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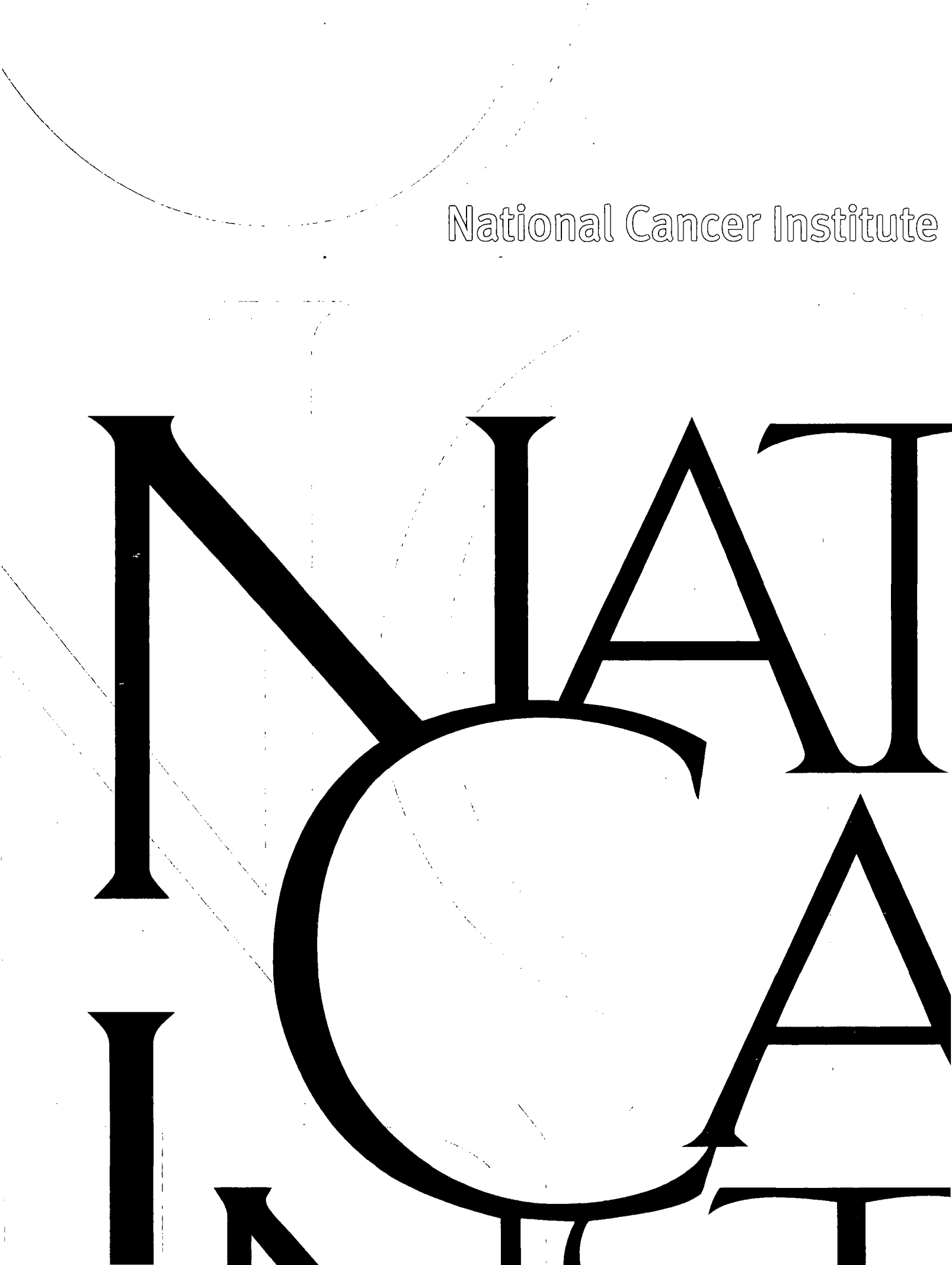
National Cancer Institute



August 1, 1997
Old Executive Office Building
Room 450

Cancer Genome Anatomy Project Website

Vice President Gore

Ellen Stovall
Director, National Coalition for Cancer Survivorship

Richard D. Klausner, M.D.
Director, National Cancer Institute
National Institutes of Health

BIOGRAPHY
Richard D. Klausner, M.D.

Richard D. Klausner, M.D., became the 11th director of the National Cancer Institute (NCI) at the National Institutes of Health (NIH) in Bethesda, Md., on Aug. 1, 1995. As director, Klausner has embarked upon a restructuring of NCI in an effort to streamline the operations of the Institute, including the consolidation of intramural research into three new divisions and a re-grouping of the extramural programs. With these streamlining efforts and a zero-based budgeting approach, he has been able to increase the funding of extramural grants by more than one-half. He has also instituted a new grant review mechanism, known as "accelerated executive review," which is designed to expedite funding for worthy grants.

Klausner has, with his new Board of Scientific Advisors, established five review groups for clinical trials, prevention, developmental therapeutics, cancer centers, and cancer control. The purpose of these groups will be to assess and provide NCI with long-range plans for these programs. Klausner is focused on improving NCI's existing programs and preparing NCI to respond to the cancer research issues of the future. To address this concern, he has established working groups to look at areas where the greatest opportunities exist, including cancer genetics, developmental diagnostics, and AIDS malignancies. In a streamlined Bypass Budget Proposal Klausner, outlines NCI's current investment, identifies areas of opportunity and predicts the outcome of funding versus waiting.

Klausner has also been instrumental in forging new alliances between payor/provider systems and NCI in an effort to improve recruitment to clinical trials. He witnessed the signing of an agreement with the Department of Defense's health care system that provides coverage for patients who are enrolled in Phase II and Phase III NCI-funded clinical trials. He also played a key role in establishing a similar alliance between the Veteran's Administration and NCI, ultimately benefitting patients and researchers alike.

Trained as an internist, Klausner combined patient care and basic research in the early days of his career. He earned his undergraduate degree from Yale University in 1973 and his Medical degree from Duke Medical School in 1976. He was a fellow in internal medicine at Duke Medical Center from 1976-1977. From 1979-1981, following additional training in internal medicine at Massachusetts General Hospital and post-graduate research at Harvard Medical School, Klausner began his research career at the NIH in the NCI's Laboratory of Mathematical Biology. He worked at NIH's National Institute of Arthritis, Diabetes and Digestive and Kidney diseases from 1981-1984, when he became chief of the Cell Biology and Metabolism Branch at the National Institute of Child Health and Human Development.

Klausner is one of the most frequently cited scientists in the world in cellular and molecular biology. His work elucidated general and novel mechanisms for the regulation of complex genetic networks in human cells. He is a leader in the study of iron metabolism and hemochromatosis, a disease of impaired regulation of iron uptake by body tissues which is associated with subsequent development of cirrhosis and liver cancer. His work has revealed the structure and function of the

T-cell antigen receptor, the central molecule of the immune system. He is an expert on how certain cell surface receptors enable antigens to activate the immune response, and he has contributed to an understanding of the molecular basis for how the cell recognizes abnormal or incompletely synthesized antigens, retrieves and eliminates them. His studies revealed novel pathways by which molecules traffic and speak to each other within the cell. Klausner has collaborated with NCI scientists to study the von Hippel-Lindau gene a member of a class of tumor suppressor genes that play a key role in the development of human kidney cancer.

