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AWARENESS ABOUT METHYLATION VIA REPAIR MECHANISMS AMONG ALLIED HEALTH SCIENCE STUDENTS

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Abstract

Introduction: The concept of DNA methylation and its function in normal cells, and to explain the possible mechanisms as to how abnormalities in this phenomenon can relate to carcinogenesis. Cytosine methylation is an epigenetically propagated DNA modification that can modify how the DNA molecule is recognized and expressed. DNA methylation undergoes extensive reprogramming during mammalian embryogenesis and is directly linked to the regulation of pluripotency and cellular identity. Aim: This survey was conducted for assessing the awareness about loss of methylation via repair of mechanisms amongst AHS students. Materials and methods: A cross section research was conducted with a self -administered questionnaire containing ten questions distributed amongst 100 ahs students.the questionnaire assessed the awareness About loss of methylation via repair of mechanisms. The responses were recorded and analysed. Result: 97.1% of respondents were aware of loss of methylation via repair of mechanisms. 67% of respondents were aware of effect of methylation. 77.7% of respondents were aware of Russell silver syndrome. 76.7% of respondents were aware of the role of methylation. 86.4% of respondents were known that the loss of methylation is an epigenetic change is true. Conclusion: There is a good awareness amongst allied health sciences students about loss of methylation via repair of mechanisms. However ,enhanced awareness initiatives and educational programmes together with increased importance for curriculum improvement that further promote knowledge and awareness of the loss of methylation via repair of mechanisms should be initiated for further understanding and benefit.

Keywords: Awareness, Loss of Methylation, Students.

INTRODUCTION

Cytosine methylation is an epigenetically propagated DNA modification that can modify how the DNA molecule is recognized and expressed. DNA methylation undergoes extensive reprogramming during mammalian embryogenesis and is directly linked to the regulation of pluripotency and cellular identity. Studying its regulation is also important for a better understanding of the many diseases that show epigenetic deregulations, in particular, cancer. In the recent years, a lot of progress has been made to characterize the profiles of DNA methylation at the genome level, which revealed that patterns of DNA methylation are highly dynamic between cell types[1].

DNA methylation occurs on cytosines and is essential for mammalian development. DNA methylation undergoes extensive reprogramming during embryogenesis.

DNA methylation is regulated by DNA binding factors, chromatin and non-coding RNAs. 5-Hydroxymethylcytosine might be an intermediate of demethylation[2].

The regulation of complex eukaryotic genomes entails not only sequence-specific DNA-binding factors, but also additional levels of regulation such as DNA modifications, histone post-translational modifications and chromatin remodeling. These modifications are often referred to as being “epigenetic” although some of them have not been shown to fulfill the strict definition of epigenetics, which implies a heritability through mitosis or meiosis [3].

During development and cellular differentiation, these epigenetic marks undergo dynamic changes that ultimately contribute to produce and maintain distinct cell types of an organism . Elucidating how these epigenetic marks participate in the regulation of cellular identity is crucial to better understand embryonic development and the etiology of many diseases[4].

Methylation is the most abundant epigenetic modification that directly affects the DNA molecule in eukaryotes. It consists in the addition of a methyl group on the carbon 5 of the cytosine, thereby creating 5-methylcytosine (5mC), and is catalyzed by enzymes of the DNA methyltransferase (DNMT) family[5].This survey was conducted for assessing the awareness about loss of methylation via repair of mechanisms amongst AHS students.

MATERIALS AND METHODS

This cross section was conducted with a self administered questionnaire Containing ten questions distributed amongst hundred allied health science students.the students randomly selected across various disciplines of allied health science students.the study setting was designated in the university campus.the survey instrument was a questionnaire pre tested and evaluated for validity and relatively concerned.

The questionnaire included ten questions selected for the democratic data throw open ended response and multiple choice questions for the other responses. The study was approved by the institutional ethical committee and informed concern was obtained from the participants. The questionnaire was posted on an online platform and the identity of the responses was kept confidential.

The questionnaire assesses the awareness about loss of methylation via repair of mechanisms among allied health science students. The responses were recorded and analyzed. There was no incomplete response and no drop out from the study; the final data option was tableted, organised and subjected to statistical analysis.

The salient questions in the study are

1. Are you aware of loss of methylation via repair of mechanisms?
2. Are you aware of the effect of methylation?
3. Are you aware of Russell silver syndrome?
4. Are you aware of the role of methylation?
5. Loss of methylation is an epigenetic change is true or false?

RESULTS

97.1% of respondents were aware of loss of methylation via repair of mechanisms. 67% of respondents were aware of effect of methylation. 77.7% of respondents were aware of Russell silver syndrome. 76.7% are aware of the role of methylation. 86.4% of respondents were known that the loss of methylation is an epigenetic change is true.

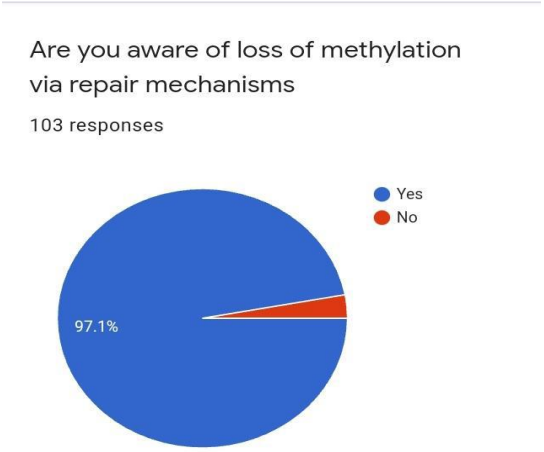

Figure 1: Awareness of loss of methylation via repair of mechanisms?

