Human Genome news

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Positional Cloning Approach Expedites Gene Hunts

For most scientists, searching for a disease gene means years of laboring over the mapping, cloning, and sequencing processes and considerably less time actually studying the gene and its function.

But this should soon change. A new approach called "positional candidate" is rapidly coming of age and should streamline the process of identifying disease genes within the next few years.

Based on the growing body of genome resources, the positional candidate strategy lets researchers combine information about a gene's chromosomal location with increasingly detailed genetic and physical maps, allowing for easier identification of a potential causative gene.

According to the latest data, positional candidate studies already have led to the identification of over 50 disease genes. Commenting recently in *Nature Genetics*, NIH National Center for Human Genome Research Director Francis Collins stated that this more efficient approach is a major reason that positional cloning is moving from the "perditional to traditional" way of finding disease genes.

Strategy Saves Time

One of the most intriguing uses of the positional candidate strategy is the recent identification of the gene causing achondroplasia (ACH), a common form of dwarfism.

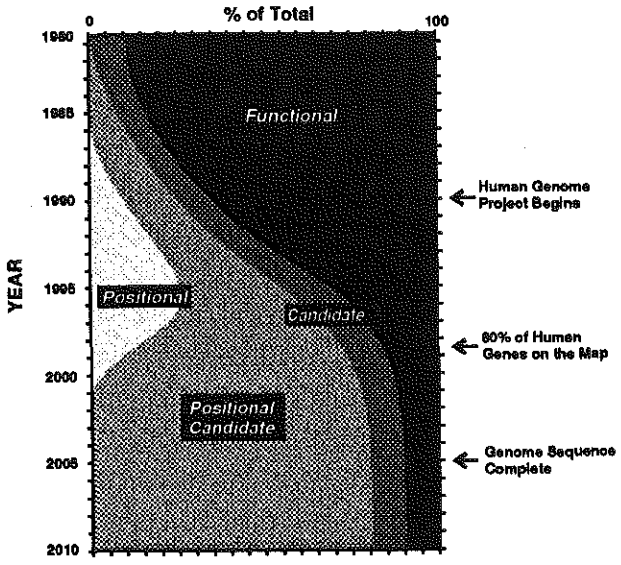
The ACH gene story began in 1991 during the marathon race for the gene responsible for Huntington's disease. That year, a group at the University of California, Irvine, reported that it had isolated an interesting cDNA that mapped to the middle of the chromosome 4 subregion possibly containing the Huntington's gene.

This was exciting news. The group, led by John Wasmuth, and other members of the Huntington's Disease Collaborative Research Group had spent nearly 8 years stalking the Huntington's gene in an initiative that *Science* once described as "a nightmare of false leads, confounding data, and backbreaking work."

The backbreaking work went on. Later studies failed to show that the gene, called FGFR3, played any role in Huntington's. Having already deposited the nucleotide sequence for FGFR3 in GenBank®, Wasmuth's group continued to search along the tip of chromosome 4.

The Irvine scientists did not realize it at the time, but this work with the FGFR3 gene would give them a head start later in the hunt for the gene involved in ACH.

Last year, three laboratories reported that linkage studies had localized the ACH gene to a 2.5-Mb stretch on the tip of chromosome 4, the region where the FGFR3 gene resides. This time, investigators had no need to construct clones of the DNA region or design complex disequilibrium studies. With the sequenced FGFR3 gene as their candidate, they acquired patient DNA samples and developed PCR primers to test for possible mutations.



Trends in methods for cloning human disease genes, 1980–2010. Projected trends after 1995 are highly speculative. Figure reprinted with permission from *Nature Genetics* [9(4), 347–50 (April 1995)].

In This Issue

Genome News

Within a matter of weeks, the Irvine scientists got their answer: 15 of 16 people with ACH had the same point mutation in the FGFR3 gene.

Positional Candidate Strategy Becoming Widely Used

The positional candidate approach relies on a three-step process that saves time and effort: (1) localizing a disease gene to a chromosomal subregion, generally by using traditional linkage analysis; (2) searching databases for an attractive candidate gene within that subregion; and (3) testing the candidate gene for disease-causing mutations.

Not so long ago, accessing a database of mapped genes seemed as futuristic as boarding the Starship *Enterprise*. With the tremendous progress in mapping human and mouse genomes and improving gene-discovery techniques, the positional candidate strategy already has amassed an impressive list of gene discoveries.

Since 1990, scientists have used this approach to find genes implicated in such conditions as Marfan syndrome, inherited nonpolyposis colon cancer, retinitis pigmentosa, long QT syndrome, Jackson-Weiss syndrome, Crouzon syndrome, Alzheimer's disease, and several others.

As impressive as this list is, recent international mapping initiatives promise to put many more human genes on the map during the next few years and make positional candidate investigations even more successful. (See related article on IMAGE Consortium, p. 3.)

In February of this year, Washington University and the pharmaceutical company Merck, Sharpe, and Dohme announced the first publicly available installment of 15,000 ESTs. Launched last summer, this ambitious effort is expected to process about 200,000 cDNAs over the next 18 months. Lawrence Livermore National Laboratory is arraying clones from a cDNA library generated at Columbia University.

Meanwhile, an international EST consortium is being coordinated at the Sanger Centre. It includes the Stanford University Genome Center, Wellcome Trust Centre for Human Genetics, Généthon, Washington University, University of Cambridge, and Whitehead Institute–Massachusetts Institute of Technology. These groups joined forces to begin mapping 70,000 ESTs to 0.5-Mb intervals or better. To help speed this important initiative along, The Institute of Genomic Research donated primers for 15,000 ESTs.

Looking to the Future

Still, several challenges remain before positional candidate strategies become firmly entrenched. One concern is the need for a more comprehensive database of mapped genes. Although well over 4000 genes have been mapped, tens of thousands more must be identified to fill in blanks in the human genome.

At the same time, standard positional cloning efforts usually result in candidate intervals of 0.5 to 5 Mb, but mapping cDNAs to traditional somatic cell hybrids or by using FISH usually will not achieve this degree of resolution. Large-insert clone libraries or radiation hybrids may be needed to provide the necessary resolution.

Despite these challenges, both of which are now being addressed successfully, most experts are encouraged by the short-term success of positional candidate studies. "With all the cDNA activity alone, it seems likely that more than half the human transcripts will be placed on the human genome map in the next 18 months," predicted Collins. "The effect on the success rate of the positional candidate approach should be profound." *[Bob Kuska, NCHGR]* ◊

"Positional Cloning Moves from Perditional to Traditional," by Francis Collins, appeared in *Nature Genetics* [9(4), 347–50 (April 1995)].

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 Sciences 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.◊

ELSI Happenings

DOE Requests ELSI Proposals

DOE invites applications for FY 1996 research grants addressing privacy issues and the development of educational materials related to ethical, legal, and social issues (ELSI) arising from information and knowledge generated by the Human Genome Project. Solicitations for proposals were announced in the *Federal Register* 60(48), 13433–34 (March 13, 1995) and in *Science* and other publications. Applications due July 13. Before submitting proposals, potential applicants should discuss their projects with Daniel Drell; Office of Health and Environmental Research, ER-72 (GTN); DOE Office of Energy Research; Washington, DC 20585 (301/903-6488, *daniel.drell@mailgw.er.doe.gov*).◊

"Diving into the Gene Pool" Exhibition in San Francisco

"Diving Into the Gene Pool" is a major, multifaceted exhibition being held at the Exploratorium in San Francisco from April 8 through September 4. The hands-on, 25-exhibit display examines DNA structure and function and the Human Genome Project from a variety of perspectives. Supported in part by the ELSI component of the DOE Human Genome Program, the exhibition concentrates on the following broad areas: DNA, tools and technology for finding genes, lessons from other species, human genetic inheritance, and social and ethical questions arising from developments in gene technologies. The Art Life section focuses on human-created hybrid plants, and events include Blooming Genes, Dog Diversity Day, Biotechnology Weekend, and DNA Dining Day. [Contact: Exploratorium; 3601 Lyon St.; San Francisco, CA 94123 (415/563-7337, Fax: /561-0307, *pubinfo@exploratorium.edu*)] ◊

Genome News

IMAGE Characterizes cDNA Clones

The Integrated Molecular Analysis of Gene Expression (IMAGE) Consortium is an international group of laboratories collaborating to characterize clones from shared arrayed cDNA libraries, integrate all data, and make clones and data publicly available. Information and resources generated by the consortium are expected to facilitate gene mapping and sequencing as well as gene-expression studies. (See related article, p. 1.)