Klausner's research has been recognized with numerous awards and honors, including the Outstanding Investigator Award from the American Federation of Clinical Research and the William Damashek Prize for major discovery in hematology. He was elected to the National Academy of Sciences in 1993, the American Academy of Arts and Sciences in 1995, and the Institute of Medicine in 1996. He has served on the editorial boards of several scientific journals, including *Chemistry and Biology*, *Analytical Chemistry*, *The New Biologist*, *Cell*, the *Annual Review of Cell Biology*, and the *Journal of Cell Biology*. He is a past president of the American Society of Clinical Investigation, and from 1993 to 1995 he served as chairman of the National Science Education Standards Project of the National Academy of Science, overseeing the first comprehensive process to provide a vision of scientific literacy in the American educational system and the criteria required to achieve it. Klausner has authored a textbook of medical immunology and a widely used textbook of internal medicine.

Klausner is the 11th director since the creation of the NCI in 1938. Previous directors were:

1938-1943	Carl Voegtlin, Ph.D.
1943-1947	Roscoe Roy Spencer, M.D.
1947-1948	Leonard Andrew Scheele, M.D.
1948-1960	John Roderick Heller, M.D.
1960-1969	Kenneth Milo Endicott, M.D.
1970-1972	Carl Gwin Baker, M.D.
1972-1976	Frank Joseph Rauscher, Jr., Ph.D.
1977-1980	Arthur Canfield Upton, M.D.
1980-1988	Vincent T. DeVita, Jr., M.D.
1988-1995	Samuel Broder, M.D.

October 1996

BIOGRAPHICAL SKETCH

ELLEN L. STOVALL

Ellen Stovall is Executive Director of the National Coalition for Cancer Survivorship (NCCS)--the largest network of individuals, organizations, and institutions, advocating on issues that affect people with all types of cancer. Prior to her appointment as Executive Director of NCCS in May 1992, she volunteered for over 20 years with organizations in the Washington, DC community as a spokesperson and advocate for quality of life issues that affect people with cancer and their families.

Ms. Stovall served as a member of the Congressionally-mandated subcommittee of the National Cancer Advisory Board to evaluate the National Cancer Program in 1993 and 1994. She has given testimony to the Senate Appropriations Committee, Senate Labor Committee, the House Commerce Committee, the Food and Drug Administration, and other governmental bodies on issues such as cancer research funding, technology transfer (CRADAs), and FDA reform. In June 1996, Ms. Stovall received the distinct honor of being appointed by President Clinton to a six-year term on the National Cancer Advisory Board.

Ms. Stovall represents NCCS's positions and policies to a variety of groups who have an interest in broadening access to quality health care for people with cancer. In December 1995, Ms. Stovall was made a member of the Board of Trustees of the Foundation for Accountability (FAcct), a purchaser and consumer driven organization that evaluates, endorses, and promotes a common set of patient-oriented measures of health care quality focused on the outcomes of care. She also serves on advisory panels, working groups, and committees of the National Cancer Institute (NCI), the American Society of Clinical Oncology (ASCO), the Association of Community Cancer Centers (ACCC), the Southwest Oncology Group (SWOG), and the United States Pharmacopeial Convention, Inc.

Recognizing a need for the voice of cancer survivors to be heard during the national debate over health care reform, a group known as the Cancer Leadership Council (CLC) was convened in 1993 under her direction. Organized to develop a consensus statement on health care reform that spoke from the cancer patient's perspective, the CLC continues to meet regularly and develops positions on health policy matters of consequence to people with cancer. In addition to the National Coalition for Cancer Survivorship (NCCS), CLC members include Cancer Care, Inc.; Candlelighters Childhood Cancer Foundation; National Alliance of Breast Cancer Organizations (NABCO); Y-ME National Breast Cancer Organization (Y-ME); Susan G. Komen Foundation; North American Brain Tumor Coalition; and the US-TOO International Prostate Cancer Support Organization (US-TOO).

Ms. Stovall is a 25-year cancer survivor, having recovered from two bouts with Hodgkin's Disease. She is a frequent panelist and requested speaker on a variety of issues related to cancer survivorship and quality health care.

Why CGAP?
A Conceptual Tour

How?
CGAP Flow Chart

View Libraries

Obtaining CGAP Reagents

Information

Methodology

Data Analysis

References

Staff

Collaborators

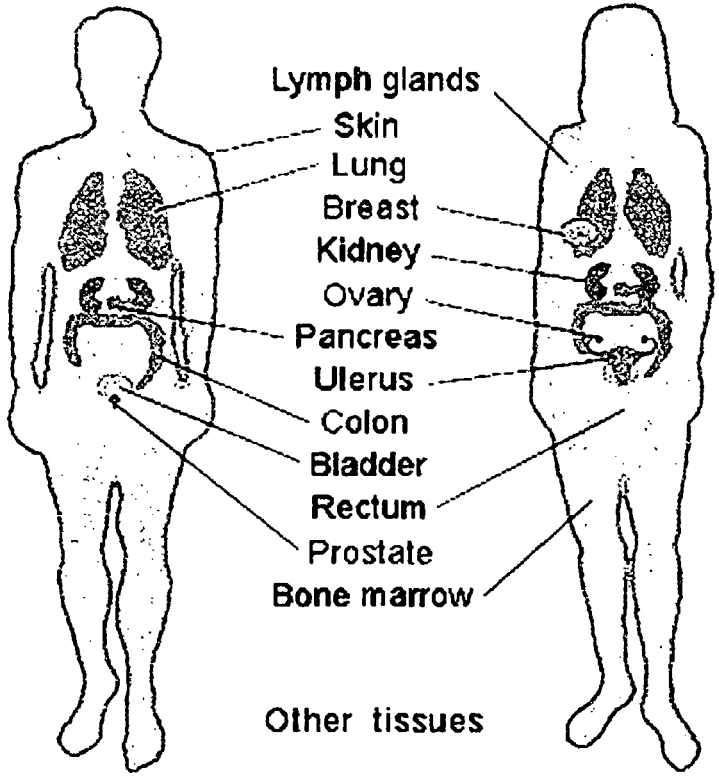
NCI Home Page

NCBI Home Page

NIH Home Page

Cancer Genome Anatomy Project

The Cancer Genome Anatomy Project (CGAP) is an interdisciplinary program to establish the information and technological tools needed to decipher the molecular anatomy of a cancer cell.



Cancer Genome Anatomy Project

Why CGAP?

In the last two decades we have learned that genetic changes lie at the root of all cancers. In response, the *Cancer Genome Anatomy Project* (CGAP) will unite the newest technologies, along with those both cost-effective and capable of high-throughput, to identify all the genes responsible for the establishment and growth of cancer.

