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Review Article

The Cancer Genomic Atlas – "TO CONQUER CANCER"

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ABSTRACT

The Cancer Genomic Atlas (TCGA) is a publicly accessible cancer data repository and tool that allows us to understand the molecular basis of cancer through the application of genomics and proteomics. So far, researchers have been able to diagnose 33 cancer types including 10 rare cancer types. The key features of TCGA are to make the data collection process publicly accessible for the better understanding of the molecular and genetic basis of cancer and its mechanism of action along with its prevention. Studies on different cancer types along with comprehensive pan cancer analysis have expanded the understanding and purpose of TCGA. Ever since its' conceptualization, its' high-throughput approach has provided a platform for the identification of genes and pathways involved in cancers and accurate classification of cancers.

Keywords: Genomics, Molecular biology, Bioinformatics, Database, Oncology

INTRODUCTION

For centuries, cancer has been affecting humans aggressively, where the first documented cases of cancer were hailed in 1500 B.C. in Egypt although the term was later proposed by Hippocrates (Father of Medicine).[1] With the advances in medical science, cancer which initially started as breast cancer has increased vastly by spreading to other organs. Cancer is generally characterized by genomic alterations such as chromosomal rearrangement, copy number aberrations, DNA sequence changes, and modification in DNA methylation which together increases the human malignancies.[1] The cell becomes cancerous when there are mutations in genes, such as the tumor suppressor p53 or *TP53*. In fact, more than 50% of cases are caused when there is a defect in p53. The continued uncontrolled cell division leads to accumulation of cells in the body which aggregate to form a tumor.

Fast forward to the 21st century, with strides made in molecular oncology, a recent advancement was the introduction of The Cancer Genomic Atlas (TCGA). Today, TCGA is a publicly accessible tool developed for better understanding of the molecular basis of cancer through genome sequencing. It was initiated in February 2005 by the National Cancer Advisory Board, and finally, it was released in 2006 by the joint collaboration of National Cancer Institute (NCI) and National Human Genome Research Institute (NHGRI).[2] It is a public platform which is designed to help researchers and clinicians to improve diagnostic methods, treatment standards, and cancer prevention. From the point of its discovery, it has brought together many researchers from various institutes to collectively and collaboratively

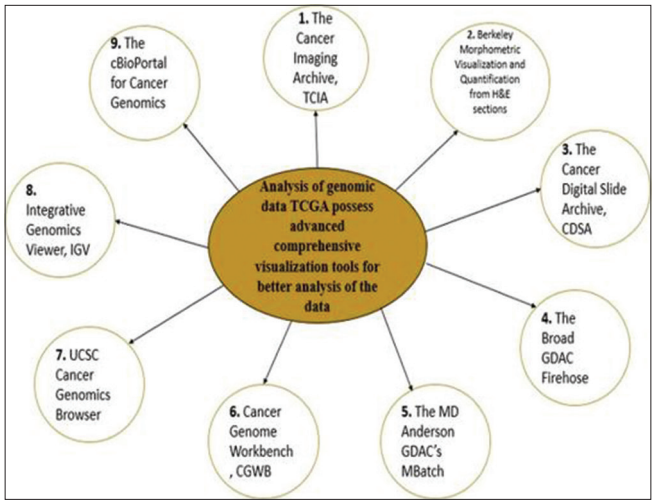

Figure 2: Analysis of genomic data: (1) It is created by National Cancer Institute (NCI) to collect and share with the public a large number of medical images of cancer form The Cancer Genomic Atlas (TCGA) cases. (2) It is a data storage of computed histology-based images of different tumor samples for TCGA cases. It is sponsored by Lawrence Berkeley National Laboratory. (3) It is an online interactive tool for viewing and annotating diagnostic and tissue slide images of different tumor types from TCGA project. (4) It is an analytical infrastructure created by the Broad Institute based on the needs of TCGA project. It provides a large amount of different quantitative algorithms such as GISTIC, MutSig, Clustering, and Correlation. (5) Used to identify and quantify the batch effects accompanying TCGA data set. (6) It is developed by NCI to integrate and display sample level genomic and transcriptional alterations in various cancers, from data from several cancer projects. (7) It is an open-access web-based tools developed and maintained by the UCSC Cancer Genomics Group to host, visualize, and analyze cancer genomics together with clinical data by utilizing genomic coordinate heatmaps. (8) Free to download, high-performance visualization tool introduced by Broad Institute for interactive exploration of large, heterogeneous, integrated data sets. (9) Developed by the Memorial Sloan-Kettering Cancer Centre for visualization, analysis, and download of large-scale cancer genomics data sets. So far, it stored data from 69 cancer genomics studies including DNA copy number data, mRNA and miRNA expression data, mutations, RPPA data, DNA methylation data, and limited clinical data related to survival.

Figure 3: DNA analyzer device and the steps involved in the DNA analyzer.

