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Review paper

Innovations in Oncology Research: A Molecular Perspective on Cancer Genetics and Treatment

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Abstract

Background and aim: Cancer initiation involves molecular events transforming normal cells into cancerous ones, paving the way for precision oncology. The global cancer burden is rising due to factors like population growth, aging, environmental exposures, and climate change. Genetic cancer, caused by inherited gene mutations, necessitates genetic testing for personalized strategies. Cancer genomes are characterized by DNA alterations affecting proto-oncogenes, tumor suppressor genes, and DNA methylation, leading to gene deregulation and abnormal expression. These insights offer targets for research and therapy in the complex disease of cancer.

Methods: A systematic search on PubMed, Scopus, and Google Scholar using keywords "oncology," "molecular," and "genetic cancer" yielded 38 relevant articles published in English after 2000. Descriptive statistics were used to analyze these papers, extracting key information on oncology, molecular, and genetic aspects of cancer research. The review offers a comprehensive overview of the field, summarizing significant molecular and genetic alterations, diagnostic approaches, therapeutic strategies, and their implications for cancer management.

Results: Several studies provide valuable insights into cancer genetics, emphasizing the significance of genetic aberrations in tumor development and the potential for personalized treatments. Advanced technologies and analytical approaches play a crucial role in understanding cancer and identifying therapeutic targets. Furthermore, the interplay between genetic and epigenetic mechanisms and the importance of RNA modifications are highlighted as key factors in cancer research. These studies contribute to our understanding of cancer genetics, molecular pathogenesis, and the need for improved diagnostics and therapies. The perspectives of oncology, molecular biology, and cancer genetics are interconnected, driving advancements in research and treatment for better patient outcomes.

Conclusion: Oncology, molecular, and genetic cancer research have advanced our understanding of cancer biology, aiding in diagnosis, treatment, and prevention. Key molecular and genetic alterations have been identified, leading to targeted therapies and personalized medicine. These discoveries have the potential to revolutionize cancer management, but unanswered questions remain. Future studies should focus on genetic-environmental interactions, immune response, early detection, and novel therapeutic targets to overcome resistance and improve outcomes.

Keywords: *Oncology, Molecular, Cancer Genetics*

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Introduction

Cancer initiation refers to the molecular events that cause a normal cell to become cancerous. These discoveries have paved the way for precision oncology and have led to advancements in understanding cancer initiation [1].

The global burden of cancer is on the rise. In 2020, there were approximately 19.3 million new cancer cases worldwide, resulting in nearly 10 million deaths. By 2040, it is projected that the number of cancer cases will increase by 47% to reach 28.4 million, leading to greater disparities between countries, ethnicities, and socio-economic groups. The increase in cancer incidence can be attributed to factors such as population growth and aging. Additionally, environmental factors play a significant role, with environmental exposures and the effects of climate change contributing to the rising risk of various types of cancer [1]. These include exposure to environmental carcinogens like air pollution and UV radiation. Climate change also leads to extreme weather events and rising sea levels, which can result in population displacement, further exacerbating disparities in cancer outcomes across different regions and social groups. Genetic cancer, also known as hereditary cancer, refers to cancers that are caused by inherited gene mutations or alterations. These specific gene mutations can increase an individual's risk of developing certain types of cancer. In genetic cancer, the mutated genes are passed down from one generation to another within a family, leading to an increased susceptibility to cancer. Examples of genetic cancer include hereditary breast and ovarian cancer (caused by mutations in BRCA1 and BRCA2 genes), Lynch syndrome (caused by mutations in DNA mismatch repair genes), and familial adenomatous polyposis (caused by mutations in the APC gene). Genetic testing and counseling are essential in identifying individuals at risk for genetic cancer, allowing for personalized screening, prevention, and treatment strategies [2].

