Review Article

Molecular Genetics of Cancer

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Abstract
Cancer is an uncontrolled cellular proliferation. It develops from a single cell with gene mutations, causing tumor growth and propagation. The genetic changes persist in the progeny of the initial cancer stem cell. Recent research has uncovered some of the mechanisms involved in the development and progression of cancer. Understanding the mechanisms of genetic mutations and their actions allows scientists to interrupt these aberrant genetic pathways and treat these diseases. This review briefly discusses evolution of knowledge in the field, technologies involved, molecular changes caused by the aberrant cancer genes, and pathways of therapeutic interventions.

Keywords: Cancer, Molecular Abnormalities, Genetics, Chromosomal Abnormalities, Carcinogenesis, Genetic Abnormalities, Therapeutic Interventions Molecular Genetics, Cancer Genome, Mutations, Oncogenes, Tumor Suppressor Genes.

Introduction
Most literature agrees that cancer arises from proliferative somatic changes in mutated cells, allowing them to outcompete and invade normal tissues.1 In molecular biology and genetics, scientists study the molecular pathways resulting from nucleotide mutations of the malignant cell, to serve as the basis for developing targeted therapies. These new targeted therapies can function as both effective and less toxic treatments, and as methods for screening and prevention. Additionally, this broad proliferation of knowledge, specifically the growing genetic predictability of cancer, raises ethical issues about the medical, emotional, and financial implications of such predictions.

History
In 1855, Rudolph Virchow published “Omnis cellula e cellula” which means “Every cell arises from another cell”.2 This idea served as the foundation for manipulating cells in researching pathologies. About a decade later Gregor Mendel observed that specific traits such as color of flowers or the height of peas could be determined mathematically between generations, serving as the foundation for the concept of genes and inheritance.3 Mendel’s work was not appreciated until the turn of the 20th century. Inheritance would eventually be attributed to genes. In 1871, Friedrich Miescher published his findings on what he called “nuclein,” a chemical which he isolated from the cell nucleus.4 He found that nuclein was composed of a discrete ratio of Hydrogen, Oxygen, Phosphorus, and Nitrogen. This later was categorized as deoxyribonucleic acid (DNA). Oswald Avery in 1994, demonstrated that DNA was the molecule that contained hereditary factor.5 Watson and Crick then famously developed a model for the structure of DNA.6 Researches have used this model of molecular inheritance to study the properties of DNA and develop gene-based therapeutics, including targeted drugs for cancer gene abnormalities.

Methodological approaches for studying Molecular Genetics
The study of molecular genetics of Cancer involves various procedures which provides information about the genetic material associated with

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malignancy. Several new laboratory techniques have transformed the science of cancer diagnosis and treatment.

**Sanger Sequencing**
The first step in genome sequencing involves heating up the DNA into two single strands. It is then placed with radiolabeled nucleotide bases and DNA polymerase. The resulting product has a radiolabeled strand to the original template making it possible to study the sequence of nucleotides. While quite useful in determining DNA sequences, one of the major drawbacks of the sanger sequencing method is its inability to determine malignant tissues from normal tissues in cancer diagnostics.  

**Complimentary DNA**
Complimentary DNA or cDNA represents the coding sequences of genes in cells. Synthesized by reverse transcription of the mRNA, cDNA is used more widely since mRNA is degraded in the cell. Once the preferred mRNA is selected, complementary DNA strands can be built with the help of the enzyme reverse transcriptase and DNA polymerase. The resulting DNA can aid in identifying mutations in the transcription and translation processes in the cell. A cDNA library comprises of collections of an organism’s reverse transcribed mRNA. Specific mutant transcription factors, oncogenes and tumor suppressors can be inserted into the cDNA library to compare resulting phenotypic changes from before and after insertion. These are commonly used to determine transcripts like fusion genes, regulatory RNAs and alternative splicing variants.  