Organized in 1993 by Gregory Lennon [Lawrence Livermore National Laboratory (LLNL)], Charles Auffray (Généthon), Bento Soares (Columbia University), and Mihael Polymeropolous (NIH National Institute of Mental Health), the consortium is now working with over 100,000 arrayed clones from 18 different libraries. LLNL is arraying these libraries for replication and distribution worldwide. Each clone in the shared libraries is given a simple, unique identifier (IMAGE CloneID) that enables integration of sequence, map, and expression data generated around the world by laboratories of various sizes, expertise, and interests.

IMAGE collaborators deposit their data into public databases. Over 70,000 sequences, at least 28,000 of which are nonoverlapping, are already in dbEST (*http://www.ncbi.nlm.nih.gov/dbEST/index.html*). Most work has focused on the normalized infant brain cDNA library from Soares. The Soares library array consists of more than 40,000 clones; more than 20,000 single-pass sequences have been generated, and over 4000 cDNAs have been mapped to chromosomes. Data from 106,394 clones have been loaded into the Genome Data Base (GDB), with more expected over the next few months. All clones in the IMAGE Consortium arrays have preassigned GDB accession numbers, so the mapping data submitted to GDB is highly amenable to cross-database coordination and integration.

Toward the Master Array

Lennon, Polymeropolous, Soares, and several other mapping and sequencing teams participated in a 1991 DOE initiative to enrich the developing physical maps with gene loci and open broad access to resulting data and resources. DOE continues to support Soares' production of cDNA libraries for other tissues, with derivative normalization and subtraction from previously characterized clones. With NCHGR support, Soares is further developing technology for generating full-length cDNA libraries. As incremental improvements are made, they will be incorporated into the continuing production of the tissue-specific libraries.

Under IMAGE auspices, the normalized Soares brain libraries are the centerpiece of the cDNA sequencing effort supported by Merck & Co. at Washington University. In February Merck announced the availability of 15,000 expressed human gene sequences; 200,000 to 300,000 are expected within the next 18 months. Rates of over 5000 sequences per week are being achieved, providing a "tremendous boost toward identifying at least one cDNA clone per human gene," Lennon said.

Later this year, the IMAGE Consortium expects to make available a "master array"—a nonredundant set of cDNA clones representing the genes identified—from each human gene transcript. "Having the genes in hand is going to allow us to put together a gene map faster than anyone thought possible," said Lennon. *[Anne Adamson, HGMIS]* ◊

Participation Welcome

The IMAGE Consortium is currently arraying other high-quality cDNA libraries and invites the participation of any laboratory willing to abide by consortium guidelines. Participants agree to place all sequence, map, and expression data arising from the use of IMAGE clones into free public databases. This data must be associated with the clone's unique identifiers. IMAGE clones are currently distributed freely and will soon be available from commercial distributors for a nominal fee.

For more information on IMAGE, send a message to *info@image.llnl.gov* or access the WWW site (*http://www-bio.llnl.gov/bbrp/genome/genome.html*).

C. elegans Sequence Data Grows

The amount of finished sequence produced by the *Caenorhabditis elegans* Genome Project grew to over 14 Mb at the end of March. This marks more than a six-fold increase from the 2.2 Mb reported in mid-1994 [see *HGN* 6(2), 1–2 (July 1994)]. Of the new total, investigators headed by Richard Wilson and Robert Waterston [Washington University (WU), St. Louis] contributed 272 cosmids (8,339,124 bases), and researchers led by John Sulston (Sanger Centre, U.K.) contributed 183 cosmids (5,634,590 bases). The St. Louis group has also finished 39 yeast cosmids (1,248,089 bases). *[Figures provided by LaDeana Hillier and David States, WU]*

Sanger Centre Ftp Site

Cosmid sequences are available by anonymous ftp (*ftp.sanger.ac.uk* in the directory *pub/databases/C.elegans_sequences* or via *http://www.sanger.ac.uk/ftpsite.html*). The ftp site, which is updated regularly, contains all the Sanger Centre *C. elegans* sequence data as well as completed contigs from St. Louis.

Sequences are divided into the following three directories.

- *EMBL_SEQUENCES:* Finished, annotated, already submitted to public databases.
- *FINISHED_SEQUENCES:* Finished but not annotated; may contain errors and change from day to day.
- *UNFINISHED_SEQUENCES:* Very preliminary, may contain contamination; major changes when updated. Useful for mapping and gene hunting.

For further information, contact Steven Jones (Fax: +44-1223/494919, *sjj@sanger.ac.uk*), who would appreciate comments on these sequences.

Washington University, St. Louis

The St. Louis group emphasizes making finished data available as rapidly as possible through the Sanger Centre ftp server (see address at left) and public sequence databases. Cosmids are processed individually; as each is finished with double stranding and the resolution of sequence conflicts and ambiguities, it is annotated (including gene prediction and BLAST searches for homology) and submitted to the public databases. ◊

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Proposed Privacy Act Presented to DOE-NIH Joint ELSI Working Group

Text of the Genetic Privacy Act is accessible via HGMIS Home Page: *http://www.ornl.gov/TechResources/Human_Genome/home.html*

Genetic Privacy Act Introduced

The Genetic Privacy Act is a proposal for legislation governing collection, analysis, storage, and use of DNA samples and the genetic information obtained from them. This first legislative product of the U.S. Human Genome Project's Ethical, Legal, and Social Issues (ELSI) component was presented to the DOE-NIH Joint ELSI Working Group in December 1994. Drafted as a federal statute to provide uniformity, the act has been introduced into six state legislatures. It could also be used as a guideline by professional societies until Congress acts.[1] George Annas, Leonard Glantz, and Patricia Roche (Boston University School of Public Health) authored the proposal with funding from the DOE ELSI program.

The Genetic Privacy Act complements and moves beyond current federal proposals for protecting medical information. It would require explicit authorization to collect DNA samples for genetic analysis, limit uses of the samples and genetic information obtained from them, and set forth penalties for violations. The act aims to protect individual privacy while permitting genetic analysis for medical and identification purposes and legitimate research.

Under the act, anyone who collects a DNA sample such as blood, saliva, hair, or other tissue for genetic analysis is required to

- provide specific verbal information and a written notice of rights and assurances before sample collection,
- obtain written authorization containing required information,
- restrict access as authorized by the sample source, and
- abide by the source's instructions regarding maintenance and destruction of DNA samples.

Special rules regarding DNA sample collection and research are set forth for minors, incompetent persons, pregnant women, and embryos. Research is permitted on nonidentifiable samples when not forbidden by the sample's source; on individually identifiable DNA samples, research is prohibited unless specifically authorized by the source.

The overarching premise of the act is that no stranger should have or control identifiable DNA samples or genetic information about an individual unless the source specifically (1) authorizes the collection of DNA samples for analysis and the creation of genetic information and (2) retains access to and control over its dissemination. Rules protecting genetic privacy must be clear and made known to the medical, scientific, business, and law enforcement communities and the public. [Contact: Marilyn Ricciardelli (617/638-4626, Fax: -5299, *mricciar@bu.edu*)] *[Anne Adamson, HGMIS]* ◊

1. Congress recently protected genetic information derived from DNA samples held by law enforcement agencies for identification purposes (P.L. 103–322, Section 210305: Violent Crime Control and Law Enforcement Act of 1994). This law would not be affected by the Genetic Privacy Act.

