Journal of Clinical Epigenetics
ISSN: 2472-1158

Open access Short Communication

Alteration of DNA Methylation in Epigenome

Olga Tokarczuk*

Department of Clinical Epigenetics, University of Białystok, Poland

INTRODUCTION

Neuroblastoma (NB) is a childhood cancer of the sympathetic nervous system and is one of the most common solid tumours in infancy. Major epigenetic changes include aberrant DNA methylation, disturbed patterns of post-translation histone modifications, chromatin composition and/or structural changes, and aberrant expression of non-coding RNAs. DNA methylation and demethylation are mediated by DNA methyltransferase (DNMT) and Teneleven Translocation Protein (TET), respectively, and histone modifications are Histone Acetyltransferases and Deacetylases (HAT, HDAC) and Histone Methyltransferases and Demethylases (HMT). This article focuses primarily on the epigenome-NB interactions and their impact on disease diagnosis and treatment.

DESCRIPTION

Plant breeding faces the challenge of increasing food demand, especially in the face of climate change. Traditional breeding has relied on genetic diversity to combine alleles to obtain the desired trait. In recent years, research on epigenetics and epitranscriptome has provided an additional source of epigenetic and epitranscriptome diversity for plant breeding, leveraging the use of biotechnology to regulate epigenetics and epitranscriptome. It has been shown to have great potential for improving crops.

Mycobacterium Tuberculosis (MTB) has co-evolved with humans for decades and has evolved multiple mechanisms to evade host immunity. Because it can efficiently alter the host's epigenome, it plays an important role in immune regulation by activating or suppressing genes involved in inducing an immune response against pathogens. Acquired modifications such as DNA methylation and chromatin remodeling regulate gene expression and affect multiple cellular processes. The involvement of epigenetic factors in the onset and onset of disease has been overlooked compared to genetic variation. Assessment of epigenetic changes is now recognized to offer significant potential in the diagnosis, prevention, and treatment strategies of a variety of diseases.

Opioid abuse poses significant risks to individuals in the United States, and epigenetic changes are the major potential biomarkers of opioid abuse. However, current evidence is primarily limited to the analysis of candidate genes in whole blood. To clarify the association between opioid abuse and DNA methylation, we performed an epigenome-wide analysis of DNA methylation in brain samples from controls that were group-matched with individuals who died of acute opioid poisoning.

CONCLUSION

Cancer is a leading cause of global mortality supported by genomic and epigenome disorders. It emphasizes the importance of multimodal data integration to understand the molecular evolution of malignant cell states throughout the life cycle of cancer. The widespread presence of driver mutations and epigenetic changes in normal-looking tissues has prompted a reassessment of the definition of carcinogenesis. In late-stage cancer, new areas are to investigate the role of clonal selection, epigenome adaptation, and persistent cells in metastasis and resistance to treatment. Finally, the importance of tumor ecosystems in the development of cancer is being elucidated through single-cell and spatial techniques at unprecedented resolution. Robust, comprehensive, integrated temporal, spatial, and multi-level tumor atlases are available throughout the cancer life cycle to improve cancer risk assessment and accelerate the discovery of treatments for patients. It defines new aspects of epigenetic regulation in placental cells associated with normal and disease and associates them with the specific biological requirements of this organ.

ACKNOWLEDGEMENT

None

CONFLICTS OF INTERESTS

The authors declare that they have no conflict of interest.

Received:	01-June-2022	**Manuscript No:**	IPJCE-22-13948
Editor assigned:	03-June-2022	**PreQC No:**	IPJCE-22-13948 (PQ)
Reviewed:	17-June-2022	**QC No:**	IPJCE-22-13948
Revised:	22-June-2022	**Manuscript No:**	IPJCE-22-13948 (R)
Published:	29-June-2022	**DOI:**	10.21767/2472-1158-22.8.29

Corresponding author Olga Tokarczuk, Department of Clinical Epigenetics, University of Białystok, Poland, E-mail: olga7234@gmail.com

Citation Tokarczuk O (2022) Alteration of DNA Methylation in Epigenome. J Clin Epigen. 8:29.

REFERENCES

1. Zhang W, Qu J, Liu GH, Belmonte JCI (2020) The ageing epigenome and its rejuvenation. Nat Rev Mol Cell Biol 21(3): 137-150.

2. Flanagan JM (2015) Epigenome-wide association studies (EWAS): Past, present, and future. Methods Mol Biol 1238: 51-63.

3. Baumbach JL, Zovkic IB (2020) Hormone-epigenome interactions in behavioural regulation. Horm Behav 118: 104680.

4. Brahma S, Henikoff S (2020) Epigenome Regulation by Dynamic Nucleosome Unwrapping. Trends Biochem Sci 45(1): 13-26.