**Whole exome Sequencing**
Post transcription the spliceosome discards the noncoding parts of the genome known as the introns. The resulting transcript is full of exons. Mutations in these exons cause around 85% of the genetic disease. Therefore, arranging all the exons of a genome, known as exome, is thought to be an effective method to study a patient’s DNA for genetic disease. Another technique known as mRNA profiling consists of mapping transcriptomes for either tumor suppressors or oncogenes. NOTCH1 was thought to be an oncogene. However, the whole exome analysis showed that NOTCH1 gene’s translation stopped early in nearly 40% of all cases, indicating that NOTCH1 may be a tumor suppressor gene instead. Together exons and whole genome sequencing has led to the discovery that DNA variations also occur outside of exons which can possibly lead to cancer.  

**Next Gen Sequencing - Whole genome sequencing**
The advent of Next Generation Sequencing (NGS) has revolutionized technological innovations in molecular genetics in the last century. It consists of DNA being broken down into 100-150 base pair (bp) segments and are then amplified by being attached to a slide via adapters. The slide holds a pool of nucleotides and DNA polymerase. Each base is associated with a corresponding color and the nucleotides are fluorescently labeled. Addition of each base emits a color indicating the order of bases at each location on the slide. Overtime, different colors aggregate at particular locations illuminating the order of the DNA bases on that particular 100-150 bp strand of DNA. The entire genome can be pieced together by recognizing the overlaps in the DNA sequences. NGS can lead to targeted gene therapies which will lead to the improvement of cancer treatment outcomes which have common molecular pathways.  

**Polymerase Chain Reaction**
In clinical practice the amount of DNA for studies is relatively small. In order to increase these small amounts of DNA for carrying multiple studies the Polymerase Chain Reaction (PCR) technique is very useful. The small quantity of DNA is heated which breaks the DNA into single strands. An initiator primer attaches to the beginning of the newly created single-stranded DNA which serves as the initial point of replication. In the presence of DNA polymerase and additional base nucleotides, the reaction is cooled to cause replication of the strands yielding more double stranded DNA. The amount of DNA can be increased by allowing continuous heating and cooling of the solution with each alternative cycle. The resulting DNA’s can be used for several analyses and procedures.  

**Molecular Alterations in Carcinogenesis**
Cell division is a process in which DNA is transferred to daughter cells without alteration. In order to ensure genomic stability, cells employ several regulatory mechanisms. DNA polymerase proofreads for replication errors during S-phase and errors that slip through are corrected by mismatch repair, base excision repair, and nucleotide excision repair. Cells with damaged DNA are channeled to the apoptosis pathway. Malfunction of these regulatory mechanisms can lead to the development of cancer. This altered genome may cause over-expression of a pro-growth gene or the suppression of a regulatory apoptosis gene. Mutations in DNA repair proteins, such as p53, will also elicit a predisposition for cancer. Inherited genes such as BRCA1 and BRCA2 carry
an 82% lifetime risk of breast cancer.\textsuperscript{12} 5-10% of all cancers are suspected to be due to abnormal inherited genes.\textsuperscript{13} In most cases however, these inherited genes do not lead to cancer without additional environmental factors coming into play. Obesity, hormones, and other environmental factors are just a few examples of additional components interacting with predisposing genes to manifest as malignant tumors.

Environmental carcinogens that can cause harmful DNA alteration include benzopyrene in tobacco smoke, ionizing radiation, and ultra-violet light. Cancer-causing infectious agents have been linked with 16% of the world’s cancer deaths.\textsuperscript{14} Examples of such oncoviruses include human papillomavirus, which causes cervical carcinoma, and the Epstein-Barr virus, which causes B-cell lymphoproliferative disease and nasopharyngeal carcinoma. Hormonal imbalance is often linked to cancer, with a strong correlation established between testosterone levels and prostate cancer. In addition, obesity has been linked to 40% of cancer deaths due to higher levels of growth hormones.\textsuperscript{15}