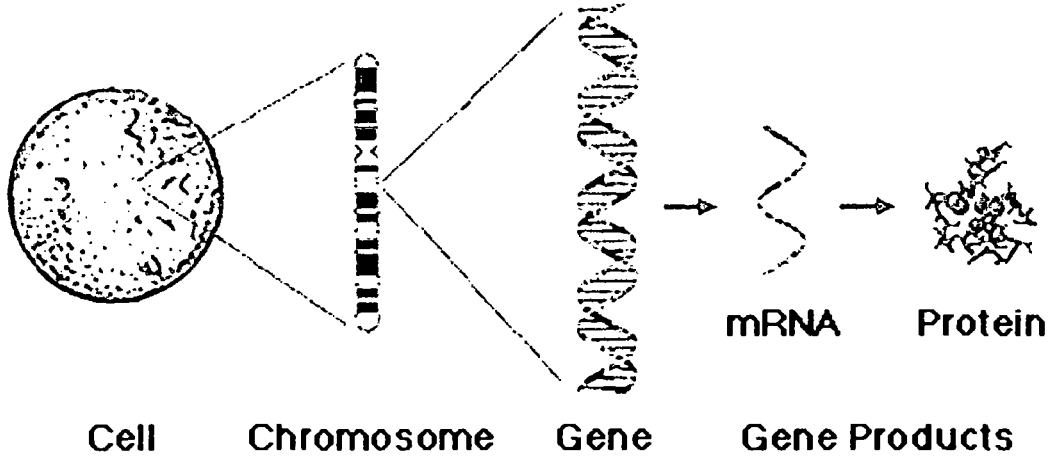
Project Goals

To achieve a comprehensive molecular characterization or normal, precancerous, and malignant cells.

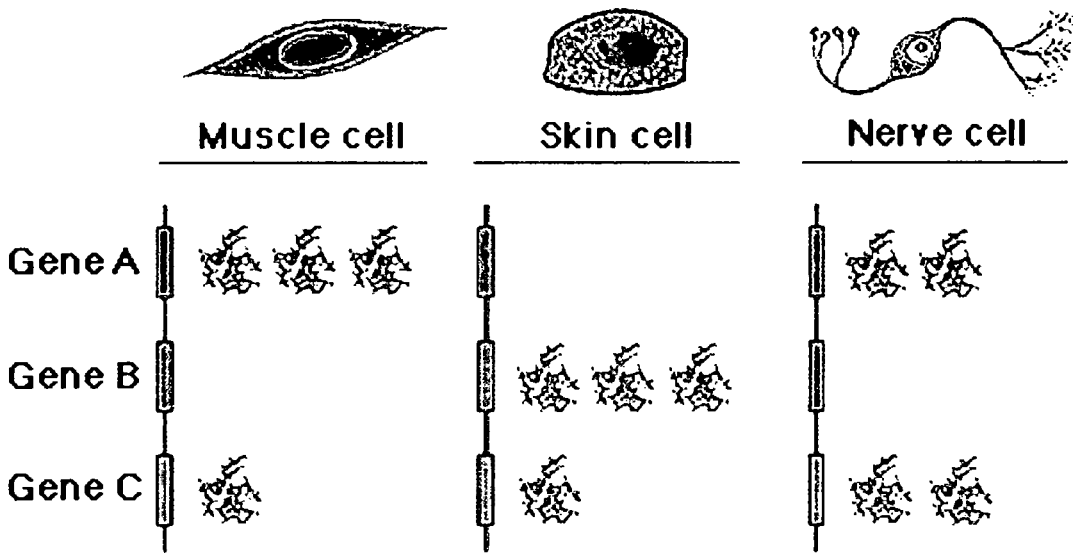
Project Resources

All data & material are made available to the research community without restrictions.

Genes Make Us Who We Are

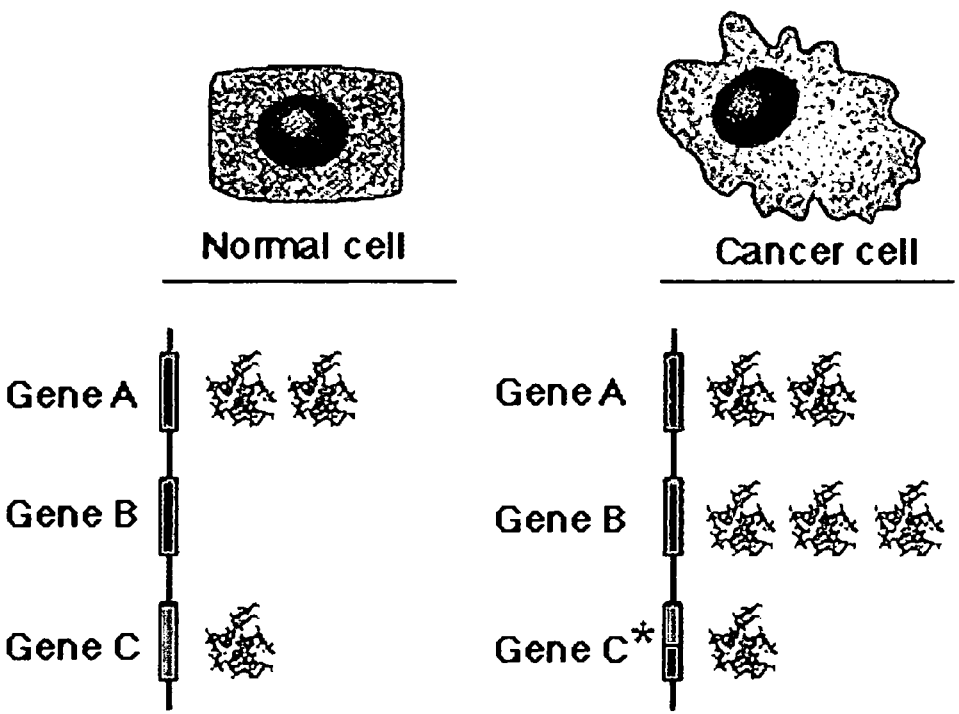


Because cancer is a genetic disease, it is important to understand what genes are and how they work. Each cell in the body contains a complete copy of the genome--the inherited genetic instructions that make us who we are. This genetic material, made of double-helical DNA molecules, is thought to contain approximately 100,000 individual genes. When genes are expressed, they produce transient messengers (mRNAs), which ultimately make proteins, the building blocks of the body.



Although every cell contians the full set of 100,000 genes, only about one tenth of them are expressed in any particular type of cell. Cells look and act the way they do because of the specific genes that they express and the amounts of gene products produced. For example, a muscle cell, a skin cell, and a nerve cell, could be distinguished by their gene expression profiles.

