ISSN: 2755-0184

Journal of Diabetes Research Reviews & Reports

SCIENTIFIC Research and Community

Research Article

Open Access

The Impact of Sequencing Human Genome on Rare Diseases of Unknown Origin

Hameed Khan, Ph.D.

Senior Scientist, Department of Genetics & Robotics, NCMRR (National Center for Medical Rehabilitation Research), National Institutes of Health (NIH), Bethesda, Maryland, USA & Adjunct Professor of NYLF (National Youth League Forum) Scholars, USA

ABSTRACT

For centuries, we have been suffering from strange diseases such as Rheumatoid Arthritis, Ankylosing Sclerosis, Multiple Sclerosis, Celiac Disease, Type I Diabetes; they were considered rare diseases of unknown origin. Since we did not know the causes of these diseases, their treatments are equally unknown and most of the treatments contain small amounts of narcotic to ease the pain. After sequencing (determining the exact order of the nucleotides in the DNA molecule) Human Genome and comparing it with the Reference Sequence, we have identified a piece of DNA, called Major Histocompatibility Complex (MHC) and Autoimmune Diseases. carrying genes which play a central role in regulating immune responses and maintaining immune tolerance. The primary function of MHC molecules is to present antigen peptides to T Lymphocytes; various MHC genes can influence how the immune system distinguishes between self and non-self -molecules. In certain situations, this process fails, leading to autoimmune diseases, where the immune system mistakenly attacks body's own tissues. The Genome comparison has revealed strong association among specific MHC allele and susceptibility to various autoimmune disorders. These associations highlight the importance of MHC polymorphism in shaping immune response determining disease risk. One of the strongest genetic risk factors for autoimmune diseases lies within the MHC region. Many autoimmune disorders show strong associations with the MHC alleles. Genome Wide Association studies have consistently identified the MHC region as the most significant genetic contributor to autoimmune risk. The next generation scientists (my students) will sequence the long polymorphic MHC DNA, letter by letter, word by word and sentence by sentence and identify genes using second and third generation sequencers responsible for all rare diseases. A gene has a start codon (AUG) which codes for amino acid Methionine. After several dozen codon the gene ends in a stop codon. There are three stop codon (AAG, UGG, UGA). Suppose identify a gene responsible for causing Rheumatoid Arthritis, we could use recombinant technology to make millions of copies of this gene. Using Restriction enzyme EcoR1 which serves as a molecular scissor, we could cut and paste this gene in Plasmid or virus which serves as Vector. Vector crosses the host cell wall and cuts the DNA of the host cell at the specific site and inserts its genome. When host cells grow and replicate, it makes millions of copies of the genes. This gene is isolated and inserted in animal model (mouse or rat) to induce Rheumatoid Arthritis. Two paths are available to us; prevention and treatments. Prevention for those individuals who are not here and treatment for those who are here and suffering from these rare diseases. Prevention applies to those couple who have a family history of these diseases. They could have a healthy child free from those rare diseases if their embryo is incubated for three days. When the embryo becomes an 8-cell, each cell could be sequenced to see if it is free from any gene of rare disease. If any of these cells carry the gene, it could be discarded. Only the cell that is free from any of those gene could be implanted.to have a healthy child. Developing treatments for those who are here is a lifelong process costing millions. If the purpose of life is not only to explore the Universe, but also to protect, preserve and spread human intelligence in every corner of the Universe, we must develop treatments no matter how long it takes and no matter how much it costs.

***Corresponding author**

Hameed Khan, Ph.D, Senior Scientist, Department of Genetics & Robotics, NCMRR (National Center for Medical Rehabilitation Research), National Institutes of Health (NIH), Bethesda, Maryland, USA & Adjunct Professor of NYLF (National Youth League Forum) Scholars, USA.

Received: October 16, 2026; **Accepted:** October 23, 2026; **Published:** October 30, 2026

Keywords: Rheumatoid Arthritis, Ankylosing Sclerosis, Multiple Sclerosis, Celiac Disease, Type I Diabetes Nitrogen Mustard, Aziridines, Carbamate, Azq

Historical Background

Soon after the discovery of double helical structure of DNA by Crick and Watson [1]. It was logical to sequence the entire human genome. In 1990, US Congress authorized three billion dollars to sequence the entire human genome. By 2003, the entire human was sequenced. We found that the Human Genome sequence contains the entire book of life, but the medical genome sequence carries only the strip of DNA in the genome which identifies the mutation responsible for a specific disease. Deleterious mutations are identified by SNIP maps, or Hap Map or Microarray. Single stranded DNA or RNA has affinity to hybridize with complimentary sequence of DNA. Genes occur on a single stranded RNA. It has a start codon AUG which codes for amino acid Methionine and several hundred codons later one of the stop codons (AAG, UGA, of GGA) appears and DNA synthesis stops. Thousands of flagrance tag are placed on a single chip. When patients DNA extracts are passed on RNA chips, it hybridized with the chip DNA. The colored hybridized DNA identifies the specific mutation responsible for the disease. That specific DNA could be obtained from the patient from the SNP data (Single Nucleotide Poly Morphism: It is a form of genotyping, which is the measurement of more general genetic variation. SNPs are one of the most common types of genetic variation. An SNP is a single base pair mutation at a specific locus at each thousand base

pairs of the genome, usually consisting of two alleles (where the rare allele frequency is > 1%).) or from RFLP data (Restriction fragment length polymorphism (RFLP) which is a technique that exploits variations in DNA sequences. DNA from differing sources will have variations or polymorphisms throughout the sequence. Using Restriction Enzymes, these differences in sequences may be teased out).

In case of cancer, most mutations occurred either due to deletion or insertion of DNA base pairs or when the nucleotide structure damage occurred in labors working in radioactive mine fields or living close to radioactive power plants exposed to radiation. Most mutation in cancer patients occurred due to rapid replication of cells. Imagine A child is conceived on day one has a single cell by the time the child is grown up to age 21, that single cell has replicated over one hundred trillion times. Mistakes occurred during fast replication.

Reference Sequence

The Human Genome: The Greatest Catalog of Human Genes on Planet Earth

When we sequenced our entire genome, we read our book of life, letter by letter word by word, sentence by sentence, chapter by chapter all forty-six volumes (chromosomes) written in six billion four hundred million genetic letters (nucleotide) of a healthy human being under the Human Genome Project. We can use our healthy Genome as a Reference Sequence for comparison. Using Nano Capillary Sequencing method, it took us 13 years to sequence the entire human genome at a cost of $3 billion. Now, we have developed next generation sequencers like Nanopore technology which will sequence the entire genome cheaper and faster. Using biopsy sample, we can take a single cell from the Lung or Oral tumor of smoker, sequence its genome, and compare it with the Reference sequence to identify the number and location of all mutations or damage genes caused by smoking. Recently, we also completed the 1000-genome project which will provide thousand copies of the same gene sequence for comparison. We also learned to convert Analog language of Biology into the Digital language of computer. Now, we can write a program and design a computer to read and compare and send the data to any country in the world at the speed of light. When comparing with the Reference Sequence with the smoker's gene sequence, it will identify all the mutations with precision and accuracy. Once the mutations responsible for causing any cancer including Lung, or Oral Carcinoma are identified, we can design drugs to shut off those genes.

There are three billion two hundred million AT/GC base pairs in every cell in humans and are arranged like a spiral staircase. We inherit each strand of the staircase from each parent. All humans have 23 pairs of chromosomes. As I mentioned above, we look different because within every 1000 to 1300 genetic letters, one base pair is located at a different place called Single Nucleotide Polymorphism (SNP). In a three billion four hundred million base pair genome of a person, there are at least 3 million SNP which make us look different from one another.