Genetic and environmental factors are responsible for the genomic lesions that cause cancer, a complex genetic disease associated with genomic instability. Studies aimed at deciphering the lesions in cancer have focused mainly on one or a few genes, despite the genomic scope of the disease. The recently decoded human DNA sequence is anticipated to foster understanding of human evolution and disease and the role of environment and heredity in the human condition. This review addresses the opportunities and challenges that the availability of the human genome sequence holds for cancer research [3].

The hallmark of a cancer genome is that it is replete with DNA alterations that perturb the normal function of proto-oncogenes and tumor suppressor genes [4], [5]. These genes normally control growth, development, differentiation, DNA repair, and DNA modification. In a neoplastic cancer cell, these genes are deregulated as a result of mutations, fusions, deletions, or epigenetic modifications. Both environmental and endogenous factors that cause gene deregulation in cancer have been reviewed extensively [5]. Allelic loss, or loss of heterozygosity, at certain chromosomal loci has been critical for the identification of tumor suppressor genes. Detection of loss of heterozygosity before cancer in solid tumors indicates that some of the losses seen in developed tumors may be crucial tumor suppressor genes lost early in development. On the other hand, proto-oncogenes are associated with recurring chromosomal aberrations, specifically, translocations, amplifications, and inversions. Nearly 100proto-oncogenes and approximately 30tumor suppressor genes have been isolated. Abnormalities in DNA methylation are also associated with cancer genomes. The net genomic alterations in a cancer cell are manifested in gene expression at the RNA and the protein level, including differences in posttranslational modification, such as phosphorylation [6].

Methods

For this literature review paper, a systematic search was conducted on PubMed, Scopus, and Google Scholar using the keywords "oncology," "molecular," and "genetic cancer." The inclusion criteria involved selecting articles published in English after 2000. A total of 38 papers met the inclusion criteria, while 25 papers were excluded based on pre-determined exclusion criteria. Descriptive statistics were employed to analyze the included papers, focusing on extracting and summarizing key information related to oncology, molecular, and genetic aspects of cancer research. The findings from this review provide a comprehensive overview of the current state of the field, highlighting significant molecular and genetic alterations, diagnostic approaches, therapeutic strategies, and their implications for cancer management.

Literature of Review

In 2001, cancer genetics research expanded its focus to include epigenetic events, cellular interactions, and common genetic variation in individual susceptibility to cancer. These new research directions have the potential to identify determinants of cancer outside the cancer cell, inform preventive strategies, and identify new intervention targets [7].

The 2002 study highlights the potential of technical advancements and insights into the molecular pathways of colorectal cancer to develop new clinical tools for diagnosis, classification, and treatment. The goal is to achieve individualized medicine based on the molecular taxonomy of tumors [8]. The availability of the human DNA sequence holds promise for advancing our understanding of human evolution, disease, and the role of environment and heredity in cancer, as described in the 2002 study [9].

In 2007, advances in molecular biology empowered healthcare providers to predict and prevent certain cancers, offering prospects for improving patient outcomes [10].

The 2007 study focuses on the cancer genetics of epigenetic genes, highlighting the genes involved in DNA methylation and chromatin modifications as potential targets for mutations and expression changes in human cancers [11].

The field of cancer pharmacogenomics emerged in 2007, utilizing genetic profiling to predict the response of tumors and normal tissue to therapy. Understanding genetic polymorphisms related to DNA repair can enhance individualized cancer therapy [12].

Genetic and epigenetic heterogeneity play crucial roles in cancer progression and drug resistance, providing population diversity, complexity, and robustness. The appreciation of new types of epigenetic regulation and the genome-centric concept of evolution contribute to a better understanding of cancer heterogeneity [13].

In 2012, studies were underway to assess the clinical validity and utility of multigene assays in breast cancer management. Incorporating genetics and genomics into clinical practice can refine risk stratification and enable individualized therapy [14].

High-throughput omics technologies have proven powerful in differentiating disease subtypes and identifying genetic events in cancer progression. These techniques offer potential in oncogenic detection, but roadblocks need to be overcome [15].

