Extended Abstract
Volume 5:4, 2021

Journal of Genetics and DNA Research

Open Access

Epigenetics role in cancer with considerations for regulatory reform

Jorma A Jyrkkanen

UBC Zoology Grad and SFU Education, Canada , E-mail: jormabio@hotmail.com

Abstract

Transcriptional variability is necessary for normal gene expression but it is also a liability when the gene profiles generated are cancer profiles. This is true for DNA transcription as well as RNA translation. Methylation can interfere with transcription and alter micro RNA translation or cleave RNA. This can lead to cellular transformation and tumorigenesis as in HPV. Viral oncogene methylation can repress tumor suppressor genes. We also see epigenetic potential of known carcinogens and mutagens needs to be assessed and included in carcinogen determinations and their regulation. Generational heritability also needs assessment.

Epigenetics is dynamic and heritable modifications to the genome that occur independently of DNA sequence. It requires interactions cohesively with various enzymes and other molecular components. Aberrant epigenetic alterations can lead to inappropriate onset of genetic expressions and promote tumorigenesis. As the epigenetic modifiers are susceptible to extrinsic factors and reversible, they are becoming promising targets in multiple cancer therapies. Recently, various epi-drugs have been developed and implicated in clinical use. The use of epi-drugs alone, or in combination with chemotherapy or immunotherapy, has shown compelling outcomes, including augmentation of anti-tumoral effects, overcoming drug resistance, and activation of host immune response.

The term, “epigenetics,” was first used to refer to the complex interactions between the genome and the environment that are involved in development and differentiation in higher organisms. Today, this term is used to refer to heritable alterations that are not due to changes in DNA sequence. Rather, epigenetic modifications, or “tags,” such as DNA methylation and histone modification, alter DNA accessibility and chromatin structure, thereby regulating patterns of gene expression. These processes are crucial to normal development and differentiation of distinct cell lineages in the adult organism. They can be modified by exogenous influences, and, as such, can contribute to or be the result of environmental alterations of phenotype or pathophenotype. Importantly, epigenetic programming has a crucial role in the regulation of pluripotency genes, which become inactivated during differentiation. Here, we review the major mechanisms in epigenetic regulation; highlight the role of stable, long-term epigenetic modifications that involve DNA methylation; and discuss those modifications that are more flexible (short-term) and involve histone modifications, such as methylation and acetylation. We will also discuss the role of nutritional and environmental challenges in generational inheritance and epigenetic modifications, concentrating on examples that relate to complex cardiovascular diseases, and specifically dissect the mechanisms by which homocysteine modifies epigenetic tags. Lastly, we will discuss the possibilities of modifying therapeutically acquired epigenetic tags, summarizing currently available agents and speculating on future directions.

This work is partly presented at International Conference on STRUCTURAL BIOLOGY AND PROTEOMICS