Genome Education Workshops Held

Scientists, ELSI Experts Sought as Mentors

Some 90 middle and secondary school science teachers from 40 states attended a June 20–25, 1994, workshop on genome education in Kansas City, Kansas. Organized by Debra Collins (University of Kansas Medical Center), the meeting was supported by the Ethical, Legal, and Social Issues (ELSI) component of the DOE Human Genome Program.

The workshop was part of an ongoing project to prepare teachers to demonstrate instructional materials in their classrooms and at local, state, and national education meetings; serve as resource professionals; and help students understand complex choices they may face as modern medicine and the knowledge of human genetics progress. Participants must commit to attending 1-week workshops during two successive summers, using workshop materials in the classroom, and sharing information and networking with other teachers.

All 115 teachers who have attended the three workshops so far are expected to reach 25 peers, each of whom has about 140 students. Thus, these teachers could reach over 400,000 students every year. As diagnostic capabilities expand, teachers can also serve as important liaisons between genetic professionals and the general public in distributing information about human genetics. Collins would like to receive names of scientists and ELSI experts willing to serve as mentors for networking with teachers.

The fourth workshop will be held June 19–24 in Kansas City. For more information, contact Collins or Lindsay McAnany [3901 Rainbow Blvd.; 4023 Wescoe; Kansas City, KS 66160-7318 (913/588-3886 or -6043, Fax: -3995, *geneduc@ukanvm.cc.ukans.edu* or *collins@ukanvm.cc.ukans.edu*, *http://www.kumc.edu/instruction/medicine/genetics/homepage.html*)]. *[Anne Adamson, HGMIS]* ◊

☛ NIGMS Distributes Cell Lines

The Human Genetic Mutant Cell Repository of the NIH National Institute of General Medical Sciences (NIGMS) is distributing lymphoblastoid cell lines representing the 8 CEPH reference families in the Généthon subset and the 15 CEPH reference families in the Cooperative Human Linkage Center (CHLC) subset. Family relationships have been verified by Southern blot analysis at the Coriell Cell Repositories and approved by CEPH. The NIGMS repository also distributes DNA from parents in all Généthon and CHLC subsets and from entire families 102, 884, 1331, 1333, and 1341. Information about DNA and cultures, as well as additional CEPH reference families, can be obtained from the online catalog via Internet (telnet to *coriell.umdnj.edu*; at the login prompt, type *online*). To access the catalog via modem: 609/757-9728. [Contact: NIGMS Human Genetic Mutant Cell Repository; Coriell Cell Repositories; Coriell Institute; 401 Haddon Ave.; Camden, NJ 08103 (800/752-3805 or 609/757-4848, Fax: -9737)] ◊

News from HUGO

Patenting Statement Issued

The Human Genome Organisation (HUGO) has released a 15-page statement about the patenting of DNA sequences. The statement summary reads in part, "HUGO is worried that the patenting of partial and uncharacterized cDNA sequences will reward those who make routine discoveries but penalize those who determine biological function or application. Such an outcome would impede the development of diagnostics and therapeutics, which is clearly not in the public interest. HUGO is also dedicated to the early release of genome information, thus accelerating widespread investigation of functional aspects of genes. This statement explains our concerns."

The statement was prepared by HUGO President C. Thomas Caskey (Merck Research Laboratories), Rebecca Eisenberg (University of Michigan Law School), Eric Lander (Whitehead Institute), and Joseph Straus (Max Planck Institute) and approved by the HUGO Council. It appears in HUGO Europe *Genome Digest* [2(2), 6–9 (April 1995)] and is available in hard copy by e-mail request from the HUGO Americas office.

Sutherland, van Ommen Named

The HUGO Council has elected Grant R. Sutherland (Adelaide Women and Children's Hospital, Australia) as the fourth president of HUGO. His 3-year term will begin January 1, 1996. As president-elect in 1995, Sutherland is working closely with the current president. Gert-Jan van Ommen (University of Leiden, Netherlands) has succeeded Kay Davies (John Radcliffe Hospital, U.K.) as HUGO Vice-President for Europe, effective January 1 of this year.

Membership Expands

Policies were initiated last year to make HUGO more representative by extending membership to all persons concerned with human genome research and related scientific subjects. Since then, the number of members has risen steadily to over 600 people in almost 40 countries. Membership now requires a standard application form, supporting signatures of two current HUGO members, a one-page curriculum vitae, and a list of five key publications.

Travel Awards Available

Short-term (2- to 10-week) travel awards up to $1500 are available for investigators under age 40 to visit another country to learn new methods or techniques. Applications must be submitted at least 6 weeks before a proposed visit.

Application requirements

- Work plan.
- Applicant's curriculum vitae, including publications.
- Travel expense details.
- Supporting declaration by a HUGO member.
- Supporting declaration by head of host laboratory.
- Supporting letter from applicant's department head.

For more information on HUGO travel awards or membership, contact one of the regional offices listed in the upper box.◊

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HUGO Council

Terms Ending 1995

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David Cox, U.S.A.
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Terms Ending 1996

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Terms Ending 1997

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Ellen Solomon, U.K.

URLs for Web

As a service to our readers, from time to time ***HGN*** will list pertinent uniform resource locators (URLs) for molecular biology and biology resources accessible through WWW.

NIH: *http://www.nih.gov*
DOE: *http://www.er.doe.gov/production/oher/hug_top.html*
HGMIS: *http://www.ornl.gov/TechResources/Human_Genome/home.html*
ACEDB 1995 Workshop: *http://genome.lbl.gov/ace95.html*
Baylor Biologist's Control Panel: *http://gc.bcm.tmc.edu:8088/bio/bio_home.html*
BIOSCI/Bionet Newsgroups: *http://www.bio.net*
BIOSCI/Bionet Newsgroup Archives: *http://www.ch.embnet.org/bio-www/info.html*
Chromosome 8 Workshop: *http://gc.bcm.tmc.edu:8088/chr8/home.html*
Comprehensive Biosciences Index: *http://golgi.harvard.edu/biopages.html*
DNA Sequences 100 kb or Longer: *http://golgi.harvard.edu/100kb*
ExPASy Molecular Biology: *http://expasy.hcuge.ch*
FlyBase (*Drosophila*): *http://morgan.harvard.edu*
Genome Data Base: *http://gdbwww.gdb.org*
HGMP Resource Centre (U.K.): *http://www.hgmp.mrc.ac.uk*
Information Retrieval and Genomics Workshop (May 1994): *http://info.cs.vt.edu/WIRG/WIRG.html*
Internet Directory of Biotechnology Resources: *http://biotech.chem.indiana.edu*
Japan Rice Genome Research Program: *http://www.staff.or.jp*
Johns Hopkins University Bioinformatics: *http://www.gdb.org*
Medical Research Council (U.K.): *http://www.nimr.mrc.ac.uk/MRC*
Molecular Biology Databases: *http://www.nih.gov/molbio*
Nucleic Acids Database Project (Rutgers Univ.): *http://ndbserver.rutgers.edu:80*
O Protein Crystallographic Package: *http://kaktus.kemi.aau.dk*
Organelle Genome Sequencing Program (Canada): *http://megasun.bch.umontreal.ca/ogmp/ogmp.html*
Organelle Genomes: *gopher://megasun.bch.umontreal.ca:70/11/Organelles/Genomes*
Protein Data Bank: *http://www.pdb.bnl.gov*
Protein Science: *http://www.prosci.uci.edu*
Swiss Federal Institute of Technology Peptide and Nucleotide Analysis: *http://cbrg.inf.ethz.ch*
Weizmann Institute Biological Computing Division: *http://dapsas1.weizmann.ac.il*
World Health Net: *http://oceania.org/world_health*

Genome News

Human Genome news

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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National Center for Human Genome Research

Role of Media and Genome Project Addressed

Some 300 scientists, journalists, and teachers attended the December 3, 1994, conference on "Genes that Make News, News that Makes Genes: Reporting on Complex Traits." The meeting, partially funded by DOE, was the fourth in a series of Science and Journalism conferences organized by the Genetic Screening Study Group (Boston) to explore relationships between science and the media. Discussion panels focusing on cancer, sexuality, and violence and aggression addressed challenges in communicating information about genetic research that might have important societal repercussions.