**MMR, BER, NER**

The 3 primary DNA repair mechanisms for a cell, in order from small to large DNA lesions, are: mismatch repair (MMR), base excision repair (BER), and nucleotide excision repair (NER). If the proteins involved in any of these processes are mutated, it would allow altered DNA to remain in the cell and cause malignancy. MMR aims to correct wrongly incorporated nucleotides in DNA. After DNA polymerase has made an incorrect nucleotide pairing, three “Mut” proteins nick the daughter strand, make a loop, and excise the altered DNA. DNA polymerase and ligase can then correct the error. Microsatellite instability is implicated in mutations of the Mut proteins and is present in most human cancers. Cancers with high microsatellite instability carry a better prognosis, such as colon cancer (15% better prognosis).\textsuperscript{16}

BER aims to correct chemical alterations of nucleotides such as oxidization, alklylation, or deamination.\textsuperscript{17} Malfunctioning in this process is linked with cancer. Polymerase β mutations are found in 30% of human cancers.\textsuperscript{18}

NER aims to correct large DNA aberrations that alter DNA shape. This complicated mechanism involves 9 different proteins that cut offending oligonucleotides and synthesize new repaired DNA.\textsuperscript{19} UV-light can cause thiamine dimerization in DNA and is one of the most common ways these bulky lesions are created.

**Epigenetic alterations favoring malignant transformation**

Epigenetic modification of gene expression allows malignant cells to self-renew, block differentiation, evade apoptosis, and develop tissue invading potential.\textsuperscript{20} These modifications include methylation, which can inactivate genes, histone modification, which can change gene expression, and microRNA production, which regulate 60% of transcriptional activity in protein-coding genes.\textsuperscript{21} Studies have shown that tumor suppressor genes such as APC, p16, and BRCA1 are often hypermethylated in tumor cells.\textsuperscript{22} Histone modifications can also occur frequently in tumor cells. Finally, suppressing microRNA production in tumor cells can allow for expression of normally inactive oncogenes.

**Human genome and the cancer genome**

Cancer is fundamentally a disease caused by mutations, and thus requires a deep understanding of the human genome. All 3.3 billion DNA base pairs were sequenced by 2003 providing a blueprint for comparison with cancer mutations. This allowed mutations to be linked with different forms of cancer. Currently, there are 350 cancer genes that have been catalogued.\textsuperscript{23}

**The Cancer Genome Atlas Map**

The cancer genome is a blueprint of the DNA of cancer cells and was a natural sequel to the human genome project in order to understand the mechanisms of malignancies and find therapeutic interventions. The Cancer Genome Atlas (TCGA) was started in 2006 to map cancer genomics and create a database with a compilation of cancer causing mutant genetic sequences. Although the study began with only glioblastoma, it quickly expanded to encompass many different types of cancer. The research findings provide potential loci or targeted therapy against tumors. For example, in glioblastoma, the most common mutant oncogenes are epidermal growth factor receptor (EGFR), platelet derived growth factor (PDGFR), and deletion mutations in tumor suppressor genes PTEN and p53. Understanding this genome can allow us to develop inhibitors in the pathways of cancer progression.\textsuperscript{24} Differences found between normal and cancer genomes could identify loci responsible for causing malignancy. 18 altered somatic genes were found in adenocarcinoma, which is the leading cause of cancer related deaths world-wide.\textsuperscript{25} However, targeted therapies counteracting these mechanisms are being developed rapidly. The future goal for the TCGA is to be able to provide diagnoses...
and treatment plans specific to patients’ DNA mutations. Such tailored medical care would offer significant benefits to patient improving the quality and quantity of their life.

As of 2014, TCGA has completed genome sequencing on 1000 tumor samples, leading to over 2700 publications in research journals. These have led to targeted therapy for many types of cancers. This growing database of cancer genomics will continue to provide valuable information for understand the molecular genetics of cancer and developing targeted treatment for it.

**Genetic Abnormalities in Cancer**

**Numerical Abnormalities**

The various genetic abnormalities noted in cancer cells include abnormal number and structures of chromosomes, which are responsible for mutations or abnormal genes. Numerical abnormalities include aneuploidy i.e. unequal number of chromosomes, hypodiploidy i.e. decrease in the number of chromosomes, or hyperdiploidy i.e. increase in the number of chromosomes.

