Human Genome news

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NCHGR Conducts Model Organism Studies

Model Projects To Facilitate Human Genome Mapping, Sequencing, and International Collaboration

The genomes of organisms such as the roundworm, yeast, bacteria, and mycoplasma are similar to the human genome in many ways. Because of the characteristics of these simpler organisms, investigators can use them in human gene research as models to study gene identity, organization, and function; to examine the processes and diseases that have counterparts in humans; and to aid in the search for homologous genes.

To meet DOE-NIH 5-Year Plan objectives (see box, p. 2), the NIH National Center for Human Genome Research (NCHGR) is funding studies of these nonhuman models for human genome mapping, sequencing, and international collaboration. NCHGR may fund additional model organism studies in the future.

Model Organism Projects

Roundworm

Investigators already understand more about the cellular development and physiology of one of the simplest organisms with a nervous system, the roundworm *Caenorhabditis elegans*, than of any other species. A pilot project to sequence 3Mb in 3 years, jointly funded by NCHGR and the U.K. Medical Research Council (MRC), is now beginning to sequence this tiny nematode's 100-Mb genome. Research groups led by Robert Waterston (Washington University) and John Sulston (MRC Laboratory of Molecular Biology) will collaborate in the effort, which aims at an eventual cost of about $.50 per base.

Currently the only extensive sequencing effort for a multicellular organism, this pilot project is expected to generate new sequencing strategies and data that will lead to a greater understanding of gene function. Information about the worm's DNA sequence will help scientists interpret molecular signals triggering growth and development in this animal.

C. elegans has been intensively studied for over 30 years. Building on the pioneering work of Sydney Brenner (MRC), scientists published in 1986 a diagram of the anatomy of the worm's nervous system. Sulston and his colleagues have traced the developmental lineage of each of the 959 adult somatic cells—an achievement that allows them to relate specific behaviors to particular cells.

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Waterston, Sulston, and Alan Coulson (MRC) had the wholehearted cooperation of the roundworm investigative community in developing highly detailed physical maps of *C. elegans'* six chromosomes to accompany the previously established genetic linkage map. Investigators are now working out efficient sequencing strategies to determine the entire base sequence.

The *C. elegans* physical map database, publicly available via modem or Internet since November 1988, has been set up on a VAX system running VMS in Cambridge, England, and in several places in the United States. Investigators are working on a Unix-based database that will run on workstations and allow access to generated sequences, the physical map, a genetic map, references, and strain lists.

Yeast

The widely studied common brewer's yeast—the single-celled fungus *Saccharomyces cerevisiae*—has been a valuable model because its biochemistry and cellular structure (e.g., cell membranes, a defined nucleus, and other cellular components and processes) are very similar to those of humans. Functions of many major proteins have been shown to be conserved between yeast and higher eukaryotes such as humans. The relationships between genetics and biochemistry and between structure and function are better understood in yeast than in any other eukaryote.

A Stanford University group led by David Botstein and Ronald Davis is beginning to sequence the 12.5-Mbp yeast genome. Yeast DNA sequence data will be correlated with existing chromosome maps, helping to lead researchers to important yeast genes.

Escherichia coli

The common intestinal bacterium *E. coli* has been the most frequently studied model organism for many decades. With the discovery of restriction enzymes in the early 1970s, *E. coli* became the first genetically engineered organism and now underpins the international biotechnology industry.

Fred Blattner (University of Wisconsin) and his colleagues are sequencing the complete *E. coli* genome that consists of 5 Mb on a single circular chromosome. Because much is already known about *E. coli* genetics, sequence data will enable researchers to investigate biochemical mechanisms responsible for the control of gene expression.

Mycoplasma

Walter Gilbert (Harvard University), a Nobel laureate who pioneered DNA sequencing in the mid-1970s, is leading efforts to sequence the genome of *Mycoplasma capricolum*. Strains of this mycoplasma cause pneumonia in a number of animals, including humans. *M. capricolum*, a wall-less bacterium whose genome is estimated to be about 750 kb and to contain only 600 genes, is among the smallest free-living organisms. Although it lacks the complexity of *E. coli, M. capricolum* contains all the essential genes for cell growth and division.

Gilbert's group plans to sequence the one-chromosome mycoplasma without first constructing a map of its genome, which is about 4 times larger than that of the 240-kb cytomegalovirus—the largest genome completely sequenced so far. (Larger genomes require strategies for isolating, cloning, mapping, and sequencing the DNA piece by piece.)

Mouse

A group led by Eric Lander (Whitehead Institute and Massachusetts Institute of Technology) has established a Center for Genome Research to develop a yeast artificial chromosome (YAC) library of the mouse genome, using YACs to construct physical maps of chromosomes 1, 11, and X, with the eventual goal of making a detailed comparison between the mouse and human genomes. The YACs will be available to the mouse genetics community.

David Housman and coworkers will work to achieve continuity across selected regions of the mouse genome by developing ways to connect ordered contigs into a complete physical map. The project will also begin to sequence mouse DNA to detect microsatellite repeats. ◊

Written by Leslie Fink, NCHGR
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and
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The DOE-NIH 5-Year Plan summarized the value of model organism studies to scientific investigation and the Human Genome Project in the following words:

> Experience has shown many times over that information derived from studies of the biology of model organisms is essential to interpreting data obtained in studies of humans and in understanding human biology. Research involving microbial, animal, and plant models will continue to provide a basis for analyzing normal gene regulation, genetic diseases, and evolutionary processes. For this reason, the human genome program will support mapping and sequencing of the genomes of a select number of nonhuman organisms.

Human Genome II Examines Progress

Human Genome II, the second international conference on the status and future of research on the human genome, was held October 22–24, 1990, in San Diego. The meeting, sponsored by the Human Genome Organisation and *Science* magazine, was chaired by James Watson (Director, NIH National Center for Human Genome Research) and Charles Cantor (Lawrence Berkeley Laboratory). The purpose of the conference was to examine progress made in Human Genome Project planning and implementation since the 1989 conference and to provide a forum for communication among the project's administration and scientists, the larger scientific community, and the general public.