Gene Expression and Cancer

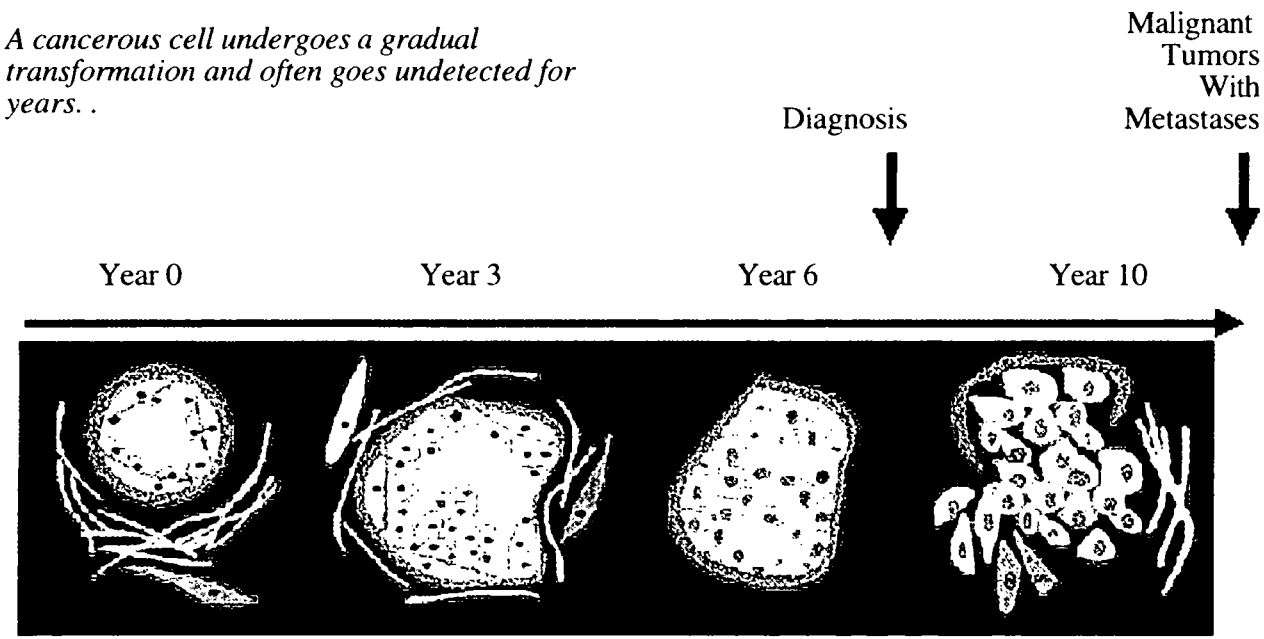


The repertoire of gene products produced by *a cancer cell* might differ in two ways from its normal counterpart:

- **Quantitatively**, as shown for gene B, which is expressed at an abnormally high level
- **Qualitatively**, as shown for gene C*, which is mutated such that it produces an altered gene product

Genes and Cancer Diagnosis

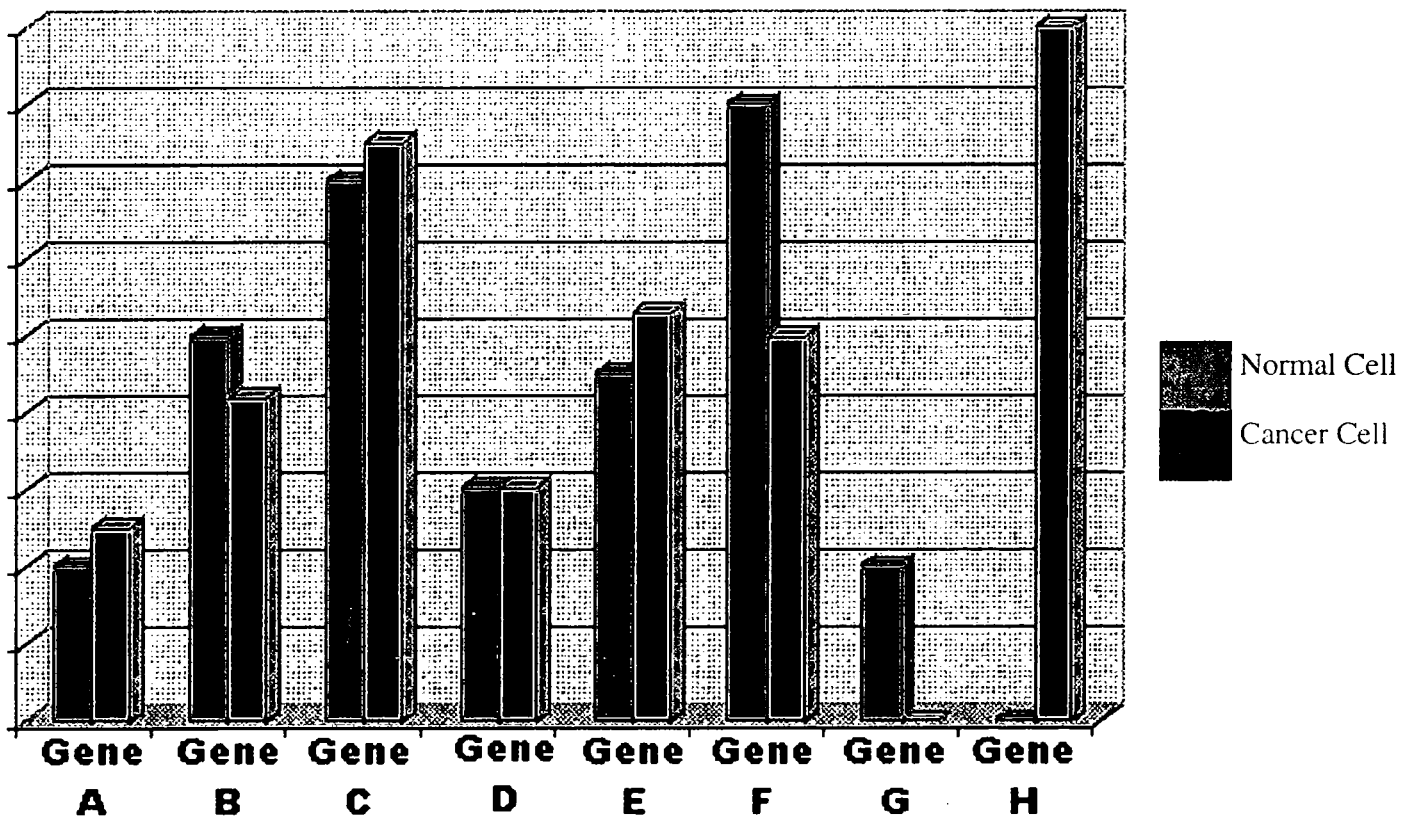
A cancerous cell undergoes a gradual transformation and often goes undetected for years. .



