IJARSCT
ISSN (Online) 2581-9429
International Journal of Advanced Research in Science, Communication and Technology (IJARSCT)
International Open-Access, Double-Blind, Peer-Reviewed, Refereed, Multidisciplinary Online Journal
Impact Factor: 7.301
Volume 3, Issue 2, September 2023

Analyzing Cancer through Molecular Perspectives: A Comprehensive Review

Anil Kumar Gurjar[1] and Dr. Shivnath Yadav[2]
Research Scholar, Department of Bioinformatics[1]
Associate Professor, Department of Bioinformatics[2]
Sunrise University, Alwar, Rajasthan, India

Abstract: *More than 277 distinct forms of cancer illness are referred to be cancer in the broadest sense. Researchers have discovered many cancer stages, suggesting that a number of gene alterations have a role in the genesis of cancer. Anomalous cell proliferation results from these gene alterations. A key component in the rise in cell proliferation is the presence of genetic diseases brought on by inheritance or heredity. Technological developments in bioinformatics and molecular approaches have helped to gather more data that may be helpful for early diagnosis and appropriate therapy. Certain adverse effects of medication may be anticipated and even managed in cancer patients. Molecular genetic investigations have identified pathways of cancer in recent years. These research' findings have enhanced our knowledge of how genetic abnormalities contribute to the development of cancer. Our goal in this work was to evaluate the molecular components of cancer.*

Keywords: Tumor suppressor genes, Passenger mutations

I. INTRODUCTION

Cancer ranks as the second most prevalent cause of mortality worldwide. The incidence of cancer has generally increased; in the United States alone, there were about 1,665,540 cancer patients in 2014, and 585,720 of them had died from the disease. Thus, in human civilizations, cancer is a serious problem that affects everyone's health. Unfortunately, the disease is variable at the tissue level, which presents major obstacles to accurate diagnosis and effective treatment. Males are more likely to be affected by prostate, lung and bronchus, colon and rectum, and urinary bladder cancers, in that order. Women are more likely to get cancer in the breast, lung and bronchus, colon and rectum, uterine corpus, and thyroid. This study indicates that prostate and breast cancer, respectively, account for a significant portion of cancer cases in men and women. The two types of cancers that most often afflict children are blood cancer and brain and lymph node cancer, respectively. Cancer is caused by a series of gradually developing gene mutations that change how cells function. It is clear that chemicals play a part in the development of cancer cells and the changes that occur to genes. Lung cancer is also caused by a variety of chemicals that are involved in smoking and are carcinogenic. It's noteworthy to note that environmental chemicals with the potential to cause cancer may directly or indirectly damage the cytoplasm and nucleus of cells, causing genetic abnormalities and mutations. Together, bacteria, viruses, and radiation contribute 7% of cancer cases and are considered additional carcinogenic factors. Essential genes often cease functioning and cellular interactions break down as a result of cancer. The cell cycle is impacted and abnormal cell division results from this disturbance. Proto-oncogenes normally regulate cell division and proliferation; however, when a genetic mutation takes place, they change into oncogenes, which are very harmful to a cell's ability to survive. In addition, the lack of tumor suppressor genes causes uncontrolled cell division. Approximately thirty distinct types of repair proteins have been found; repair genes often produce proteins and/or enzymes with the ability to repair. In essence, repair genes play two functions in the efficient repair of DNA: they prevent UV light-induced DNA damage and eradicate the original UV-induced DNA lesions by removing uracil from DNA.

Epigenetics is the study of cell fate and epigenetic changes, which play a major role in the development of cancer. These changes include DNA methylation, histone modifications, and nucleosome positioning. In cancer cells, DNA methylation has significantly decreased. Mono-acetylated H4K16 is often down regulated in cancer cells, which is the primary source of most histone alterations. Even if the majority of the time the underlying molecular pathways are still

ISSN 2581-9429 IJARSCT

IJARSCT
ISSN (Online) 2581-9429
International Journal of Advanced Research in Science, Communication and Technology (IJARSCT)
International Open-Access, Double-Blind, Peer-Reviewed, Refereed, Multidisciplinary Online Journal
Impact Factor: 7.301
Volume 3, Issue 2, September 2023

unknown, every family of chromatin-modifying proteins has a relationship to cancer. In this study, we looked at cancer from a molecular perspective to get a better understanding of the disease.