In Peru, genetic counseling plays a crucial role in identifying hereditary cancers and preventing diseases and deaths caused by these conditions. Expanding and strengthening the training process in genetics and genetic counseling for healthcare professionals can have a significant impact on cancer prevention [16].

In 2013, the clinical management of solid tumor patients has recently undergone a paradigm shift as a result of accelerated advances in cancer genetics and genomics. Molecular diagnostics is now

an integral part of routine clinical management in lung, colon, and breast cancer patients. However, molecular biomarkers remain largely excluded from current management algorithms of urologic malignancies. The need for new treatment alternatives and validated prognostic molecular biomarkers is pressing [17].

New DNA-sequencing technologies can play an important role in planning and implementing cancer prevention and screening strategies, as highlighted in the 2014 study. Further research is needed, especially in investigating new biomarkers and measuring gene-environment interactions [18].

In 2015, the growing incidence and mortality of cancer worldwide demand the development of accurate biomarkers for detection, diagnosis, prognostication, and monitoring. Epigenetic alterations hold great potential as innovative cancer biomarkers due to their stability, frequency, reversibility, and accessibility in body fluids [19].

Gastric cancer is a complex disease with high mortality. Understanding the genomic landscape of gastric cancer is critical for improving patient outcomes. The years following 2015 have seen considerable progress in deciphering the genomic aberrations associated with gastric cancer. The challenge lies in translating these molecular findings into clinical utility and enabling novel strategies for early detection [20].

The 2016 study discusses cancer drug resistance, particularly acquired resistance, and the various mechanisms that may contribute to it. These mechanisms include altered expression of drug transporters, impaired DNA repair and apoptosis, epigenetic alterations, mutation of drug targets, and alterations in the tumor microenvironment [21].

In 2017, cancer cytogenetics and cytogenomics emerged as important fields, providing key information for improving cancer patient care and identifying genes responsible for the development of neoplastic states. These advancements have also led to the emergence of molecularly targeted therapies in personalized medicine [22].

In a 2019 study by Miranda Furtado et al. [23], the focus is on epigenetic regulation of gene function in cancer and its potential as a target for therapy. The review highlights the emerging field of pharmaco(epi)genomics and the use of epidrugs to reprogram the epigenetic landscape in cancer cells. The authors discuss the clinical implications of targeting epigenetic markers in cancer treatment.

Moving on to a 2019 study by Hristova and Chan [24], the authors discuss the challenges and advancements in cancer biomarker discovery and translation. The review focuses on proteomics and other omics approaches for biomarker detection, emphasizing the integration of multiple techniques to address tumor heterogeneity and improve sensitivity.

In a 2019 study by Sweet-Cordero and Biegel [25], the authors explore the genomic landscape of pediatric cancers. They highlight the differences between pediatric and adult cancers, with pediatric tumors showing fewer somatic mutations but a higher prevalence of germline alterations in cancer predisposition genes. The study emphasizes the implications of these findings for diagnosis and treatment in pediatric oncology.

Next, in a 2019 study by Strelnikov and Zaletaev [26], the authors discuss the evolution of cancer DNA methylotyping. They highlight the discovery of methylation-sensitive restriction endonucleases and the use of PCR-based assays to analyze DNA methylation patterns. The authors describe their laboratory's use of methylation-sensitive restriction enzyme PCR (MSRE-PCR) protocols to diagnose abnormal DNA methylation in genetic diseases and characterize methylotypes in various cancers.

These studies provide valuable insights into different aspects of cancer genetics, including the role

of epigenetic regulation, biomarker discovery, pediatric cancer genomics, and DNA methylation analysis. They contribute to our understanding of cancer biology and have implications for the development of targeted therapies and diagnostic approaches.

In a 2020 study by Basset et al. [27], the authors discuss the future of clinical cancer genetics, highlighting the importance of strengthened partnerships between molecular pathologists, medical oncologists, and cancer genetics teams. They emphasize the routine use of somatic genetic analyses in metastatic cancer and the identification of germline variants in tumor samples. The authors suggest that mainstreaming programs allowing oncologists to prescribe germline testing under supervision will become unavoidable.