The diverse topics covered, the technological improvements and data accumulation reported, and the ambitious plans revealed at the conference testify to the international genome effort's vitality and productivity. Over 700 scientists attended the conference, whose program sessions covered the following topics:

- Genome project organization and funding mechanisms.
- Ethical, legal, and social issues related to the use of data produced by the Human Genome Project.
- Study of model organisms: primarily yeast, roundworm, fruit fly, and mouse.
- New methods: lasers and fluorescent labels; sequencing by hybridization; cloning techniques for expressed or genomic sequences; solid supports for template preparation and sequencing; and computing devices for high-speed sequence comparisons.
- Genetic diversity in humans: disease genes, human leucocyte antigen alleles, mitochondrial sequences, interspersed repetitive sequences, and flow karyotypes of individual chromosomes.
- Genetic regions of interest: a variety of tumor suppressor alleles (e.g., neurofibromatosis, polyposis coli, Wilms' tumor); the cystic fibrosis gene sequence and implications; the fragile X region; oncogenes; and developmental regulator genes.
- Large-scale DNA sequencing projects: design, automation, error handling, and computing needs.

Some 100 posters reported details of technical developments and recently acquired data from around the world; more than a dozen industry-sponsored workshops presented new products and technologies for genome research.

Several major themes emerged from the conference:

- The human DNA sequence is proving extremely interesting to applied and basic molecular biologists alike; indicators of genetic susceptibility to disease and clues to developmental regulation and evolutionary processes have already begun to appear.
- The crucial importance of model organism studies is continually underscored by work on protein sequence homologies and regulatory elements; human genes are now being recognized and isolated by their homologies with genes of model organisms.
- Major improvements in sequencing technologies have been made in a short time. Yet, the sequencing production rate must increase significantly, and the cost must decrease at least tenfold. High throughput and achievement of capabilities for adding finished data directly into sequence databases remain high-priority items.
- New emphasis is being placed on informatics development. Sophisticated methods are needed for sequence assembly and for managing the complex flow of information and materials through a large-scale sequencing project. Other needs include databases and analysis applications capable of handling the enormous quantity of data that will be generated.

Reports presented and events of the past year suggest that answers to basic biological questions regarding structure/function relationships and health and disease may be within grasp. ◇

Reported by Kathleen H. Mavournin
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Human Genome III: October 21–23 San Diego, CA

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Genome Effort Seen Vital, Productive

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

DOE Centers Facilitate Technology Transfer

Industry representatives are invited to attend the February DOE Human Genome Program Contractor-Grantee Workshop to learn more about DOE-funded genome projects.

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Sylvia Spengler
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As the Human Genome Project is implemented, an unprecedented flow of new resources and technologies will be released, many with wide-ranging applications to clinical medicine or to improvements in economically important animals, plants, and microorganisms. Because of the vast potential for commercial development of these technologies, the U.S. Congress views the Human Genome Project as an opportunity to strengthen the nation's ability to compete with other countries industrially and economically.

Benefits Economy

By creating new products, markets, and jobs, rapid deployment of technology from the research laboratory to the marketplace can play an important role in vitalizing the U.S. economy. Application of genome technology to clinical medicine has already begun, with several biotechnology companies predicting an annual $200-million market in genetic tests and personal identification. The pharmaceutical industry is using the new genetic information to improve drug design [see *HGN* **2**(4): 10–11 (November 1990)]. In addition to the impact on medical technologies for humans, investigators and businessmen are anticipating a billion-dollar business in genetically altered animals and plants.

Furthers Human Genome Project Goals

Progress of the genome effort depends on technology development to enable researchers to map and sequence DNA more efficiently and economically. Collaboration between human genome laboratories and the private sector can engender a more focused approach to the technology challenge and allow the project to expand its capital and expertise base.

Transfer Activities at DOE Centers

One mission of the DOE Human Genome Centers at Lawrence Livermore National Laboratory (LLNL), Lawrence Berkeley Laboratory (LBL), and Los Alamos National Laboratory (LANL) is to facilitate the transfer of new genome technologies and resources to industry and small businesses for broader application by the commercial sector. To accomplish this mission, all three laboratories are exploring ways to increase cooperation with the private sector.

A number of projects involving interaction between the centers and the private sector are now under way, and additional interactions (not listed) are in the preliminary stages. In some instances, private industries are marketing technologies developed at research laboratories and are providing research funds or other resources; other collaborative programs involve joint development of technologies and their applications to achieve project goals.

Resource Development, Marketing

- LLNL pioneered chromosome painting using hybridization probes derived from their Charon 21A flow-sorted libraries and repackaged the flow-sorted libraries into a Bluescript® vector for ease of amplification and for use in chromosome painting. Amoco, Inc., will market the amplified libraries and provide funding for further painting technology development.
- LANL pioneered chromosome-specific repetitive sequence hybridization probes for detecting individual human chromosomes.
- Life Technologies, Inc., developed new bacterial host strains that give greater stability to several new cosmid cloning vectors produced by LLNL. Life Technologies is interested in marketing the LLNL vectors.
- Dynal Corporation and LBL are evaluating the use of monodisperse beads in isolating mRNA, chromosomes, and restriction fragments. They are also exploring the use of

The Ultimate Technology Transfer

Perhaps the ultimate technology transfer occurs when one large project creates tools and technologies useful for the initiation of other related projects, whose research in turn produces data that benefits the originating project.

Plant Improvement

The Agricultural Research Service of the U.S. Department of Agriculture is launching its own research effort to study selected traits of key food and forest crops, using methods developed in the Human Genome Project. The agricultural plant genome project will not focus on mapping an entire genome but will search instead for genes that control economically important traits such as yield, nutritional content, and resistance to disease, insects, and drought.

Animal Breeding

Recognizing that gene mapping can contribute toward improving livestock, animal scientists are now making a concerted effort to launch their own genome projects; their efforts will concentrate on mapping genes that control traits such as fat deposition, increased disease resistance, and litter size. Animal researchers are convinced that human chromosome mapping efforts can help direct their own search for genes, since considerable homology has been found to occur between the genomes.

Future Benefits

As technology transfer comes full circle, human genome mapping efforts will reap benefits from the implementation of these plant and animal projects as they reveal information fundamental to the search for specific human genes. ◊

beads to amplify hybridization signals and extend DNA molecules.

- Multichromophore fluorescent probes using DNA intercalation complexes, originated at LBL, are licensed to Molecular Probes, Inc., and will be used to develop new types of fluorescent probes and stains for DNA detection.
- LANL is negotiating with a major biotechnology company the joint development of a technology for sequencing DNA using fluorescent base-specific tags. The tagged DNA fragments will be detected and identified by laser-induced fluorescence.

