



THE CANCER GENOME ATLAS

The Cancer Genome Atlas (TCGA) Pilot Project

Charting a new course for prevention, diagnosis, and treatment of cancer

Every day more than 1,500 Americans die from cancer — about one person every minute. As the U.S. population ages, this rate is expected to rise significantly unless researchers can develop new strategies to stop the growth and spread of cancer cells within a patient.

Among the most promising strategies are efforts to identify key genetic “targets” within cancer cells and then create therapeutics designed to zero-in on those targets. This approach for attacking cancer through its genetic vulnerabilities stems from recent advances made possible by the sequencing of the human genome. Yet, the successful completion of the Human Genome Project in 2003 represents just the first step in the quest to fully understand the biology of cancer.

Building upon the foundation laid by researchers, the National Institutes of Health (NIH) launched The Cancer Genome Atlas (TCGA) Pilot Project to further scientific understanding of cancer and create a comprehensive “atlas” of the genomic changes involved in cancer.

The Pilot Project is a three-year collaboration of NIH’s National Cancer Institute (NCI) and National Human Genome Research Institute (NHGRI).

Today, scientists at more than a dozen institutions across the nation are collaborating on the Pilot Project. Using innovative tools and technologies, they are working together in a coordinated, systematic manner to create an atlas of genomic changes in three specific cancers: brain, lung, and ovarian.

TCGA May Help Define the Future of Cancer Research

Scientific understanding of the molecular roots of cancer is improving daily. However, cancer is an extremely complex disease and, from a genetic standpoint, may someday prove to be unique for each cancer patient. Scientists expect that a deeper, systematic exploration of cancer will provide important insights into the mechanisms responsible for the uncontrolled growth of cancer cells and their spread throughout the patient's body.

Data from the Pilot Project will provide researchers and clinicians with a glimpse of what may grow into a comprehensive atlas of molecular information listing the genomic changes in all types of cancer.

What Causes Cancer?

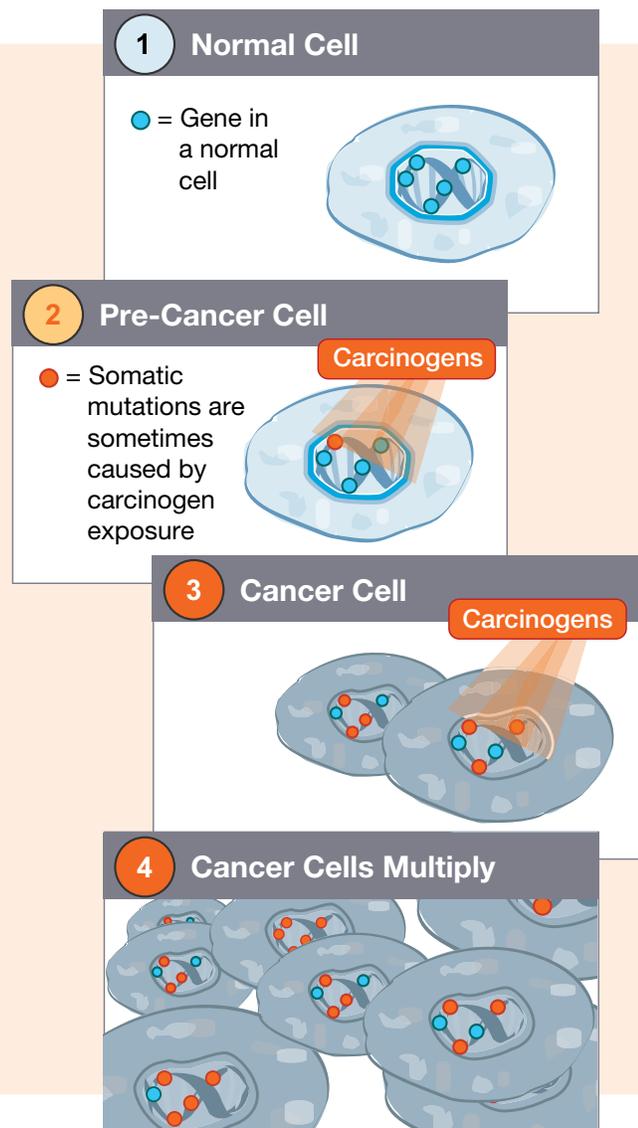
The development of cancer is a multi-step process in the life of a cell. Cancer can be initiated by mutations in a cell's DNA. DNA is the molecule in our body that carries genetic information we inherit from our parents. A mutation in DNA is simply a change in DNA, but these changes can occur through a variety of mechanisms, some that are inherited and some that are acquired after birth.

All children are born with some genetic mutations that they inherit from their parents. These are called germline mutations. Other DNA mutations occur sporadically throughout our lifetime. These mutations are called somatic mutations. They are sometimes caused by exposure to carcinogens from the environment or from lifestyle choices, such as tobacco use. Somatic mutations are responsible for the vast majority of cancers. The purpose of TCGA is to create an "atlas" of the significant somatic mutations associated with most cancers.

The genomic information generated by TCGA could stimulate advances in cancer research and provide opportunities for the discovery and development of new targets for cancer therapeutics. It could also provide new ways to help clinicians develop personalized treatment plans for each patient and allow clinical trials to focus on patients who are most likely to respond to specific treatments.

TCGA Starts by Studying Three Cancers

The Pilot Project will focus on three types of cancers: brain (glioblastoma), lung, and ovarian. Together, these cancers account for more than 210,000 cancer cases each year in the United States.