Identifying the genetic differences among normal cells, precancerous cells, and cancer cells, will contribute to our understanding of cancer as it

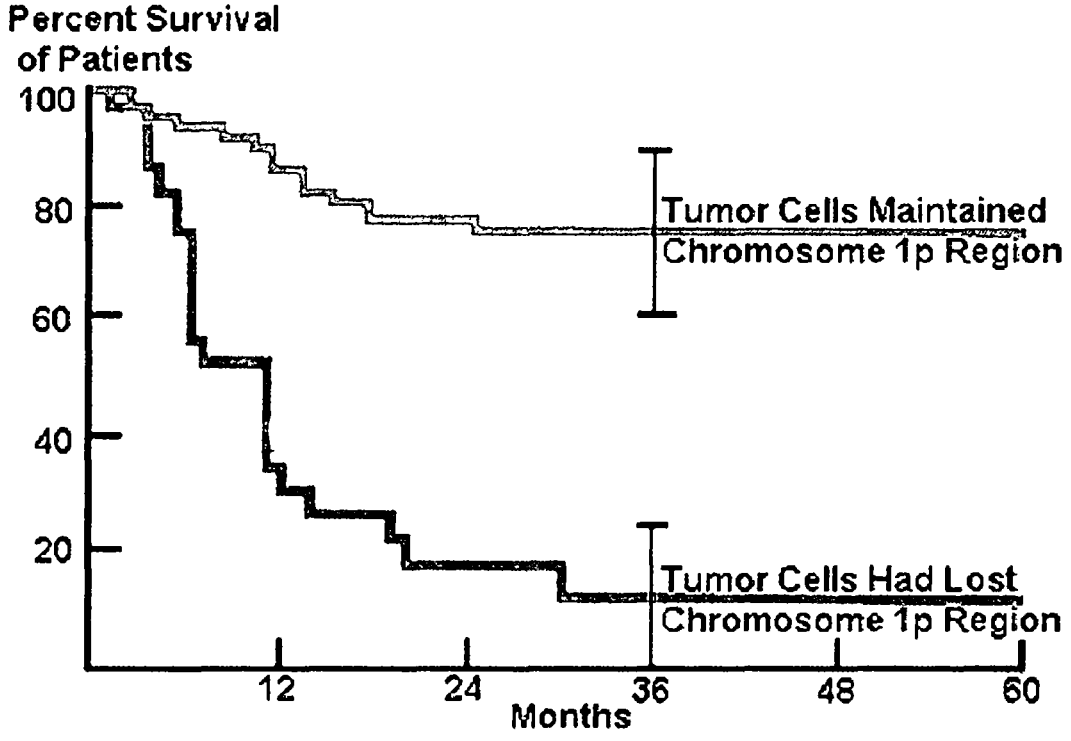
- fosters the discovery of genes that directly cause cancer
- provides us with a way to identify early precancerous cells and thus enhances our methods for early detection
- improves our ability to match patients with appropriate treatment

Gene Profiling: Getting The Fingerprint Of The Cell



Establishing for a cell the repertoire of genes expressed, together with the amount of gene products produced for each, yields a powerful "fingerprint". Comparing the fingerprints of a normal versus a cancer cell will highlight genes that by their suspicious absense or presence (such as Gene H) deserve further scientific scrutiny to determine whether such suspects play a role in cancer, or can be exploited in a test for early detection.

An Example of How Gene Expression Differences Can Determine Therapy Choice



Source: Caron, H, *et al.* , New England Journal of Medicine, 1996 PubMed.

Often, patients suffering from tumors that by traditional criteria are indistinguishable, nevertheless can experience very different outcomes despite having received the same treament. The research results displayed in this graph demonstrate that for patients suffering from the cancer neuroblastoma, the presence or absence of a specific set of genes found on Chromosome 1 strongly correlates with patient outcome. Therefore, in the future this characteristic of the tumor can be used to identify those patients that would benefit from more aggressive treatment, and those best served by the current treatment protocol.

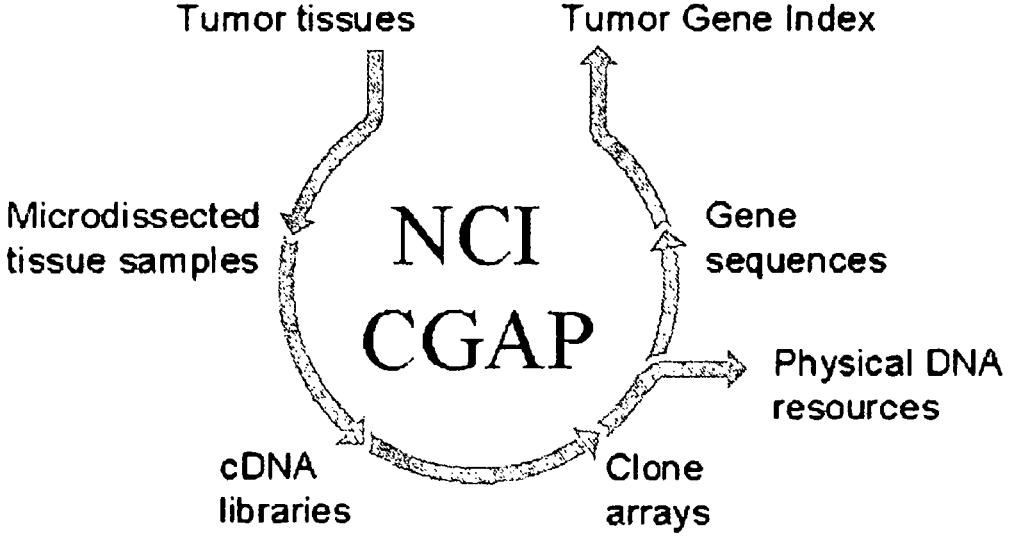
NCI | CGAP NCBI

Cancer Genome Anatomy Project

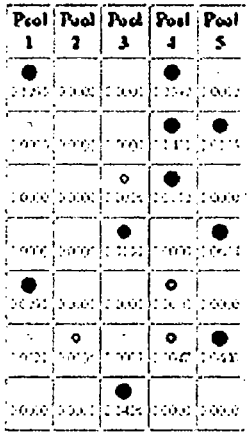
The Cancer Genome Anatomy Project (CGAP) is an interdisciplinary program to establish the information and technological tools needed to decipher the molecular anatomy of a cancer cell.

Browse Libraries and Tissues

Look at an Example



Compare Gene Expression



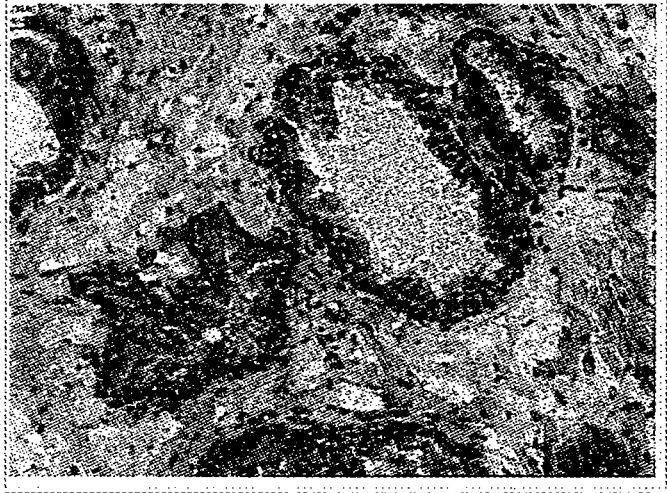
Look at an Example

For additional information on CGAP, contact Robert Strausberg, 301-496-1550.

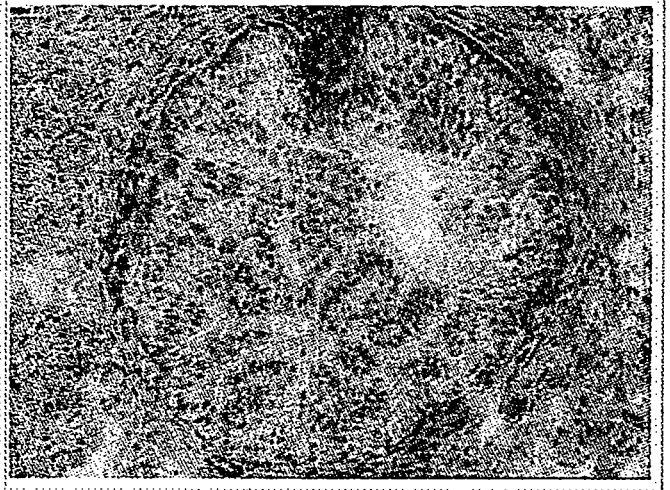
If you have comments or questions on this Web Site, contact the NCBI Help Desk.