**Structural Abnormalities**

A second type of chromosomal abnormalities is structural, which include deletions, translocations, inversions, rearrangements, and amplifications. A deletion is a removal of a chromosomal segment from the set, which can cause activation of an oncogene or inactivation of a tumor suppressor gene.

Translocation results from one piece of chromosome detaching and attaching to a different nonhomologous chromosome, or on a new site off the same chromosome. Translocation can be most commonly found in lymphomas, sarcomas, and leukemias, with the most well-known being chronic myelogenous leukemia (CML). In CML the long arm of chromosome 22 becomes attached to chromosome 9 which creates the oncogene BCR-ABL.

Inversion involves a segment of a chromosome detaching and re-inserting in the opposite direction leading to either activation of an oncogene or deactivation of a tumor suppressor gene. An example involves the juxtaposition of the Mixed-Lineage Leukemia gene (MLL) to the Clathrin Assembly Lymphoid Myeloid Leukemia (CALM), leading to acute myeloid leukemia (AML) seen in infants.

**Oncogenes**

Oncogenes are capable of transforming regular cells into tumor cells. The pre-mutated form, proto-oncogenes, functions to promoting cell growth, regulating differentiation, and minimizing apoptosis. Proto-oncogenes can mutate into oncogenes when there are mitogens and carcinogens involved.

The three mechanisms involved in converting a proto-oncogene to an oncogene are mutations in the DNA or in a regulatory region of a gene such as a promotor, gene amplification, and chromosomal rearrangement such as translocations.

Activation of oncogenes can come from translocation, a well-known example is the BCR-Abl fusion gene, which is associated with chronic myelogenous leukemia. BCR-Abl results from the translocation between chromosome 9 and 22 and is called the Philadelphia chromosome. This translation causes the continuous and unregulated production of tyrosine leading to an excess of cell growth.

**Tumor Suppressor Gene**

A tumor suppressor gene is involved in repairing DNA mistakes, controlling the rate of cell division based on the need, and regulating the process of apoptosis. A notable tumor suppressor gene is the p53 gene which is linked to leukemias, lymphomas, sarcomas, brain tumors, and carcinomas of the breast, colon, and lung. When a tumor suppressor gene goes through mutation or inactivation it loses its function, eliminating the regulatory protein. This, if is combined with activation of an oncogene could lead to the development of cancer.

**Fusion Gene**

A fusion gene is created by two different genes coming together through structural abnormalities in the chromosome, leading to cancer through multiple pathways. These pathways include overexpression, suppression, changing the location of a protein, and removing the regulatory domains of specific genes. 20% of cancer in humans arise from gene fusion abnormalities, but with advances in technology scientist are able to disrupt the effects these malfunctions.

**Passenger and Driver Mutations**

Driver mutations are required for maintenance and survival of cancer cells. “Passenger mutations” are classified as such when the cancer has multiple nonfunctional mutations that continue to persist in the cancer cells. These passenger mutations are frequently present with driver mutations and could be of value in cancer diagnosis and research.

**Mutations in Metabolic Enzymatic Pathways**

Mutations in the metabolic enzymatic pathways can provide the cancer cells with a favorable environment to proliferate. Under hypoxic conditions the cell is able to convert pyruvate to lactic acid, which is an inefficient system for generating energy. However, cancer cells are
able to effectively use this method because they are separated from the underlying stroma and blood vessels. Due to an increase in non-aerobic glycolysis, an acidic microenvironment is created, which is toxic to normal cells but the malignant cancer cells are able to adapt and resist to the acid induced cell toxicity. Abnormalities can also occur during cell division and metabolism during certain cellular checkpoints. Whenever these checkpoints become deranged or defective, the potential for developing cancer increases.

Metastasis
Cancer cells have the potential to spread to other parts of the body, a process known as metastasis. Approximately 90% of cancer deaths are caused by metastasis, most commonly spreading to the bone, liver, and lung.

