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DNA Methylation: An Overview

Leena Cindy*

Department of Biotechnology, Adhiyamaan College of Engineering, Hosur, Tamil Nadu, India

Introduction

An epigenetic 'code' modifies gene-expression patterns by permitting or restricting the transcriptional potential of genomic regions based on the pattern of DNA and histone modifications. Histone alterations, specifically the absence of histone H3 lysine 4 methylation (H3K4me0) and the presence of H3K9 methylation, are linked to DNA methylation. The functional significance of domain design in the processes linking histone methylation and DNA methylation in mammalian cells are discussed in this article. The H3K4me0-interacting ADD domain of the DNA methyltransferase DNMT3a and its accessory protein Dnmt 3L connects the DNA methylation process with unmodified H3K4. The CpG-interacting CXXC domain of the H3K4 methyltransferase MLL1 may connect the H3K4 methylation response to unmethylated DNA. SET1, another H3K4 methyltransferase that lacks an inherent CXXC domain, interacts directly with the similar domain-containing accessory protein CFP1. The putative MBD in the H3K9 methyltransferase SETDB1 may interact with the MBD-containing protein MBD1 to link the H3K4 methylation process to methylated DNA. Finally, we look at the domain structure of the DNA methyltransferase DNMT1, its accessory protein UHRF1, and their associated proteins, and propose a mechanism for coordinating DNA methylation and histone methylation during mitotic cell division, allowing parental DNA to be transmitted while histone methylation patterns are copied to newly replicated chromatin [1,2].

Description

Methylation of DNA, RNA, and proteins is involved in a variety of cellular processes and is linked to a variety of differentiation events, physiological activities, and human disorders. This review gives a compact yet comprehensive overview of methylation at many levels, including the mechanisms, cross-talking, and clinical consequences, with a special focus on malignancies, to help in the diagnostic and therapeutic design for cancer treatment using methylation. We conclude that DNA methylation is the only kind of methylation that has been widely adopted in clinics and is mostly employed for early detection. The translation of RNA and protein methylation's oncotherapeutic and prognostic values into clinical usage requires a lot of work [3].

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Conclusion

These treatments are frequently quite precise and consequently only work in a fraction of cancer patients. This has raised the necessity for the physician to determine the therapeutic method that benefits the patient the most while also avoiding overtreatment. This condition has a significant influence on diagnostic tumour pathology procedures, as it necessitates precise pre-therapeutic tumour characterisation to enable clinical case management. Aberrant DNA methylation within gene regulatory areas, which affects a number of genes with varied functions, is a common and early occurrence in cancer.

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***Address for Correspondence:** Leena Cindy, Department of Biotechnology, Adhiyamaan College of Engineering, Hosur, Tamil Nadu, India; E-mail: leena.c@gmail.com*

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