Moving on to a 2020 study by Nasir et al. [28], the authors explore the field of nutrigenomics and its potential in cancer prevention and management. They emphasize the impact of lifestyle and dietary habits on the risk of diet-related diseases, including cancer. The review highlights the significant role of dietary modifications in reducing disease risk and discusses the potential applications of nutrigenomics in preventing diet and lifestyle-related cancers.

Discussion

These studies provide insights into the complexity of cancer genetics, emphasizing the significance of genetic aberrations in tumor development and the need for better understanding for improved diagnosis and treatment. Specific genes and alterations are discussed, such as BRCA in breast cancer and DNA repair genes in prostate cancer, highlighting their potential as targets for therapy. The studies also underscore the importance of advanced analytical approaches and the potential for personalized treatments based on individual cancer types [29], [30], [31], [32].

These studies provide valuable insights into cancer research and highlight the importance of advanced technologies. Recillas-Targa (2022) emphasizes the role of genetic and epigenetic alterations in cancer development and their interaction with environmental factors. Bhati et al. (2012) focuses on the application of omics technologies in cancer research, showcasing their potential for differentiating disease subtypes and identifying genetic events. Together, these studies contribute to our understanding of cancer and the possibilities for improved diagnostics and treatments [15], [33].

These studies offer valuable insights into cancer research. Orsolic et al. (2023) highlights the interplay of dysregulated genetic and epigenetic mechanisms in cancer and the critical role of RNA modifications in regulating cellular pathways. They also identify alterations in the RNA modification machinery as potential therapeutic targets or diagnostic markers. On the other hand, the 2007 study discusses the impact of molecular biology advances on cancer prevention and treatment, including the potential for tailored treatments based on genetics. Together, these studies contribute to our understanding of cancer and the potential for personalized interventions [10], [34].

These studies provide insights into cancer research. Balmain et al. (2003) emphasizes the complexity of human malignancies, with multiple gene aberrations and differential gene expression. They discuss the role of both high-penetrance and low-penetrance genetic variants in cancer development and the need for advanced analytical approaches. In contrast, the 2019 study focuses on the challenges of cancer biomarker discovery, particularly in late-stage diagnosis, and highlights the potential of proteomics and integrating multiple omics approaches. Together, these studies contribute to our understanding of cancer genetics, molecular pathogenesis, and the need for improved diagnostic and therapeutic strategies [24], [35].

The perspectives of oncology, molecular biology, and cancer genetics are interconnected and vital

in cancer research and treatment. Oncology focuses on diagnosing, treating, and managing cancer patients, while molecular biology delves into the molecular processes underlying cancer development, identifying biomarkers and targets for intervention. Cancer genetics investigates genetic factors contributing to cancer risk and inheritance patterns. Together, these perspectives enhance our understanding of cancer biology, guide personalized treatment approaches, and drive advancements in research, aiming to improve patient outcomes and quality of life.

Conclusion

In conclusion, the fields of oncology, molecular, and genetic cancer research have significantly advanced our understanding of cancer biology and provided valuable insights into diagnosis, treatment, and prevention strategies. Through extensive studies, researchers have identified key molecular and genetic alterations that drive cancer initiation and progression. These findings have facilitated the development of targeted therapies, personalized medicine approaches, and improved prognostic tools. The significance of these discoveries lies in their potential to revolutionize cancer management, leading to more effective treatments with reduced side effects. However, there are still many unanswered questions, and future studies should focus on elucidating the complex interplay between genetic alterations, environmental factors, and immune response in cancer development. Additionally, efforts should be directed towards enhancing early detection methods and exploring novel therapeutic targets to overcome treatment resistance and improve patient outcomes.

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Conflict of interests

The authors declare that there are no competing interests.

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