NCI CGAP Cancer Genome Anatomy Project NCBI

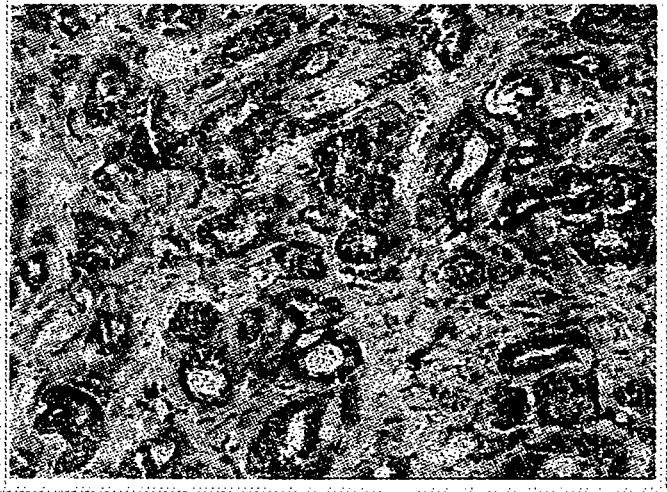
Normal prostate epithelial cells



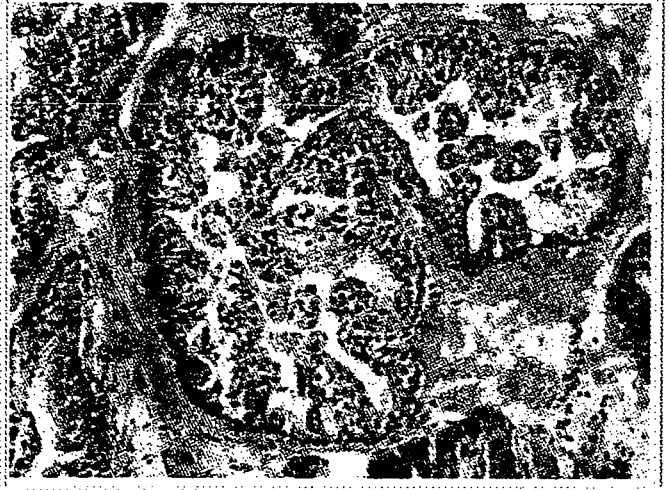
Prostatic Intraepithelial Neoplasia - low grade



Invasive prostatic tumor



Prostatic Intraepithelial Neoplasia - high grade



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NCI CGAP Cancer Genome Anatomy Project NCBI

Digital Differential Display (DDD)

DDD is a computational method for comparing sequence-based gene representation profiles among individual cDNA libraries or pools of libraries. The following table describes the pools that have been defined so far.

Comparison of Normal versus Tumor Prostate Cell Gene Expression

Normal	Precancerous	Malignant	Gene index	Gene description
0.0163	0.0630	0.0078	Hs.1548	Prostate specific antigen (APS)
0.0163	0.0024	0.0104	Hs.73487	Beta-microseminoprotein (prostate secreted) (MSMB)
0.0000	0.0000	0.0156	Hs.82186	V-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3 (alternative products) (ERBB3)
0.0000	0.0000	0.0130	Hs.5417	ESTs
0.0069	0.0071	0.0000	Hs.62954	Ferritin heavy chain (FTH1)
0.0059	0.0071	0.0000	Hs.38972	ESTs
0.0000	0.0047	0.0000	Hs.18910	ESTs

Questions or comments? Write to the NCBI Help Desk

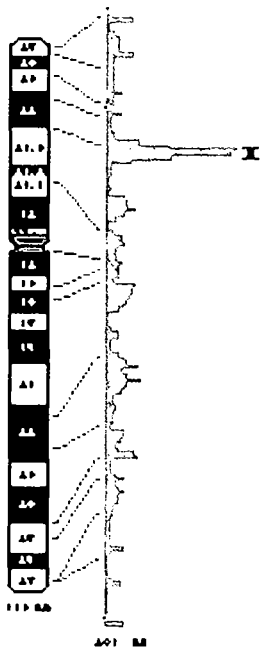
Document: Done

Map Search

Chromosome

6

Go to:
1 2 3 4 5
6 7 8 9 10
11 12 13 14 15
16 17 18 19 20
21 22 X



Search Interval

Enter the names of the Genethon markers which define the desired search interval.

Select Markers

Interval: D6S276-D6S439

176 cDNA markers in this interval

Between D6S273 and D6S1666 [44-45 cM]

SHGC-2492 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-1 CW*0101 ALPHA CHAIN PRECURSOR

SHGC-9818 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DQ(W1.1) BETA CHAIN PRECURSOR

Cancer Research
BECAUSE LIVES DEPEND ON IT

National Institutes of Health

EMBARGOED FOR RELEASE
10:00 a.m. EDT
Friday, August 1, 1997

Bob Kuska
NCI Press Office
(301) 496-6641

New CGAP Website: A Powerful New Tool in the Study of Cancer

With a few clicks of a computer mouse, scientists now can access a free online index that will soon show tens of thousands of genes expressed in common cancers, including lung, prostate, colon, breast, and ovarian.

The website, part of the recently launched Cancer Genome Anatomy Project (CGAP) and which was developed by the National Cancer Institute (NCI) and National Library of Medicine, offers a powerful new tool to study cancer. Now scientists literally can click on the CGAP website from their office computers and submit specific queries about genes expressed during the development of cancer. In response, the CGAP database will sort through its gene index in seconds and provide a list of genes relevant to the query, data that just a few years ago researchers might have contemplated devoting their entire careers to obtain.

Then, researchers can go back to the laboratory to investigate more completely the role of these genes or sets of genes and their protein products in cancer. "CGAP highlights the rapid progress that can be made when technology development and scientific discovery work hand in hand," said Vice President Al Gore, who officially launched the CGAP website today at a ceremony in Washington, D.C. "We hope this project will eventually have an impact on every aspect of the fight against cancer."

(more)

The CGAP homepage is located at **www.ncbi.nlm.nih.gov/ncicgap**. The website now contains information on thousands of genes in a few cancers, but it will constantly add new data as they become available, making the gene index very much a work in progress over the next few years. All CGAP resources--including cDNA libraries, clones, and sequence data--are publicly accessible to scientists.

"CGAP will add thousands of new pieces to the cancer puzzle," said Richard Klausner, M.D., director of NCI. "As we access where each piece fits into the process, we can begin to target these key pieces, or molecules, in detecting and treating cancer."

CGAP is a historic, multi-year project that will assemble the first index of genes involved in cancer. In tandem with the indexing project, CGAP will push to develop high-speed technologies to analyze the genes, proteins, and other biomarkers linked to cancer and disseminate these tools to researchers.