In his keynote address, Francis Collins (NIH National Center for Human Genome Research) spoke of issues requiring public input and called for clinical trials to evaluate social and personal burdens of genetic information.

Cancer panelists discussed potential benefits and harms of predictive testing, public expectations about human genome research, and the roles of scientists and the press in generating those expectations. Fred Li (Dana Farber Cancer Institute) pointed out the need to consider predictive cancer testing as research, address issues in testing children, and undertake public education. He recommended that general population screening not be done and stressed the importance of assessing carefully the usefulness of any predictive test and of providing counseling both before and after testing.

Neil Holtzman (Johns Hopkins University School of Medicine) expressed his belief that press coverage of genetic discoveries has generated unrealistic public expectations. He blamed some of these problems on journalists' esteem for scientists and suggested they use an investigative reporting model.

Sandra Steingraber (Women's Community Cancer Project) noted that focusing on cancer's hereditary aspects may allow people to maintain emotional distance from victims. The media reinforce this attitude by underplaying possible environmental factors in disease development. Laurie Garrett (*Newsday*) observed that most people do not understand gene function and view new developments with a mixture of fear and optimism. She called for accuracy in reporting but acknowledged many constraints on journalists, including space, time, and the necessity to sell a product.

The panel on human sexuality focused largely on press coverage of a possible genetic basis for homosexuality. Dean Hamer (National Cancer Institute) described measures taken by his group to encourage responsible reporting of their study linking some male homosexuality to the X chromosome. William Byne (Mount Sinai Medical School) pointed out that views critical of research into the biological basis of sexuality were not reported adequately. Chandler Burr, freelance writer, found that reporters and scientists tend to sensationalize and oversimplify discoveries, an opinion shared by several other speakers.

During the panel discussion on aggression and violence, Xandra Breakefield [Harvard Medical School (HMS)] expressed dismay over inaccurate reporting of her study examining correlations between monoamine oxidase deficiency and aggressive or violent behavior. Gregory Carey (University of Colorado) discussed difficulties and limitations in twin and adoption studies exploring genetic factors in violent behavior. He and others argued strongly against dichotomizing nature and nurture in these analyses.

Joseph Alper (University of Massachusetts, Boston) criticized scientists and journalists for overstating findings in monoamine oxidase studies and in research relating serotonin levels and aggressive behavior. Felton Earls [Harvard School of Public Health (HSPH)] described a longitudinal study to identify social, economic, and biomedical factors that might correlate with violent behavior. Freelance writer Susan Ince observed that the lack of scientific criticism in press coverage creates the impression that there is none. She also offered the opinion that some researchers may be promoting their own social agenda.

Jonathan Beckwith (HMS), David Smith (DOE Office of Health and Environmental Research), and B.D. Colen (HMS) summarized the conference from their perspectives as scientist, scientist/administrator, and journalist, respectively. Some common themes included a growing concern over raising false public expectations about predictive genetic screening and the importance of emphasizing gene-environment interaction. Attendees generally agreed that both scientists and journalists must assume greater responsibility in promoting accurate reporting. *[Jonathan Beckwith and Lisa Geller (HMS) and Kathleen Glass (HSPH)]* ◊

☛ dFLASH Supports Databases

Release 1.1.0 of the dFLASH electronic mail server, a homologous sequence retrieval program for protein and DNA sequences, now supports the latest release of the GenBank®, PIR, and SWISS-PROT databases. Full bibliographic references are optional, and new dFLASH features are described in the Help file. The server, which is still under development, is accessible through the Internet directly and through genQuest of Oak Ridge National Laboratory. To use dFLASH, send an e-mail message to *dflash@watson.ibm.com* with the server name in the subject line. Comments and reports of problems can be sent to the same address with *bug* or *comments* in the subject line. [Contacts: Andrea Califano: 914/784-7827, *acal@watson.ibm.com*; Isidore Rigoutsos: -7968, *rigoutso@watson.ibm.com*; Fax: -7455)] ◊

GDB WWW Server Enhancements

GDB Home Page (*http://gdbwww.gdb.org*)*

- Reorganized into three categories: Query Tools, Links to Related Resources, and Information about GDB and OMIM.
- Frequently Asked Questions (FAQ) page added, to be updated periodically.

GDB Browser

- Detail information is retrieved directly from the database rather than from WAIS files. This may cause a slight delay for queries retrieving a large number of entries.
- "mailto" links in Contact Detail allow direct e-mail to contact person. This feature is currently supported by Netscape and Lynx browsers but not Mosaic.
- The most important citations associated with retrieved entries are now indicated by asterisks (**) beside the publication year.

*GDB and OMIM are available via WWW from the GDB Home Page. The HUGO/GDB Chromosome Editors list is located at */editors.html*.

GDB Version 6.0 Goals

Goals and enhancements of GDB Version 6.0, to be released this autumn, are accessible via the GDB Home Page under Future Plans (*http://gdbwww.gdb.org/gdb6-goals.html*). The new system architecture and details of enhancement implementation will be available in future documents.

☛ FASTLINK 2.2 Accessible from Rice University

Alejandro Schaffer (Rice University) reported in the February issue of *Linkage Newsletter* that since May 1993 his group has been distributing faster versions of the genetic linkage analysis programs in LINKAGE 5.1. Dubbed FASTLINK, Version 2.2 has corrected several bugs in LINKAGE 5.1 and offers such enhancements as more dynamic memory allocation; additional diagnostics to detect user errors; crash recovery for LINKMAP and MLINK as well as LODSCORE and ILINK; information about FASTLINK portability; and a document explaining the preprocessor program UNKNOWN. To retrieve the code for FASTLINK 2.2, ftp to *ftp softlib.sc.rice.edu*; log in as *anonymous* and leave full e-mail address as password. Retrieve the file *fastlink.tar.Z* from the directory *pub/fastlink*; outside of ftp, use the commands *uncompress fastlink.tar.Z* and *tar xvf fastlink.tar*. FASTLINK is also available now for DOS; retrieve the file *README.DOS* for more details. [Contact: Schaffer (713/527-8101 ext. 3813, Fax: /285-5930, *schaffer@cs.rice.edu*)] ◊

GDB USER SUPPORT, REGISTRATION

To become a registered user of GDB and OMIM, contact one of the User Support offices listed 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.

The Help Line in Baltimore is staffed from 9 a.m. to 5 p.m. EDT 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.

GDB, OMIM Training Schedule

"GDB/OMIM and Genomic Data on the Internet" class will be held in Baltimore on June 5–6, September 25–26, and December 4–5. These courses offer thorough coverage of the structure, content, and roles of GDB and OMIM; discuss the strengths and weaknesses of various interfaces for searching the data; and explore related genomic resources available worldwide on the Internet. In addition to using GDB and OMIM application software, participants will learn how to retrieve phenotype, mapping, and sequence data with ftp, e-mail, Gopher, and WWW. Contact the U.S. GDB User Support Office.

