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AWARENESS ABOUT GENOMIC INSTABILITY VIA HYPOMETHYLATION OF LINE 1 AMONG ALLIED HEALTH SCIENCES STUDENTS

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Abstract

Introductıon: Intestinal and colorectal cancers are multifactorial diseases with various inputs including diet, environment, genetic mutations, and epigenetic abnormalities. The disease first manifests as an over-proliferation defect in the form of polyps that, if not removed, can progress to precancerous adenomas. Aım: This survey was conducted for assessing the awareness about genomic instability via hypomethylation of LINE 1 among allied health Sciences students. Materıals and Methods: This cross-sectional research was conducted with a self-administered questionnaire containing ten questions distributed amongst 100 Allied Health science students.The students were randomly selected across various disciplines of Allied Health Sciences.The study setting was designated in the university campus.The survey instrument was a questionnaire pre tested and evaluated for validity and reliability concerns. Results: 84.5% of the respondents were aware about genomic instability and hypomethylation of line 1. 69.8% of the respondents were aware about DNA hypomethylation. 70.7% of the respondents were aware about hypomethylation increase gene expression. 72.4% of the respondents were aware about genomic stability is important. 69% of the respondents were aware about DNA include RNA. 69% of the respondents were aware about radiation cause damage to DNA. Conclusıon: There is moderate awareness amongst allied health Sciences student about genomic instability via hypomethylation of LINE 1. Enhanced aware initiatives and educational programs together with iincreased importance for curriculum improvements that future promote knowledge and awareness of genomic instability via hypomethylation of LINE

Keywords: Awareness, Health Science, DNA, Hypomethylation.

INTRODUCTION

Ionizing radiation is a well-known carcinogen resulting in a large spectrum of DNA lesions, including double-strand breakages (DSB). Radiation-induced genomic instability (RIGI) is a driving force underlying radiation carcinogenesis. Several experiments support a new paradigm of radiation biology in which RIGI can be transmitted from the surviving cell through multiple cell generations to be expressed in the progeny as a delayed and persistent effect[1].

The delayed aneuploidy--numerical chromosome aberrations are induced by low doses of x-radiation in human fibroblasts. Fifty and 100 mGy of x-rays induce delayed aneuploidy of chromosomes 1 and 4 in the progeny of irradiated fibroblast cells. Therefore, unexpected health effects likely result from delayed genomic instability after

radiation exposure, raising concerns regarding the most appropriate dose limit for radiation exposure in both the public and industrial workers[2].

Furthermore, delayed genomic instability can partially explain the mechanisms underlying radiation-induced carcinogenesis, which is poorly understood. However, despite the important implications associated with the biological effects of low-dose ionizing radiation and the impact on radiation safety and protection protocols, there are very few studies regarding delayed genomic instability after low-level radiation exposure among the general population or radiographers[3].

Genome-wide epigenetic alterations are known to hold substantial potential as biomarkers for environmental exposures; this, in turn, may provide insight into mechanisms of environmentally related diseases and allow for a better understanding of disease etiology. DNA methylation, a well-defined epigenetic mechanism, plays an important role in cancer development by adding or removing methyl (-CH3) groups at CpG dinucleotides, which influences gene regulation[4].

Genomic DNA hypomethylation resulting from demethylation in repeats or transposable elements or across the genome is associated with genomic instability, an increased number of mutational events, and subsequent development of cancer. In particular, some studies report that changes in genomic DNA methylation are associated with a striking form of genomic instability known as chromosome instability, including centromeric aberrations, chromosome aberrations, and aneuploidy[5]

MATERIALS AND METHODS

This cross-sectional research was conducted with a self-administered questionnaire containing ten questions distributed amongst 100 Allied Health science students.The students were randomly selected across various disciplines of Allied Health Sciences.The study setting was designated in the university campus.The survey instrument was a questionnaire pre tested and evaluated for validity and reliability concerns. The questionnaire included ten questions eliciting the demographic data through open ended responses and multiple choice questions for the other responses.The study was approved by the Institutional Ethical Committee and informed consent was obtained from the Participants. The questionnaire was posted in an online platform and the identity of the respondents were kept confidential.

The questionnaire assessed the awareness about Genomic Instability and hypomethyliation of LINE 1. The responses were recorded and analysed. There were no incomplete responses and no dropouts from the study. The final data obtained was organized, tabulated and subjected to statistical analysis. The salient questions in the study are:

1. Are you aware of genomic instability and hypomethylation of line 1?
2. Are you aware of DNA hypomethylation?
3. Does hypomethylation increase gene expression?
4. Do you think genomic stability is important?
5. Does DNA include RNA?
6. Does radiation cause damage to DNA?

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RESULTS

84.5% of the respondents were aware about genomic instability and hypomethylation of line 1. 69.8% of the respondents were aware about DNA hypomethylation. 70.7% of the respondents were aware about hypomethylation increase gene expression. 72.4% of the respondents were aware about genomic stability is important. 69% of the respondents were aware about DNA include RNA. 69% of the respondents were aware about radiation cause damage to DNA.