II. REVIEW METHOD

Using terms like "cancer and molecular process," "cancer and treatment," and "molecular aspects," we first looked for research publications. The publications that met these word requirements were then thoroughly evaluated, and the results were appropriately reported.

Cancer from the molecular prospective

Oncogene production and genetic illnesses are caused by a variety of genetic changes, including chromosome translocation, point mutation, deletion amplifcation, and insertion activation. An exchange of genetic material between chromosomes 9 and 22 is the cause of the high rate of chronic blood cancer diagnoses in the elderly. Ninety-five percent of patients have Ph1, a biomarker generated by this condition that might aid in a precise diagnosis. The Bcr gene's association with the Abl oncogene resulted in the creation of a unique gene combination that translated into a protein with kinase activity.

An unusual protein produced by a p53 gene mutation is crucial in upsetting the biochemical mechanism associated with p53. Research indicates that p53 anomalies are present in 60% of instances of cancer. Consequently, aberrations in these molecular and biological processes have a role in the development of cancer cells, explaining the complex relationship between the p53 gene and cancer. Under normal conditions, p53 plays a major role in angiogenesis, differentiation, senescence, cell division, and DNA metabolism. Additionally, most mutations connected to p53 impact the site where DNA binds, and p53 controls the impairment of genes caused by replication. The collaboration of p53 with CDK1–P2 and CDC2 maintains cancer cells in the G1 and G2 phases of the cell cycle. As a matter of fact, p53 either promotes or prevents cancer cell proliferation. After other genes cause damage to DNA, the p53 protein binds to the damaged DNA and activates the WAF1 gene. Through this mechanism, p53 and CDK2 are linked, preventing p21 from influencing the cell cycle's next phase. Apoptosis induction, DNA repair protein activation, and cell cycle arrest in the G1/S phase are the three ways that p53 prevents cancer.

All things considered, chromosomal instability, gene loss, and displacement are caused by hypomethylation, which is often the outcome of repeated sequences. L1 of the LINE family, which has been connected to a number of cancers including bladder, lung, and breast cancers, is one of the greatest examples of hypomethylation. Hypomethylation in certain promoters may cause the ectopic expression of oncogenes; the tumor suppressor gene MASPIN displays this condition in breast and prostate cancer cases. DPP6 and MAGE in melanoma, SNCG in ovarian and breast cancer, and S100P in pancreatic cancer are more examples. Hypermethylation, as opposed to widespread hypomethylation, is restricted to a particular CpG site. Transcription inactivation caused by hypermethylation of the promoter impacts genes involved in repair, apoptosis, cell cycle control, and vitamin response. These events play a critical role in the development of cancer. Hypermethylated promoters may thus be considered as novel biomarkers for the diagnosis and prognosis of cancer, as the majority of research focuses on the CpG regions of promoters. It's also important to keep in mind that aberrant methylation, such as hypermethylation in the CpG region, often happens during cancer. Poor control of DNMT may be the source of the general disturbance of DNA methylation patterns; in fact, it has been shown that DNMT1 and DNMT3b are substantially expressed in a range of tumor types. Moreover, it has been shown that DNMT3a, DNMT3b, and DMNT1 expression are all downregulated by the MIR-29 family. DNMT expression is regulated by miRNA as well.

Since acetylation is caused by HDAC, this condition impacts several cancers. The Sirtuin family comprises one of the main families of HDAC enzymes. Increases in SirT1 expression and activity may take many different forms. Moreover, the cooperation of SirT1 and DNMT1 affects DNA methylation. HDAC expression may be regulated by microRNAs. For example, in prostate cancer, miR-449a inhibits HDAC-1 expression to regulate cell survival and proliferation. In addition to altering the expression of HDAC in a number of cancers, including lung, leukemia, and colon cancer, ectopic mutations and deletions in HAT and related genes cause problems with histone acetylation. These events could be the main reason why cancer develops. Furthermore, cancer cells lost H4K16ac, H3K4me3, H4K20me3, and H3K27me3. Changes in the distribution of histone methylation are mainly caused by histone methyltransferases and

IJARSCT
ISSN (Online) 2581-9429
International Journal of Advanced Research in Science, Communication and Technology (IJARSCT)
International Open-Access, Double-Blind, Peer-Reviewed, Refereed, Multidisciplinary Online Journal
Impact Factor: 7.301
Volume 3, Issue 2, September 2023

histone demethylases. Furthermore, crippling mutations in UTX and SETD2 arise during kidney cancer. In leukemia, MLL oncoprotein results in abnormal H3K4 and H3K29 methylation patterns, which in turn impacts the expression of the MLL target genes.