User Support Offices

UNITED STATES
GDB User Support
Genome Data Base
Johns Hopkins University
2024 E. Monument Street
Baltimore, MD 21205-2100
410/955-9705
Fax: /614-0434
help@gdb.org

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Fax: -2956
mika@gdb.gdbnet.ad.jp

NETHERLANDS
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Fax: -652977
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GDB User Support
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+ 44/1223-494511
Fax: -494512
admin@hgmp.mrc.ac.uk

¶ LANL Publishes ELSI Supplement

The *ELSI Bibliography: Ethical Legal & Social Implications of the Human Genome Project* (Second Edition) and its 1994 supplement provide comprehensive lists of publications on major topics related to ethical, legal, and social issues (ELSI) of the Human Genome Project. Michael Yesley, Michael Roth, and Pilar Ossorio extracted the bibliography and supplement from a database compiled at Los Alamos National Laboratory (LANL) with support by the ELSI component of the DOE Human Genome Program. Both volumes are available on request from LANL; MS A187; Los Alamos, NM 87545 (Fax: 505/665-4424, *msy@lanl.gov*). Requests for custom searches should be directed to the same address.◊

Genome News

Alternatives in Technological Controversies

A conference on "Which Scientist Do You Believe? Process Alternatives in Technological Controversies" attracted almost 40 people from the United States and Canada to Concord, New Hampshire, on October 6–7, 1994. The meeting was organized by Arthur Kantrowitz (Dartmouth College) and Thomas Field [Franklin Pierce Law Center (FPLC)] to consider the resolution of technical disputes in a variety of settings. It was funded partially by the Ethical, Legal, and Social Issues component of the DOE Human Genome Program.

Presentation topics included processes for resolving medical controversies [Itzhak Jacoby (Uniformed Services University of the Health Sciences)], the need to separate scientific facts from social values in public controversies (Kantrowitz), congressional regulations on risks to humans and the environment [Dalton Paxman (Congressional Office of Technology Assessment)], DNA evidence in the courtroom [Albert Scherr (FPLC)], and nontechnical input in framing scientific issues [Kristin Schrader-Frechette (University of South Florida)].

Interest was particularly strong in the admissibility of DNA trial evidence. Only recently has the use of DNA "fingerprints" been possible, and basic issues concerning their admissibility are being resolved. As with other technologies, legislators, judges, and regulatory personnel will have to sort out competing claims of equally qualified scientists and expert witnesses.

The conference also devoted a great deal of attention to negotiation and to mediation and arbitration by neutrals regarding the rights and obligations of the parties. These procedures are known as alternative dispute resolution (ADR). Rena Steinzor (University of Maryland) credited ADR—in particular, a skilled mediator—and the sponsorship of a private foundation in settling a conflict over major environmental legislation. She also stated that excluding public authorities and their representatives from negotiations had been helpful in reaching agreement among very divergent private stakeholders.

Norman Balmer (Union Carbide Corporation) and Field discussed ADR in patent disputes and recent federal legislation encouraging regulatory use of ADR. For example, mediation received little attention 20 years ago but now has become popular in a number of settings and warrants even more use. Balmer emphasized that ADR has the advantage of minimizing litigation expense and resolving disputes relatively quickly.

One option that received considerable attention was the "Science Court," which could be used in legislative, regulatory, and court settings to allow resolution of technical issues by technical people. In this procedure, which was first proposed more than 25 years ago, competing sides would present their cases to a technically trained, neutral panel for an informed decision based on merit. Because similar approaches have been tried in the United States and Canada without dire results, many earlier concerns have diminished. No Concord conferee voiced fundamental opposition to the concept, and several indicated the need for renewed consideration.

Participants made no recommendations as a group but individually suggested that mechanisms for resolving technical components of public controversies could use improvement; several agreed to found a multidisciplinary association to address this and related topics. A conference summary, including presented papers, will appear in the Spring issue of *Risk*, which will be available in mid-May (Fax: 603/224-3342, *tfield@fplc.edu*). *[Thomas Field, FPLC]* ◊

Beijing Hosts 2nd South-North Conference

The Second South-North Conference, held in Beijing on November 6–10, 1994, demonstrated that developing countries are participating meaningfully in the Human Genome Project. Both in overall session structure and the high level of scientific content, the conference exemplified the goals of its sponsors—United Nations Educational, Scientific, and Cultural Organization (UNESCO), Peking University, and the Chinese National Commission for UNESCO.

In this and previous conferences, UNESCO has established three major ways in which developing countries and populations can participate in the genome project:

- Give special attention to genetic traits, including inherited diseases or susceptibilities in native populations. Isolated populations are especially important in genetic analyses.
- Organize scientific work using the best available technologies for mapping and sequencing at least some representative sites. Special attention would be given to organisms or traits of particular value or interest to societies.
- Take part in moral and ethical discussions on beneficial uses of genetic technology and safeguards of individual privacy.

The First South-North conference, held in Brazil in 1992, emphasized planning and initial work at a number of sites. [See *HGN* 4(4), 12–13 (November 1992).] This second conference concentrated on an update of scientific work and demonstrated substantive Chinese contributions, including a number of presentations on the genetic diversity of some 50 ethnic groups. Many delegates emphasized the sense of responsibility shared by the Chinese government and investigators regarding human genome studies in a country with more than 20% of the total world population.

Chinese researchers presented significant scientific achievements in the following areas:

- Rice genome studies, from long-range mapping to blight resistance;
- Human genome research, including long-range mapping of portions of the X chromosome; and
- Technology development, with contributions to YAC cloning and bioengineering.

Disease-gene presentations were comparable to studies from the United States, Canada, and Europe. Delegates from Brazil, Kenya, and Shanghai made impressive presentations, respectively, on molecular biology techniques for genome research, studies of the intracellular protozoan parasite *Theileria parva*, and YAC cloning and mapping of the Duchenne muscular dystrophy gene region.

These South-North conferences have established that genome analysis is thriving globally, with some high-quality laboratory groups functioning in developing countries. *[David Schlessinger (Washington University School of Medicine) and Santiago Grisolia (Instituto de Investigaciones Citologicas)]* ◊

Genome News

Interoperable Tools Working Group Meets

An informal off-site informatics meeting was held on November 15, 1994, as an adjunct to the DOE Human Genome Program Contractor-Grantee Workshop in Santa Fe, New Mexico. The discussion at the National Center for Genome Resources involved about 25 NIH and DOE investigators. Its purpose was to develop ideas and a working plan for an interoperable framework of genome-analysis tools. An earlier discussion on this topic was organized by David States at the Cold Spring Harbor Genome Mapping and Sequencing meeting in May 1994 [see *HGN* 6(4), 16 (November 1994)]. As in the earlier session, the group strongly agreed about the desirability of a framework to provide researchers with seamless and transparent access to an array of sequence-analysis tools and databases.

The Santa Fe meeting centered around a plan to develop a multiple-client environment that could access a variety of Internet servers. It would facilitate genome analysis and data retrieval, entry, and annotation, transparently passing data types and control among the various tools. In this approach, individual tool designers would attach their servers to the framework by submitting a client code and information about their server and input-output data types to a central library. The modular, flexible framework would allow growth and new types of analysis and data and facilitate community-wide interoperability.

Several goals were reached at the meeting:

1. Agreement that semantic issues could be overcome and would not prevent framework construction, a divisive issue at previous sessions.
2. An understanding that large centers often require "batch mode" processing, whereas individual users most often want interactive analysis. Both should be incorporated by design.
3. Discussion of ASN.1 and other systems for standard format description.
4. Consideration of data-type or object-exchange mechanisms such as CORBA.
5. Identification of an initial suite of tools to be included in a prototype framework.

Participants also agreed on the importance of building and testing a prototype for evaluating methods and comparing approaches. With this in mind, several groups are beginning to work on systems that would incorporate tools to fetch entries from Genome Sequence Data Base, GenBank®, and perhaps the Genome Data Base; access sequence-analysis systems such as XGRAIL; provide links to such sequence-comparison tools as BLAST, genQuest, and Biopoet; and facilitate data entry and annotation.

The prototype would demonstrate several major project goals, including the ability to navigate and access distributed Internet tools within a single environment, exchange data among tools, and use interoperable systems for data retrieval, analysis, and annotation. The group hoped the prototype would be available by May, when members will reconvene at the Cold Spring Harbor meeting.