Although all living creatures have the same AT/GC base pairs, the numbers of chromosomes are different in each species. A unit or a large number of AT/GC base pairs that are arranged to produce a protein is called genes (usually from a few hundred genetic letters to a few thousand.) When we eat food, each ingredients are broken down by proteins or enzymes produced by these genes to extract energy needed by our body. You can chemically connect AT/GC base pairs together.

We deciphered all 46 chromosomes, 23 from each parent. The 46 chromosomes present in each cell of our body are the greatest library of the Human Book of Life on planet Earth. The Human Genome Project has identified the following genes on each chromosome: We found that the chromosome-1 is the largest chromosome carrying 263 million A, T, G and C nucleotide bases and it has only 2,610 genes. The chromosome-2 contains 255 million nucleotides bases and has only 1,748 genes. The chromosome-3 contains 214 million nucleotide bases and carries 1,381 genes. The chromosome-4 contains 203 million nucleotide bases and carries 1,024 genes. The chromosome-5 contains 194 million nucleotide bases and carries 1,190 genes. The chromosome-6 contains 183 million nucleotide bases and carries 1,394 genes. The chromosome-7 contains 171 million nucleotide bases and carries 1,378 genes. The chromosome-8 contains 155 million nucleotide bases and carries 927 genes. The chromosome-9 contains 145 million nucleotide bases and carries 1,076 genes. The chromosome-10 contains 144 million nucleotide bases and carries 983 genes. The chromosome-11 contains 144 million nucleotide bases and carries 1,692 genes. The chromosome-12 contains 143 million nucleotide bases and carries 1,268 genes. The chromosome-13 contains 114 million nucleotide bases and carries 496 genes. The chromosome-14 contains 109 million nucleotide bases and carries 1,173 genes. The chromosome-15 contains 106 million nucleotide bases and carries 906 genes. The chromosome-16 contains 98 million nucleotide bases and carries 1,032 genes. The chromosome-17 contains 92 million nucleotide bases and carries 1,394 genes. The chromosome-18 contains 85 million nucleotide bases and carries 400 genes. The chromosome-19 contains 67 million nucleotide bases and carries 1,592 genes. The chromosome-20 contains 72 million nucleotide bases and carries 710 genes. The chromosome-21 contains 50 million nucleotide bases and carries 337 genes. The chromosome-22 contains 56 million nucleotide bases and carries 701 genes. Finally, the sex chromosome of all females called the chromosome-X contains 164 million nucleotide bases and carries 1,141 genes. The male sperm called chromosome-Y contains 59 million nucleotide bases and carries 255 genes.

If you add up all genes in the 23 pairs of chromosomes, they come up to 26,808 genes and yet we keep on mentioning 24,000 genes needed to keep us function normally. There are 16,000 good genes, 6,000 defected or mutated genes and 2,000 Pseudogenes. A gene codes for a protein, not all 24,000 genes code for proteins at the same time. (Alternative splicing could generate thousands of new combinations of proteins. (The cells use new combination to generate new proteins as needed). It is estimated that less than 19,000 genes are code for protein. Because of the alternative splicing, each gene codes for more than one protein. As needed by our body, a small number of genes interact to make specific proteins. All the genes in our body make less than 50,000 protein which interact in millions of different ways to give a single cell. Millions of cells interact to give a tissue and hundreds of tissues interact to give an organ and several organs interact to make a human [2-6].

The Human Genome is made of four nucleotides, the bio-bricks, of life. They are neither alive nor dead. They can be cut paste and copied. Out of four-letter text, three letters code for an amino acid called codon. Hundreds of codons join to code for a protein called gene. A gene is a unit of inheritance. Using Restriction Enzyme like EcoR1, we could cut the sequence at a specific site. We can move gene from man to mouse and from mouse to mosquitos and from mosquitos to microbes. Once in microbes, we can insert into a plasmid which acts as a vector which and carry the gene across the

cell membrane into a bacteria where it cuts the bacterial genome at a specific site and insert the gene and enzyme DNA ligase join the plasmid with the bacterial genome. Bacteria replicate every 20 minute. Within few days, it makes millions of copies of the gene.

The nucleus of every living cell carries complete genetic information to make a species. The basic flow of genetic information in any cell is as follows. The DNA replicates (makes its own copies). The information from DNA is transcribed or copied into a form known as "RNA". The complete set of RNA (also known as its transcriptome) is subject to some editing (cutting and pasting) to become messenger mRNA, which is translated in the ribosome, to its coded protein. DNA carries information, and the protein carries all the body function.

Walter Ross

Designing drugs to shut off genes is a real challenge. The pioneering work on cross-linking double stranded DNA to shut off genes were done by W. C. J. Ross (Walter C. J. Ross) who was professor at the London University and a prominent British cancer researcher and chemist at the Chester Beaty Institute of Royal Cancer Research Hospital, a postgraduate medical center of London University. He is best known for his pioneering work on biological alkylating agents and chemotherapy development, including co-authoring scientific literature and major reference texts like Biological Alkylating Agents (1962) and contributing to volumes of The Terpenes. I worked for him for almost ten years, as his assistant, then as his student and then his postdoctoral fellow.

Ross' Rationale for Using War Chemicals to Treat Cancers

Soon after the discovery of double helical structure of DNA by Crick and Watson, Professor WCJ Ross (a true intellect) of London University realized that during replication, the double strand DNA separates, and each strand takes the complimentary nucleotide forming two cells. Since the cancer cells divide faster than normal cells by cross-linking both strands of DNA. He could prevent the replication of cancer cells.

Nitrogen Mustard was mercilessly used as a weapon during the WWI by both German and Italian Armies against Allied forces. Most soldiers exposed to Nitrogen Mustard were freeze to death. Their blood analysis showed a sharp decline in White Blood Cell (WBC). Since patients with the cancer of the blood called Leukemia showed a sharp increase in WBC, Professor Ross and his group at London University, England, wondered if minimum amount of Nitrogen Mustard could be used to control Leukemia in cancer patients. It was indeed found to be true. During the following 30 years, Ross developed hundreds of derivatives of Nitrogen Mustard to treat a variety of cancers. His most successful drugs are Chlorambucil, Melphalan and Myrophine As his graduate student, during the following ten-year period, I made for Professor Ross dozens of analogs of Nitrogen Mustards. The deadliest among them was the Phenylenediamine Mustard. We use these compounds to check the sensitivity of the Experimental Tumors in the Tumor Bank. If tumors in the Tumor Bank become resistant, we must replace resistant tumor cells with fresh more sensitive tumors for testing other compounds.

Ross was the first person who conducted Radiolabeled study to show that Nitrogen Mustard shut off a gene by cross-linking both strands of DNA that we inherit one strand from each parent. It was the same Cross-linking agents such as Nitrogen mustard made by Haber. Solders exposed to Nitrogen Mustard showed a sharp decline of White Blood Cells (WBC) from 5000 cell/CC to 500/CC. Children suffering from Childhood Leukemia have a very high WBC count (over 90,000/CC). Most of the WBCs are premature, defected, and unable to defend the body from microbial infections. Ross rationale was that cancer cells divide faster than the normal cell; by using Nitrogen Mustard he could use cross linking DNA and prevent cell division. Once he demonstrated that he could shut off a gene by cross-linking DNA; he could shut off any mutated gene including the genes of all 220 tissues present in a human by finding a dye that could specifically color that tissue. He could attach the Nitrogen Mustard group to the dye and attack the cancer genes in any one those 220 tissues.

