Commentary
Volume 7:5, 2023

Journal of Genetics and DNA Research

ISSN: 2684-6039 Open Access

DNA Methylation in Gene Regulation, Disease, and Environmental Influences

Lisa Moore*

Department of Human Genetics, David Geffen School of Medicine, University of California, Los Angeles, USA

Description

DNA methylation is a crucial epigenetic modification that occurs in all living organisms. It is a process that involves the addition of a Methyl group ($-CH_3$) to the cytosine base of DNA, which alters the way that the DNA is read and transcribed. DNA methylation is an essential mechanism for gene regulation and plays a vital role in many biological processes, including development, differentiation, and disease.

DNA methylation is carried out by a group of enzymes known as DNA Methyltransferases (DNMTs). These enzymes transfer a methyl group from S-Adenosylmethionine (SAM) to the fifth carbon atom of the cytosine ring, producing 5-methylcytosine (5 mC). Methylation typically occurs in CpG dinucleotide, where a cytosine is followed by a guanine, but it can also occur in non-CpG sites.

DNA methylation is a stable modification that can be inherited from one cell generation to the next. During cell division, the methylation pattern is maintained by a process called maintenance methylation, where the newly synthesized DNA strand is methylated by DNMT 1 to match the methylation pattern of the parental strand.

The function of DNA methylation in gene regulation is complex and varies depending on the location and context of the methylation. In general, methylation of promoter regions, which are typically located up-stream of the transcription start site, is associated with gene repression. Methylation of enhancer regions, which are typically located upstream or downstream of the transcription start site, can either enhance or repress gene expression, depending on the specific enhancer and the genes it regulates.

In addition to gene regulation, DNA methylation also plays a crucial role in genomic imprinting, X-chromosome inactivation, and transposon silencing. Genomic imprinting is a process where specific genes are expressed depending on whether they are inherited from the mother or the father. DNA methylation at imprinted genes plays a critical role in maintaining the parent of origin specific gene expression. X-chromosome inactivation is a process that occurs in females to equalize the expression of X-linked genes with males. DNA methylation of the X-chromosome is required for proper X-inactivation. Transposon silencing is the process of silencing transposable elements, which are mobile genetic elements that can cause genomic instability if left unchecked. DNA methylation plays a critical role in the silencing of transposable elements.

Aberrant DNA methylation patterns have been associated with many human diseases, including cancer, neurodegenerative disorders, and autoimmune diseases. In cancer, global hypo methylation, which is a reduction in overall DNA methylation levels, and hyper methylation of specific promoter regions have been observed. Global hypo methylation can cause genomic instability and activation of oncogenes, while hyper methylation of tumor suppressor genes can lead to their silencing and contribute to cancer development. In neurodegenerative disorders, DNA methylation changes have been observed in the brains of affected individuals, and in some cases, the DNA methylation changes are specific to certain regions of the brain. In auto-immune diseases, DNA methylation changes have been observed in immune cells, and these changes may contribute to the dysregulation of the immune system.

DNA methylation is a dynamic process that can be influenced by a variety of factors, including environmental exposures, diet, and lifestyle. For example, exposure to environmental toxins, such as cigarette smoke, can alter DNA methylation patterns in the lungs and increase the risk of lung cancer. Diet and lifestyle factors, such as folate intake and exercise, have also been shown to influence DNA methylation patterns.

How to cite this article: Moore, Lisa. "DNA Methylation in Gene Regulation, Disease, and Environmental Influences." *J Genet DNA Res* 7 (2023): 171.

***Address for Correspondence:** Lisa Moore, Department of Human Genetics, University of California, Los Angeles, USA; E-mail: Moore.lisa@gmail.com*

Received: 06 May, 2023, Manuscript No. JGDR-23-97964; **Editor assigned:** 09 May, 2023, PreQC No. JGDR-23-97964 (PQ); **Reviewed:** 24 May, 2023, QC No. JGDR-23-97964; **Revised:** 06 July, 2023, Manuscript No. JGDR-23-97964 (R); **Published**: 14 July, 2023, DOI: 10.37421/2684-6039.2023.7.171

(MRPFT)