Hardware Development, Marketing

- LLNL and Autogen, Inc., have been working to extend Autogen's automated plasmid DNA extractor capabilities to include cosmid DNA extraction. LLNL is a test site for this apparatus and will continue to evaluate the system.
- Applied Biosystems, Inc., (ABI) and LLNL developed a fluorescence-based chemistry to automate clone fingerprinting for physical map construction, using a polyacrylamide gel electrophoresis system and software for automated data collection and analysis. ABI is marketing the chemistries and software. To eliminate the use of radioisotopes, ABI and LLNL are developing automated restriction-fragment analysis on a horizontal agarose system using fluorescence tags on DNA, a methodology that can also be applied to Southern blotting procedures.
- LLNL, LANL, and Beckman Instruments, Inc., are redesigning and testing the high-density replica plater attachment for the Biomek® Workstation. This device, as presently configured, automatically creates high-density arrays of plasmids, lambda, cosmids, or YACs on agarose or filters.
- Bio-Rad Corporation and LANL are developing and applying Bio-Rad's pulsed-field gel electrophoresis technology to enhance resolution of multimegabase DNA fragments.
- LBL and Hewlett-Packard (HP) are devising advanced applications for HP robotic systems. HP is providing technical assistance and lending some advanced robotic hardware.
- LBL is working to generate DNA templates for the ABI automated DNA sequencer. LBL is also devising methods to obtain sequence tagged sites from YAC clones, using *Alu*-vector, inverse, and anchored PCR to obtain YAC end-specific templates.
- LBL and Cruachem, Inc., are collaborating on an advanced low-cost, high-volume, 20-channel DNA synthesizer

(see Technology Transfer, p. 6)

Steps in the Technology Transfer Process

Finding Opportunities

Because industry also benefits from opportunities to develop the technologies and resources that will eventually be required for genome project work, these interactions can be viewed as two-way technology transfers. National laboratory human genome centers provide a variety of opportunities for the private sector to collaborate on joint projects or to obtain direct access to technology.

Private-sector involvement in research and development can determine how successfully the technology transfers to the marketplace, and collaborative efforts can speed development of essential tools for genome research. Effective publication of opportunities for collaboration is, therefore, particularly important. Opportunities for cooperative work or licensing are communicated in several ways:

- Announcements in **Commerce Business Daily** (a government publication used by many private businesses) and in various technology transfer journals.
- Center-sponsored workshops and seminars, announced mainly in scientific journals, to facilitate interaction with the scientific community, including industry researchers. Over 50 industry representatives attended the 1988 Human Genome Workshop, sponsored by the LANL Technology Transfer Office, to learn about opportunities arising from genome work. Communication among academic and national laboratory researchers fosters continuing dialogues and collaboration.
- Human Genome Project research reports presented at conferences and in scientific and technical publications.

STEP 1. CONTACT: To receive general information about laboratories and specific data about ongoing programs and their current output, persons interested in technology transfer should first contact the technology transfer offices of the DOE human genome centers:

- LANL: Ronald Barks, 505/667-3839
- LLNL: Peter Matlock, 415/422-6416
- LBL: Pepi Ross, 415/486-6462

The company will be asked to send general information to the center, possibly including an annual report. Technology transfer offices may initiate discussions between a company and appropriate scientists or engineers after receipt of this information.

STEP 2. MEETING: Interested companies may be invited to the centers to view facilities and to continue discussions; laboratory and company representatives then work together to develop collaborative programs. If there is a large response from the private sector to a particular project, a workshop may be held to discuss opportunities for collaborations or licenses.

STEP 3. PROPOSAL: After a proposal for the collaborative program or licensing plan is submitted for evaluation, the center may request a business development plan to eliminate technically unqualified companies from consideration and to ensure the appropriateness of the planned resource or technology use.

STEP 4. APPLICANT SELECTION: Reviewers, including representatives from noncompeting businesses and the centers' legal and technical/scientific offices, consider all aspects of each proposal, after which the company most appropriate for the interaction is selected.

National Competitiveness Technology Transfer Act of 1989

Last year, in the continuing effort to facilitate interaction between the public and DOE national laboratories, the U.S. Congress passed the National Competitiveness Technology Transfer Act. When implemented, this law will allow more direct interaction among the research laboratories, industry, academia, and state and local government agencies. ◊

Genome News

Human Genome news

NATIONAL INSTITUTES OF HEALTH

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

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DEPARTMENT OF ENERGY · UNITED STATES OF AMERICA

Technology Transfer *(from p. 5)*

and on control software design and implementation. LBL will evaluate instrument prototypes.

- A laser-excited confocal fluorescence gel scanner, designed at LBL, is being licensed by Molecular Dynamics and will be developed into a commercial gel scanner for reading DNA sequencing and fingerprinting gels.

Software Development, Marketing

- IBM and LANL have jointly tested computer-developed programs for efficiently calculating the probability of clone overlap, based upon fingerprint characteristics that the clones have in common. Management of heterogeneous networks and databases of interest to the genome program are also being investigated.
- LLNL and Amoco, Inc., are collaborating on an image-analysis system for semi-automated chromosome karyotyping and on user-friendly application programs for karyotype analysis. They plan to transfer the application to clinical and research laboratories. With Delft University (the Netherlands), hardware and software were produced for a Macintosh-based karyotyping system.
- LANL has negotiated with Sybase and Servio Corporation to make available to Human Genome Project investigators their respective products, namely, relational and object-oriented database management systems, at greatly reduced costs. Hands-on use of these products will show the originators where modifications need to be made.
- ABI is marketing the "Contig Browser," a prototype version of software developed at LLNL for analysis of overlapping clones (contigs) and graphical display of those contigs.
- LBL and DiaQuest, Inc., developed data-capture software for images from video screens, in conjunction with a single DNA molecule imaging system. The software will be marketed by DiaQuest.
- Oracle Corporation and LANL are investigating the applicability of object-oriented database methods to human genome data. A formal collaboration is under consideration.
- LBL and Photometrics, Inc., developed a number of image-analysis programs (based on the X-window system) that have been transferred to Photometrics for its high-resolution charged-coupled display development work. ◇

Written by Denise K. Casey
HGMIS, Oak Ridge National Laboratory

Chromosome 22 Newsgroup Established

An electronic bulletin board has been established as part of the international BIOSCI network to allow more frequent contact among persons interested in chromosome 22 mapping and sequencing, specific genes, chromosomal abnormalities, and related disease phenotypes. It will also serve as a forum to distribute information concerning new clones, references, cell lines, genes, polymorphisms, and scientific meetings. [See *HGN* **2**(1): 10 (May 1990) for information on the BIOSCI Human Genome newsgroup.]

The Chromosome 22 Newsgroup can be received worldwide via USENET as "bionet.genome.chrom22", with USENET software running. To obtain a news source or "feed," contact Internet: "biosci@genbank.bio.net".