As I said above, Ross was the first person who used Nitrogen Mustard, a chemical weapon used as a chemical weapon during WWI, to attack DNA for preventing cancer growth. Radiolabeled study showed that Nitrogen Mustard shut off a gene by cross-linking both strands of DNA that we inherit one strand from each parent. It was the same Cross-linking agents such as Nitrogen mustard made by Haber. Solders exposed to Nitrogen Mustard showed a sharp decline of White Blood Cells (WBC) from 5000 cell/CC to 500/CC. Children suffering from Childhood Leukemia have a very high WBC count (over 90,000/CC). Most of the WBCs are premature, defected, and unable to defend the body from microbial infections. Ross rationale was that cancer cells divide faster than the normal cell; by using Nitrogen Mustard he could use cross linking DNA and prevent cell division. Once he demonstrated that he could shut off a gene by cross-linking DNA; he could shut off any mutated gene including the genes of all 220 tissues present in a human by finding a dye that could specifically color that tissue. He could attach the Nitrogen Mustard group to the dye and attack the cancer genes in any one those 220 tissues.

Although Nitrogen Mustard is highly toxic, Ross thought more cancer cell would be destroyed than normal cells. Over decades, Ross made several hundred derivatives of Nitrogen Mustard as cross-linking agents. Some of the Nitrogen Mustards are useful analog such as Chlorambucil used for treating childhood leukemia (which brought the WBC level down to 5,000/CC) and Melphalan and Myrophine for treating Pharyngeal Carcinomas. Because of the high toxicity of Nitrogen Mustard, new drugs could not be developed to treat other types of Oral or Lung Cancers [7-13].

As I said above, Ross was the first person to use war chemicals successfully to treat cancer. Although such drugs are highly toxic, more cancer cell will be destroyed than the normal cells. Over decades, Ross made several hundred derivatives of Nitrogen Mustard as cross-linking agents. Some of the Nitrogen Mustards are useful analog such as Chlorambucil used for treating childhood leukemia (which brought the WBC level down to 5,000/CC) and Melphalan and Myrophine for treating Pharyngeal Carcinomas. Because of the high toxicity of Nitrogen Mustard, new drugs could not be developed to treat other types of Oral or Lung Cancers.

Toxic Effect of Nitrogen Mustard

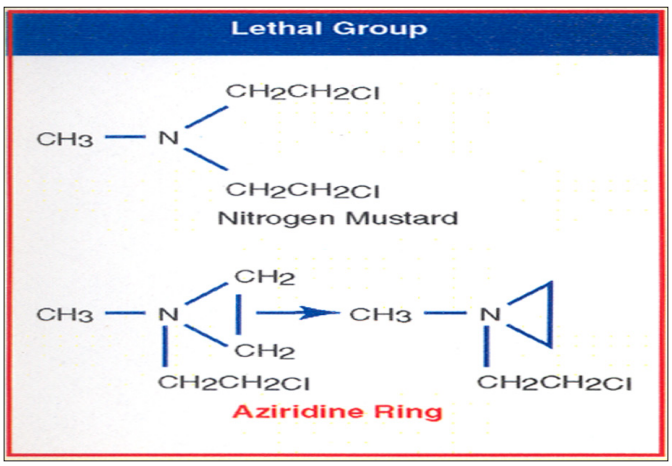
As his Assistant, I had made several dozens of previously synthesized analogs of Nitrogen Mustards for Professor Ross. I will describe how to make the Nitrogen Mustard by using Haber's crudest method. Haber reacted to Methylamine with Ethylene oxide to make 2-bis dihydroxy ethyl methyl amine. It was chlorinated by heating Phosphorus Penta Chloride in Phosphoric Acid. If you noticed a faint smell of Mustard Seed, Congratulations, you got Nitrogen Mustard; you cooled the solution and diluted with ice cold water, the oil floating in the aqueous solution was extracted with Chloroform. The solution is dried, and Hydrogen chloride

gas is passed through to make its solid Hydrogen-Chloride salt of Nitrogen Mustard Hydrogen Chloride salt is separated. No matter how many precautions you take, after the completion of the experiment, if you would take an alcohol swab of working bench or walls, doors, knobs and run a mass spectrum of the alcohol extract, you find a spectrum corresponding to Nitrogen Mustard. If you are exposed to Nitrogen Mustard and cross the threshold level, your WBC drops sharply and the energy providing Mitochondria die and you are most likely to freeze to death even during summer. Someone in the Defense department may make it, now-a-day. Safety committee will not approve this study in the University Research Lab. Your IRB (Institutional Review Board) and the safety committee will reject your proposal; and who will provide the funds for such an expensive study. The drug sensitivity between normal cells to cancer cells gives a ratio of toxicity called the Chemotherapeutic Index (CI). The higher the ratio the more toxic chemicals are to cancer cells. When tested against Walker Carcinoma 256 in Rats, most Nitrogen Mustards cross-link both strands of DNA and give a CI of ten.

Drug Design to Shut Off Genes to Treat Animal Cancer

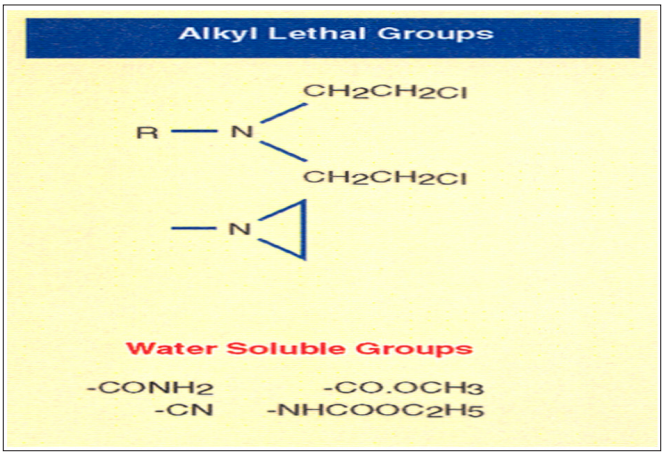
Aziridine Analogs as Anti-Cancer Agents Serving as Pro-Drugs

A radiolabel study to understand the mechanism of action of Nitrogen Mustard Ross showed that cross-linking of DNA occurred in two steps. The first step is involved in the formation of a three-member aziridine intermediate which remains stable and inactive in the neutral media (acts as a pro-drug). The second arm of the Nitrogen Mustard generates a highly reactive carbonium ion by enzyme which attacks the first arm of the double stranded DNA. The second arm is attacked, as the cancer cells grow; they use Glucose as a source of energy. Glucose is broken down Lactic Acid. In the presence of acid, the Aziridine ring becomes activated by generating the carbonium ion which attacks the second arm of the DNA resulting in the cross-linking. This study result showed that cross-linking both strands of DNA is not necessary to shut off a gene, only binding to a single strand of DNA by aziridine could also shut off a gene with half the toxicity. To attack a single strand of DNA, aziridine analogs are separately synthesized. As a part of my doctoral thesis, I was assigned a different path. Instead of cross-linking DNA strands, I am to design drugs to attack only one strand of DNA. The following chart describes the formation of Aziridine ring intermediate. Ross demonstrated that cross=linking both strands of DNA to shut off a gene is not necessary, binding to single strand of DNA by intermediate Aziridine could also shut off a gene. It has a great advantage over Nitrogen Mustard; Aziridine acts as a Pro-drug. The Aziridine ring opens in the acidic medium. The true drug is released a Carbonium ion which attack DNA once the Aziridine opens.