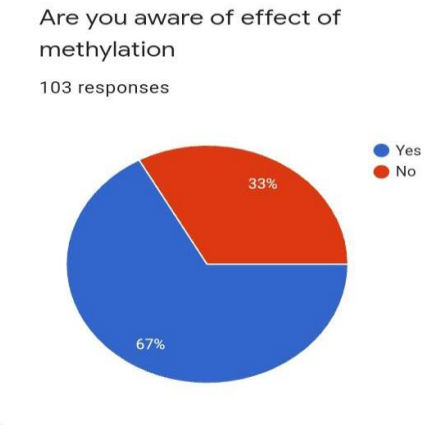

Figure 2: Awareness of effect of methylation?

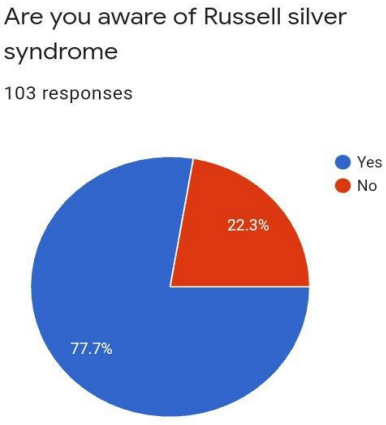

Figure 3: Awareness of Russell silver syndrome?

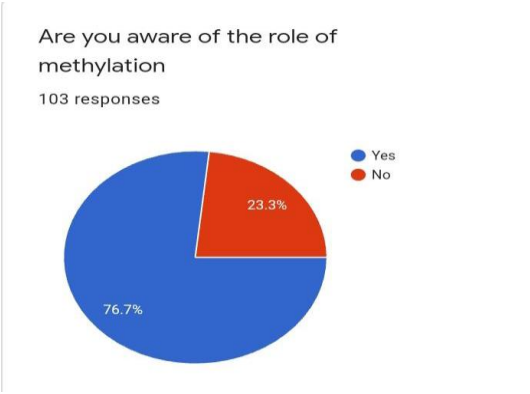

Figure 4: Awareness of the role of methylation?

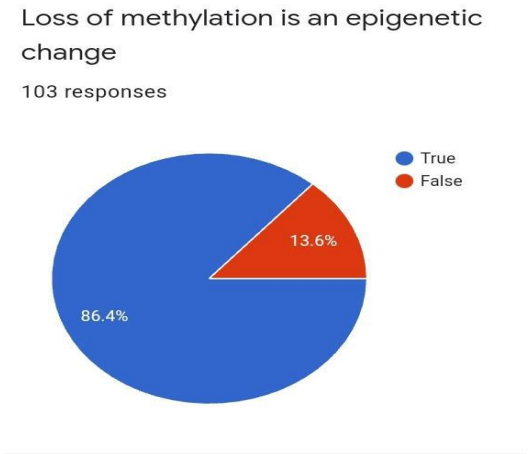

Figure 5: Loss of methylation is an epigenetic change?

DISCUSSION

DNA damage has been long recognized as causal factor for cancer development. When erroneous DNA repair leads to mutations or chromosomal aberrations affecting oncogenes and tumor suppressor genes, cells undergo malignant transformation resulting in cancerous growth. Genetic defects can predispose to cancer: mutations in distinct DNA repair systems elevate the susceptibility to various cancer types[6]. 97.1% of respondents were aware of loss of methylation via repair of mechanisms.

DNA damage not only comprises a root cause for cancer development but also continues to provide an important avenue for chemo- and radiotherapy. Since the beginning of cancer therapy, genotoxic agents that trigger DNA damage checkpoints have been applied to halt the growth and trigger the apoptotic demise of cancer cells. An overview about the involvement of DNA repair systems in cancer prevention and the classes of genotoxins that are commonly used for the treatment of cancer[7]. 67% of respondents were aware of effect of methylation

Cytosine methylation is generally viewed as a repressive mark that inhibits transcriptional initiation, either by preventing the binding of certain transcription factors, or by recruiting methyl-binding proteins (MBPs) and generating a repressed chromatin environment. These patterns of DNA methylation can be stably propagated during cell division, which makes it a paradigm for epigenetic regulation that can

mediate long lasting changes in gene expression even when the initial triggering signal has disappeared[8]. 77.7% of respondents were aware of Russell silver syndrome

In addition, profiles of DNA methylation are perturbed in many diseases, in particular all types of cancer that show both genome-wide hypomethylation and aberrant hypermethylation of tumor-suppressor genes or non-coding RNAs . An illustration of the key roles of DNA methylation in cancer is that mutations in some of the enzymes that methylate (DNMT3A) and hydroxymethylation (TET2) DNA are frequent in leukemia[9]. 76.7% are aware of the role of methylation.

Cytosine methylation is found in many species of the plant, fungi and animal kingdoms, but has apparently undergone a very complex evolutionary history. In fungi for example, cytosine methylation is absent in Saccharomyces cerevisiae but present in other species such as Neurospora crassa. Similarly, in insects, cytosine methylation is absent in Drosophila melanogaster but present in the honey bee Apis mellifera[10] .86.4% of respondents were known that the loss of methylation is an epigenetic change is true

CONCLUSION

There is good awareness amongst allied health sciences students about loss of methylation via repair of mechanisms. However ,enhanced awareness initiatives and educational programmes together with increased importance for curriculum improvement that further promote knowledge and awareness of the loss of methylation via repair of mechanisms should be initiated for further understanding and benefits.

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