Regular electronic mail access is also available via:

- Internet, BITNET, EARN, or JANET.
- Modem through the GenBank® On-line Service (415/962-7364).

Request Chromosome 22 Newsgroup subscription via electronic mail to one of the following BIOSCI nodes:*

- Ireland – EARN/BITNET: "biosci@irlearn.ucd.ie"
- United Kingdom – JANET: "biosci@uk.ac.daresbury"
- Sweden – Internet: "biosci@bmc.uu.se"
- United States – Internet/BITNET: "biosci@genbank.bio.net"

*Users in other parts of the world may contact either the U.S. or Ireland nodes. ◇

Working Group Hears Sequencers

The second meeting of the NIH-DOE Joint Sequencing Working Group was held on September 29 in Hilton Head, South Carolina. Several scientists engaged in large-scale sequencing projects were invited to present the current status of their sequencing efforts and to participate in discussions.

DOE and NIH staff also reported briefly on new program activities:

- DOE has embarked on a project to produce sequence tagged sites from human cDNAs.
- NIH has issued a Request for Applications for "Feasibility Studies for Large-Scale DNA Sequencing of Regions of High Biological Interest."

Cost Determination

The actual cost of DNA sequencing, particularly large-scale sequencing, is not easy to determine at the moment. In an attempt to come to terms with this issue, the investigators who reported on their sequencing projects were asked to include cost estimates. Participants agreed that for purposes of assessing costs, sequencing begins with an isolated cosmid (or equivalent) with the DNA ready to be subcloned into M13 and ends with assembly of the final sequence, ready for publication or submission to a database.

Working group discussions made clear that estimating costs is difficult for a number of reasons. Lab-to-lab sequencing costs vary because of these factors:

1. Use of different sequencing technologies,
2. Amount of technology development in a given project,
3. Level of accuracy of finished sequence, and
4. Overhead costs.

The committee felt that sequencing cost estimates should incorporate technology development because the only sequencing projects being funded are those that include significant technology development.

The working group recommended that the NIH National Center for Human Genome Research (NCHGR) attempt to establish a standard means for determining current costs as a baseline to which future charges can be realistically compared. Accordingly, NCHGR has contracted with a fiscal consultant to review sequencing costs in a number of laboratories and to help establish a model for measuring the impact of new technologies on reducing sequencing costs.

Invited Participants

Frederick R. Blattner	University of Wisconsin
George M. Church	Harvard Medical School
Richard A. Gibbs	Baylor College of Medicine
Bruce A. Roe	University of Oklahoma
J. Craig Venter	National Institutes of Health
Richard K. Wilson	Washington University School of Medicine

Technology Development

The working group discussed ways to stimulate new sequencing technology development. They agreed that NIH and DOE should encourage grantees to seek out investigators from other disciplines who might contribute to technology advancement. Most new development will take place in the context of established sequencing efforts.

Finally, participants discussed how DOE and NIH could communicate more effectively with the larger scientific community to counteract the mistaken impression that large-scale sequencing of human DNA is a major component of the current research program. The working group agreed that articles should be published in prominent journals to publicize these facts:

1. Most NIH Human Genome Program funds are devoted to genetic and physical mapping, with only 15% going to sequencing technology development.
2. Most NIH sequencing technology development projects, namely, yeast, *Caenorhabditis elegans*, and *Escherichia coli*, are examining model organisms, which are of interest to many investigators,

The next meeting of the working group will be held in conjunction with the Cold Spring Harbor Genome meeting in May.

For a list of members, see *HGN* **2** (2): 4 (July 1990). Invited participants are listed above. ◇

Reported by Jane L. Peterson
Chief, Research Centers Branch
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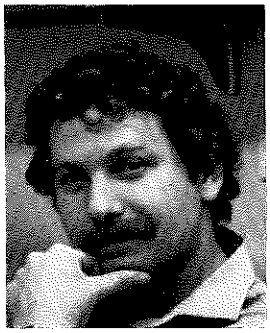

Eric S. Lander
Chairman
NIH Research Review Committee

Lander To Chair NIH Genome Research Review Committee

Eric S. Lander was recently appointed chairman of the 18-member NIH Genome Research Review Committee. The committee provides the National Center for Human Genome Research with a primary review of research and training grants-in-aid, grant applications, cooperative agreements, and contract proposals for special research programs.

These programs include projects and centers, institutional fellowships, conference proposals, special developmental award programs, and contract proposals for research related to human and model organism characterization.

Such research covers:

- construction of genetic and physical maps;
- technology development for DNA sequencing, data management, and analysis; and
- development of innovative support technologies, tools, and resources.

Eric Lander, a member of the Whitehead Institute for Biomedical Research and of the faculty at the Massachusetts Institute of Technology, is Director of the MIT Center for Genome Research. He received a B.A. degree from Princeton University and a Ph.D. from Oxford University, where he was a Rhodes Scholar. Lander is a MacArthur Prize Fellow for 1987 to 1992.

Lander serves on the editorial boards of *Genomics* and *Mammalian Genome* and is a member of the Joint Informatics Task Force of the Joint NIH-DOE Subcommittee on the Human Genome.

Research Review Committee members are appointed to 4-year terms by the NIH Director from the fields of human genetics, quantitative genetics, molecular biology, cell biology, biochemistry, and computer science. ◇

Reported by Anne E. Adamson
HGMIS, Oak Ridge National Laboratory

W. David Benton
NCHGR Assistant to the Director for Scientific Data Management

NCHGR Names Benton To Oversee Computing Needs

A big challenge facing the Human Genome Project is the development of new computer software and hardware to gather, store, and analyze the vast amount of information from the project's mapping and sequencing research. The 50,000 to 100,000 genes in the human genome are estimated to contain information, which, if printed in dictionary type, would require a 220,000-page volume about 25 feet thick.

Informatics—a new scientific discipline—uses mathematics, computer science, and biology to create tools for acquiring and managing genome research data and for analyzing biological information contained in human and model organism genomes. Although computing has become more common in biomedical research, further software development and integration of machines and databases are needed.

To oversee the informatics program, which will develop computer technologies capable of meeting Human Genome Project needs, W. David Benton has joined the National Center for Human Genome Research (NCHGR) as Assistant to the Director for Scientific Data Management.

