Pharmaspire

SHORT COMMUNICATION

Cancer's initiation and progression: Deciphering the role of genetic and epigenetic alterations

Keshav Taruneshwar Jha, Pooja A. Chawla

Department of Pharmaceutical Chemistry, ISF College of Pharmacy, Moga, Punjab, India

ABSTRACT

Cancer is a complex disease involving both genetic and epigenetic alterations that drive the transformation of normal cells into malignant ones. In this review, we discuss how genetic mutations and epigenetic changes contribute to cancer initiation and progression. Genetic changes such as mutations, deletions or amplifications of oncogenes and tumor suppressor genes are crucial for the development of most cancers. In addition, epigenetic mechanisms such as DNA methylation, histone modifications and non-coding RNAs are also frequently dysregulated in cancer and contribute to its heterogeneity. A better understanding of the interplay between genetic and epigenetic events will shed light on the molecular mechanisms underlying cancer initiation and progression, and may help identify new therapeutic.

KEY WORDS: Cancer, Genetics, Mutations, Progression

Exploring the complex interconnection between genetic and epigenetic changes presents significant prospects for expanding our understanding of cancer biology and devising precise treatment strategies. Genomic modifications, encompassing mutations, and abnormalities in chromosomes have long been acknowledged as pivotal catalysts in cancer genesis.[1] The unveiling of oncogenes and tumor suppressor genes has brought forth valuable elucidation of the molecular mechanisms involved in the emergence and advancement of tumors. Moreover, the advent of high-throughput sequencing technologies has facilitated extensive genomic profiling, yielding valuable observations into the mutational patterns prevalent across diverse types of cancer.[2,3] In recent times, it has become increasingly apparent that epigenetic modifications also assume a central role in cancer.[4] Epigenetic changes, which involve DNA methylation, modifications to histones, and gene regulation mediated by non-coding RNA, possess significant influence over gene expression patterns and cellular behavior. These alterations contribute to the disruption of crucial cellular processes such as cell cycle regulation, DNA repair, and apoptosis, ultimately promoting the development of tumors.[5] Of utmost importance is the intricate and dynamic interplay between genetic and epigenetic alterations in cancer. Genetic modifications have the capacity to directly impact epigenetic markers, resulting in widespread changes in gene expression profiles. Conversely, abnormal epigenetic modifications can interfere with normal cellular functions and contribute to genomic instability, thereby facilitating the accumulation of additional genetic alterations.[6,7] Gaining a comprehensive understanding of the precise genetic and epigenetic changes that propel the onset and progression of cancer is indispensable for the advancement of targeted therapeutic approaches. Precision medicine methodologies strive to identify and exploit the distinct genomic and epigenomic characteristics exhibited by individual tumors, thereby enabling more effective and personalized treatment strategies. Moreover, comprehending the capacity of cancer cells to undergo epigenetic modifications opens up possibilities for therapeutic intervention by specifically targeting the reversible nature of these alterations.[1,8] Nonetheless, challenges persist in attaining a thorough comprehension of the intricate interplay between genetic

Address for Correspondence:
Prof. (Dr.) Pooja A. Chawla,
E-mail: pvchawla@gmail.com

Access this article online

Website: http://isfcppharmaspire.com

DOI: 10.56933/Pharmaspire.2023.15116

Date of Submission: 19 May 2023
Date of Revision: 30 May 2023
Date of Acceptance: 31 May 2023

and epigenetic alterations. The integration of extensive sets of genomic and epigenomic data, along with sophisticated computational analyses, will play a pivotal role in deciphering the intricate regulatory networks that underlie the biology of cancer. In addition, conducting functional studies and utilizing preclinical models will aid in unraveling the functional repercussions of specific genetic and epigenetic changes, as well as their influence on the development of tumors and response to treatment.[9,10] In conclusion, the investigation of genetic and epigenetic alterations in cancer initiation and progression represents a promising frontier in cancer research. The integration of genetic and epigenetic information holds tremendous potential for improving our understanding of tumor biology and developing novel therapeutic approaches. Continued efforts in this field are crucial to advance our knowledge and ultimately improve outcomes for cancer patients.

CONFLICT OF INTEREST

None.

REFERENCES

1. CastroMuñoz LJ, Ulloa EV, Sahlgren C, Lizano M, De La Cruz-Hernández D, ContrerasParedes A. Modulating epigenetic modifications for cancer therapy (Review). Oncol Rep 2023;49:59.
2. Hartmaier RJ, Albacker LA, Chmielecki J, Bailey M, He J, Goldberg ME, *et al*. High-throughput genomic profiling of adult solid tumors reveals novel insights into cancer pathogenesispublic release of adult cancer pathogenesis. Cancer Res 2017;77:2464-75.
3. Kerick M, Isau M, Timmermann B, Sültmann H, Herwig R, Krobitsch S, *et al*. Targeted high throughput sequencing in clinical cancer settings: Formaldehyde fixed-paraffin embedded (FFPE) tumor tissues, input amount and tumor heterogeneity. BMC Med Genomics 2011;4:68.
4. Feinberg AP, Levchenko A. Epigenetics as a mediator of plasticity in cancer. Science 2023;379:eaaw3835.
5. Kay J, Thadhani E, Samson L, Engelward B. Inflammation-induced DNA damage, mutations and cancer. DNA Repair (Amst) 2019;83:102673.
6. Scully R, Panday A, Elango R, Willis NA. DNA double-strand break repair-pathway choice in somatic mammalian cells. Nat Rev Mol Cell Biol 2019;20:698-714.
7. Alves-Fernandes DK, Jasiulionis MG. The role of SIRT1 on DNA damage response and epigenetic alterations in cancer. Int J Mol Sci 2019;20:3153.
8. Louwies T, Ligon CO, Johnson AC, Meerveld BG. Targeting epigenetic mechanisms for chronic visceral pain: A valid approach for the development of novel therapeutics. Neurogastroenterol Motil 2019;31:e13500.
9. Jühling F, Hamdane N, Crouchet E, Li S, El Saghire H, Mukherji A, *et al*. Targeting clinical epigenetic reprogramming for chemoprevention of metabolic and viral hepatocellular carcinoma. Gut 2021;70:157-69.
10. Ilango S, Paital B, Jayachandran P, Padma PR, Nirmaladevi R. Epigenetic alterations in cancer. Front Biosci (Landmark Ed) 2020;25:1058-109.