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# Cancer and its Genomics in Transformation Era



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## Introduction

Cancer is a disease of the genome, genomics deals with the characterization of point mutations and other structural alterations in a wide range of cancers with the help of next-generation sequencing advanced technologies. All the (deoxy ribonucleic acid) DNA contained in our cells makes up our genome. In most cells, the genome is packaged into two sets of chromosomes: 1 set from our mother and another set from our father. These chromosomes are composed of six billion individual DNA letters. In the English alphabet there are 26 letters: A through Z. In the alphabet of our genes there are four letters: A, C, G and T. Just like the letters in a book make words to tell a story, so do the letters in our genomes. Genomics is the study of the sequence of these letters in your DNA and how each string of letters passes information to help each cell in your body work properly [1].

For centuries, scientists have been searching for better ways to treat cancer. The development of radiation therapy in the early 1900s and chemotherapy in the 1940s were two milestones. At the starting Chemotherapy drugs lacked the selective capacity to distinguish between cancer cells and normal cells, leading to toxic and sometimes intolerable side effects for patients [2]. Medical advances, both therapies have become more targeted, and researchers have found ways to minimize side effects and maximizes the results [3]. Today, radiation therapy and chemotherapy and multimodal treatments are considered the standard of care in treating cancer patients, helping millions of survivors to live longer [4].

In cancer cells, small changes in the genetic letters can change what a genomic word or sentence means. A changed letter can cause the cell to make a genome that doesn't allow the cell to work as it should. These proteins can make cells grow quickly and cause damage to neighboring cells. By studying the cancer genome, scientists can discover what letter changes are causing a cell to become a cancer. The genome of a cancer cell can also be used to tell one type of cancer from another. In some cases,

studying the genome in a cancer can help identify a subtype of cancer within that type, such as breast cancer, gastric cancer, colon cancer, ovarian cancer etc. Understanding the cancer genome may also help your doctor select the best treatment for that cancer of that patient [5].

The study of cancer genomes has revealed abnormalities in genes that drive the development and growth of many types of cancer. This knowledge has improved our understanding of the biology of cancer and led to new methods of diagnosing and treating the diseases. For example, the discovery of cancer-causing genetic and epigenetic changes in tumors has enabled the development of therapies that target these changes as well as diagnostic tests that identify patients who may benefit from these therapies. One such targeted drug is vemurafenib which was approved by the for the treatment of patients with melanoma who have a specific mutation in the *BRAF* gene as detected by an approved test [6].

## History

Over the past decade, large-scale research projects have begun to survey and catalog the genomic changes associated with a number of types of cancer. These efforts have revealed unexpected genetic similarities across different types of tumors. For instance, mutations in the *HER2* gene distinct from amplifications of this gene, for which therapies have been developed for breast, esophageal, and gastric cancers that have been found in a number of other cancers, including breast, bladder, pancreatic, and ovarian to name a few [7]. Researchers have also shown that a given type of cancer, such as breast, lung, and stomach, may have several molecular subtypes. For some types of cancer, the existence of certain subtypes had not been known until researchers began to profile the genomes of tumor cells. The results of these illustrate the diverse landscape of genetic alterations in cancer and provide a basic foundation for understanding the molecular basis of this new group of diseases.

Available advanced technologies and the knowledge gained from previous genomic studies could be used to define the full set of driver mutations and other alterations to DNA and RNA in many cancers. These studies that compare genomic information from tumors and normal tissue from the same patient allow researchers to discover genomic changes that may drive cancer. A large number of genetic alterations that drive the development and progression of many types of cancer have been identified through large-scale research in these studies. Given this opportunity is to expand the current use of genomic methods to investigate the molecular basis of different clinical sub-phenotypes. These new approaches could help researchers identify genetic changes that may distinguish aggressive cancers, indolent and very indolent ones. Similar approaches could be used to study the molecular basis of response to a given therapy, as well as mechanisms of resistance to treatment available [8].

### Conclusion

The data wealth emerging from these cancer genomic studies will be increasingly integrated with patients' medical, clinical and the diagnostic data. This integrated results could be used to develop more tailored made approaches to cancer diagnosis and treatment, as well as to improve methods in predicting cancer risk, prognosis, response to treatment, prevention, screening common as well as rare cancer types. Comprehensive analysis of few cancer genomes has revealed the great deal of diversity in the genetic abnormalities found within cancers of a single type and moreover, recurrent genetic alterations within these cancers are often involved in large percentage of cases. Identifying which genetic changes initiate cancer development and discovering rare genetic alterations that drive cancers are therefore challenging and good for the development of this field.

Development of cell lines and animal models that capture the diversity of human cancer is also the immediate need. Models of

these cancer subtypes may be nonexistent or under represented, and there are no models for many recurrent genetic lesions in human cancer. Analyzing and managing this vast amounts of data involved in genomic studies are additional challenges for the field. Research in this area requires an efficient and manageable bioinformatics infrastructure and increasingly involves contributions of data and expertise from cross and inter disciplinary teams [9].

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