, 301/230-0052, Fax: -0054]

15–17. *Chromosome Coordinating Meeting 1992; Baltimore, MD [P. Pearson, 410/955-9705, Fax: -0054]

19. NCHGR Lecture Series. Leroy Hood: The Genome Project and Biotechnology in the 21st Century; Bethesda, MD [see contact: Oct. 15]

December

7. *DOE Human Genome Coordinating Committee; Bethesda, MD

7–8. DOE/NIH Joint Subcommittee on the Human Genome; NIH Program Advisory Committee on the Human Genome; Bethesda, MD [J. Ades, 301/402-2205, Fax: -2218]

17. NCHGR Lecture Series. Neil Holtzman: Getting Genetic Tests to the Public—Safely and Effectively; Bethesda, MD [see contact: Oct. 15]

January 1993

5–8. Biotechnology Computing Track of the 26th Hawaiian International Conference on System Sciences; Kauai, HI [L. Hunter, 301/496-9300, Fax: -0673, Internet: hunter@nlm.nih.gov]

7. NCHGR Lecture Series. Norman Arnheim: Analysis of DNA Sequences in Single Cells; Bethesda, MD [see contact: Oct. 15]

17–22. "Advances in Gene Technology: Protein Engineering and Beyond" at the 1993 Miami Bio/Technology Winter Symposia; Miami Beach, FL [S. Black, 305/547-3597, Fax: /324-5665]

24–25. *National Advisory Council for Human Genome Research; Bethesda, MD [see contact: Dec. 7–8]

February 1993

1–6. Oncogenes and Anti-Oncogenes in Cell Differentiation, Development, and Human Cancer; AACR, Big Sky, MT [see contact: Nov. 4–8]

7–11. *Third DOE Contractor-Grantee Workshop; Santa Fe, NM (abstract deadline: Nov. 16) [S. Spengler, 510/486-4879, Fax: -5717]

15–19. *15th Annual Conference on the Organization & Expression of the Genome; Lorne, Victoria, Australia [S. Easteal, (Int.) 61/6-249-4719, Fax: -4712]

18. NCHGR Lecture Series. Richard Durbin: ACEDB Genome Database and Data Analysis from the Nematode Sequencing Project; Bethesda, MD [see contact: Oct. 15]

March 1993

6–8. Chromosome 20 Workshop; Paris, France [C. Smith, 510/643-6376, Fax: -1188]

11–12. First International Workshop on Human Chromosome 1; Cambridge, MA (abstract deadline: Dec. 15) [N. Dracopoli, 617/253-8575, Fax: /258-8728]

18. NCHGR Lecture Series. Steve Warren: Triplet Repeat Expansion Mutations—Example of the Fragile X; Bethesda, MD [see contact: Oct. 15]

25. NCHGR Lecture Series. Francis Collins: Identification of Human Disease Genes by Positional Cloning; Bethesda, MD [see contact: Oct. 15]

April 1993

12–18. 1993 Keystone Symposia Meetings: Gene Therapy; Keystone, CO (abstract deadline: Dec. 2) [Keystone Symposia, 303/262-1230, Fax: -1525]

12–18. 1993 Keystone Symposia Meetings: Genetically Targeted Research & Therapeutics-Antisense & Gene Therapy; Keystone, CO (abstract deadline: Dec. 2) [see contact: April 12–18, above]

15. NCHGR Lecture Series. Troy Duster: Socio-Historical Context of Genetic Explanations of Behavior; Bethesda, MD [see contact: Oct. 15]

May 1993

9–12. *Fourth Annual X Chromosome Workshop; St. Louis, MO [M. Thomas, 314/362-7259, Fax: -1232]

14–15. Fourth International Workshop on Chromosome 3; Groningen, Netherlands [C. Buys, (Int.) 31/50-632-925, Fax: -947]

16. Chromosome 3 & Cancer; Groningen, Netherlands [see contact: May 14–15, above]

16–17. *National Advisory Council for Human Genome Research; Bethesda, MD [see contact: Dec. 7–8]

19–22. 84th Annual Meeting of AACR; Orlando, FL [see contact: Nov. 4–8]

