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# **Analyzing Cancer through Molecular Perspectives: A Comprehensive Review**

Anil Kumar Gurjar<sup>1</sup> and Dr. Shivnath Yadav<sup>2</sup>

Research Scholar, Department of Bioinformatics<sup>1</sup> Associate Professor, Department of Bioinformatics<sup>2</sup> 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

### 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: genomewide 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.
- [15]. Seto M, Honma K, Nakagawa M. Diversity of genome profiles in malignant lymphoma. Cancer Sci. 2010;101:573e578.

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#### Volume 3, Issue 2, September 2023

- [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.
- [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.

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#### Volume 3, Issue 2, September 2023

- [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