1. Broad Institute of MIT and Harvard – ABI (TCGA platform code); Applied Biosystems Sequence data (DCC Platform Name); DNA Analyzers (Instrument Support Materials); Primers (Sequence Download)
2. McDonnell Genome Institute at Washington University McDonnell Genome Institute at Washington University – ABI (TCGA platform code); Applied Biosystems Sequence data (DCC Platform Name); DNA Analyzers (Instrument Support Materials); Primers (Sequence Download)
3. Human Genome Sequencing Center at Baylor College of Medicine – ABI (TCGA platform code); Applied Biosystems Sequence data (DCC Platform Name); DNA Analyzers (Instrument Support Materials); Primers (Sequence Download)
4. University of North Carolina – AgilentG4502A_07_1(TCGA platform code); Agilent 244K Custom Gene Expression G4502A-07-1(DCC Platform Name); SurePrint G3 CGH+SNP Microarray (Instrument Support Materials); FASTA (Sequence Download)
5. University of North Carolina – AgilentG4502A_07_2 (TCGA platform code); Agilent 244K Custom Gene Expression G4502A-07-2 (DCC Platform Name); SurePrint G3 CGH+SNP Microarray (Instrument Support Materials); FASTA (Sequence Download)
6. University of North Carolina – AgilentG4502A_07_3 (TCGA platform code); Agilent 244K Custom Gene Expression G4502A-07-3 (DCC Platform Name); SurePrint G3 CGH+SNP Microarray (Instrument Support Materials); FASTA (Sequence Download)
7. Memorial Sloan Kettering Cancer Centre – CGH-1x1M_G4447A (TCGA platform code); Agilent SurePrint G3 Human CGH Microarray Kit 1x1M (DCC Platform Name); SurePrint G3 CGH+SNP Microarray (Instrument Support Materials); FASTA (Sequence Download)
8. Broad Institute of MIT and Harvard – Genome_Wide_SNP_6 (TCGA platform code); Affymetrix Genome-Wide Human SNP Array 6.0 (DCC Platform Name); Genome-Wide Human SNP Array 6.0 (Instrument Support Materials); FASTA (Sequence Download)
9. McDonnell Genome Institute at – Genome_Wide_SNP_6 (TCGA platform code); Affymetrix Genome-Wide Human SNP Array 6.0 (DCC Platform Name); Genome-Wide Human SNP Array 6.0 (Instrument Support Materials); FASTA (Sequence Download)
10. University of North Carolina – H-miRNA_8x15K (TCGA platform code); Agilent 8 x 15K Human miRNA-specific microarray(DCC Platform Name);Human

Table 1: Types of genome sequencing methods and its characteristics.

Types of genome sequencing methods	Characteristics
1. RNA sequencing (RNAseq)	• Used for transcriptome profiling, and deriving strand information with very high precision • Rapidly identifies and quantify rare and common transcripts, isoforms, novel transcripts, gene fusions, and non-coding RNAs, among a wide range of samples, including low-quality samples • The TCGA deposits data containing information about both nucleotides sequence and gene expression
2. MicroRNA sequencing (miRNAseq)	• It utilizes materials enriched in small RNAs • The detection of specific sets of short, noncoding RNAs that have the capacity to regulate hundreds of genes within or across diverse signaling devices is further carried out
3. DNA sequencing (DNAseq)	• Nucleotides are determined within a DNA molecule, for providing information about DNA alterations such as insertions, deletions, polymorphism as well as copy number variation, mutation frequencies or viral infection events • The TCGA uses DNA sequencing systems based on sanger sequencing
4. SNP-based platforms	• Analyses genome-wide structural variation across multiple cancer genomes • Array-based detection of single-nucleotide polymorphisms includes platforms able to define SNP, CNV, and loss of LOH across multiple samples
5. Array-based DNA methylation sequencing	• TCGA utilizes DNA methylation assay based on the Illumina platform, assuring single base-pair resolution, high accuracy, easy workflows, and low input DNA requirements • This method is based on highly multiplexed genotyping of bi-sulfite-converted genomic DNA • The TCGA DNA methylation data files contain information for signal intensities, detection confidence, and calculated beta value for methylated and unmethylated probes
6. Reverse-phase protein array	• Method for large-scale protein expression profiling, biomarker discovery, and cancer diagnostics • It is an antibody-based technique allowing for the analysis of more than 1000 samples with up to 500 different antibodies at a time • The TCGA DCC data include original images of protein arrays, calculated raw signals, relative concentration of proteins, and normalized protein signals

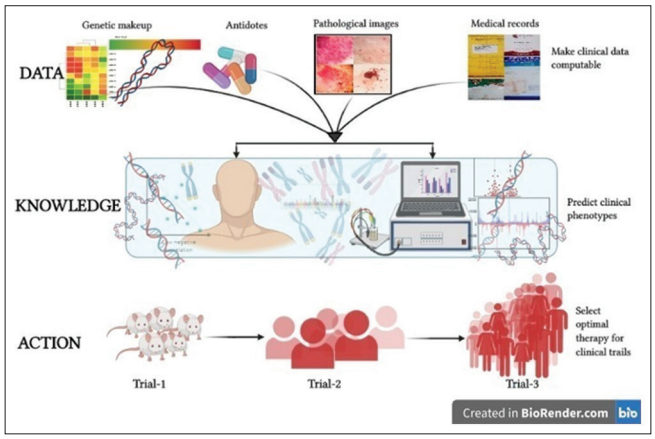

Figure 4: Artificial intelligence is being implemented in various fields of science to assist medical professionals, to detect diseases at an early stage and diagnose with the best treatment possible. This also helps them to modify the traditional methods of treating a particular disorder in an appropriate way.

Acknowledgment

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Declaration of patient consent

Patient's consent not required as there are no patients in this study.

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Nil.

Conflicts of interest

There are no conflicts of interest.

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