DNA Binding Aziridine Group

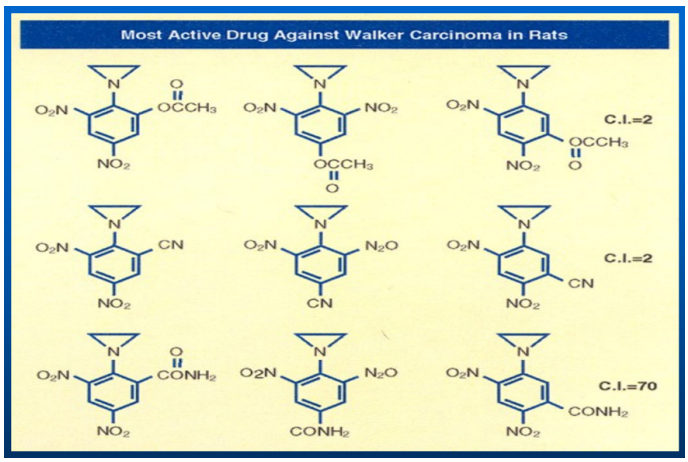
This study showed that to attack a single strand of DNA, we must synthesize Aziridine in the Lab by using ethyl amino methyl sulphonate in sodium hydroxide. Pure Aziridine was distilled off. Synthesis of Aziridine analogs will give two advantages over Nitrogen Mustard: first, instead of cross-linking, Aziridine binds to one strand of DNA, reducing its toxicity of the double stranded Nitrogen Mustard by half. Second, it gives selectivity, the Aziridine ring serves as a prodrug. Its ring opens only in the acidic medium. Once the active ingredient Aziridine was determined to attack DNA, the next question was what drug delivery method should be used to deliver Aziridine at the tumor site.



The Above Structures are Nitrogen Mustard (2-Bischloroethyl Methyl Amine) and Aziridine

Designing Drugs to Bind to a Single Stranded Dna to Treat Animal Cancers

As a part of my doctoral thesis, I was assigned a different path. Instead of cross-linking both strands of DNA by Nitrogen Mustard, I am to design drugs to attack only one strand of DNA by making Aziridine analogues. We decided to use Aziridine moiety (as an intermediate of Nitrogen Mustard) that would be an excellent active component to shut off a gene by binding to a single strand of DNA. To deliver Aziridine to the target site which is the N-7 Guanine of DNA, we decided to use Dinitrophenyl (DNP) moiety as a drug delivery agent. DNP is a dye which colors the tumor tissues of the experimental animal tumor such as Walker Carcinoma 256 in Rats. It is well known that analogs of DNP such as Dinitrophenol disrupt the Oxidative Phosphorylation (OXPHOS) of the ATP (Adenosine Triphosphate) which provides energy to perform all our body functions. To provide energy for our body function, the high energy phosphate bond in ATP is broken down to ADP (Adenosine Diphosphate) which is further broken down to AMP (Adenosine Mono Phosphate), the enzyme Phosphokinase put the inorganic phosphate group back on the AMP giving back the ATP. This cyclic process of Oxidative Phosphorylation is prevented by Dinitrophenol. As a part of my doctoral thesis, I decided to use Dinitrophenol as drug delivery method for the active ingredient aziridine. The analog of DNP such as Aziridine Dinitrophenol could also serves as a dye which stains Walker Carcinoma 256, a solid and most aggressive tumor in Rat. The first compound I made by attaching the C-14 radiolabeled Aziridine to the DNP dye. The Dinitrophenyl Aziridine was synthesized using Dinitrochlorobenzene with C-14 radiolabeled Aziridine in the presence of Triethyl amine which removes the Hydrochloric.



The Most Water-Soluble Substituent

The first three compounds on top line of the above chart carry all three isomer of the most water-soluble Ethyl Ester group attached to 2,4-Dinitropehny aziridine. The compound in vivo is hydrolyzed Ethyl Ester to produce most water-soluble carboxylic group. Since it is the most water-soluble substituent, within 24 hours of injection in Rats, the entire radioactive compound was passed down from in the Rat urine, and it can be extracted by Chloroform. Since the Ortho position was not available for DNA binding, it showed no biological activity, but the third compound in which Ortho position was free to bind to DNA showed some anti-tumor activity in Rats.

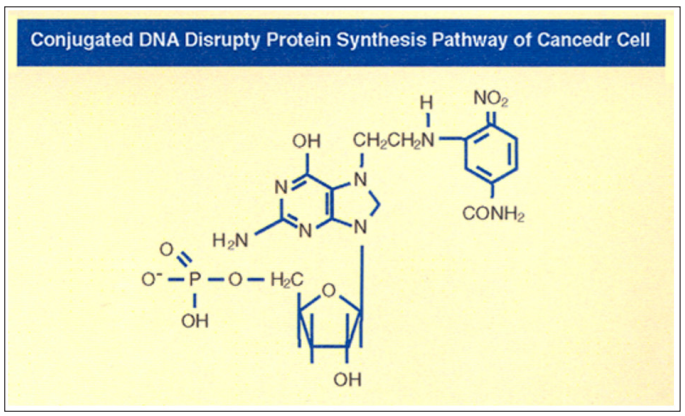
The Least Water-Soluble Substituent

On the other hand, when the least water-soluble Cyano-group was attached to all three isomers of the 2,4-Dinitrophenyl aziridine compound as shown in the second line of the above chart, most of the compound stayed at the injection site. Only the last Cyano-derivative attached to DNA showed some anti-tumor activity.

The Moderately Soluble Amido-Substituent

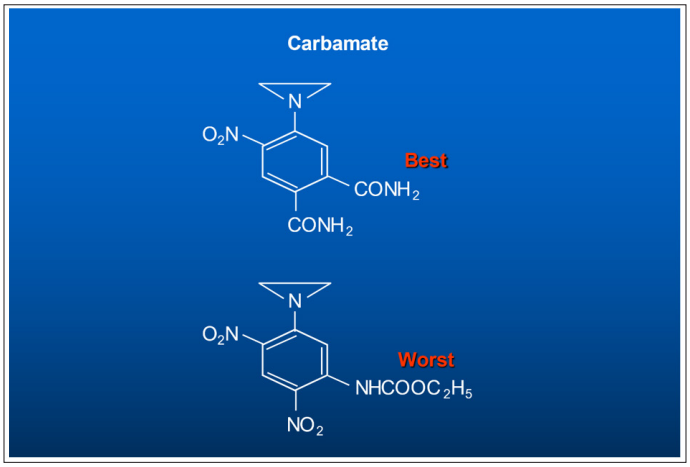
The last line of the above chart showed that the first two Amido groups were sterically hindered and did not bind to DNA and showed no biological activity, but the last compound presents the perfect drug delivery method. The entire drug was delivered from the injection site to the tumor site. The drug 1-Aziridine, 2,4-dinitro, 5-benzamide (CB1954) showed the highest anti-tumor activity. It has a CI of seventy; it is seventy times more toxic to cancer cells, highest toxicity ever recorded against Walker Carcinoma 256 in Rats [14-16]. The tumor was wiped out and the animals were returned to cages.

As I said above, Nitrogen Mustards are highly toxic because they have neither specificity nor selectivity. They attack all dividing cells whether they are normal or abnormal. On the other hand, the analogs of Aziridines and Carbamates serve as prodrugs and remain inactive in the basic and neutral media. They become activated only in the presence of acid produced by growing cancer cells. Aziridine attacks DNA in acidic medium, particularly the N-7 Guanine. The dye Dinitro benzamide has great affinity for Walker Tumor. The Aziridine Dinitro benzamide (CB1954) has the highest toxicity to Walker Tumor cells ever recorded. As the tumor grows, it uses Glucose as a source of energy. Glucose is broken down to Lactic Acid. It is the acid which activates the Aziridine ring. The ring opens to generate a carbonium ion which attacks the most negatively charged N-7 Guanine of DNA (as shown below) shutting off the Walker Carcinoma gene in Rat. The following conjugate structure shows how CB1954 binds to a single strand of DNA shutting off the gene.



Conjugated Dna Disrupting Protein Synthesis Pathway of Cancer Cell

For the discovery of CB1954, The University of London, honored me with the Institute of Cancer Research (ICR) post-doctoral fellowship award to synthesize more analogs of CB1954. Over the years, I made over a hundred additional analogs of Dinitro phenyl aziridines. To increase the toxicity of CB1954 to Walker Carcinoma, I made additional 20 analogs as a postdoctoral fellow. When I attached one more Carbonium ion generating moiety, the Carbamate moiety to the Aziridine Dinitrobenzene, the compound Aziridine Dinitro benzamide Carbamate was deadliest. It was so toxic that its Therapeutic Index could not be measured. We stopped the work. Further work at London University was discontinued for safety reasons.



