



DNA Methylation in Cancer: Review

Sidhartha Singh, Deepika Rai^{*}, Ayush Praveen

G.B. Pant Engineering College, Pauri-Garhwal, U.K.-246194, India

Address for Correspondence: Deepika Rai; dipikarai@gmail.com

ABSTRACT: Mammalian genome has a profound effect of DNA methylation or covalent addition of a methyl group to cytosine with reference to CpG dinucleotide. These modifications are very stable but reversible. The effect of mutation of a number of Tumor suppressor gene (TSGs) can be mimicked by the change in methylation of promoter. Hypomethylation and hypermethylation of promoter of proto-oncogenes are aberrations of genomic DNA which can result in carcinogenesis. Proper embryonic development also requires DNA methylation. Global hypomethylation has been found to disrupt the normal methylation pattern in cancer cells along with region specific hypermethylation. If the promoter of a TSG are involved in hypermethylation event then silencing of that gene occurs which in turn gives cell a growth advantage in a manner similar to mutations. However the transcription of retrotransposons, protooncogene and gene involved in the malignant cell metastasis has been observed to be activated if the event of hypomethylation occurs. A high level of DNA methyltransferase DNMT1 and DNMT3B which plays a crucial role in the catalysis of methylation of genomic DNA in malignant cells is present in different types of cancers. This review will provide an overview of cancer, methylation, its various types, what leads to the malfunction in certain gene due to methylation and various methods how DNA methylation occurs which leads to oncogenesis. © 2014 iGlobal Research and Publishing Foundation. All rights reserved.

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