Explaining Cancer Genome Research [1]

A growing area of cancer research, called cancer genome research, compares genes found in tumors and genes found in healthy tissue in order to understand how these genes differ and which ones are important. To do this, researchers collect samples from all types of tumors to find out a tumor?s genetic ?fingerprint? and then compare it to the fingerprints of healthy tissue from the same person. Different genes are involved in different tumor types, and understanding what genes are important to the development of cancer may lead to improvements in detecting, diagnosing, and treating cancer.

About cancer and cancer genomes

Cancer begins when normal cells start to change and grow uncontrollably, forming a mass called a tumor. All of these changes take place at the most basic level of the cell?its genes. Genes are made up of deoxyribonucleic acid (DNA), which contains all of the chemical instructions that tell cells what to do and when to do it. When these instructions have mistakes, cells may not function normally. Sometimes these mistakes result in uncontrolled, abnormal cell growth and the ability to invade and spread to other tissues and organs in the body. This is the beginning of cancer.

All of the genes in a cancer cell are known as a cancer genome. Many of these genes are like those in healthy cells; however, a few genes have specific mutations (changes) that are responsible for turning a previously healthy cell into a cancer cell. While some of these mutations are inherited (passed down from your parents), most happen during your lifetime. Many of these changes occur as a result of being exposed to environmental factors, such as chemicals, or from lifestyle choices, such as smoking. Others appear to happen at random as cells divide.

Researchers are learning that different tumors have different mutations, even if the cancer started in the same organ. In other words, not all lung tumors or breast tumors have the same genetic fingerprint. There is also evidence that a recurrent cancer (a cancer that comes back after treatment) has different mutations than the original cancer. This variation is what makes treating cancer so difficult, but it is also what provides opportunities for new treatments.

If you have been diagnosed with cancer, you might have had some tissue removed in a biopsy [2] . The biopsy sample provides doctors with information about the best way to treat your cancer. Now doctors often use additional tests to learn whether the tumor has specific mutations that may affect your treatment options. For example, ASCO recommends [3] that a person with

advanced non-small cell lung cancer have the tumor tested for the epidermal growth factor receptor (EGFR) when a doctor is considering giving a treatment known as a tyrosine kinase inhibitor (TKI).

The Cancer Genome Atlas project

One of the biggest efforts underway to understand the cancer genome is The Cancer Genome Atlas [4] (TCGA) project. This project was started in 2006 by the National Cancer Institute and the National Human Genome Research Institute. The idea is to create a ?map? of various cancer genomes in order to better understand what turns a normal cell into a cancer cell and what makes one cancer different from another.

As part of TCGA, researchers are collecting tissue samples from patients treated at cancer centers across the United States. By studying hundreds of these tissue samples and comparing them to tissue samples from people who do not have cancer, researchers are mapping the genomes of glioblastoma (a malignant brain tumor [5]), lung cancer [6], and ovarian cancer [7]. TCGA expanded the range of its research; find a complete list of all the cancer genomes that TCGA is mapping here [8].

In the first results mapping the glioblastoma genome [9], researchers found several mutated genes that are responsible for the development and growth of glioblastoma, including three genetic mutations researchers previously did not know were common in this type of cancer. This information may help researchers determine if patients with a particular gene that is mutated may benefit from treatments that target that gene but not from other treatments. Researchers also pinpointed a mutated gene that may cause chemotherapy to not work in some people with glioblastoma.

Another important finding from TCGA is that tumors from the colon and the rectum, judging by their DNA fingerprints, are really a single type of cancer, not two different cancers as previously thought. This information helps doctors better understand how cancer begins and may improve future treatment for people with this cancer.

What this means for patients

Although some results of cancer genome mapping may not be ready for use in cancer treatment today, discoveries from this research may lead to better tests to diagnose cancer and new treatments that are more effective. Talk with your doctor to learn more about the role of genes in cancer, including whether your tumor should be tested for mutated genes and if there are any treatment options that target those genes.

More Information

Understanding Targeted Treatments [10]

Facts About Personalized Cancer Medicine [11]

Understanding Pharmacogenomics [12]

Links:

[1] http://www.cancer.net/research-and-advocacy/introduction-cancer-research/explaining-cancer-genome-research
[2] http://www.cancer.net/node/24406
[3] http://www.cancer.net/node/24512
[4] http://cancergenome.nih.gov/
[5] http://www.cancer.net/node/18562
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