Angiogenesis
Angiogenesis, the creation of new blood vessels, is a pivotal step in growth and spread of cancer. It involves a complex multi-step cascade regulated through different angiogenic factors, such as the vascular endothelial growth factor (VEGF) and the hepatocyte growth factor (HGF). When there is an overproduction or increasing sensitivity to these growth factors and their receptors, malignant cells are able to grow and metastasize.

Apoptosis
Apoptosis is a generally controlled process of programmed cell death that is activated when there is unrepairable damage to a cell, or when the cell is no longer necessary for the body’s function. When a cell’s apoptotic pathway becomes nonfunctional such as P53, a tumor suppressor gene, becoming deactivated, a cell could proliferate and manifest as cancer.

Drug Resistance
Intrinsic or acquired resistance to chemotherapy develop because like humans, tumors are capable of adapting for survival. An intrinsic resistance means that the tumor contains resistance-mediating factors. While an acquire resistance is developed during treatments. Several studies have shown that the primary mechanism of resistance involves over expression of the P-glycoprotein and the multidrug resistance-associated protein (MRP).

Cancer genome and new taxonomy of Tumors
Traditionally malignant tumors have been classified based on the site of origin, and sometimes morphology. With the advancement of technology, many current genomic analyses are able to clarify the reasons for heterogeneity for tumors arising from the many different organs of the body. With all this knowledge, it is allowing us to redefine the way we currently classify tumors with potential new classification and nomenclature. It also will provide a more rational understanding of the biology, prognosis, and appropriate treatment options of new malignant tumors.

Molecular basis of Cancer genetics
Cancer diagnostics involve different classifications on the basis of histopathology, site of origin and biological behavior. Researcher and physicians have been able to take advantage of the ever-advancing molecular technology in cancer diagnostics and treatments with greater success and less risk of toxicity.

CML
Chronic Myeloid Leukemia or (CML) is an uninhibited production of the granulocyte. Peter Nowell and David Hungerford made a discovery about a small common chromosome in CML patients. Known as the Philadelphia Chromosome (Ph), it is caused by the translocation between chromosomes 9 and 22. Changes in the molecular makeup resulted in a fusion gene known as break point cluster region/ ableson murine leukemia (BCR/ABL). BCR/ABL serves as an oncogene where it leads to constitutive production of tyrosine kinase leading to mass production of white blood cells. A BCR/ABL tyrosine kinase inhibitor, Imantinib, is a very successful drug in the treatment of chronic CML and has set the standard for genotype targeted therapy for other neoplastic diseases.

Breast Cancer
Some mutations commonly seen in clinical setting are the Human Epidermal Growth Factor receptor 2 gene (HER2) and Estrogen Receptor (ER). They lead to uninhibited proliferation, and apoptotic resistance. In the presence of estrogen, ER is activated and turns on the transcription by oncogenes c-MYC and cyclin D1. Additionally, the two most common genes responsible for the inheritance of breast cancer have been breast cancer susceptibility gene 1 and 2 (BRCA1 and BRCA2). Found in over 80% of familial breast cancer cases, BRCA1 and BRCA 2 are tumor suppressor genes that repair DNA breaks. Prevalence of these genes not only increased the risk but also caused an earlier onset of the cancer.

Colorectal Cancer (CRC)
Neoplasms of the colorectal area are inherited in around 10-25% of the cases. Familial adenomatous polyposis (FAP) is caused by a mutation in APC, a tumor suppressor gene in which
thousands of polyps’ form in an individual as early as in their 20s which can progress to carcinoma.\textsuperscript{45} Another disorder that progresses to carcinoma is the hereditary nonpolyposis colorectal cancer (HNPCC) caused by a mutation in the mismatch repair genes. Some of the other commonly seen mutations include the tumor suppressor gene p53 and KRAS. While p53 is responsible for cellular apoptosis\textsuperscript{46}, KRAS is responsible for cellular proliferation. KRAS is commonly found in a total of one third of all human cancers.\textsuperscript{47}