NCI launched CGAP last winter in collaboration with the National Library of Medicine, U.S. Department of Energy, and several pharmaceutical companies, including Bristol Myers-Squibb, Genentech, Glaxo-Wellcome, and Merck.

According to Klausner, CGAP is currently building cDNA libraries, collection of cloned gene transcripts, in normal, precancerous, and malignant cells from the lung, prostate, colon, breast, and ovary. "If a gene transcript represented a book, one could think of CGAP as collecting and ordering into individual libraries all of the books that a normal, a precancerous, and a malignant cell prints at one time," said Klausner. "With further analysis of each library, it will be possible ultimately to read and contrast the full genetic text of a normal cell with that of a cancer cell, critical information in trying to understand the molecular causes of cancer."

Klausner said CGAP is employing a powerful, new research tool to create many of its cDNA libraries. Called laser capture microdissection, or LCM, the new technique allows researchers to select specific tumor cells for analysis, and assess which genes they are expressing in their environment inside the body.

Lance Liotta, M.D., Ph.D., chief of NCI's Laboratory of Pathology, said researchers in the past typically have had to spend hours isolating and culturing cells before they were ever able to study the genes and proteins inside them. As a result, the cells often have begun to react to their

new laboratory environment, expressing genes differently than they would inside in the body and making analyses difficult.

LCM works on the same, basic aim-and-shoot principle as a camera:

- A scientist looks through a microscope at a tissue biopsy, which typically contains hundreds of different types of cells.

- Upon spotting a group of interesting cells (normal, pre-cancerous, or cancerous), the scientist presses a button attached to the side of the microscope. The button activates a laser, which flashes a beam of light that has an intensity slightly greater than a laser pointer.

- The laser beam passes through the plastic film placed above the tissue sample and focuses onto the cells. In the process, the beam melts the film, causing it to fuse to the underlying cells. When the film is removed, the selected cells are immediately extracted from the plastic and ready for analysis.

After performing LCM, researchers apply other powerful technologies to gather thousands of gene transcripts at once from inside the tumor cells. The transcripts are cloned and catalogued into cDNA libraries, then they are sequenced. Ultimately, useful data from the libraries is collected and uploaded into the CGAP database, where researchers for the first time can access an index of genes, both new and previously known, that are expressed throughout the cancer process.

Mike Emmert-Buck, M.D., Ph.D., an NCI scientist who was instrumental in developing LCM and building the prostate libraries used in CGAP, noted the new database has another powerful feature. He said the database shows not only which genes are expressed, but also the levels--high, low, or undetectable--at which the sequences are transcribed at different stages of cancer. "Sometimes it is just as important to know what's not in a cell as it is to know what's there," said Emmert-Buck. "The breadth of analysis that CGAP will open up to researchers is going to be incredible."

# # #

For general information on cancer, contact:

Cancer Information from the Office of Cancer Communications
National Cancer Institute news releases are available via the Internet through the World Wide Web (http://rex.nci.nih.gov). Click on Mass Media.

Cancer Information Service

The Cancer Information Service (CIS), a national information and education network, is a free public service of the NCI, the Nation's primary agency for cancer research. The CIS meets the information needs of patients, the public, and health professionals. Specially trained staff provide the latest scientific information in understandable language. CIS staff answer questions in English and Spanish and distribute NCI materials.

Toll-free phone number: 1–800–4–CANCER (1–800–422–6237)
TTY: 1–800–332–8615

CancerFax®

For NCI information by fax, dial (301) 402–5874 from the telephone on a fax machine and listen to recorded instructions.

CancerNet™

For NCI information by computer:

CancerNet Mail Service (via E-mail)

To obtain a contents list, send E-mail to cancernet@icicc.nci.nih.gov with the word "help" in the body of the message.

Internet

CancerNet is also accessible via the Internet through the World Wide Web (http://cancernet.nci.nih.gov) and Gopher (gopher://gopher.nih.gov) servers.

Cancer Research

BECAUSE LIVES DEPEND ON IT

National Institutes of Health

EMBARGOED FOR RELEASE
10:00 a.m. EDT
Friday, August 1, 1997

NCI Press Office
(301) 496-6641

Cancer Genome Anatomy Project

The National Cancer Institute (NCI), in partnership with government, academic, and industrial laboratories, has launched the Cancer Genome Anatomy Project. This revolutionary project promises to put into place new information and technologies that will create an important platform from which to understand, prevent, and treat cancer. CGAP also has launched its new online website, developed by the NCI and National Library of Medicine. It allows scientists to rapidly access data generated through the project and apply it to their studies.

Background: The Promise of "Fingerprinting" Tumor Cells

Over the last 25 years, it has become clear that cancer is fundamentally a disease involving changes in the genes of cells that become cancerous. This discovery not only answers a long-standing biological question, it also indicates that genes and the proteins that they encode hold the key to improved cancer prevention, detection, diagnosis, and treatment. The challenge now is to define, as physiologists have defined human anatomy, the complete molecular anatomy of tumor

(more)

cells. This means looking into these cells and defining the location, structure, and function of the genes, proteins, and protein networks that drive the development of cancer.

With this molecular anatomy as a blueprint, researchers hope to embark on a new era in the development of tools to fight cancer. Cancer is now often detected relatively late in its development and classified by its site of origin and appearance under a microscope. Health professionals in the future will look inside cells and collect their molecular characteristics, much like a detective gathers fingerprints left at the scene of a crime. They will analyze these fingerprints, looking for abnormal patterns of activity in the genes, proteins, or protein networks that power our cells. These clues will tell doctors whether a tumor is likely to grow fast or slow and whether it will spread to other parts of the body, critical information that currently is often impossible to ascertain. Through enhanced understanding of the molecular basis of cancer development, treatment also will change. By knowing the molecular profile of a person's tumor, it is anticipated that health professionals in the future will be able to develop and select treatments designed specifically to work in fighting individual cancers.

Improving Cancer Diagnostics: Overall Goals

To pursue this vision of the future, the NCI has developed a multi-faceted plan to advance the discovery of new diagnostic tools. The first project is the Cancer Genome Anatomy Project, which marks the discovery phase for improved cancer diagnostics.

Launched in early 1997, CGAP has two overall goals:

- Enhance discovery of the acquired and inherited molecular changes in cancer.
- Evaluate the clinical potential of these discoveries. This requires the creation and dissemination of technologies that can read and interpret the molecular features of cancer.

CGAP is the first step towards constructing a research infrastructure for the molecular analysis of cancer. The next step will be to apply these new research tools and biomarkers to clinical research, where their diagnostic and prognostic use can be evaluated and integrated into clinical care.

Cancer Genome Anatomy Project: Initial Programs

The initial programs of the Cancer Genome Anatomy Project will aim to:

- Begin compiling an index of all tumor genes. NCI will coordinate the production of gene libraries and DNA sequences of genes from normal and cancerous tissue. The first cancers to be studied will include breast, colon, prostate, lung, and ovary.

- Make the gene sequences compiled in the tumor index publicly available on the CGAP website (**www.ncbi.nlm.nih.gov/ncicgap**).