The Best and the Worst Dinitro Phenyl Aziridine Analogs

Although Aziridine Carbamate is extremely toxic, it is also very useful in testing the sensitivity of tumors in Tumor Bank. Over the years, some tumors in the tumor bank could become resistant. If a tumor culture survives in a petri dish by adding a solution of Aziridine Dinitrobenzene Carbamate, it means that this tumor has become resistant over the years and must be replaced by new sensitive tumor cells. The combination of Aziridine and Carbamate is the deadliest to cells.

In developing drugs for treatments, we poison bad DNA selectively. All poisons are a class of chemicals that attack all DNA good and bad alike. Chemicals that cause cancer, at a safe level, can also cure cancer. Science teaches us to selectively attack bad sets of DNAs without harming the good sets of DNAs. Poisons are injurious to living creatures. There is a small class of chemicals, when exposed to humans, disrupt the function of DNAs, and make normal cells abnormal and they are called cancer causing chemicals or carcinogens. I must confess, we still use surgery to cut off cancerous breasts; we still burn cancer cells by radiation;

and we still poison cancer cells by chemicals. The largest killer of women is breast cancer. After all the treatment, the remaining cancer cells return as metastatic cells and kill breast cancer patients in three years. A decade from now, these methods could be considered brutal and savage, but today that is all we have. We hope to develop new treatment for Breast Cancer. Hope means never ever giving up [17,18].

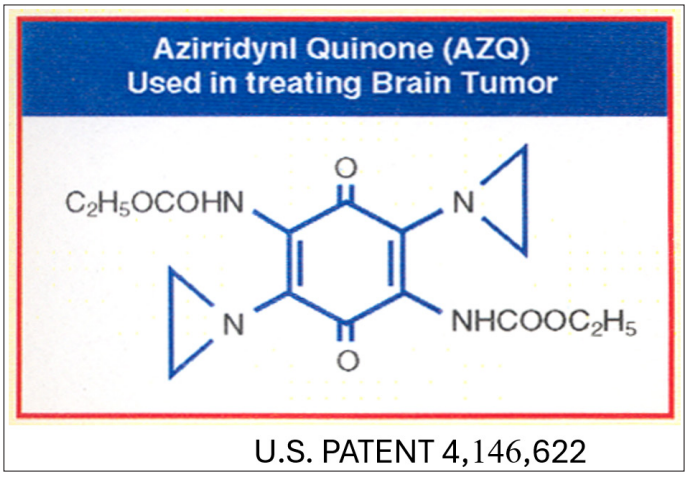
Drug Design to Treat Human Cancer

The Rational for Designing Drugs to Treat Glioblastoma, Human Brain Cancers

I designed drugs to treat Glioblastoma the brain cancer. In the pre-genome era, if the sequence in the Brain tumor confirms the presence of a mutation in the SNP responsible for causing the Glioblastoma, since there was no treatment, the patient dies within fourteen months of diagnosis. Glioblastoma is a solid aggressive tumor. It grows so rapidly, it crushes the neuronal circuits, it cushes the synapses and most patients internally bleed to death within fourteen months.

Glioblastoma (GBM) is a primary type of brain cancer which originates in the brain, rather than traveling to the brain from other parts of the body, such as the lungs or breasts. GBM is also called glioblastoma multiforme which is the most common type of primary brain cancer in adult humans. Attaching Nitrogen Mustard group to a carrier dye will produce highly toxic compound which will have neither specificity nor selectivity. Such a compound will attack all dividing cells whether they are normal or abnormal. On the other hand, the analogs of Aziridines and Carbamates serve as prodrugs that are that they remain inactive in the basic and neutral media. They become activated and produce powerful carbonium ions which attack DNA only in the presence of acid produced by cancer cells.

One day, I heard an afternoon lecture at the NIH in which the speaker described that radio labeled Methylated Quinone crosses the Blood Brain Barrier (BBB) in mice. When injected in mice, the X-ray photograph showed that the entire radioactivity was concentrated in the Mice's brain within 24 hours. I immediately realized that Glioblastoma multiforme, the brain tumor in humans, is a solid aggressive tumor like Walker Carcinoma in Rats. I decided to use Quinone moiety as a novel drug delivery molecule to cross BBB (Blood Brain Barrier) delivering Aziridine rings to attack Glioblastomas. By introducing an additional Carbamate [17-19].



Single Strand DNA Binding Aziridine and Carbamate

As I said above, Glioblastomas, brain cancer, is a solid and aggressive tumor and is caused by mutations on several sites in chromosomal DNA. Deleterious genetic mutations are the result of damaging DNA nucleotides by exposure to radiation, chemical and environmental pollution, viral infections, or genetic inheritance. The other factors responsible for causing DNA mutations are due to the fast rate of replication of DNA. For example, the bacteria E-coli grows so rapidly that within 24 hours, a single cell on a petri dish containing nutrients forms an entire colony of millions when incubated on the Agar Gel. Mistakes occur in DNA during rapidly replication such as Insertion of a piece of DNA, Deletion, Inversion, Trans location, Multiple Copying, Homologous Recombination etc. When an additional piece of nucleotide is attached to a DNA string, it is called Insertion, or a piece of DNA is removed from the DNA string; it is called Deletion or structural Inversion of DNA is also responsible for mutations. Since the gene codes for Proteins, Insertion and Deletion on DNA have catastrophic effects on protein synthesis. With the Quinone ring as a carrier across BBB, I could introduce different combinations of Aziridine rings and Carbamate moieties to Quinine and could create havoc for Glioblastomas. My major concern was how toxic this compound would be to the human brain cells. Fortunately, brain cells do not divide, only cancer cells divide. Attempting to find the site of mutations on Glioblastomas represents the greatest challenge. In Glioblastomas, three major changes occur on Chromosomes (C-7, C-9 & C-10) and two minor changes occur on Chromosomes (C-1 & C-19). These mutations are responsible for causing brain cancers in humans. Let us examine the effect on each chromosome. In a normal human cell, Chromosome-7 which is made of 171 million nucleotide base pairs, and it carries 1,378 genes. When Insertion occurs on Chromosome-7. Ninety-seven percent of Glioblastoma patients are affected by this mutation. On the other hand, a different mutation occurs on Chromosome-9 which is made of 145 million nucleotide base pairs, and it carries 1,076 genes. A major Deletion of a piece of DNA occurs on Chromosome-9 which results in eighty- three percent patients who are affected by this mutation. A minor Deletion of DNA also occurs on Chromosome-10 which is made of 144 million base pairs, and it carries 923 genes. Although it is a minor deletion of a piece of DNA and yet it contributes to ninety-one percent patients with Glioblastoma. To a lesser extent, small mutation occurs on Chromosome-1 (the largest Chromosome in our Genome). It is made of 263 million nucleotide base pairs and carries 2,610 genes) and Chromosome-19 (it is made of 67 million base pairs and carries 1,592 genes) are also implicated in some forms of Glioblastomas.

All known Glioblastomas causing genes are located on five different chromosomes and carry a total of 9,579 genes. It appears impossible to design drugs to treat Glioblastomas since we do not know which nucleotide on which gene and on which chromosome is responsible for causing the disease. It becomes possible by using C-14 radiolabeled Aziridines, we can confirm the binding site of a nucleotide on a specific gene and on a specific chromosome. By comparing with the Reference Sequence described above. We can further confirm the sites of mutations.

