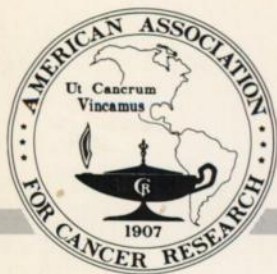


March 15, 1992

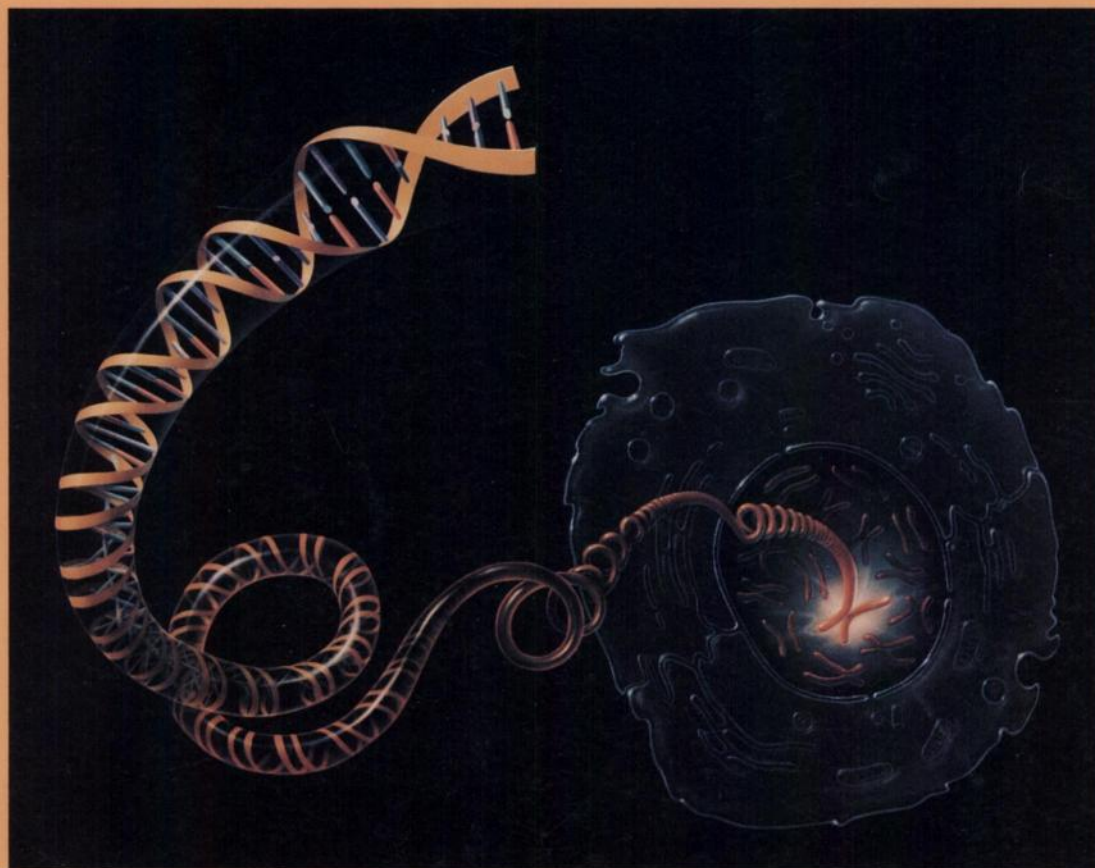


# Cancer Research

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**Department of Microbiology  
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The Comprehensive Cancer Center**

Applications are invited for a vacant faculty position in Molecular Immunology jointly supported by the Department of Microbiology and the Ohio State University Comprehensive Cancer Center. Preference will be given to established investigators applying for a position at the Associate Professor or Professor level. The successful applicant will be expected to maintain an internationally recognized, molecular-oriented research program in cancer immunology and to participate in graduate and undergraduate teaching. This is one of several new cancer related positions that will be filled in the near future to expand the research program of the O.S.U. Comprehensive Cancer Center coincident with the establishment of the Arthur G. James Cancer Hospital and Research Institute.

Applicants should submit a curriculum vitae, statement of current research interests and future plans, and the names of three references to Professor John N. Reeve, Chair, Department of Microbiology, The Ohio State University, Columbus, OH 43210; Tel. 614-292-2301 or FAX 614-292-1538. Review of applications will begin immediately and continue until the position is filled. Women and minority candidates are very strongly encouraged to apply. The University is an Affirmative Action/Equal Opportunity Employer.

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of the

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**September 21-22, 1992**

to be held at

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Chicago, Illinois, USA**

This important meeting is being convened in honor of Dante G. Scarpelli, Magerstadt Professor and Chairman, Department of Pathology, Northwestern University Medical School, in recognition of his lifelong contributions to the field of chemical carcinogenesis. The program is designed to identify and explore new directions of papilloma virus tumorigenesis, DNA repair, and chemical carcinogenesis.