Benton comes to NCHGR from IntelliGenetics, Inc., where he managed the DNA sequence database GenBank®. Benton received his B.A. degree in chemistry from St. Olaf College and his Ph.D. in cell biology from the University of Minnesota, where he studied the sequence of ribosomal RNA genes in plants. From 1980 to 1985, he worked as a molecular and cell biologist for the Atlantic Richfield Plant Cell Research Institute in Dublin, California. In the Stanford University laboratory of Ronald Davis, Benton developed the method now widely used for screening bacteriophage DNA for recombinant sequence. ◇

DOE HGCC Discusses YACs and cDNAs

The DOE Human Genome Coordinating Committee (HGCC) met November 20 in Livermore, California. Discussion topics included yeast artificial chromosomes (YACs), cDNAs, the contractor-grantee workshop, and study section reviews.

Elbert Branscomb became the newest member of HGCC in October. Responsible for the computations and informatics effort at the Lawrence Livermore National Laboratory Human Genome Center, Branscomb brings substantial informatics expertise to HGCC. He received his Ph.D. in theoretical physics from Syracuse University in 1964. Sylvia Spengler is representing the Lawrence Berkeley Human Genome Center on the committee until the center's director is appointed.

For additional information about HGCC membership, please refer to *Human Genome Quarterly* 1(1): 3–4 (Spring 1989) and 1(3): 5 (Winter 1990).

YAC Goals

DOE roles regarding YACs include support of the following:

- YAC distribution by contract.
- Establishment of a new size-selected library in strains with many markers. A number of companies could handle this on a contract basis.
- Basic YAC research, such as enhancement of transformation efficiency as it applies to library construction; testing would be required.

cDNA Initiative

Charles Cantor (HGCC Chair and Principal Scientist, DOE Human Genome Program) will contribute to the section of the Request for Proposals related to cDNAs. With coordinated exchanges of cDNAs among laboratories, cDNA mapping would cost about the same as creating STSs within random regions of the genome. The added benefit is that sequencing of cDNAs would yield important biological information early in the Human Genome Project. A major goal of the cDNA initiative is to establish STS sites within unique cDNA clones to aid the mapping effort. Suggested activities to support this goal include:

1. Developing new libraries, both those normalized and those reduced by other techniques.
2. Developing mapping tags, such as STSs; that is, conversion of DNA sequences to STSs.
3. Mapping of cDNA/STSs to the chromosome.
4. Tying maps, sequences, and STSs to a database.
5. Initiating or significantly improving techniques to localize cDNAs to a chromosome or region.
6. Exploring methods to produce a master cDNA set.

Other possible areas of support involve the usefulness of mouse cDNAs to map human regions and the impact of multigene families on mapping and STSs.

HGCC met December 4 in Bethesda, Maryland, to review study section results and to further discuss the DOE cDNA initiative with invited experts.

The next HGCC meeting will be in Santa Fe, New Mexico, on February 21, following the DOE Human Genome Program contractor-grantee workshop. Discussions will focus on progress and overall program coordination. ◊

Reported by Sylvia J. Spengler
Executive Officer, HGCC

Manuscripts Requested

Bioethics is planning a 1991 special issue on "The Human Genome Project: Where Will the Map Land Us?" Manuscripts for major articles, reports, short discussion papers, and book reviews are invited. Contributions—from any relevant discipline—should be related to ethical aspects of the genome project. A prior letter of inquiry or abstract is recommended before manuscript submission. The deadline is January 15. ◊

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NCHGR ELSI Program Plans Productive Year

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Eric Juengst, Director
NCHGR Ethical, Legal, and Social Implications Program
Building 38A, Rm. 614
9000 Rockville Pike
Bethesda, MD 20892
301/496-7531

The Human Genome Project is faced not only with formidable scientific challenges but also with important ethical, legal, and social questions arising from the availability of new genetic information. Questions related to genetic testing, counseling, access to genetic information, and insurability have led to the funding of projects designed to study these issues.

In FY 1990 the National Center for Human Genome Research (NCHGR) allocated $1.6 million to such projects initiated by the Center's Ethical, Legal, and Social Implications (ELSI) program, headed by Eric Juengst.

Studies, conferences, and research projects funded by NCHGR include the following activities:

- Two-year study, conducted by the Institute of Medicine, to examine questions of quality control in genetic test administration and interpretation.
- March 1991 conference at the University of Houston Health Law Center to summarize studies in antidiscrimination law, privacy rights, and property rights law and to assess the application of these laws.
- Three interdisciplinary meetings focusing on scientific, ethical, and legal problems and cosponsored with the American Association for the Advancement of Science.
- International conference at the University of Wisconsin, Madison, to examine such questions as military use of genetic information, international sharing of research benefits and burdens, and the definition of issues most in need of the international community's attention.
- Conference at the University of California, Berkeley, to encourage historians, social scientists, and philosophers to consider the social impact of new genetic information.
- January 1991 workshop in Washington, D.C., to establish areas of agreement and disagreement regarding

(see NCHGR ELSI, p. 11)

Genetics, Religion, and Ethics Initiative Holds Conferences

Initiative Contact:
J. Robert Nelson
Texas Medical Center
P.O. Box 20569
Houston, TX 77225
713/797-0600

Among the spin-off studies and activities of the Human Genome Project is the unique, 3-year initiative "Genetics, Religion, and Ethics." The undertaking is designed to provide an ongoing inquiry and creative dialogue among some 150 genetic researchers, physicians, ethicists, theologians, public policymakers, and representatives of churches and religions interested in the uses of data produced by genetic science.

As the first stage of the project, a conference was held March 30–April 1, 1990, at the Institute of Religion of the Texas Medical Center in Houston. Groups formed at this conference are now meeting in Chicago, Boston, Washington, and Houston to study identified social, ethical, and religious questions arising from the Human Genome Project. The second conference, using position papers prepared by the four groups, will take place in Houston March 13–15, 1992; the project will conclude with preparation and distribution of a book for use by the scientific, medical, and religious communities, as well as the general public. ◇

Speakers at the March 30–April 1 Conference:

J. Robert Nelson (Director of the Institute of Religion, Texas Medical Center): "Changing Concepts of Human Life, Nature, and Identity."

Francis S. Collins (Director of the Center for Genome Research, University of Michigan): "Implications of the Human Genome Project for Medical Practice."

William R. Hendee (Vice President for Science and Technology, American Medical Association): "Public Attitudes Toward the Human Genome Project: Endorsement, Indifference, Opposition."

John C. Fletcher (Professor of Biomedical Ethics and Religious Studies, University of Virginia): "The Ethical Futures of Autonomy and Privacy in a World Where the Human Genome Is Mapped."

C. Thomas Caskey (Director of the Institute for Molecular Genetics, Baylor College of Medicine): "Updating the Human Genome Project."

Robert M. Cook-Deegan (HUGO): "Updating Public Policy."