With the completion of 1,000 Human Genome Project, it becomes easier. by simply comparing the patient's genome with the sequence of 1000-genomes, letter by letter, word by word and sentence by sentence, we could identify the differences called the variants with precision and accuracy, the exact variants, or mutations responsible for causing the disease. Once the diagnosis is confirmed, the next step is how to treat the disease. As I explained above, by making

CB 1954 to treat the solid Walker Carcinoma in Rats, I established the structure activity relationship. I also demonstrated that by adding Aziridine and Carbamate to the dinitro-phenyl moieties, I could make the most toxic compound. Since Quinone crosses the Blood Brain Barries. I decided to attach these toxic moieties to Quinone making AZQ to treat human Glioblastoma. Since these moieties serve as Pro-drug, they become active drug in acidic medium. Tumors grow faster than normal cells; they use glucose as a source of energy. Glucose breaks down to produce lactic acid. It is acid which breaks down the prodrug and releases the active drug attacking the tumor. We have demonstrated that all bad genes can be shut off using Aziridine or Carbamate or both as attacking the tumors shutting off the genes. If you plan to develop drugs to treat other cancers, all we need to do is to identify carriers such as coloring dyes which stains a specific tumor. By attaching Aziridines and Carbamate moiety to carriers' dyes, we could attack other tumors.

One of the greatest challenges of nanotechnology is to seek out the very first abnormal cell in the presence of billions of normal cells of our brain and shut off the genes before it spread. I worked on this assignment for about a quarter of a century; conducted over 500 experiments which resulted in 200 novel drugs. They were all tested against experimental animal tumors. Forty-five of them were considered valuable enough to be patented by the US Government (US Patent 4, 146, 622 & 4,233,215). One of them is AZQ which not only stops the growth of Glioblastoma, but also the tumor starts shrinking. For the discovery of AZQ, I was honored with, "The 2004 NIH Scientific Achievement Award." One of America's highest Award in Medicine. I was also honored with the India's National Medal of Honor, "Vidya Ratna" a Gold Medal. (see Exhibits 1,2,3,4)

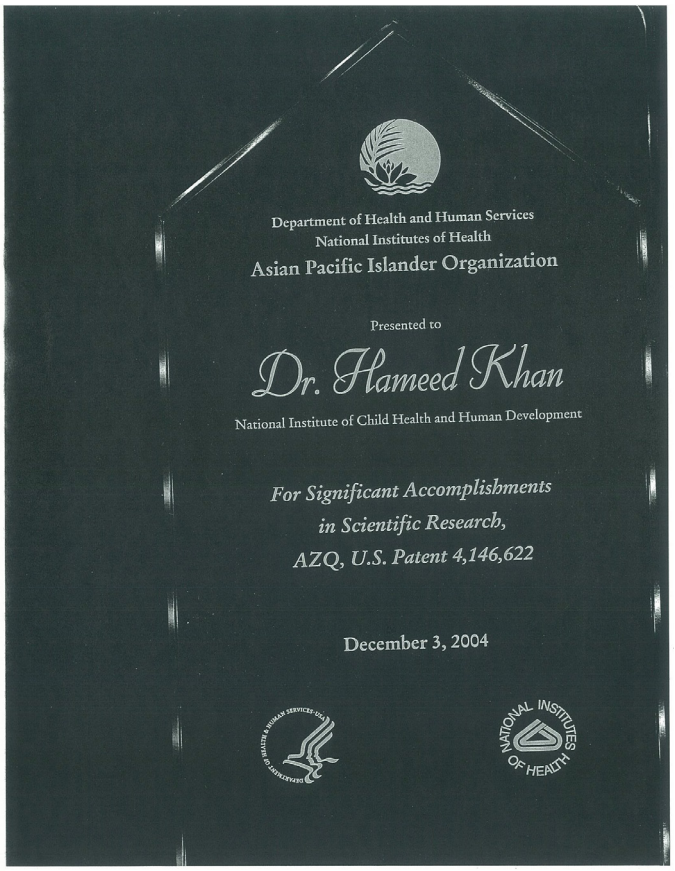
Exhibit # 1

2004 NIH Scientific Achievement Award
Presented to
Dr. Hameed Khan
By
Dr. Elias Zerhouni,
The Director of NIH

During the NIH/APAO Award Ceremony held on December 3, 2004.



Dr. Khan is the Discoverer of AZQ (US Patent 4,146,622 & 4,233,215), a Novel Experimental Drug Specifically Designed to shut off a Gene that causes Brain Cancer for which he receives a 17-year Royalty for his invention (License Number L-0I9-0I/0). To this date, more than 300 research papers have been published on AZQ. The award ceremony was broadcast live worldwide by the Voice Of America (VOA). Dr. Khan is the first Indian to receive one of America's highest awards in Medicine.



2004 NIH Scientific Achievement Award

Exhibit # 2

His Excellency, Dr. A.P.J. Abdul Kalam,
The President of India
Greeting
Dr. A. Hameed Khan



Discoverer of anti-cancer AZQ, after receiving 2004, Vaidya Ratna, The Gold Medal, One Of India's Highest Awards in Medicine At The Rashtrapathi Bhavan (Presidential Palace), in Delhi, India, During a Reception held on April 2, 2004.

Exhibit # 3

Dr. Khan was invited to give Maharaja Theromal Memorial Lecture. After the lecture, the Royal Family invited Dr. and Mrs. Khan for tea at the Royal Palace.

The Royals of Travancore



Dr. Hameed Khan of NIH was invited to give the "Maharaja Thrumal Memorial Award Lecture" "On the Impact of Genetic Revolution on our lives during 21st Century and Beyond" at the University of Trevandrum. After the lecture, His Royal Highness Sree Padmanabha Dasa Marthanda Varma (the brother-in-law) of Her Royal Highness Maharani Travancore (on his left) invited Dr. Hameed Khan and Mrs. Vijayalakshmi Khan for the Tea at the Pattom Palace at Thiruvanthapuram on May 12, 1999. Standing on Dr. Khan's right is the Son-in-law of Her Royal Highness, the Maharani.

Exhibit # 4

Gold Medal for Dr. Khan



Dr. A. Hameed Khan, a Scientist at the National Institutes of Health (NIH) USA, an American Scientist of Indian Origin was awarded on April 2, 2004. Vaidya Ratna; The gold Medal, one of India's Highest Awards in Medicine for his Discovery of AZQ (US Patent 4,146,622) which is now undergoing Clinical Trials for Treating Bran Cancer.

Glioblastoma (GBM) has no cure because of its aggressive, infiltrative growth pattern, extreme cellular diversity, and location behind the blood-brain barrier. These factors allow the tumor to aggressively evade standard treatments, such as surgery and chemotherapy, causing rapid regrowth. AZQ does not cure Glioblastoma. It simply shrinks the tumor. Most Glioblastoma patients die within fourteen months of their diagnosis. After the treatment with AZQ life of Glioblastoma patients may extend to two additional years. Sequencing the single cell and comparing it with Reference Sequence from the embryo will not help because too many mutated genes are involved. Identified mutations included CHEK2 (c.1477G>A, p.E493K), IDH1 (c.395G>A, p.R132H), and TP53 mutations. Non-coding regions exhibited variants in the TERT promoter (c.-146C>T, c.-124C>T) and TP53 RNA splicing site (c.376-2A>C, c.376-2A>G).

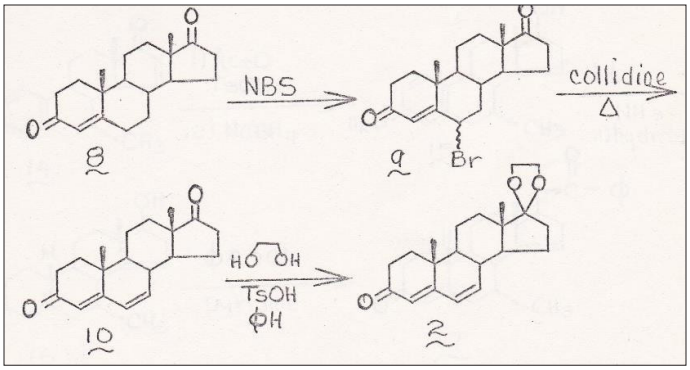
It may be that AZQ is shutting few genes not all. To shut off other genes, we must continue to develop more effective drugs. It is up to the Manufacturer of AZQ to take the next to conduct further studies and submit the safety data of AZQ to FDA for approval.