Training Calendar**†

October

1–2. *Molecular Cytogenetics: Chromosome In Situ; Oncor, Inc., Gaithersburg, MD (also offered Dec. 10–11) [M. Williams, 800/77-ONCOR or 301/963-3500, Fax: /926-6129]

5–9. Cell Culture Techniques; Germantown, MD (also offered at later dates) [Life Technologies, Inc. (LTI), 800/952-9166 or 301/921-2250, Fax: /258-8212]

5–9. In Situ Hybridization and rDNA Technology; Exon-Intron, Inc., Columbia, MD [Workshop Coordinator, 410/730-3984, Fax: -3983]

8–21. †Analysis & Genetic Manipulation of YACs; Cold Spring Harbor, NY [CSHL, 516/367-8343, Fax: -8845]

9–22. †Molecular-Cell Biology Techniques: Advanced In Situ Hybridization and Immunocytochemistry; CSHL, Cold Spring Harbor, NY [see contact: Oct. 8–21]

12–14. PCR Techniques; Lake Tahoe, NV [Ctr. for Advanced Training in Cell and Molecular Biology/Catholic University of America (CATCMB/CUA), 202/319-6161, Fax: -5721]

12–14. Recombinant DNA Methodology (CATCMB/CUA); Lake Tahoe, NV [see contact: Oct. 12–14, above]

18–Nov. 1. Carolina Workshops on cDNA and Gene Expression; Chapel Hill, NC [W. Litaker, 919/966-1730, Fax: -6821]

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

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

†NCHGR-funded event.

19–23. †Advanced Linkage Courses; Zürich, Switzerland (application deadline: Aug. 25) [K. Montague, 212/960-2507, Fax: /568-2750]

21–22. Molecular Medicine at Michigan: Hands-on program for reporters in the human genome lab; Ann Arbor, Michigan (application deadline: Oct. 7) [C. Aisen, 313/764-2220, Fax: /747-2104]

26–27. Future Technologies for DNA Analysis; Bethesda, MD [Armed Forces Institute of Pathology (AFIP), 301/427-5231, Fax: -5001]

26–30. Recombinant DNA: Techniques & Applications; Rockville, MD (also offered Feb. 22–26, 1993) [Am. **Type Culture** Collection (ATCC), 301/231-5566, Fax: /770-1805]

26–Nov. 4. †Essential Computational Genomics for Biologists; CSHL, Cold Spring Harbor, NY [see contact: Oct. 8–21]

27–Nov. 9. Molecular Genetics, Cell Biology & Cell Cycle of Fission Yeast; CSHL, Cold Spring Harbor, NY [see contact: Oct. 8–21]

November

3–6. PCR Applications/Cycle DNA Sequencing; ATCC, Rockville, MD (also offered Mar. 2–5, 1993) [see contact: Oct. 26–30]

7–8. Future of DNA Sequence Analysis Workshop; Oslo, Norway [H. Prydz, (Int.) 47/2-95 8754, Fax: -69 4130]

9–13. Recombinant DNA Methodology; Exon-Intron, Inc., Columbia, MD [see contact: Oct. 5–9]

11–12. Advanced Data Banks; IntelliGenetics (IG), Mountain View, CA [S. Maulik, 415/962-7342]

December

8–11. DNA Fingerprinting; ATCC, Rockville, MD [see contact: Oct. 26–30]

8–11. Molecular Modeling: Methods and Techniques; Athens, GA [Am. Chemical Society (ACS), 202/872-4508, Fax: -6336]

14–18. Advanced Recombinant DNA Methodology; ATCC, Rockville, MD [see contact: Oct. 26–30]

15. Introduction to PCR; Biotechnology Training Programs (BTP), Gainesville, FL [BTP, 800/821-4861, Fax: 515/232-8306]

16–18. Cloning & Hybridization of PCR Products; BTP, Gainesville, FL [see contact: Dec. 15]

21–22. Clinical Diagnosis Using PCR & Hybridization Analysis; BTP, Gainesville, FL [see contact: Dec. 15]