RELIGIOUS PERSPECTIVES REPRESENTED

Albert Moraczewski (Pope John XXIII Medical-Moral Research and Education Center, Houston): The Roman Catholic Church.

Stanley S. Harakas (Holy Cross Greek Orthodox School of Theology, Brookline, MA): The Greek Orthodox Church.

Hartwig von Schubert (World Council of Churches, Heidelberg, Germany): Protestant Churches of Europe.

Maimon M. Cohen (University of Maryland Medical School): Judaism.

Hassan M. Hathout (The Genetics Institute): Islam.

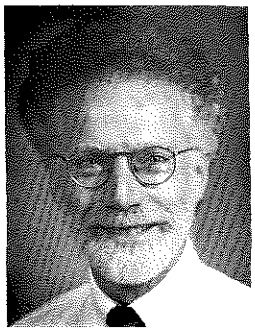
DOE Appoints Yesley To Oversee ELSI Program

Michael S. Yesley, staff attorney at Los Alamos National Laboratory (LANL), will assist in the administration of the DOE program on Ethical, Legal, and Social Issues (ELSI) related to the use of data produced in the Human Genome Project.

Yesley, who also conducts an ELSI program at the LANL Center for Human Genome Studies, has extensive experience in bioethics. He was Staff Director of the National Commission for the Protection of Human Subjects (NCPHS) at the Department of Health, Education, and Welfare from 1974 to 1978 and chaired the human studies review board at The Rand Corporation from 1978 to 1980. While at Rand, he taught courses at the University of California, Los Angeles, on ethical issues in biomedical and social science research.

"Michael is a welcome addition to the DOE human genome program. He brings an expertise and background of knowledge that complements our technical capabilities," says Benjamin Barnhart, Manager of the DOE program.

After moving to Santa Fe to practice law in 1980, Yesley served on the New Mexico Medical Malpractice Commission and the Bioethics Committee of St. Vincent Hospital. He has worked at LANL for the past 2 years on safety and environmental matters, taxation, R&D contracting, and review of human studies, in addition to the ELSI program. He earned a B.A. degree in philosophy and a J.D. degree from Harvard University.



Michael S. Yesley
DOE ELSI Program

Michael S. Yesley
Los Alamos National Laboratory
MS A187, P. O. Box 1663
Los Alamos, NM 87545
505/665-2523, Fax: 505/665-2301
Internet: "yesley_michael_s@ofvax.lanl.gov"

Yesley will serve as corepresentative with DOE program staff to the DOE-NIH Joint ELSI Working Group and, when requested, as DOE liaison with other U.S. and worldwide public and private programs and institutions. He will also assist DOE staff in managing the review of ELSI grant proposals submitted to the DOE Office of Energy Research.

According to Yesley, acquiring and analyzing relevant information will help develop the means to resolve major societal concerns raised by potential uses of vastly increased genetic knowledge. This will require a cooperative effort from many disciplines, including the biological and social sciences, health care, law, and the humanities; representatives of the sectors of society that will be most affected by the new genetic knowledge must be included in the deliberations.

Basic principles for protecting human research subjects as set forth by NCPHS in its Belmont Report (1978) will provide guidance, Yesley believes. Those principles are:

1. Beneficence: maximizing benefits while minimizing harm.
2. Respect for persons: assuring individual autonomy while protecting those with limited capacity for self-determination.
3. Justice: allocating benefits and burdens fairly. ◊

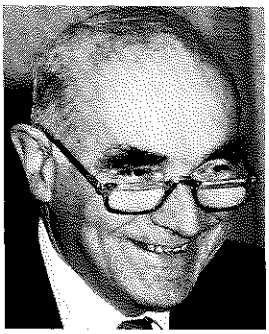
NCHGR ELSI *(from p. 10)*

responsible use of genetic information and to seek ways of reaching consensus in areas of greatest disagreement.

- April 1991 meeting at the Center for Biomedical Ethics, University of Minnesota, to examine and review professional standards in genetic counseling and to explore the impact that genomic research may have on the counseling profession.
- Research project focusing on physicians' attitudes and preparedness for widespread genetic testing.
- Research project designed to minimize misinterpretation of genetic test results and to clarify the genetic disease concept and analyze its role in ethical and social issues.
- Production of a public television series, in cooperation with the National Science Foundation, to inform the public about the role of genetic research in future health care.

The NCHGR ELSI program is also working with the DOE Human Genome Program and other organizations to disseminate information about the implications of genetic research. ◊

Genome News



Hubert Curien
Minister of Research
and Technology

France Launches Human Genome Program

Genome-related research in France today involves more than 67 laboratories and some 500 researchers, engineers, and technicians working for public research agencies and universities, according to Hubert Curien, Minister of Research and Technology.

In outlining the French Human Genome Research Program to the Council of Ministers at its October 17, 1990, meeting, Curien said that to date the government has appropriated 150 million francs ($30 million) for human genome research; in 1990 funding by the Research and Technology Fund (Fonds de la Recherche et de la Technologie) included the following allocations:

- 7 million francs ($1.4 million) for research on methodologies adapted to genome research. These awards were based on competitive bids solicited in 1988.
- 16 million francs ($3.2 million) to the Centre d'Etude du Polymorphisme Humain (CEPH).
- 30 million francs ($6 million) to the 4-year European Eureka Program to design and produce a series of robots that will increase the speed of molecular biology operations such as nucleic acid extraction, circular DNA preparation ("Miniprep"), molecular hybridization, cloning, cloned-DNA fragment mapping, and DNA sequencing. The Miniprep robot should be marketed in 1991.

Formal Program – GIP

To spur research efforts on human gene analysis, France is launching this month a formal national human genome research program, piloted by a special committee called a Groupement d'Interet Public (GIP). In addition to the funds already allocated, the committee will have at its disposal 50 million francs ($10 million) in 1991 and 100 million francs ($20 million) annually, beginning in 1992. In total, France has pledged 200 million francs ($40 million) for human genome research in 1991 and 250 million francs ($50 million) in 1992.

Presided over by a leading scientist, GIP will be an autonomous body that will coordinate planning and execution of laboratory research projects and organize international cooperation, notably with other European countries and the United States. Its executive board will be composed of participating industrialists and representatives of concerned research agencies and involved ministries, such as Research, Health, National Education, and Industry. The executive board will be assisted by a scientific board charged with defining programs and evaluating research projects and their results. A GIP subcommittee will oversee the program's medical, technological, and economic applications.

France will concentrate research activity on the genome's coding regions, only 5 to 10% of the genome. To this end, authorities plan to:

- speed up development of automated mapping methods used in molecular biology;
- expand computer capabilities (hardware and software for data processing and analysis);
- train highly qualified personnel; and
- distribute biological specimens to laboratories for analysis, reproduction, and storage.