Comments to the group and information requests may be sent to *FTFNAMES@mars.epm.ornl.gov*. A Mosaic page related to the project can be accessed at *http://avalon.epm.ornl.gov:80/FTF. [Edward Uberbacher, Oak Ridge National Laboratory]* ◊

¶ Newsletter for Mouse Researchers

Neurology News, a newsletter for mouse researchers, is available via WWW (*http://www.jax.org/resources/documents/NeuroNews.html*) and hard-copy subscription (800/422-6423).

☛ *More Informatics Resources*

Boston University Provides Gopher, Web Servers

Gopher and WWW servers are available for the BioMolecular Engineering Research Center and Molecular Biology Computer Research Resource (BMERC) at Boston University (*http://bmerc-www.bu.edu*, Gopher: *bmerc-gopher.bu.edu*). These servers provide access to (1) the Protein Sequence Analysis System, an e-mail server for analyzing amino acid sequences; (2) ProLink, an integrated database of protein structure, sequence homology, and functional pattern data installed in a relational format under Sybase; and (3) specially designed software, data files, and support information. [Contact: Bill Schmidt; BMERC; Boston University; 36 Cummington St.; Boston, MA 02215 (617/353-7123, Fax: -7020, *gophradm@darwin.bu.edu* or *wwwadmin@darwin.bu.edu*)] ◊

Jackson Laboratory Announces Mouse Genome Database

The Jackson Laboratory in Bar Harbor, Maine, has announced that the Mouse Genome Database (MGD) superseded the Genomic Database of the Mouse (GBASE) on January 31. MGD will accommodate rapid data growth and changing information needs, taking advantage of software and network improvements. MGD includes all former GBASE data and is integrated with the Encyclopedia of the Mouse Genome, an application that generates a graphical display of mouse genetic linkage maps using MGD mouse locus and homology information. [Bioinformatics Home Page: *http://www.informatics.jax.org*, user support: *mgi-help@informatics.jax.org* (207/288-3371 ext. 1900, Fax: -2516)]

Release #9 of the Whitehead Institute–Massachusetts Institute of Technology (MIT) mouse genetic maps is available through MGD and the mouse encyclopedia. Data have been incorporated into locus information tables, PCR primer RFLP tables, and a new set of MIT data files for the encyclopedia. Files may be downloaded from the encyclopedia Home Page (*http://www.informatics.jax.org/encyclo.html*) or via ftp (*ftp.informatics.jax.org* from the directory *pub/informatics/encyclo/data/3.0/mit.jan.1995*). ◊

CEPH Genotype Database Downloads to PC and UNIX via Ftp

The CEPH database of genotypes for all genetic markers tested in the reference families [*Genomics* 6, 575–77 (1990)] can be downloaded for PC and UNIX via ftp (*ftp ftp.cephb.fr* from the directory *pub/ceph_genotype_db*). V7.1 includes genotypes for some 6000 genetic markers (over 2500 of which are microsatellite markers), pairwise LOD scores between marker loci on the same chromosome, and database-management programs. The server also contains databases for published CEPH consortium maps.◊

CEPH Viewer Browses, Manipulates Data

CEPH Viewer is a client-server database for browsing and manipulating CEPH physical mapping and linkage data [Nadkarni et al., *Genomics* 25, 318–20 (1995)]. Data imported into CEPH Viewer was downloaded by anonymous ftp from *ceph-genethon-map.genethon.fr* in the directory *pub/ceph-genethon-map*. [CEPH Viewer contact: Prakash Nadkarni; Yale School of Medicine; 333 Cedar St.; New Haven, CT 06510 (203/785-7403, Fax: /737-2243)] ◊

Calendar of Genome Events*

April 1995

8–Sept. 4. Diving Into the Gene Pool; San Francisco [Exploratorium, 415/563-7337, Fax: /561-0307, *pubinfo@exploratorium.edu*]

June 1995

5–7. Bioinformatics & Genome Res. Conf.; San Francisco [CHI, 617/487-7989, Fax: -7937, *http://www.xensei.com/users/chi/homepg.html]*

14–16. High-Throughput Screening for Drug Discovery; CHI, San Diego (poster deadline: May 19) [see contact: June 5–7]

16–18. 6th Intl. X Chromosome Workshop; Banff, Canada [T. Bech-Hansen, 403/229-7243, Fax: -7243, *ntbech@acs.ucalgary.ca* or D. Nelson, 713/798-4787, Fax: -6370, *nelson@bcm.tmc.edu*]

19–20. Nucleic Acid–Based Therapeutics; CHI, San Diego (poster deadline: May 18) [see contact: June 5–7]

20–21. Molecular Genet. In Early Diagnosis & Prevention of Cancer; Bethesda, MD [GMCRF, N. Krakora, 202/636-8740, Fax: -8755]

20–22. IGES 4th Annu. Meeting; Snowbird, UT [M. Austin, 206/685-9384, Fax: -3407, *maustin@u.washington.edu*]

24–29. Genet. Recombination and Genome Rearrangements; Snowmass Village, CO [FASEB Summer Conf., 301/530-7095, Fax: /571-0650, *src@faseb.org*]

July 1995

5–8. 10th Intl. Conf. on Math. and Comput. Model. and Sci. Comput.; Boston (abs. deadline: Jan. 15) [X. Avula, 314/341-4585, Fax: /364-3351, *avula@umr.edu*]

16–19. ISMB-95; Cambridge, UK (abs. deadline: Feb. 15) [C. Rawlings, +44-0171/269-3639, Fax: -3067, *ismb95@biu.icnet.uk*]

17–18. **DIMACS Spec. Yr.: Geom. Methods for Conformational Model. Mini-Workshop; New Brunswick, NJ [M. Farach, 908/445-4580, Fax: -5932, *special@dimacs.rutgers.edu* or *http://dimacs.rutgers.edu*]

18–Aug. 1. 11th World Cong. on Med. Law; Pilansberg, South Africa [D. Friedman, +27-140/84-2470 or -2471, Fax: /24894]

20–22. MIMBD '95; Cambridge, UK [P. Karp, Fax: 415/859-3735, *pkarp@ai.sri.com* or *http://www.ai.sri.com/people/pkarp/mimbd.html*]

August 1995

2–5. 7th Intl. Workshop on Fragile X and X-linked Mental Retardation; Tromso, Norway (reg. deadline: May 1) [L. Tranebjaerg, +47-77/645-410, Fax: -430]

4–6. 3rd Intl. Workshop on Chromosome 15; Vancouver, Canada [W. Robinson, 604/875-3229, Fax: -2376, *wendyr@unixg.ubc.ca*]

6–10. 46th Annu. AIBS Meeting: Sci. and Ethics; San Diego [AIBS, 800/992-2427, Fax: 202/628-1509, *meetings@aibs.org*]

13–18. FEBS '95; Basel, Switzerland [Convention Ctr. Basel, +41-61/686-2828, Fax: -2185]

15–20. Yeast Cell Biol.; CSHL (abs. deadline: May 31) [CSHL, 516/367-8346, Fax: -8845, *meetings@cshl.org* or *http://www.cshl.org*]

22–27. Molecular Genet. of Bacteria & Phages; CSHL (abs. deadline: June 7) [see contact: Aug. 15–20]

23–27. Math. Model. and Info. Syst. in Biol., Ecol., and Med.; Sofia, Bulgaria (abs. deadline: June 30) [S. Markov, +359-2/707-460 or /713-3704, *biomath@bgearn.bitnet*]

24–25. 13th Annu. Botechnol. Patent Forum; Rockville, ME [ATCC, 301/231-5566, Fax: /770-1805, *internet@atcc.org*]

September 1995

6–10. Eukaryotic DNA Replication; CSHL (abs. deadline: June 21) [see contact: Aug. 15–20]

11–12. Natl. Adv. Council for Hum. Genome Res.; Washington, DC [J. Ades, 301/402-2205, Fax: -2218, *ja51b@nih.gov*]