TCGA is starting as a pilot project because the approach and infrastructure for a project of this scale have to be tested thoroughly before it is feasible to study a large number of tumors. Brain, lung, and ovarian cancers were selected for the Pilot Project because of the availability of

high-quality human tissue collections, known as biorepositories, that met TCGA's strict scientific, technical, and ethical requirements, and because these cancers have poor prognoses for diagnosed patients.

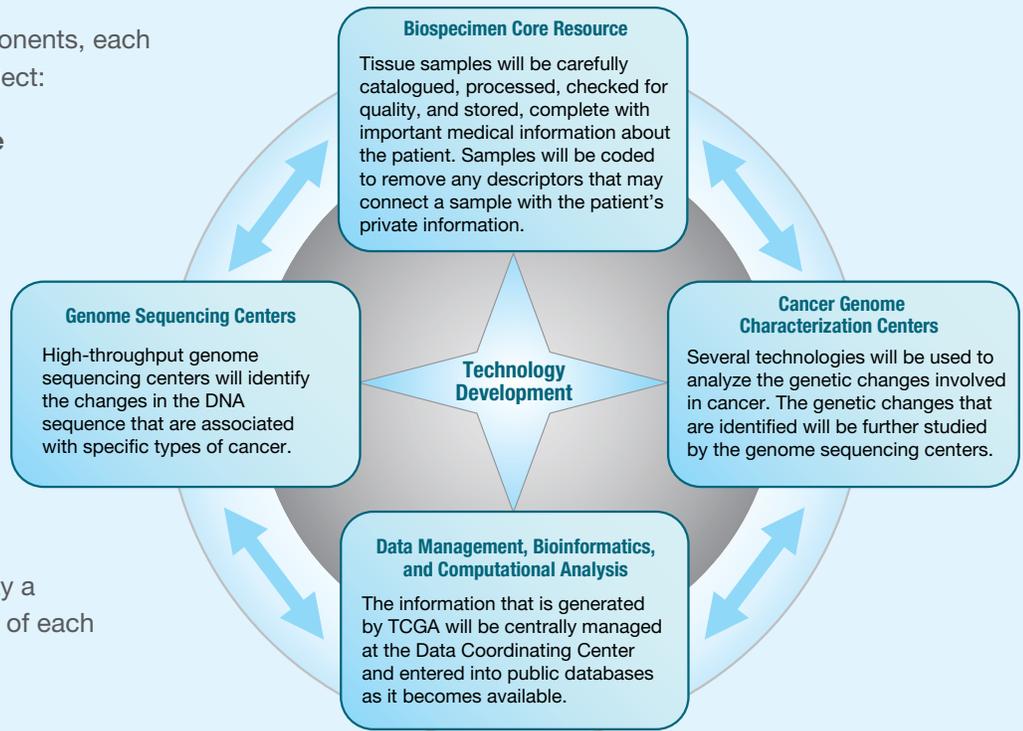
TCGA Process

Beginning with the critical first step of patient participation, TCGA involves a broad cross-section of the cancer research community, including basic researchers, clinical researchers, bioethicists, doctors, nurses, cancer patients, and advocates.

TCGA is a network of four components, each critical to the success of the project:

- **Biospecimen Core Resource**
- **Cancer Genome Characterization Centers**
- **Genome Sequencing Centers**
- **Data Management, Bioinformatics, and Computational Analysis, including a TCGA Data Coordinating Center**

Technology development will play a vital role in advancing the efforts of each of the four TCGA components.



The specific steps in TCGA process are:

1. Patient Volunteerism	Eligible cancer patients are asked to donate tissue and/or blood samples.	
2. Biospecimen Distribution	A centralized facility processes tissue samples and then sends genetic materials to TCGA research centers.	
3. Research and Discovery	TCGA components work together to identify genomic changes associated with cancer.	
4. Data Sharing	Genomic information generated by TCGA is made widely available through public databases. Researchers around the world can use the information to speed advancements in cancer biology and related technologies.	
5. Goals	Advances made by researchers using TCGA data pave the way for targeted strategies for diagnosing, treating, and preventing cancer.	

How Do NCI and NHGRI Receive Input About TCGA?

A group of outside experts, called TCGA External Scientific Committee, provides input to NCI and NHGRI on all aspects of the pilot project. The committee provides perspectives from all communities, including patient advocates, clinicians, and scientists, and facilitates communication across all communities.

Prior to undertaking the project, NCI and NHGRI held a series of meetings to gather input from the scientific and advocacy communities about TCGA. In addition, specific forums are being held to bring together members of TCGA network and experts in brain cancer, lung cancer, and ovarian cancer so they can collaborate as TCGA studies these cancers.

In the Future, How May TCGA Improve Diagnosis, Treatment, and Prevention of Cancer?

TCGA will help the cancer research community better understand the genetic changes associated with cancer.

This improved understanding may lead to:

- New targets for cancer therapeutics
- Better tools for assigning patients to clinical trials
- More personalized treatment plans for each patient
- Better diagnostics to assess risk for specific cancers
- Improved strategies for cancer prevention

How Will NCI and NHGRI Evaluate TCGA?

Success factors for the Pilot Project include completion of genomic analysis of the three initial types of cancer, identification of specific alterations in genes associated with cancer, and the ability to differentiate cancer subtypes based on genomic changes.

How Can I Get More Information?

For more information about TCGA, including policies, participating institutions, and progress, please visit <http://cancergenome.nih.gov>.

Or contact us at:

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For more information about the National Cancer Institute and its programs, please visit <http://cancer.gov>.

For more information about the National Human Genome Research Institute, please visit <http://genome.gov>.



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