Drug Approval Process

An oversimplified picture of the New Drug approval process is described below. For more accurate information, check 21 CFR. The manufacturer conducts a 90-toxicity study to determine a safe level followed by a 2-year chromonic study to see that it is neither a carcinogen nor allergen. The data is submitted to the Food & Drug Administration (FDA). Scientists at FDA follow the rules described in CFR (Code for Regulation) by setting up an expert review committee. Members of the committee could recommend additional safety tests If they are satisfied, FDA issues a, IND (Investigational New Drug). When IND is approved, it permits clinical trial. In Phase-I, 30 patients are treated. If it is safe, Phase-II is recommended in which 300 patients are tested. If no adverse effects are observed, the drug is tested in Phase-III screening in which 3,000 patients are tested. Even after the approval of Phase-III testing, a yearly Adverse Reaction report is required. If Adverse Reaction is observed, the drug is withdrawn. If safe an NADA, new drug approval issued. The drug will go to clinical trials. Here is an example from my doctoral thesis.

How to Design Drugs to Treat Metastatic Breast Cancer

Recent, Radiolabeled studies in mice showed that male hormone Testosterone has great affinity for female organs like Breast, Ovary, and Fallopian tube cells. On the other hand, Estrogen, the female hormone, has great affinity for male Prostate gland. By attaching multiple Aziridine rings and Carbamate ions to both Hormones, I could design novel drugs to attack both the Breast and the Prostate cancers. Now, I found that I could increase its toxicity several folds to abnormal cells by attaching more than four Aziridine and Carbamate moieties to both Male and Female Hormones. In a Breast tumor, within the start and stop codon, BRCA1 gene has captured over two hundred thousand nucleotide bases. The BRCA1 gene carries about three thousand mutations. These mutations are caused by exposure to radiation, chemical or environmental pollutants, viral infection or genetic inheritance. To attack the mutated nucleotides among the three thousand mutations in BRCA1 gene, we could use male hormone, Testosterone, and bind multiple radio-labeled Aziridine and Carbamate ions to attack BRCA1 mutations. By using three-dimensional MRI [19], we could show how many radio-labeled nucleotides were bound to which mutations. Out of seventeen positions available for substitutions on Testosterone ring system. There are only three positions that are 1,3 and 17 are available for substitution on Testosterone ring system.



Carl Djerassi had demonstrated that we could activate additional positions for substitutions on hormone ring system such as the position 9 and 10 by reacting with Bromo-acetamide which introduce a Bromo ion on position 10 which could be de-brominated by Collidine to introduce a 9,10 double bond which we could further brominate to produce 9,10 dibromo compound. These bromo ion could be replaced by additional Aziridines or Carbamateions [23]. We could increase or decrease the number of Aziridine and Carbamate ions to get maximum benefit by further brominating position 15 and 16 to introduce additional Aziridine and Carbamate moieties.

Similarly, we could use the female hormone Estrogen and by attaching multiple Aziridine and Carbamate ions to attack Prostate tumor in Men. Since there are seventeen positions also available on Estrogen ring as well; again, we could increase or decrease the number of Aziridine and Carbamate ions to get the maximum benefit by using Djerassi' method as we did with Testosterone. The above methods are novel approach to designing drugs to treat Breast and Prostate cancers using genetic make-up of a patient to treat metastatic cancers.

Conclusion

If the purpose of life of mankind on Earth is to protect, preserve and spread human intelligence in every corner of the Universe, we must find treatments of all diseases well-known as well we rare no matter how much it cost and no matter how long it takes. To succeed in our aim, we need outstanding men and women who among you would be vanguard of research and technology in the greatest country in the world. We bequeath the future of this country in your hands. We know you will do your best to keep America the sole remaining superpower in the Western world, a jewel in the crown, a beacon of light, a shining city on the hill.

The ideas expressed in this article are mine and do not represent NIH policy.



The Author

Dr. Hameed Khan was born in Hyderabad, India, educated in England and received his doctorate degree in Chemistry from the University of London. He is a recipient of the Institute of the Cancer Research postdoctoral award of the Royal Cancer Hospital, University of London and a recipient of the Fogarty International postdoctoral award of the National Institutes of Health (NIH), and the National Cancer Institute of USA. He is a discoverer of AZQ (US Patent 4,146,622 & 4,233,215) for which he was honored with the "2004 NIH Scientific Achievement Award", one of America's highest awards in Medicine. He was also honored with a National Medal of Honor, the Gold Medal by the Government of India. He is a Fellow of the American Institute of Chemistry and was elected to the American Science Advisory Board.

A Note to my Readers

The Impact of Sequencing Human Genomes is a series of lectures to be delivered to the scholars of the National Youth League Forum (NYLF) and the International Science Conferences. After rewarding me with the "2004 NIH scientific Achievement" NIH Speaker's Bureau advised me to continue to teach critical thinking to the NYLF scholars who would join NIH in future. NYLF scholars are the very best and brightest students selected from all over the USA and the world brought to Washington by Envision, an outstanding organization that provides future leaders of the world. I am reproducing here part of the lecture which was delivered over the years at the International Science Conference that was PCS 6the Annual Global Cancer Conference held on November 15-16, 2019, in Athens, Greece, as well as Johns Hopkins University, Georgetown University and the University of Maryland. These lectures are released online and are available to my students and readers on their cell phone.

References

1. Watson JD, Crick FHC (1953) Molecular Structure of Nucleic Acids: A Structure for Deoxyribose Nucleic Acid. Nature 171: 737-738.
2. Hameed Khan (2021) The Impact of Sequencing Human Genome on Genomic Food & Medicine. Int. J. Genet. Genomics 9: 6-19
3. ES Lander, LM Linton, B Birren, C Nusbaum, MC Zody, et al. (2001) Initial sequencing and analysis of the human genome. Nature 409: 860921
4. (2004) Finishing the euchromatic sequence of the human genome. Nature 431: 931-945.
5. Kerstin Lindblad-Toh, Claire M Wade, Tarjei S Mikkelsen, Elinor K Karlsson, David B Jaffe, et al. (2005) comparative analysis and haplotype structure of the domestic dog. Nature 438: 803-819.
6. Jay Shendure, Shankar Balasubramanian, George M Church, Walter Gilbert, Jane Rogers, et al. (2017) DNA sequencing at 40: past, present and future. Nature 550: 345-353.
7. WCJ Ross (2015) Drug Information: Description, User Reviews, Drug Side Effects, Interactions – Prescribing Information J. Am. Chem. Soc 136: 5860-5863.
8. WC ROSS (1953) The chemistry of cytotoxic alkylating agents. Adv Cancer Res 1: 397-449.
9. Ross WCJ (1962) In vitro reactions of biological alkylating agents. Ann N Y Acad Sci 68: 669-681.
10. 10.Ross WCJ (1949) 43. Aryl-2-halogenoalkylamines. Part I. J. Chem. Soc 152: 183-191.
11. 11.Ross WCJ (1950) 464. The reactions of certain epoxides in aqueous solutions. J. Chem. Soc 153: 2257-2272.
12. Ross WCJ, Mitchley BCV, Ann. Rep. Brit (1964) The Impact of Sequencing Human Genome on Genetic Determinism.

Is our Behavior Controlled by our Genes? Empire Cancer Campn 42: 70.