It is well recognized that the tumor suppressors BRG1 and BRM are important in 15–20% of instances of lung cancer. Interestingly, studies have shown that BRG1 regulates the expression of genes locally and disrupts the p53 and SWI/SNF complex. The development of many malignancies is influenced by the SWI/SNF complex via its interactions with RB, p53, MYC, MLL, and BRCA1. Therefore, inhibiting the SWI/SNF complex stops cells from proliferating. Moreover, transcription is suppressed by promoter hypermethylation brought on by changes in nucleosome positioning. Promoter hypermethylation, which results in TSS occupancy by nucleosomes, has been linked to MLH1 in colon cancer. CpG hypermethylation mostly targets genes that encode parts of chromatin-changing complexes, such CHD5. In this case, its expression is downregulated and the regular structure of chromatin is disturbed. In addition to the issue with nucleosome placement, histone variations—such as an upregulation of MacroH2A expression during the senescence process—are also connected to cancer. Because there is less cell proliferation, lung tumors with increased MacroH2A expression have a better prognosis.

III. CONCLUSION

Over the last thirty years, a significant amount of data about the functions of genes and proteins in the development of cancer cells has been documented by researchers. Actually, one of the most significant findings was the function of altered genes in cancer cells. Environmental variables linked to genetic mutations have been discovered recently. We can identify new cancer biomarkers and assess the strength of gene expression and faulty proteins with the aid of various molecular techniques. These results may help treat cancer and lessen its complications. Furthermore, several investigations into the role of epigenetic pathways in the onset and advancement of diverse medical conditions, including cancer, are ongoing. Furthermore, it seems that a great deal about epigenetics is yet unknown. Nonetheless, by identifying all relevant genes and environmental factors, this provides us with a thorough map for future attempts to lower the incidence of cancer.

REFERENCES

[1]. Siegel R, Naishadham D, Jemal A. Cancer statistics 2013, CA Cancer J. Clin.
[2]. 2013;63:11e30.
[3]. Meacham CE, Morrison SJ. Tumour heterogeneity and cancer cell plasticity.
[4]. Nature. 2013;501:328e337.
[5]. Fisher R, Pusztai L, Swanton C. Cancer heterogeneity: implications for targeted therapeutics. Br J Cancer. 2013;108:479e485.
[6]. Siegel RL, Miller KD, Jemal A, Cancer statistics. 2016, CA Cancer J Clin. 2016;66: 7e30.
[7]. Schottenfeld D, Fraumeni Jr JF. Cancer Epidemiology and Prevention. Oxford University Press; 2006.
[8]. Yoo KY, Shin HR. Cancer epidemiology and prevention. Korean J Epidemiol. 2003;25:1e15.
[9]. Aizawa K, Liu C, Tang S, et al. Tobacco carcinogen induces both lung cancer and non-alcoholic steatohepatitis and hepatocellular carcinomas in ferrets which can be attenuated by lycopene supplementation. Int J Cancer. 2016;139: 1171e1181.
[10]. Poon SL, McPherson JR, Tan P, Teh BT, Rozen SG. Mutation signatures of carcinogen exposure: genome-wide detection and new opportunities for can- cer prevention. Genome Med. 2014;6:24.
[11]. Trafialek J, Kolanowski W. Dietary exposure to meat-related carcinogenic substances: is there a way to estimate the risk? Int J Food Sci Nutr. 2014;65: 774e780.
[12]. Cumberbatch MG, Cox A, Teare D, Catto JW. Contemporary occupational carcinogen exposure and bladder cancer: a systematic review and meta- analysis. JAMA Oncol. 2015;1:1282e1290.
[13]. Antwi SO, Eckert EC, Sabaque CV, et al. Exposure to environmental chemicals and heavy metals, and risk of pancreatic cancer. Cancer Causes Control. 2015;26:1583e1591.
[14]. Parkin DM. The global health burden of infection-associated cancers in the year 2002. Int J Cancer. 2006;118:3030e3044.