In parallel with human DNA research, genomes of model organisms such as bacteria and yeast will be analyzed in an effort to understand the mechanisms of gene expression and species evolution.

Because of the program's ethical, legal, and social implications, the French National Ethics committee (Comite National d'Ethique) has already been consulted and will be kept informed regarding new data arising from human genome research. ◇

Reported by Michele Durand
Science Attache, French Embassy
Washington, D.C.

French Public Research Agencies Involved in Genome Research:

- Centre National de la Recherche Scientifique (CNRS)
- Institut National de la Sante et de la Recherche Medicale (INSERM)
- Institut National de la Recherche Agronomique (INRA)
- Commissariat a l'Energie Atomique (CEA)
- Institut Pasteur de Paris
- Institut National de la Recherche en Informatique et en Automatique (INRIA)

NSF Grants Offered

The National Science Foundation (NSF) Directorate of Biological, Behavioral, and Social Sciences (BBS) has announced that grants are being offered in the following areas:

1. A cross-disciplinary effort to foster the design, development, implementation, and use of information resources for managing the large amounts of archival information generated by research programs. Eligible activities include:
   - Planning and development of new public-use databases and software, methods, and tools.
   - Scientific data management research.
   - BBS data management training, including conferences and workshops.
   - BBS information management idea exchange.
   - Genomic applications, particularly for nonhuman model species.

For information, contact Robert Robbins, 202/357-7652.

2. The *Arabidopsis* Genome Research Initiative [*HGN* **2**(3): 13 (September 1990)].

For information, contact Machi Dilworth, 202/357-7652.

To receive NSF grant applications, contact: NSF Division of Grants and Contracts; Washington, DC 20550 (202/357-7880). ◇

For more information . . .

HGMIS can provide readers with more information on many of the newsletter articles or other related material. Please contact :

- Laura Yust, 615/574-7582 (see HGMIS address, p. 16).

U.S. Genome Research Funding Information

Note: Investigators wishing to apply for NIH or USDA funding are urged to discuss their projects with agency staff before submitting formal proposals. DOE accepts preproposals without prior discussion.

NIH National Center for Human Genome Research (NCHGR)

Application receipt dates:

- R01, P01, R21, 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 Innovative Research (SBIR) grants – April 15, August 15, and December 15.
- Requests for Applications (RFAs) – receipt dates are independent of the above dates.

Program announcements are listed in issues of the weekly *NIH Guide for Grants and Contracts*, which may be obtained 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; send E-mail requests to "pjones@uncvx1.bitnet" or "jones@samba.acs.unc.edu" (Internet).

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

DOE Human Genome Program

Solicitations for proposals are published in a February or March issue of the *Federal Register*, in *Science*, and in other publications. After submitted preproposals are evaluated for programmatic relevance, formal proposals will be due in August.

SBIR Grants. DOE also invites small business firms (500 or fewer employees) to submit grant applications addressing the human genome topic of the Small Business Innovation Research (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.

Selected firms may receive up to $50,000 to explore the feasibility of their ideas. In a second phase, up to $500,000 will be available to individual firms to support those ideas judged highest in potential for meeting program objectives. For a copy of the DOE solicitation, issued on December 7, 1990, contact: Samuel Barish; SBIR Program Manager, ER-16; DOE; Washington, DC 20585; 301/353-5707.

- SBIR grant application receipt date: March 7.

U.S. Department of Agriculture (USDA)

Genome projects and proposal receipt dates:

- USDA Plant Genome Research Project – January 28, 202/401-4871.
- USDA Animal Molecular Genetics Project – February 4, 202/401-4399.

Grant Application Kits: Proposal Services Branch, 202/401-5056. ◇

Calendar of Genome Events*

January	24–25	**Human Genome Workshop: Ethics, Law, and Social Policy**; Washington, DC [*B. Weibel, 901/577-4905*]
	27–Feb. 1	**Bio/Technology Magazine Winter Symposium – Advances in Gene Technology: The Molecular Biology of Human Genetic Disease**; Miami Beach, FL [*The Miami Bio/Technology Winter Symposia, 800/642-4363, Fax: 305/324-5665*]
February	3	**"Symposium on Ethical, Legal, and Social Implications of Human Genome Research"** at the **National Association for Science, Technology, and Society Meeting**; Arlington, VA [*V. Mike, 212/535-3231*]
	17–20	***DOE Contractor-Grantee Workshop**; Santa Fe, NM [*S. Spengler, 415/486-4943, Fax: 415/486-5717*]
	18–19	**Biomedical Ethics Sessions** at **The AAAS Annual Meeting**; Washington, DC [*AAAS conference office*, 202/326-6450]
	20	***DOE Human Genome Coordinating Committee**; Los Alamos, NM
	24–28	Paper session on **"Molecular Biology Applications"** at **The Seventh IEEE Conference on Artificial Intelligence Applications**; Miami Beach, FL [*D. Searls, 215/648-2146, Fax: 215/648-2288*]
March	7–9	**Legal and Ethical Issues Raised by the Human Genome Project**; Houston, TX [*C. Tanenbaum, 713/749-3872*]
	15–16	***Workshop on a Legal Research Agenda for the Human Genome Initiative**; Tempe, AZ [*D. Karjala, 602/965-2124*]
	15–17	***Chromosome 17 Workshop**; Salt Lake City, UT (abstract required) [*P. Fain, 801/581-5070, Fax: 801/581-6052*]
	19–21	**"Development and Application of Electrophoretic Techniques in Molecular Biology"** sessions at the **International Electrophoresis Society Meeting**; Washington, DC [*J. Cunningham, 301/898-3772, Fax: 301/898-5596*]
	24–28	**Mathematical Analysis of the Human Genome: DNA Sequence to Protein Structure**; Santa Fe, NM [*S. Spengler, 415/486-4943, Fax: 415/486-5717*]
April	8–9	***The Genetic Prism: Understanding Health and Responsibilities**; Berkeley, CA [*P. Boyle, 914/762-8500*]
	12	**Technological, Ethical, Legal, and Public Policy Implications of the Emerging Genetic Knowledge**; Oklahoma City, OK [*T. Bole, 405/271-2111*]
	18–20	**Conference on Biotechnology and the Diagnosis of Genetic Disease: An Assessment Forum on the Societal, Technical, and Regulatory Issues**; Arlington, VA [*S. Wilkinson, 202/687-5391*]
	19–20	***Genetic Counseling: Ethics, Values, and Professional Responsibilities**; Minneapolis, MN [*Meetings proceedings available from D. Bartels, 612/625-4917*]
	22–24	**"Workshop on Social Issues in Human Genome Research"** at **FASEB 1991**; Atlanta, GA [*E. Juengst, 301/496-7531*]
May	8–11	***Genome Mapping and Sequencing Conference**; Cold Spring Harbor, NY
	15–18	**Genetic-Related Symposia** at the **82nd Annual Meeting of the American Association for Cancer Research**; Houston , TX [*M. Foti, 215/440-9300, Fax: 215/440-9313*]
June	1–5	**8th International *C. elegans* Meeting**; Madison, WI [*Registration materials: Memorial Union Conference Office, 608/262-2755; Technical information: P. Anderson, 608/263-8429*]
	24	**NIH Program Advisory Committee on the Human Genome**; Bethesda, MD [*C. Mohan, 301/496-0844, afternoons*]

*Attendance at meetings listed with asterisk is either limited or restricted.