13. Biochem. Soc. Colloquium: Navigating the Genome; Dublin [K. Wolfe, +353-1/702-1253, Fax: /679-8558, *khwolfe@otto.tcd.ie*]

13–15. **DIMACS Sp. Yr.: DNA Sequence Determination from Shotgun Sequence Data; New Brunswick, NJ [see contact: July 17–18]

13–17. Biol. & Genet. of Complex Mamm. Traits; Bar Harbor, ME [S. Serreze, 207/288-3371 ext. 1378, Fax: -5079, *complex95@aretha.jax.org*]

16–20. 7th Intl. Genome Sequencing and Analysis Conf.; Hilton Head, SC (abs. deadline: May 1) [Conf. Office, 301/869-9056, Fax: -9423, *seqconf@tigr.org*]

17–20. Intl. Conf. on Mol. Struct. Biol.; Vienna (abs. deadline: May 31) [A. Kungl, +43-1/587-249, Fax: -966, *msb95@helix.mdy.univie.ac.at*]

17–20. 2nd Intl. Workshop on Hum. Y Chromosome; Pacific Grove, CA [C. Lau, 415/476-8839, Fax: /502-1613, *clau@itsa.ucsf.edu* or N. Affara, +223/333–700, Fax: -346, *na@mbuc.bio.cam.ac.uk*]

19–22. Data Banks and Comput. Support of Hum. Genome Proj.; Moscow [V. Tsitovich, 7-095/135-2311, Fax: -1405, *imb@imb.msk.su*]

22–24. 2nd Single Chromosome Workshop on Hum. Chromosome 1; Vienna [A. Weith, +43-1/797-30-625, Fax: /798-7153, *weith@aimp.una.ac.at*]

28–29. 2nd Annu. Self-Assembling Nanostructures for Gene Transfer; CHI, Wakefield, MA [see contact: June 5–7]

29–Oct. 1. 1st Intl. Chromosome 10 Workshop; Crete, Greece (abs. deadline: July 31) [J. Mao, 617/893-5007 ext. 242, Fax: /642-0310, *mao@cric.com* or N. Moschonas, +30-81/212-469, Fax: /230-469, *moschon@victor.imbb.forth.gr*]

October 1995

10–11. 2nd Annu. Gene Therapy Technol.; CHI, Washington, DC [see contact: June 5–7]

13–14. Workshop on Gene Finding and Gene Struct. Prediction; Philadelphia (abs. deadline: May 1) [D. Searls, 215/573-3107, Fax: -3111, *dsearls@cbil.humgen.upenn.edu*]

22–23. Chromosome 3 Workshop; Minneapolis [S. Naylor, 210/567-3842, Fax: -6781, *naylor@thorin.uthscsa.edu*]

23–25. BioWest/BioPacifica '95; San Jose, CA [BioConf. Intl., 301/652-3072, Fax: -4951]

24–28. ASHG 95; FASEB, Minneapolis [see contact: June 24–29]

29–31. 3rd Intl. Chromosome 13 Workshop; Tarrytown, NY [D. Warburton, 212/305-7143, Fax: –7436, *cuh@cuccfa.ccc.columbia.edu*]

29–Nov. 1. Natl. Soc. of Genet. Counselors 14th Annu. Educ. Conf.; Minneapolis [B. Leopold, 610/872-7608, Fax: -1192]

November 1995

5–7. 5th Intl. Workshop on Identification of Transcribed Sequences; Marseilles, France (abs. deadline: Aug. 15) [N. Matthews, 303/333-4515, Fax: -8423, *nanm@druid.hsc.colorado.edu*]

5–8. 3rd Intl. Conf. on Autom. in Mapp. & DNA Sequencing; Berkeley, CA (abs. deadline: June 30 to *LCRebrovich@LBL.gov*) [M. Field, 510/486-6386, Fax: -5548, *MOField@LBL.gov*]

12–16. 9th Intl. Mouse Genome Conf.; Ann Arbor, MI (abs. deadline: Aug. 1) [D. Miller, 716/845-4390, Fax: -8169, *dmiller@mcbio.med.buffalo.edu*]

13–14. 4th Intl. Workshop on Hum. Chromosome 16; Leiden, Netherlands [M. Breuning, +31-71/276-048 or -293, Fax: -048, *breuning@rullf2.LeidenUniv.nl*]

16–17. 3rd Intl. Workshop on Hum. Chromosome 12; Leuven, Belgium [P. Marynen, +32-16/34-5891, Fax: -5997, *peter.marynen@med.luleuven.ac.be*]

18. Chromosome 12 Genes in Hum. Cancer; Leuven, Belgium [see contact: Nov. 16–17]

December 1995

2-6. Mol. Basis of Gene Transcription; San Diego [AACR, 215/440-9300, Fax: -9313]

Training Calendar*

June 1995

5–6. GDB/OMIM and Genomic Data on the Internet; Baltimore [see box, p. 7]

10–16. **Protein Purification: Isolation, Analysis, Characterization; New Brunswick, NJ (also offered later) [Rutgers Univ. Off. Continuing Prof. Educ., 908/932-9271, Fax: -8726]

12–16. **Introductory Linkage Course; New York [K. Montague, 212/960-2507, Fax: /568-2750, *jurg.ott@columbia.edu*]

19–24. Human Genome Networking Proj. for Mid. and Sec. Sci. Tchrs.; Kansas City, KS [D. Collins, 913/588-6043, Fax: -3995, *collins@ukanvm.cc.ukans.edu*]

July 1995

17–18. Med. and Exptl. Mamm. Genet.; Bar Harbor, ME [Jackson Lab., 207/288-3371 ext. 1253, 7:30 a.m. to 3:30 p.m. EDT]

31–Aug. 11. Genomic Res. Short Course; Bethesda, MD (Faculty from institutions with substantial minority enrollment eligible.) [P. Gregory, 301/496-3978, Fax: -7157, *edcore@helix.nih.gov*]

August 1995

13–18. Genome Technol. and Implications; Ann Arbor, MI [A. Pott, 313/747-1827, Fax: /764-4133] ◊

*Dates and meeting status may change; courses may also be offered at other times and places; check with contact person.
**Attendance is either limited or restricted.

For Your Information

Ongoing Training Courses

Courses are being held in the following selected subject areas during June, July, and August. Check with contact person for specific course titles, places, and times.

ACS (P. Orton, 202/872-4508, Fax: -6336). *Molecular modeling and computational chemistry, molecular biology and recombinant DNA technology, analytical methods for proteins.*

AFIP/ARP (J. Centeno, 202/782-2839, Fax: -9215, *CENTENO@email.afip.osd.mil*). *Analysis and molecular biology techniques in environmental toxicology and forensic science.*

BTCI (K. Borgh, 608/273-9737, Fax: -6992, *kborgh@promega.com*). *Gene hunting and molecular characterization.*

BTP (S. Chance, 800/821-4861, Fax: 603/267-1993, *biotraining@delphi.com*). *PCR and clinical applications, basic cloning and hybridization, quantitative RNA-PCR.*

Carolina Workshop (W. Litaker, 919/962-8920, Fax: /966-6821). *Gene targeting in ES cells and transgenic mice.*

CATCMB/CUA (M. Miller, 202/319-6161, Fax: -4467, *millerm@cua.edu*). *In situ hybridization, DNA-binding proteins and transcriptional regulators, protein purification and analysis, capillary electrophoresis, immunochemistry, expression of recombinant DNA in mammalian cells.*

CSHL (516/367-8346, Fax: -8845, *meetings@cshl.org* or *http://www.cshl.org*). *Arabidopsis molecular genetics, molecular cloning of neural genes, expression of eukaryotic genes, yeast genetics, bacterial genetics.*