ISSN 2581-9429 IJARSCT

IJARSCT
ISSN (Online) 2581-9429
International Journal of Advanced Research in Science, Communication and Technology (IJARSCT)
International Open-Access, Double-Blind, Peer-Reviewed, Refereed, Multidisciplinary Online Journal
Impact Factor: 7.301
Volume 3, Issue 2, September 2023

[15]. Seto M, Honma K, Nakagawa M. Diversity of genome profiles in malignant lymphoma. Cancer Sci. 2010;101:573e578.
[16]. Cigudosa JC, Parsa NZ, Louie DC, et al. Cytogenetic analysis of 363 consecutively ascertained diffuse large B-cell lymphomas. Genes, Chromosomes Cancer. 1999;25:123e133.
[17]. Shtivelman E, Lifshitz B, Gale RP, Canaani E. Fused transcript of abl and bcr genes in chronic myelogenous leukaemia. Nature. 1985;315:550e554.
[18]. Matlashewski G, Lamb P, Pim D, Peacock J, Crawford L, Benchimol S. Isolation and characterization of a human p53 cDNA clone: expression of the human p53 gene. EMBO J. 1984;3:3257.
[19]. Wei Q, Li L, Chen D. DNA Repair, Genetic Instability, and Cancer: World Scientific. 2007.
[20]. Wood RD, Mitchell M, Sgouros J, Lindahl T. Human DNA repair genes. Science. 2001;291:1284e1289.
[21]. Alvarez-Buylla ER, Chaos A´, Aldana M, et al. Floral morphogenesis: stochastic
[22]. explorations of a gene network epigenetic landscape. PLoS One. 2008;3:e3626.
[23]. Portela A, Esteller M. Epigenetic modifications and human disease. Nat Bio- technol. 2010;28:1057e1068.
[24]. Goelz SE, Vogelstein B, Hamilton SR, Feinberg AP. Hypomethylation of DNA from benign and malignant human colon neoplasms. Science. 1985;228: 187e191.
[25]. Fraga MF, Ballestar E, Villar-Garea A, et al. Loss of acetylation at Lys16 and trimethylation at Lys20 of histone H4 is a common hallmark of human cancer. Nat Genet. 2005;37:391e400.
[26]. Sharma S, Kelly TK, Jones PA. Epigenetics in cancer. Carcinogenesis. 2010;31: 27e36.
[27]. Joensuu H, Dimitrijevic S. Tyrosine kinase inhibitor imatinib (STIS71) as an
[28]. anticancer agent for solid tumours. Ann Med. 2001;33:451e455.
[29]. King CR, Kraus MH, Aaronson SA. Amplification of a novel v-erbB-related gene in a human mammary carcinoma. Science. 1985;229:974e977.
[30]. Heinrich MC, Blanke CD, Druker BJ, Corless CL. Inhibition of KIT tyrosine kinase activity: a novel molecular approach to the treatment of KIT-positive malig- nancies. J Clin Oncol. 2002;20:1692e1703.
[31]. Thomas RK, Baker AC, DeBiasi RM, et al. High-throughput oncogene mutation profiling in human cancer. Nat Genet. 2007;39:347e351.
[32]. Chae SW, Sohn JH, Kim D-H, et al. Overexpressions of Cyclin B1, cdc2, p16 and p53 in human breast cancer: the clinicopathologic correlations and prognostic implications. Yonsei Med J. 2011;52:445e453.
[33]. Taylor WR, Stark GR. Regulation of the G2/M transition by p53. Oncogene. 2001;20:1803.
[34]. Bukholm IK, Nesland JM. Protein expression of p53, p21 (WAF1/CIP1), bcl-2, Bax, cyclin D1 and pRb in human colon carcinomas. Virchows Arch. 2000;436:224e228.
[35]. Roninson IB. Oncogenic functions of tumour suppressor p21 Waf1/Cip1/Sdi1: association with cell senescence and tumour-promoting activities of stromal fibroblasts. Cancer Lett. 2002;179:1e14.
[36]. May P, May E. Twenty years of p53 research: structural and functional aspects of the p53 protein. Oncogene. 1999;18:7621.
[37]. McBride O, Merry D, Givol D. The gene for human p53 cellular tumor antigen is located on chromosome 17 short arm (17p13). Proc Natl Acad Sci. 1986;83: 130e134.
[38]. Isobe M, Emanuel B, Givol D, Oren M, Croce CM. Localization of gene for human p53 tumour antigen to band 17p13. Nature. 1986;320:84e85.
[39]. Miller C, Koeffler H. P53 mutations in human cancer. Leukemia. 1993;7: S18eS21.
[40]. Koshland Jr DE. Molecule of the year. Science. 1991;254:1705e1706.
[41]. Muller PA, Vousden KH. Mutant p53 in cancer: new functions and therapeutic opportunities. Cancer Cell. 2014;25:304e317.
[42]. Selivanova G. p53: fighting cancer. Curr Cancer Drug Targets. 2004;4:385e402.
[43]. Kanai Y, Hirohashi S. Alterations of DNA methylation associated with abnor- malities of DNA methyltransferases in human cancers during transition from a precancerous to a malignant state. Carcinogenesis. 2007;28:2434e2442.
[44]. Wilson AS, Power BE, Molloy PL. DNA hypomethylation and human diseases.
[45]. Biochim Biophys Acta. 2007;1775:138e162.