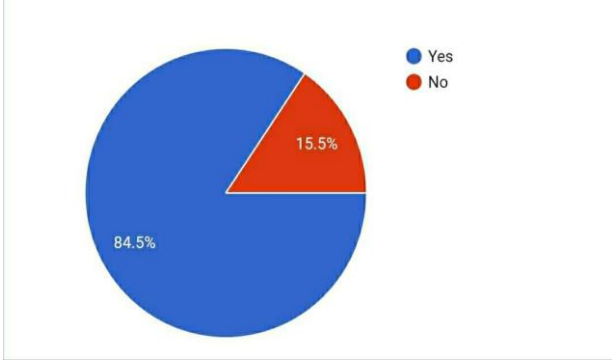

Figure 1: Awareness about genomic instability and hypomethylation of line 1

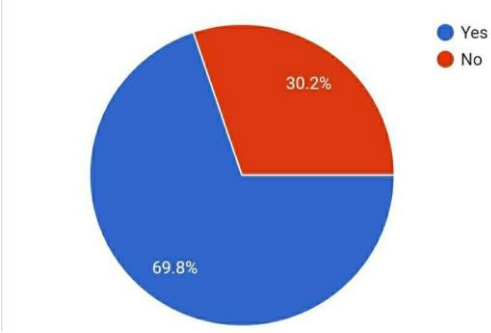

Figure 2: Awareness about DNA hypomethylation

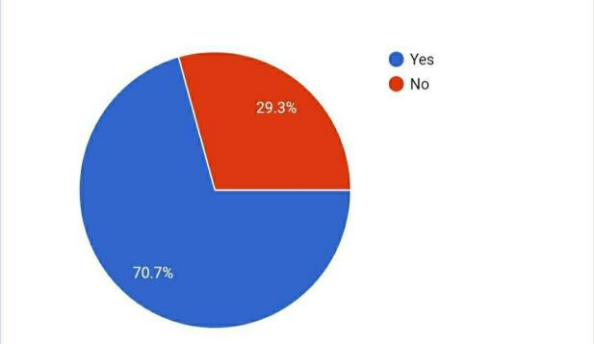

Figure 3: Awareness about hypomethylation increase gene expression

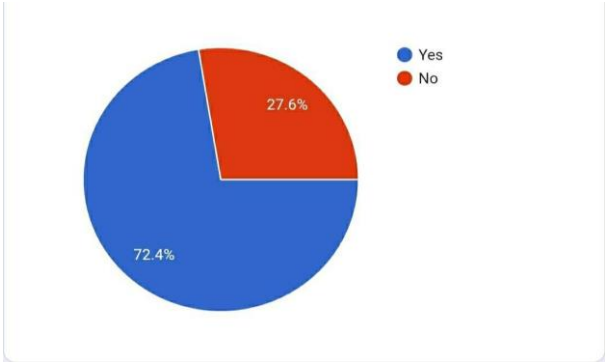

Figure 4: Awareness about genomic stability is important

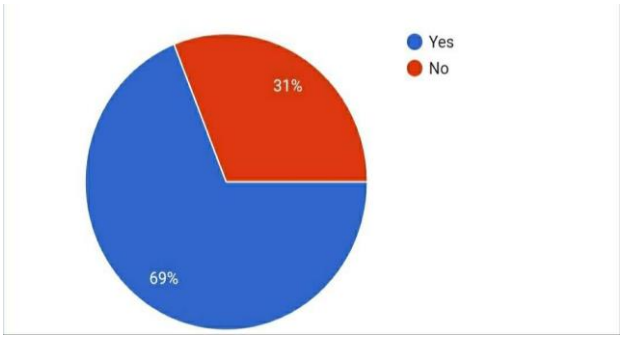

Figure 5: Awareness about DNA include RNA

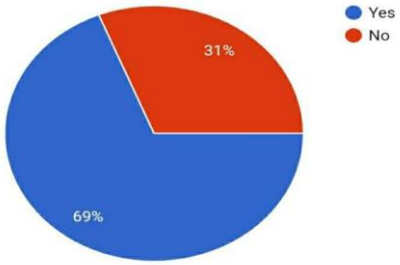

Figure 6: Awareness about radiation cause damage to DNA

DISCUSSION

Long interspersed element-1 (LINE-1) is a repetitive DNA retrotransposon that duplicates via a copy-and-paste genetic mechanism. As LINE-1 constitutes approximately 17% of the human genome, the extent of LINE-1 methylation is regarded as a surrogate marker of global DNA methylation[6]. 84.5% of the respondents were aware about genomic instability and hypomethylation of line 1.

DNA hypomethylation refers to the loss of the methyl group in the 5-methylcytosine nucleotide. Methylation is a natural modification of DNA, and mainly affects the cytosine base (C) when it is followed by a guanosine (G) in mammals (Methylation)[7]. 69.8% of the respondents were aware about DNA hypomethylation.

Although downregulation of gene expression was found to be the most pronounced effect of hypermethylation in the present study, we also show that hypermethylation in the promoter region can be associated with upregulation of gene expression[8]. 70.7% of the respondents were aware about hypomethylation increase gene expression.

When DNA is methylated, nearby histones are deacetylated, resulting in compounded inhibitory effects on transcription. Likewise, demethylated DNA does not attract deacetylating enzymes to the histones, allowing them to remain acetylated and more mobile, thus promoting transcription[9]. 72.4% of the respondents were aware about genomic stability is important.

DNA methylation is essential for silencing retroviral elements, regulating tissue-specific gene expression, genomic imprinting, and X chromosome inactivation. Importantly, DNA methylation in different genomic regions may exert different influences on gene activities based on the underlying genetic sequence[10].69% of the respondents were aware about radiation cause damage to DNA.

CONCLUSION

There is moderate awareness amongst allied health Sciences student about genomic instability via hypomethylation of LINE 1. Enhanced aware initiatives and educational programs together with iincreased importance for curriculum improvements that future promote knowledge and awareness of genomic instability via hypomethylation of LINE

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