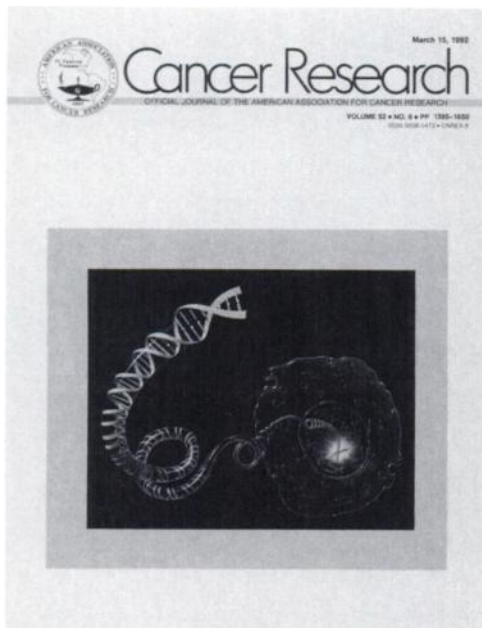
#### **Speakers will include:**

H. zur Hausen, Heidelberg    L. Laimins, Chicago    P. Howley, Bethesda    M. Topal, Chapel Hill    L. Loeb, Seattle  
D. Hanahan, San Francisco    S. Hecht, Valhalla    N. Drinkwater, Madison    C. Harris, Bethesda

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# COVER LEGEND



The Human Genome Project (HGP), an enterprise of mind-boggling magnitude and significance, culminates a revolution in biology that has taken place with the birth of molecular genetics a scant 40 years ago. The success of this project will have extraordinary effects on the theory and practice of biology and medicine and is bound to have an impact on virtually every biological aspect of humanity. Its impact on the understanding and conquest of cancer is readily apparent with the discoveries in recent years of cancer-causing and cancer-repressing genes. The *FASEB Journal*, Vol. 5, January 1991, has devoted 72 pages to the history of the HGP and to its current status. The issue contains 16 articles by many of those involved in planning and management of the HGP and covers many features of the program including pros and cons. Although enthusiasm is not universal among scientists, the sheer audacity of the project has in great measure overcome lingering doubts, and it is now operating with increasing worldwide participation, even though a successful conclusion will still necessarily depend on technical advances not yet available.

Sequencing of the human genome was initially conceived by Charles DeLisi of the United States Department of Energy in 1985 (DOE) as a means of detecting mutations inherited by offspring of survivors of the atomic bomb dropped over Japan during World War II. After a series of international meetings and much discussion in scientific and political circles in the ensuing 3 years, the United States Congress endorsed the effort by appropriating funds to both the DOE and the NIH. To reach its 15-year goals, the HGP is expected to cost as much as \$200 million per year. Headed by James D. Watson, the National Center for Human Genome Research (NCHGR) has put in place funding mechanisms for the NIH program, which will comprise a multiplicity of coordinated, highly sophisticated programs of data collection, management, storage, dissemination, etc. Paul Berg is Chairman of the Advisory Committee to the NIH program.

Meanwhile, independent efforts have begun in other scientifically advanced countries, notably in the United Kingdom, Italy, Japan, France, and the former U.S.S.R. A coordinated international program, known by the acronym HUGO (Human Genome Organization), got off to an auspicious beginning in 1988 under UNESCO. After 3 years of acrimony between the

NCHGR and HUGO over respective prerogatives and responsibilities (*Science*, November 15, 1991, p. 932), a mutually satisfying arrangement is now in place. Under Sir Walter Bodmer of The Medical Research Council (United Kingdom), President, HUGO will assist in coordination of research and collaboration in the collection and exchange of data and will provide a forum for discussion of scientific, ethical, social, legal, and commercial implications. A number of private foundations are also contributing in various ways.

As might be expected, many concerns have been voiced and dissent is not negligible, despite a great deal of enthusiasm within the scientific and political communities. The sheer magnitude of the effort is daunting. The human genome comprises about 3 billion base pairs and somewhere around 50 to 100,000 expressed genes. Only about 1900 of these have been mapped and assigned to 12 of the 23 chromosomes; altogether there are about 5000 genes for which some information exists. About 40 genes associated with human disease have been mapped to particular chromosomes. These are collected and maintained in a data base at Johns Hopkins developed by Victor McKusick; this data base, OMIM, which includes information concerning disease genes, and a second large mapping data base called the Genome Data Base, which includes research mapping data, are now supported by the NCHGR and the DOE.

Although there is agreement that new techniques are necessary for completion of the project in a reasonable time frame of about 15 years, a discouraging picture was drawn by Bart Barrell of the MRC Molecular Biology Laboratory in Cambridge, United Kingdom. He claims that technical progress has been slower than expected over the last 5 years. Since perhaps only about 5% of the total genome is involved in coding for proteins, there is concern that an overwhelming proportion is "junk" and not worthy of a special effort to sequence. As Paul Berg has stated, however, this is a myopic view that ignores the many still unknown roles of noncoding genes in all-important aspects of gene regulation and expression. Bernard Davis has raised a number of points in dissent: (1) The sense of urgency is not scientifically justified and will crowd out more productive programs of individual investigators. (2) It was conceived for a different purpose by the DOE, and the engine is running on political hype rather than scientific necessity. (3) The procedures and goals are not necessarily the best way to advance the science. (4) The sequence-based approach raises serious political and social problems. Moreover, Richard Roberts of the Cold Spring Harbor Laboratory has recently brought up a disturbing note on the frequency of DNA sequence errors in the current data bases (*Science*, May 31, 1991, p. 1255).

Policy questions are also raised by Robert Weinberg, who asks "... which aspects of normal phenotypic variability will be linked to distinct markers during this decade and the next. Good guesses might include certain physiological responses, morphological variation, and even certain aspects of cognitive function, temperament and perception." He continues, "... they have the potential of affecting reproductive decisions, education policy, hiring practices, insurance practices, marriageability, and may even lead, more ominously, to genetically templated differences between different ethnic groups and races." The NCHGR is well aware of the ethical, legal, and social questions arising from the new technology and is setting aside at least 5% of its annual budget and has established a joint NIH-DOE subcommittee to address these issues. Granting all of the unprecedented advantages of this new knowledge of our genome, are we wise enough to deal with the Pandora's box that it will open? However, Pandora's box held an important ingredient, hope, and hope shall drive the project to as yet unimagined benefits to humankind.

We are indebted to Leslie Fink of the NCHGR for assistance.

Sidney Weinhouse