Table 1: Target therapies drugs for specific cancers

<table>
<thead>
<tr>
<th>Gene Target</th>
<th>Generic Name (Trade Name)</th>
<th>Indication</th>
</tr>
</thead>
<tbody>
<tr>
<td>ALK\textsuperscript{48}</td>
<td>Crizotinib (Xalkori) -oral</td>
<td>•Non-small cell lung cancer</td>
</tr>
<tr>
<td>Ceritinib (Zykadia) -oral</td>
<td>•Non-small cell lung cancer</td>
<td></td>
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<tr>
<td>BCR/ABL\textsuperscript{49,50,51}</td>
<td>Imatinib (Gleevec) -oral</td>
<td>•Chronic myeloid leukemia</td>
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<td></td>
<td>•Acute lymphoblastic leukemia</td>
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<tr>
<td></td>
<td>•Dermatofibrosarcoma protuberans</td>
<td></td>
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<tr>
<td></td>
<td>•Gastrointestinal stromal tumors</td>
<td></td>
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<tr>
<td>Nilotinib (Tasigna) -oral</td>
<td>•Chronic myeloid leukemia</td>
<td></td>
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<tr>
<td>Bosutinib (Bosulif) -oral</td>
<td>•Chronic myeloid leukemia</td>
<td></td>
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<tr>
<td>Dasatinib (Sprycel) -oral</td>
<td>•Chronic myeloid leukemia</td>
<td></td>
</tr>
<tr>
<td></td>
<td>•Acute lymphoblastic leukemia</td>
<td></td>
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<tr>
<td>CD2\textsuperscript{52}</td>
<td>Rituximab (Rituxan) -IV</td>
<td>•Non-Hodgkin’s lymphoma</td>
</tr>
<tr>
<td>BRAF\textsuperscript{53}</td>
<td>Dabrafenib (Tafinlar) -oral</td>
<td>•Melanoma</td>
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<tr>
<td>EGFR\textsuperscript{54}</td>
<td>Afatinib (Gilotrif) -oral</td>
<td>•Non-small cell lung cancer</td>
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<tr>
<td></td>
<td>•Non-small cell lung cancer</td>
<td></td>
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<tr>
<td></td>
<td>•Advanced pancreatic cancer</td>
<td></td>
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<tr>
<td>Gefitinib (Iressa) -oral</td>
<td>•Non-small cell lung cancer</td>
<td></td>
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<tr>
<td>HER2\textsuperscript{55}</td>
<td>Trastuzumab (Herceptin) -IV</td>
<td>•Breast cancer</td>
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<td></td>
<td>•Breast cancer</td>
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<td></td>
<td>•Gastric adenocarcinoma</td>
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<tr>
<td>Laptitinib (Tykerb) -oral</td>
<td>•Breast cancer</td>
<td></td>
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<tr>
<td>JAK2\textsuperscript{56}</td>
<td>Ruxolitinib (Jakafi) -oral</td>
<td>•Myelofibrosis</td>
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<tr>
<td></td>
<td>•Polycythemia vera</td>
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<tr>
<td>Multi-Kinase\textsuperscript{57,58,59}</td>
<td>Axitinib (Inlyta) -oral</td>
<td>•Renal cell carcinoma</td>
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<tr>
<td></td>
<td>•Hepatocellular carcinoma</td>
<td></td>
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<tr>
<td></td>
<td>•Renal cell carcinoma</td>
<td></td>
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<tr>
<td>Sorafenib (Nexavar) -oral</td>
<td>•Gastrointestinal stromal tumors</td>
<td></td>
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<tr>
<td>Sunitinib (Sutent) -oral</td>
<td>•Renal cell carcinoma</td>
<td></td>
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<td></td>
<td>•Pancreatic neuroendocrine tumors</td>
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<tr>
<td>PD1\textsuperscript{56}</td>
<td>Nivolumab (Opdivo) -oral</td>
<td>•Melanoma</td>
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<td></td>
<td>•Non-small cell lung cancer</td>
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<tr>
<td></td>
<td>•Renal cell carcinoma</td>
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<tr>
<td>PI3K\textsuperscript{51,62}</td>
<td>Idelalisib (Zydelig) -oral</td>
<td>•Chronic lymphocytic leukemia</td>
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<td></td>
<td>•Follicular lymphoma</td>
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<tr>
<td></td>
<td>•Small lymphocytic lymphoma</td>
<td></td>
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<tr>
<td>VEGF\textsuperscript{58,63,64,65,66}</td>
<td>Bevacizumab (Avastin) -IV</td>
<td>•Colorectal cancer</td>
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<tr>
<td></td>
<td>•Non-squamous non-small cell lung cancer</td>
<td></td>
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<tr>
<td></td>
<td>•Breast cancer</td>
<td></td>
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<tr>
<td></td>
<td>•Glioblastoma</td>
<td></td>
</tr>
<tr>
<td></td>
<td>•Renal cell carcinoma</td>
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</tbody>
</table>
Targets for Therapeutic Interventions
The table provides a list of some of the currently available targeted drug therapies for specific malignant diseases. The United States Federal Drug Administration (FDA) has approved them based on their safety and efficacy. Many new drugs are currently in development or in clinical trials for approval for other neoplastic diseases.