13. Thierry Facon, Jean Yves Mary, Cyrille Hulin, Lotfi Benboubker, Michel Attal, et al. (2007) Melphalan and prednisone plus thalidomide versus melphalan and prednisone alone or reduced-intensity autologous stem cell transplantation in elderly patients with multiple myeloma (IFM 99-06): a randomised trial. Lancet 370: 1209-1218.
14. LM Cobb, TA Connors, LA Elson, AH Khan, BC Mitchley, et al. (1969) 2,4-dinitro-5-ethyleneiminobenzamide (CB 1954): a potent and selective inhibitor of the growth of the Walker carcinoma 256. Biochem Pharmacol 18: 1519-1527.
15. AH Khan, WCJ Ross (1969) Tumour-Growth Inhibitory Nitrophenylaziridines and related compounds: Structure-Activity Relationships PART I. CHEM.-BIOL INTERACTIONS 1: 27-47.
16. AH Khan, WCJ Ross, Tumour-Growth Inhibitory Nitrophenylaziridines and related compounds: Structure-Activity RelationshipsPART II. CHEM.-BIOL INTERACTIONS 4: 11-22.
17. A Hameed Khan, John Driscoll (1976) Potential Central Nervous System Antitumor Agents: Aziridinylbenzoquinones PART I. JOURNAL OF MEDICINAL CHEMISTRY 19: 2.
18. Ed Chou, A Hameed Khan, John Driscoll (1976) Potential Central Nervous System Antitumor Agents: Aziridinylbenzoquinones. PART II. JOURNAL OF MEDICINAL CHEMISTRY 19: 1302.
19. AH Khan, B Shaikh, EH Allen, EA Sokoloski (1988) Californium-252 Plasma Desorption Mass Spectrometry of Aminoglycoside Antibiotics. Biomed Environ Mass Spectrom 17: 329-335.
20. A Hameed Khan (2021) The Impact of Diagnostic MRI on the Early Detection of Lethal Genes in Human Genome and to Develop Genomic Medicine to Treat Brain Cancers. J Med - Clin Res & Rev 5: 1-9.
21. A Hameed Khan (2021) The Impact of Diagnostic MRI on the Early Detection of Lethal Genes in Human Genome and to Develop Genomic Medicine to Treat Brain Cancers. J Med - Clin Res & Rev 5: 1-9.
22. (2020) A chapter was Published in the Book entitled, Prevention, Detection and Management of Oral Cancer: Chapter entitled, "The Impact of Sequencing Human Genome on Drug Design to Treat Oral Cancer: Published in the IntechOpen https://www.intechopen.com/chapters/63395.
23. Ala-Eddin Al Moustafa (2017) Development of Oral Cancer: Risk Factors and Prevention Strategies. Published by Springer & Edited by Ala-Eddin Al Moustafa https://www.researchgate.net/publication/315706760_Development_of_Oral_Cancer_Risk_Factors_and_Prevention_Strategies.
24. 23.Hameed AK (2021) The Impact of Diagnostic MRI on the Early Detection of Lethal Genes in Human Genome and to Develop Genomic Medicine to Treat Brain Cancers. J Med - Clin Res & Rev 5: 1-9.
25. Leon V. Berhardt (2021) The Impact of Sequencing Human Genome on Genomic Medicine and the Discovery of AZQ (US Patent 4,146,622) Specifically Designed to shut off genes that cause Brain Cancer. e-Book 180: 1-63.
26. Abdul Hameed Khan (2005) The Rational Drug Design to Treat Cancers: Drug Design - Novel Advances in the Omics Field and Applications: Edited by Arli Aditya Parikesit. A book published in London https://www.intechopen.com/chapters/73119.
27. Hameed Khan (2021) The Impact of Sequencing Human Genome on Genomic Food & Medicine Int. J. Genet. Genomics 9: 6-19.
28. Hameed Khan (2021) The Impact of Sequencing Genomes on The Human Longevity Project. J Med - Clin Res & Rev 5: 1-12.
29. Hameed AK (2021) The Impact of Diagnostic MRI on the Early Detection of Lethal Genes in Human Genome and to Develop Genomic Medicine to Treat Brain Cancers. J Med - Clin Res & Rev 5: 1-9.
30. Khan H (2021) The Impact of Sequencing Genomes on The Human Longevity Project. J Med - Clin Res & Rev 5: 1-12.
31. Hameed Khan (2021) The Impact of Sequencing Human Genome on Genomic Food & Medicine. J. Genet. Genom 9: 6-19.
32. Hameed Khan (2021) ADVANCES IN MEDICINE AND BIOLOGY, The Impact of Sequencing Human Genome on Genomic Medicine and the Discovery of AZQ (US Patent 4,146,622) Specifically Designed to Shut off Genes That Cause Brain Cancer https://novapublishers.com/shop/advances-in-medicine-and-biology-volume-180/.
33. Arli Aditya Parikesit (2021) Drug Design - Novel Advances in the Omics Field and Applications. The Rational Drug Design to Treat Cancers 95: 115.
34. T Selvankumar (2026) Abbreviated Key Title: EAS J Biotechnol Genet ISSN: 2663-189X (Print) & ISSN: 2663-7286 (Online) Published By East African Scholars Publisher, Kenya EAS Journal of Biotechnology and Genetics Abbreviated Key Title: EAS J Biotechnol Genet ISSN: 2663-189X (Print) & ISSN: 2663-7286 (Online) Published By East African Scholars Publisher, Kenya https://www.easpublisher.com/journal/easjbg/home.
35. Hameed Khan (2021) Genomic Medicine: Using Genetic Make-up of the Human Genome, Genomic Medicine: Using Genetic Make-up of the Human Genome, AZQ was Designed to Treat Glioblastoma, the Brain Tumoz. Crimsonpublishers 6: 2.
36. A Hameed Khan (2021) The Impact of Sequencing Human Genome on Cancer Chemotherapy. J Can Res Rev https://www.researchgate.net/publication/358209642_The_Impact_of_Sequencing_Human_Genome_on_Cancer_Chemotherapy.
37. A Hameed Khan (2021) The Impact of Sequencing Human Genome on Cancer Chemotherapy. J Can Res Rev https://www.researchgate.net/publication/358209642_The_Impact_of_Sequencing_Human_Genome_on_Cancer_Chemotherapy.
38. A Hameed Khan (2021) The Impact of Sequencing Genomes on the understanding of the Origin of Life on Earth. Bi¬omed J Sci & Tech Res 40: 2.
39. A Hameed Khan (2022) The Impact of Sequencing Human Genome on the Genetically Engineered Life. J. Cancer Research and Cellular Therapeutics 6: 1.
40. A Hameed Khan (2022) Sequencing the Human Genome to Study the correlation between Genes and Violence, Horizon publishers.
41. A Hameed Khan (2022) The Impact of Sequencing Human Genome on the 2nd Genesis on Earth. JCTAES 3: 1-18.
42. A. Hameed Khan (2022) Assessment of Human Genome Sequencing on the New-World Order. HAL open science https://hal.science/hal-05188855.
43. A. Hameed Khan (2022) The Impact of Sequencing Human Genome on Novel Drug Delivery Method to Treat Cancers. J. Genet. Genom 10: 64-78.
44. A Hameed Khan (2022) The Impact of Sequencing Human Genome on the 2nd Genesis on Earth. J Cur Tre Agri Envi Sust 5: 1-21.

45. Hameed Khan A (2023) The Impact of Sequencing Human Genome on Idiopathic Diseases. Biomedical Sciences 5: 2.
46. A Hameed Khan (2023) The Impact of Sequencing Human Genome on Darwinian Evolution. J Can Ther Res 3: 26.
47. A Hameed Khan (2024) The Impact of Sequencing Human Genome is not only to treat all Genetic Diseases, but also to extend human life to travel into deep space in search of exo-planets to protect, preserve and spread human intelligence across the Universe. J. Cancer Res. Rev. Rep 6: 1.
48. A Hameed Khan (2024) The Impact of Sequencing Human Genome on Epigenetic Diseases. J Cur Tre Clin Bio Res 4: 1-19.

Copyright: ©2026 Hameed Khan. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.