



## Role of Epigenetic alterations in the development of cancers

Riffat Mehboob<sup>1</sup>

<sup>1</sup>Lahore Medical Research Center LLP

\*[mehboob.riffat@gmail.com](mailto:mehboob.riffat@gmail.com)

### ARTICLE INFO

#### How to Cite:

Mehboob, R. (2022). Role of Epigenetic alterations in the development of cancers . Pakistan BioMedical Journal, 5(2). <https://doi.org/10.54393/pbmj.v5i2.346>

Many different factors are involved in the progression of cancers. Genes mutations and chromosomal abnormalities are normally considered main cause of cancers but there are some other reason for the development of cancers. Other cancer causing factors are known as epigenetic alterations [1,2]. Epigenetic modification of genome is known as epigenetic alterations, lead toward cancer cells production. Epigenetic modification does not cause change in sequences of nucleotide. Similar to genetic alteration epigenetic alteration can't be ignored [3]. Basically mechanisms behind epigenetic modifications are deregulation of DNA proteins, change in CpG island methylation, change in histone, oncogenes activation and deactivation of tumor suppressor [4]. Epigenetic alterations is directly linked with functional alterations of genome. Alteration in DNA methylation, histone degeneration and functional and structural abnormalities of chromosomes are the major examples of epigenetic modifications [5]. The main function of all epigenetic alterations is to modulate gene expression with same DNA sequences. Means these changes never effect main basal sequence of DNA [6], which remain same in cell division [7]. Many different types of cancers contains large number of epigenetic alterations, the most important of these are epigenetic alterations that occurs in DNA repair genes. These DNA repair genes drive slow expression of DNA proteins. These abnormalities cause genetic unreliability, which is mainly considered as characteristic of various cancers .

### REFERENCES

- [1] 1. Baylin SB, Ohm JE. Epigenetic gene silencing in cancer—a mechanism for early oncogenic pathway addiction?. *Nature Reviews Cancer*. 2006 Feb;6(2):107-16.
- [2] 2. Bedi GC, Westra WH, Gabrielson E, Koch W, Sidransky D. Multiple head and neck tumors: evidence for a common clonal origin. *Cancer research*. 1996 Jun 1;56(11):2484-7.
- [3] 3. Novak K. Epigenetics Changes in Cancer Cells: Highlights of the American Association for Cancer Research Special Conference on Chromatin, Chromosomes, and Cancer Epigenetics; November 10-14, 2004; Waikoloa, Hawaii. *Medscape General Medicine*. 2004;6(4).
- [4] 4. Suzuki K, Yamaji H, Kobashigawa S, Kawauchi R, Shima K, Kodama S, Watanabe M. Epigenetic gene silencing is a novel mechanism involved in delayed manifestation of radiation-induced genomic instability in mammalian cells. *Radiation research*. 2011 Apr;175(4):416-23. <https://doi.org/10.1667/RR2391.1>.
- [5] 5. Kanwal R, Gupta K, Gupta S. Cancer epigenetics: an introduction. *Cancer epigenetics*. 2015:3-25.
- [6] 6. Horsthemke B. Epimutations in human disease. DNA methylation: Development, genetic disease and cancer. 2006:45-59. [https://link.springer.com/chapter/10.1007/3-540-31181-5\\_4](https://link.springer.com/chapter/10.1007/3-540-31181-5_4).
- [7] 7. Macfarlane GJ, Boyle P, Scully C. Oral cancer in Scotland: changing incidence and mortality. *British Medical Journal*. 1992 Nov 7;305(6862):1121-3. <https://doi.org/10.1136/bmj.305.6862.1121>.