Prevention
Progress in molecular genetics cancer research will allow us to screen a healthy individual, predict the probability of onset, and intervene before the disease manifests. The research would apply to chronic diseases such as cancer, diabetes, and hypertension, which involve multifactor etiologies like genetic predisposition and lifestyle.

Ethics
Cancer in majority of the cases is a result of sporadic mutations in somatic cells, while only a fraction of them are inherited genetically. Currently tests are available for identifying healthy people who are at risk for developing certain cancers from inherited or familial factors. This knowledge while providing advance information to allow preventive measures also creates stress, anxiety and social stigma.

Additionally, such knowledge if made available to others could be exploited for denying employment and insurance. Laws have been enacted to protect such individuals. However, the potential for misuse of this information exists. Predicating the future may have its benefits but society has to learn how to handle such information in an ethically and socially responsible way.

Islamic Perspective
“Iqra,” meaning to read, was the first word revealed in the Quran. The command to read has been interpreted by scholars as an obligation to seek knowledge. In one of the early revelations, the Quran states, “Oh my Lord, advance me in knowledge.” The Quran is referring to all knowledge, not simply spiritual knowledge as clarified in the hadith. A desert dweller once asked the Prophet (PBUH), “Oh Messenger of Allah, should we seek medical treatment?” The Prophet (PBUH) replied, “Seek medical treatment, for Allah has not sent a disease without sending a cure for it. Those who have the knowledge of the cure know it and those who are ignorant of it do not.” “There are nearly 750 verses in the Quran directing and encouraging mankind to ponder and fully utilize the wonderful creations of the Almighty. Thus, it is clear that seeking knowledge, including medical knowledge, is a part of the faith. The ultimate goal of medical knowledge and research is to save lives. The Quran emphasizes the value of saving a life, stating, “...whosoever killeth a human being for other than manslaughter or corruption in the earth, it shall be as if he had killed all mankind, and whoso saveth the life of one, it shall be as if he had saved the life of all mankind...” This was revealed when Adam’s son Cain killed his younger brother Abel. Humanity today is about 7.2 billion people. Saving a life is the greatest reward one can seek in this world. The pursuit of knowledge to discover and administer treatments to save people from deadly diseases is an act of worship of the highest order. Currently, tests are available for identifying healthy people who are at risk for developing certain cancers from inherited or familial factors. While medically advantageous, this knowledge could also create stress, anxiety and social stigma.

An extreme case of social stigma would be denial of employment or insurance based on these genetic risk factors. While laws have been enacted to protect against such abuse, the potential for misuse still exists. Detecting predictable genetic factors may have its benefits but society must develop ethical and social responsibility in parallel to scientific developments.

Future prospects
Continuing research in cancer management appears hinges on understanding the pathophysiology of malignancy. Past achievements and future prospects for therapeutics are promising due to the progress in uncovering the molecular mechanisms at play.
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70. Glorious Quran: 20:114.

71. Musnad Ahmad: 18456.