January 1993

4–8. Recombinant DNA Methodology; CATCMB/CUA, Washington, DC (also offered Mar. 8–12) [see contact: Oct. 12–14]

9–11. PCR Techniques; CATCMB/CUA, Washington, DC [see contact: Oct. 12–14]

11–15. †Advanced Linkage Courses; New York, NY (application deadline: Nov. 16) [see contact: Oct. 19–23]

12–15. Recombinant DNA Techniques; New Brunswick, NJ (early registration: Dec. 31) [Office of Continuing Professional Education, 908/932-9271, Fax: -8726]

March 1993

2–5. PCR Reaction/Cycle DNA Sequencing; ATCC, Washington, DC [see contact: Oct. 26–30]

16–19. Recombinant DNA Techniques; New Brunswick, NJ (early registration: Mar. 1) [see contact: Jan. 12–15]

For Your Information

U.S. Genome Research Funding Guidelines

Note: Investigators wishing to apply for NIH and DOE funding are urged to discuss their projects with agency staff before submitting proposals.

NIH National Center for Human Genome Research (NCHGR)

Application receipt dates:

- R01, P01, R21, R29, P30, P50, K01,* 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.

*Expedited review possible. Check with NCHGR staff during application development phases.

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

- Hard-copy subscription: call 301/496-7441.
- Electronic version (E-Guide): Access through one of the following methods.

1. Institutional Hubs. A designee receives automatic updates and distributes them locally to researchers. To use this NIH-preferred method, send a message naming the responsible person to Rebecca Duvall (BITNET: q2c@nihcu, Internet: q2c@cu.nih.gov).
2. NIH Grant Line (also known as DRGLINE). User reads electronic bulletin board for weekly updates. Connection is through a modem, and a new feature allows files to be transmitted rapidly via BITNET or Internet. For more information, contact John James (301/496-7554 or BITNET: zns@nihcu).

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

DOE Human Genome Program

Solicitations for proposals will be announced in early spring issues of the *Federal Register* and *Science* and in other publications. Formal proposals are due in August.

For further information, contact the program office via

- 301/903-5037, Fax: 301/903-5051, or Internet: drell@mailgw.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: fall 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, 1993. For further information, see *p. 4 or contact*

- Linda Holmes, Oak Ridge Institute for Science and Education: 615/576-4805.◊

Mapping the Mouse Genome–Technology Emphasis

RFA HG-92-002

NCHGR invites applications for support of projects to increase the production rate, resolution, and usefulness of genetic and physical maps of the mouse genome. Specific goals are to (1) incorporate into the genetic map significant numbers of genes identified by sequence tagged sites, (2) develop technology to speed the construction of physical maps, and (3) facilitate the progress of other map-based genetic and molecular biology projects by making mapping resources available to the community.

Receipt Timetable

Letter of intent: October 16; applications: November 13.

For additional information or to discuss proposals, contact Bettie J. Graham, Chief; Research Grants Branch; NIH NCHGR; Building 38A, Room 610; Bethesda, MD 20892 (301/496-7531; Internet: b2g@cu.nih.gov). For a copy of the complete RFA, send a self-addressed label to Mouse RFA at the same mailing address.◊

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3. ___ *Report of the DOE Contractor-Grantee Workshop, February 17–20, 1991* (complete report with abstracts)

AAAS Am. Assoc. for the Advancement of Science
AACR Am. Assoc. for Cancer Research
AAP Association of American Physicians
ACEDB *Caenorhabditis elegans* Database
ACS Am. Chemical Soc.
AFIP Armed Forces Institute of Pathology
AFCR American Federation of Clinical Research
ASHG Am. Soc. of Human Genetics
ASIS American Society for Information Science
ATCC Am. *Type Culture* Collection
BTP Biotechnology Training Programs
CATCMB/CUA Center for Advanced Training in Cell and Molecular Biology/ Catholic Univ. of America
CSHL Cold Spring Harbor Laboratory
ELSI Ethical, Legal, and Social Issues
IG IntelliGenetics
LTI Life Technologies, Inc.
NCHGR National Center for Human Genome Research
NSGC National Society of Genetic Counselors

Reader Comments:

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