IJARSCT
ISSN (Online) 2581-9429
International Journal of Advanced Research in Science, Communication and Technology (IJARSCT)
International Open-Access, Double-Blind, Peer-Reviewed, Refereed, Multidisciplinary Online Journal
Impact Factor: 7.301
Volume 3, Issue 2, September 2023

[46]. Futscher BW, O Meara MM, Kim CJ, et al. Aberrant methylation of the maspin promoter is an early event in human breast cancer. Neoplasia. 2004;6: 380e389.
[47]. Esteller M. Epigenetic gene silencing in cancer: the DNA hypermethylome.
[48]. Hum Mol Genet. 2007;16:R50eR59.
[49]. Li M, Chen W-D, Papadopoulos N, et al. Sensitive digital quantification of DNA methylation in clinical samples. Nat Biotechnol. 2009;27:858e863.
[50]. Doi A, Park I-H, Wen B, et al. Differential methylation of tissue-and cancer- specific CpG island shores distinguishes human induced pluripotent stem cells, embryonic stem cells and fibroblasts. Nat Genet. 2009;41:1350e1353.
[51]. Miremadi A, Oestergaard MZ, Pharoah PD, Caldas C. Cancer genetics of epige- netic genes. Hum Mol Genet. 2007;16:R28eR49.
[52]. Vaquero A, Sternglanz R, Reinberg D. NAD -dependent deacetylation of H4 lysine 16 by class III HDACs. Oncogene. 2007;26:5505e5520.
[53]. Espada J, Ballestar E, Santoro R, et al. Epigenetic disruption of ribosomal RNA genes and nucleolar architecture in DNA methyltransferase 1 (Dnmt1) defi- cient cells. Nucleic Acids Res. 2007;35:2191e2198.
[54]. Noonan E, Place R, Pookot D, et al. miR-449a targets HDAC-1 and induces growth arrest in prostate cancer. Oncogene. 2009;28:1714e1724.
[55]. Kondo Y, Shen L, Suzuki S, et al. Alterations of DNA methylation and histone modifications contribute to gene silencing in hepatocellular carcinomas. Hep- atology Res. 2007;37:974e983.
[56]. Dalgliesh GL, Furge K, Greenman C, et al. Systematic sequencing of renal car- cinoma reveals inactivation of histone modifying genes. Nature. 2010;463: 360e363.
[57]. Wang P, Lin C, Smith ER, et al. Global analysis of H3K4 methylation defines MLL family member targets and points to a role for MLL1-mediated H3K4 methylation in the regulation of transcriptional initiation by RNA polymerase II. Mol Cell Biol. 2009;29:6074e6085.
[58]. Mulero-Navarro S, Esteller M. Chromatin remodeling factor CHD5 is silenced by promoter CpG island hypermethylation in human cancer. Epigenetics. 2008;3:210e215.
[59]. Sporn JC, Kustatscher G, Hothorn T, et al. Histone macroH2A isoforms predict the risk of lung cancer recurrence. Oncogene. 2009;28:3423e3428