- Support the development of novel technologies that scan genes, proteins, or protein networks linked to cancer. The program aims to develop efficient systems that fully integrate and automate the various steps involved in molecular analysis, such as sample preparation, sample analysis, data collection, and data analysis. NCI will rapidly disseminate these new tools to all researchers.

# # #

For general information on cancer, contact:

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Toll-free phone number: 1-800-4-CANCER (1-800-422-6237)
TTY: 1-800-332-8615

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National Institutes of Health

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NCI Press Office
(301) 496-6641

Questions and Answers About the Cancer Genome Anatomy Project

1. What is the Cancer Genome Anatomy Project?

The Cancer Genome Anatomy Project (CGAP) is a program that will generate an unprecedented body of information about the genetic changes that accumulate in a normal cell as it turns into a cancer cell. Research teams from the National Cancer Institute (NCI), academic centers and private companies will create a database and develop new technologies that will be immediately available to scientists throughout the world on the Cancer Genome Anatomy Project web page, a sophisticated website maintained by the National Library of Medicine. Using the molecular signature of tumors, CGAP's goal is to lay the foundation for a new era of cancer prevention, detection, diagnosis and treatment.

2. How will this be accomplished?

Researchers will clone and sequence the active genes present in cancers at various stages of tumor development, and make the data available immediately to scientists on the CGAP website.

With these new data, scientists will be able to discover new genes that play a role in cancer. Or they will be able to find out when known genes become active or silent in the development of tumors

(more)

Because of the far-reaching scope of the CGAP program, new technologies related to all aspects of the project will emerge. Information about these technologies will also be available through the CGAP website.

3. What will be the specific steps involved in achieving the goals of CGAP?

CGAP researchers will collect high quality tissue samples from normal, precancerous, and tumor cells for many cancers. A cDNA library will be prepared from each tissue sample. A cDNA library is the subset of genes -- out of the 100,000 human genes -- that are active in a particular cell.

The genes from the libraries will be sequenced and the sequence will be made available to scientists around the world on the CGAP website. **(www.ncbi.nlm.nih.gov/ncicgap)**.

Besides providing the actual sequences, the website will link each sequence to databases of scientific papers, protein products, related genes, and maps of the human genome. Scientists will also find a description of the methods used to prepare the tissue samples and gene libraries as well as the levels of expression for the active genes.

Also included at the website is a broad overview of the CGAP program, opportunities for researchers to participate in CGAP, the latest technology breakthroughs, and information about how to obtain cDNA libraries and arrays of these libraries for further research.

4. Why is it important to know the genetic profile of a cancer cell?

The information collected by CGAP researchers will provide scientists many new opportunities for prevention, early detection, and treatment of cancers. Knowing the patterns of genes that are active in cancer cells compared with normal cells will help researchers identify genes that may later prove useful in the clinic.

For example, it is anticipated that these data will eventually enable researchers to determine, at the earliest possible stage of cancer development, those tumors that will respond to therapy, which therapies they will respond to, and whether a particular cancer will grow quickly or slowly, or whether it will spread.

5. What aspects of CGAP are currently in place?

The CGAP website **(www.ncbi.nlm.nih.gov/ncicgap)** which plays a central role in ensuring the rapid availability of the data generated by CGAP scientists, is currently in place. Besides being easily accessible and user-friendly, the CGAP website is electronically integrated to other important biological databases, such as Genbank and PubMed.

In addition, an infrastructure for producing cDNA libraries for CGAP and for sequencing DNA from these libraries has been established. A number of libraries from cancer, precancer, and normal cells have already been produced. Over 40,000 DNA sequences have already been generated from libraries representing a variety of cancer types. This information, already available via the website, is linked electronically to relevant papers, protein structures, and related genes.

It is estimated that laboratories involved in CGAP will sequence 1 million clones over the next two years, or roughly 10,000 clones per week.

6. Who is involved in CGAP?

In addition to the approximately $3.5 million in support for CGAP by NCI in the current fiscal year, the National Center for Biotechnology Information (part of the National Library of Medicine) and the Department of Energy are participating in the development of CGAP. Support for the project is also being provided by Bristol-Myers Squibb, Genentech, Glaxo Wellcome, and Merck & Co. Preparation of libraries and DNA sequencing are being performed at several academic centers and companies, and in time, even more will likely be involved.

7. Who will be the primary users of CGAP?

The primary users of CGAP will be research scientists who are interested in how normal, precancerous, and tumor cells differ from one another. These scientists will be able to obtain information relevant to this question from the CGAP website. The information on the CGAP website will be linked to other databases around the world such as those that contain information arising from the Human Genome Project. By bringing together all of the information about active or silent genes in specific tumor-types, CGAP will help scientists make more progress against cancer.

8. Why is CGAP being launched at this time?

Over the past 20 years, it has become clear that all cancer arises from the gradual accumulation of multiple genetic changes within a cell. This knowledge provides the basis for a new approach in our fight against cancer. The ability to determine the genetic profile of a cell at all stages of cancer development is the key step to rapid advances in cancer prevention, early detection, diagnosis, and selection of optimal treatment.

In CGAP, the revolutions in cancer biology, web-based informatics, and human genomics converge to make it possible for the first time to uncover the molecular basis of cancer. It is hoped that the combined efforts of experts in all of these fields will quickly provide the

international scientific community with an unprecedented volume of data and new technologies, which will, in turn, stimulate research aimed at eradicating cancer.

9. What cancers are included in CGAP?

Initially, CGAP is concentrating on five major cancers -- breast, colon, lung, prostate, and ovarian cancers. However, CGAP is designed to collect data for all cancers. The rate at which scientists around the world take advantage of CGAP will set the pace for expansion of the project into other cancers.

10. What are the immediate benefits to CGAP?

The CGAP database will provide the cancer research community with several candidate genes that are involved in the development of cancer. The identification of these candidate genes will stimulate further research to assess their long-term usefulness as tools in the fight against cancer.

11. What will be the longer-term benefits to CGAP?

The NCI's vision for CGAP is that it will eventually have an impact on every aspect of the fight against cancer. Ultimately, it is an understanding of the genetic alterations in cancer cells that will enable better cancer prevention, earlier cancer detection, more accurate cancer diagnosis, and more effective cancer treatments. CGAP will provide the infrastructure to allow those types of discoveries.

12. How can I get more information about CGAP?

The first thing to do is to visit the CGAP website **(www.ncbi.nlm.nih.gov/ncicgap)** where additional information including a conceptual tour of CGAP is provided. The site contains a link to the Help Desk of the National Center for Biotechnology Information. If you still have questions about CGAP, contact the NCI press office at (301) 496-6641.

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For general information on cancer, contact:

Cancer Information from the Office of Cancer Communications
National Cancer Institute news releases are available via the Internet through the World Wide Web (http://rex.nci.nih.gov). Click on Mass Media.

Cancer Information Service

The Cancer Information Service (CIS), a national information and education network, is a free public service of the NCI, the Nation's primary agency for cancer research. The CIS meets the information needs of patients, the public, and health professionals. Specially trained staff provide the latest scientific information in understandable language. CIS staff answer questions in English and Spanish and distribute NCI materials.

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