Exon-Intron (800/407-6546, Fax: 410/730-3983). *PCR understanding and methodologies, RNA isolation and gene expression, rDNA, tissue culture and baculovirus, in situ hybridization, chemiluminescence principles.*

GRC (401/783-4011, Fax: -7644). *Molecular genetics, nucleic acids.*

IU (J. Clay, 812/855-6329, Fax: -8997, *jclay@indiana.edu*). *Recombinant DNA technologies and applications.*

LTI (L. Kerwin, 800/952-9166, Fax: 301/258-8212). *In situ hybridization; gene expression systems; analysis of gene expression; cDNA library, PCR, recombinant baculovirus, recombinant DNA, and cell culture techniques.*

MBL (508/548-3705 ext. 401, Fax: /457-1924, *admissions@mbl.edu* or *http://www.mbl.edu*). *Cellular and molecular biology, molecular evolution.*

PSC (N. Blankenstein, 412/268-4960, *biomed@psc.edu*). *Nucleic acid and protein sequence analysis, methods of molecular mechanics and dynamics of biopolymers, structural determination from NMR.*

Oncor (800/556-6267, Fax: 301/926-6129). *Introduction to molecular cytogenetics.*

UMBC (C. Harriger, 410/455-2336, Fax: -1074, *Carolyn_Harriger@umbcadmn.bitnet*). *Recombinant DNA.*

UMDS (P. Faik, +44-171/403-6998, Fax: /407-5281, *wss@umds.ac.uk*). *Genetic analysis from YAC to gene, analysis of multifactorial diseases.*

UWS (M. Barnard, 206/616-1864, Fax: /685-7515, *mbarnard@u.washington.edu*). *Genomic information and its ethical implications.*◊

Extended calendars are available at *http://www.ornl.gov/TechResources/Human_Genome/home.html* or from HGMIS (see p. 6 for contact information).

U.S. Genome Research Funding Guidelines

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

DOE Human Genome Program

See p. 2 for DOE funding announcement

- Contact for funding information or general inquiries: *genome@er.doe.gov* or 301/903-6488.
- Relevant documents: ftp: *oerhp01.er.doe.gov* in directory */genome* or *http://www.er.doe.gov/production/oher/hug_top.html*

DOE Human Genome Distinguished Postdoctoral Fellowships

Next deadline: February 1, 1996.

- Contact: Linda Holmes, Oak Ridge Institute for Science and Education (615/576-9934, Fax: /241-5219).

NIH National Center for Human Genome Research (NCHGR)

Program announcements listed in *NIH Guide for Grants and Contracts* (*gopher.nih.gov* and *http://www.nih.gov* or 301/496-0844). Bracketed numbers below refer to application due dates. [1] February 1, June 1, and October 1; [2] April 5, August 5, and December 5; [3] May 10; [4] on a continuous basis; and [5] May 1 and November 15.

Program Categories

Research

- Ethical, legal, and social implications (ELSI) of human genome research, Fellowships (PA 92-21) [1].
- Genome science and technology centers (PAR 94-044) [1].
- Informatics (PA 92-59) [1].
- New and improved technologies for genomic research and analysis (PA 94-045) [1].
- Pilot projects or feasibility studies for genomic analysis (PAR 94-046) [1].

Training

- Courses related to genomic analysis (PA 91-88) [1].
- Individual postdoctoral and senior fellowships in genomic analysis and technology (PA 92-21) [2].
- National research service awards:
  - Institutional training grants in genomic science (PA 94-085) [3].
  - Individual predoctoral student fellowships for disabled (PA 95-028) [5] and minorities (PA 95-029) [5].
- Special emphasis research career awards in genomic research (PA 91-89) [1].

Special Programs

- Minority institution travel awards (PA 91-17) [4]
- Research supplements for underrepresented minorities and disabled [4].

NCHGR: 301/496-7531, Fax: /480-2770.

- ELSI: *Elizabeth_Thomson@nih.gov* or 301/402-4997.
- Genetic linkage mapping, annotation, and single-chromosome workshops: *Elise_Feingold@nih.gov*
- Informatics: *David_Benton@nih.gov*
- Large-scale mapping, sequencing of human and mouse genomes: *Jeff_Schloss@nih.gov*
- Physical mapping technology, training, and special programs: *Bettie_Graham@nih.gov*
- Sequencing technology development, technology transfer, nonmammalian model organisms: *Carol_Dahl@nih.gov* or *Robert_Strausberg@nih.gov*

Small Business Innovation Research (SBIR) Grants

DOE and NIH invite small business firms (less than 500 employees) to submit grant applications addressing the human genome topic of SBIR programs. The two agencies also support the Small Business Technology Transfer (STTR) program to foster transfers between research institutions and small businesses. Contacts:

- Kay Etzler; c/o SBIR Program Manager, ER-16; DOE; Washington, DC 20585 (301/903-5867, Fax: -5488). DOE SBIR due March 1, 1996; STTR, early 1996.
- Bettie Graham (see contact, NCHGR). NIH SBIR due April 15, August 15, and December 15. STTR, December 1.

National SBIR/STTR conferences: Washington, DC (October 16–18); Salt Lake City, UT (October 30–November 1); Dallas, TX (April 29–May 1, 1996). Conference hotline: 407/791-0720; electronic registration: 203/379-9427.◊

NCHGR Offers Grants for Sequencing Projects

NCHGR invites applications for the following research projects. For information on obtaining program announcements, see box above.

- RFA HG-95-004: Novel automated sequence technology for large-scale genomic sequencing through scale reduction and increased parallelization of existing approaches that use Sanger sequencing reactions with electrophoretic fragment separation. This is a reissuance of RFA-HG-95-001. Letter of intent due June 15; applications, August 29. [Contact: Carol Dahl or Robert Strausberg; Sequencing Technology Branch; NIH NCHGR; Bldg. 38A, Room 610; 38 Library Drive MSC 6050; Bethesda, MD 20892-6050 (see box for telephone and fax numbers, e-mail address)]
- **RFA HG-95-005:** Pilot projects to test strategies leading to full-scale production sequencing of mammalian DNA. Letter of intent due June 1; applications, August 4.◊

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3. ___ DOE *Human Genome 1993 Program Report* ___DOE *Primer on Molecular Genetics*
4. ___ Reprint of "Report of the Invitational DOE Workshop on Genome Informatics; 26–27 April 1993; Baltimore, Maryland" [*J. Comp. Biol.* 1(3), 173–90], edited by Robert Robbins.

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SELECTED CALENDAR ACRONYMS

AACR Am. Assoc. for Cancer Res.
ACS Am. Chem. Soc.
AFIP/ARP Armed Forces Inst. of Pathol./Am. Registry of Pathol.
AIBS Am. Inst. of Biol. Soc.
ASHG Am. Soc. of Hum. Genet.
ATCC Am. *Type Culture* Coll.
BTCI BioPharm. Technol. Ctr. Inst.
BTP Biotechnol. Train. Programs
CATCMB/CUA Ctr. for Adv. Train. in Cell and Mol. Biol./Cathol. Univ. Am.
CHI Cambridge Healthtech Inst.
CSHL Cold Spring Harbor Lab.
DIMACS Discrete Math. & Comp. Sci.
FASEB Fed. of Am. Soc. for Exptl. Biol.
FEBS Fed. of Eur. Biochem. Soc.
GDB/OMIM Genome Data Base/Online *Mendelian Inheritance in Man*
GMCRF Gen. Motors Cancer Res. Found.
GRC Gordon Res. Conf.
IGES Intl. Genet. Epidemiology Soc.
ISMB Intelligent Syst. for Mol. Biol.
IU Indiana Univ.
LTI Life Technologies, Inc.
MBL Marine Biol. Lab.
MIMBD Meet. on the Interconnection of Mol. Biol. Databases
PSC Pittsburgh Super Comput. Ctr.
UMBC Univ. of Md. Baltimore Co.
UMDS United Med. & Dental Schools
UWS Univ. of Wash., Seattle

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