

Scientific and Technological Advances that will Contribute to the Cure of Cancer in the Next Ten Years

Adrian P Hunis*

Emeritus Member of ASCO, Emeritus Member of ESMO, Professor of Oncology at the School of Medicine of the University of Buenos Aires, Argentina

***Corresponding Author:** Adrian P Hunis, Emeritus Member of ASCO, Emeritus Member of ESMO, Professor of Oncology at the School of Medicine of the University of Buenos Aires, Argentina.

Received: April 12, 2023

Published: May 01, 2023

© All rights are reserved by **Adrian P Hunis**.

In accordance with the medical and scientific advances that we are experiencing and the results that are already being seen with digital technologies, such as Artificial Intelligence, added to my experience of more than forty years in the management, care and treatment of cancer patients, I understand that these eight elements are going to mean a before and after in the cure for cancer.

Deep sequencing is a technique that allows the identification of mutations and variations in the human genome. DNA sequencing is done using technologies such as sequencing by synthesis, which uses fluorescence detection to read the nucleotide sequence of a piece of DNA. Coverage depth refers to the number of times each base of the genome has been sequenced on average, allowing the identification of DNA mutations with high precision. Deep sequencing is useful for studying genetic diseases, cancer, and genetic variability in human populations.

Liquid biopsy is a non-invasive technique that makes it possible to detect tumor cells or DNA fragments of circulating tumors in the blood, without the need to perform a solid biopsy of the tumor. This is accomplished by analyzing bodily fluids such as blood, urine, or cerebrospinal fluid. Liquid biopsy is being used to diagnose cancer, monitor disease progression, and assess response to treatment. It is also being investigated for other diseases, such as autoimmune diseases and infectious diseases.

Proteomics and Alpha Fold: Proteomics refers to the study of all proteins in a particular cell or tissue. Alpha Fold is an artificial intelligence computer program developed by Google that can

predict the 3D structure of proteins based on their amino acid sequence. Proteomics and Alpha Fold are driving the discovery of new therapies and the understanding of diseases at the molecular level. For example, proteomics is being used to identify biomarkers for diseases such as cancer and Alzheimer's disease, and Alpha Fold is being used to predict protein structure in non-model organisms and in the identification of new therapeutic proteins.

The single cell technique allows for the study of genetic differences between individual cells in a population of cells. This is especially useful in genetic disease and cancer research, where the specific cells that lead to disease progression can be identified. The single cell technique is performed using technologies such as RNA sequencing at the single cell level, which allows analysis of gene expression at the single cell level. This may help to better understand how cells behave in different disease states and to identify new therapies.

Organoids are small artificial organs created in the laboratory from pluripotent stem cells or cells of a particular organ. These organoids can be used to study human disease, test drugs and therapies, and perform toxicity tests. Organoids are useful for studying diseases that are difficult to model in animals, such as colon cancer and pancreatic cancer. They are also being used to study neurodegenerative diseases such as Alzheimer's and Parkinson's.

CAR-T cells are a type of cell therapy that uses genetically modified T cells to attack cancer cells in the body. T cells are a type

of immune system cell that normally help protect the body against infection and disease. In CAR-T cell therapy, T cells are taken from the patient and genetically modified to express a specific chimeric antigen receptor (CAR) for the cancer cell. The modified cells are grown in the laboratory and infused back into the patient so they can attack cancer cells.

Epigenetic drugs are a class of drugs that act on epigenetics, which refers to changes in gene expression that do not involve changes in the DNA sequence. These changes are regulated by chemical modifications in the DNA and the histones that package it. Epigenetic drugs can modify these modifications and therefore influence gene expression. They are being used to treat diseases such as cancer, Huntington's disease, and multiple sclerosis.

Spatial transcriptomics is a technique that allows analysis of gene expression in a specific section of tissue in three dimensions. This allows the identification of specific cells that express certain genes and how these cells interact with each other in a tissue. Spatial transcriptomics is performed using technologies such as fluorescence microscopy and RNA sequencing at the single cell level. This technique can help to better understand how cells function in a tissue and how changes in gene expression can contribute to diseases such as cancer.

Obviously, these data and these techniques will go a long way in the fight against cancer and other prevalent diseases. It is probable that many of them can be cured, others chronicled, and other patients will die despite the advances that I present here.

Research continues and it is the only way to live longer and better.