Calendar of Genome Events*

July	14–18	***Workshop at AAAI-91 Conference: AI Approaches to Classification and Pattern Recognition in Molecular Biology**; Anaheim, CA; attendance applications deadline: March 8 [*M. Noordewier, 201/932-3698*]
	22–26	**"High Performance Computing in Biology and Medicine"** and **"Computational Molecular Biology and Genetics"** at the **13th IMACS World Congress on Computation and Applied Mathematics**; Dublin [*M. Witten, USA, 512/471-2472, Fax: 512/471-2445, E-mail: "xxvb742@utchpc.bitnet" or "xxvb742@morpheus.chpc.utexas.edu"*]
August	18–22	**11th International Workshop on Human Gene Mapping (HGM 11)**; London [*M. Probert, (Int.) 44-71/269-3052, Fax: 44-71/430-1787*]
September	22–25	**Genome Sequencing Conference** III; Hilton Head, SC [*S. Wallace, 301/480-0634, Fax: 301/480-8588*]

*Attendance at meetings listed with asterisk is either limited or restricted.

Training Calendar: Workshops and Coursework

February	4–9	**cDNA Library Workshop**; LTI, Germantown, MD (also offered Mar. 4–9) [*G. Tinney, 800/828-6686 or 301/921-2250, Fax: 301/258-8212*]
	18–22	**Recombinant DNA Techniques**; LTI, Germantown, MD [*see contact: Feb. 4–9*]
March	4–8	**Recombinant DNA Methodology: Lecture/Demonstration**; Washington, DC [*Catholic University of America, 202/319-6161, Fax: 202/319-5721*]
	11–26	**Carolina Workshop: In Vitro Mutagenesis Technology**; Chapel Hill, NC [*P. Carl, 919/962-8920, Fax: 919/966-6821*]
	18	**DNA Amplification by PCR: Hands-On Training in Molecular Biology Laboratory Techniques**; BTP, Norton, MA (also offered at other times and locations) [*S. Chance, 515/232-8306 1:00–5:00 p.m.CST*]
	18–22	**Transfection Techniques**; LTI, Germantown, MD [*see contact: Feb. 4–9*]
	19–22	**Basic Cloning Techniques**; Norton, MA [*see contact: Mar.18*]
April	2–5	**Linkage and Chromosome Mapping/Sequence Analysis**: Courses at U.K. Human Genome Mapping Project Resource Centre; Harrow, England (also offered at later dates) [*C. Bates, (Int.) 44/81-869-3446, Fax: (Int.) 44/81-869-3807*]
	8–22	**Cloning & Analysis of Large DNA Molecules**; Cold Spring Harbor, NY (applications were due 1/15/91) [*CSHL, 516/367-8343, Fax: 516/367-8845*]
	15–19 & 22–26	**Recombinant DNA: Techniques and Applications**; ATCC, Rockville, MD [*D. Drabkowski, 301/231-5566, Fax: 301/770-1805*]
May	7–10	**RFLP Analysis: Hands-On Training in Molecular Biology Laboratory Techniques**; New Orleans, LA [*see contact: Mar. 18*]
June	24–28	**Principles of Flow Cytometry: Hands-On Training in Molecular Biology Laboratory Techniques**; Ames, IA [*see contact: Mar. 18*]
July	5–13	**DNA Related Methods in Human Genetics: YAC Cloning in Genome Analysis**; London [*P. Faik, (Int.) 44/71-403-6998*]
	22–Aug. 2	**Short Course in Medical and Experimental Mammalian Genetics**; Jackson Laboratory, Bar Harbor, ME [*J. Musetti, 207/288-3371, ext. 1253, Fax: 207/288-5079*]
August	5–12	**Genetic Approaches to Human Disease Using DNA Markers**; Cold Spring Harbor, NY [*see contact: April 8–22*]

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.

ABI	Applied Biosystems, Inc.
AAAI	American Association for Artificial Intelligence
AAAS	American Association for the Advancement of Science
ATCC	American Type Culture Collection
BBS	Biological, Behavioral, and Social Sciences (NSF)
BTP	Biotechnology Program
cDNA	complementary DNA
DNA	deoxyribonucleic acid
DOE	Department of Energy (U.S.)
ELSI	Ethical, Legal, and Social Issues/ Implications
FASEB	Federation of American Societies for Experimental Biology
GDB	Genome Data Base (HHMI)
GIP	Groupement d'Interet Public
HERAC	Health and Environmental Research Advisory Committee
HGCC*	Human Genome Coordinating Committee
HGM	Human Genome Mapping
HGN*†	**Human Genome News**
HGMIS*	Human Genome Management Information System (ORNL)
HHMI	Howard Hughes Medical Institute
HP	Hewlett-Packard
HUGO	Human Genome Organisation [International]
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.
MIT	Massachusetts Institute of Technology
MRC	Medical Research Council
NCHGR†	National Center for Human Genome Research (NIH)
NCI†	National Cancer Institute (NIH)
NCPHS	National Commission for the Protection of Human Subjects
NCRR†	National Center for Research Resources (NIH)
NIH†	National Institutes of Health
NLGLP*	National Laboratory Gene Library Project (LANL, LLNL)
NSF	National Science Foundation
OER*	Office of Energy Research
OHER*	Office of Health and Environmental Research (OER)
ORNL*	Oak Ridge National Laboratory, Oak Ridge, Tenn.
PACHG†	Program Advisory Committee on the Human Genome (NIH)
SBIR	Small Business Innovative Research
STS	sequence tagged site
UCSF	University of California, San Francisco
USDA	U.S. Department of Agriculture
YAC	yeast artificial chromosome

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