



Epigenetics Impacts on Human Diseases

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Received: 02-Jun-2023, Manuscript No. IRJBB-23-103024; Editor assigned: 05-Jun-2023, PreQC No. IRJBB-23-103024 (PQ); Reviewed: 19-Jun-2023, QC No. IRJBB-23-103024; Revised: 23-Jun-2023, Manuscript No. IRJBB-23-103024 (R); Published: 30-Jun-2023, DOI: 10.14303/2250-9941.2023.56

Abstract

Epigenetics is the study of how environmental factors and behaviour may alter how your genes function. While epigenetic alterations are reversible and do not alter your DNA sequence like genetic changes do, they can alter how your body interprets a DNA sequence.

Keywords: DNA, RNA, Histone, Chromatin, Epigenetic enzyme, HAT, HDAC, Epigenetics, Chronic disease

INTRODUCTION

The field of epigenetics investigates how cells regulate gene function without altering the DNA sequence. In Greek, "epi-" means on or above and "epigenetic" refers to variables other than the genetic code. Epigenetic alterations to DNA control whether or not genes are activated. These alterations are connected to DNA and do not alter the order in which the DNA building blocks are arranged. The epigenome, which is all of the changes that control how genes are expressed inside a cell's whole set of DNA, is referred to as the genome. An area of research termed epigenetics, sometimes known as epigenomics, focuses on DNA modifications without affecting the underlying sequence. The degrees to which genes are switched on and off can be altered chemically in the DNA letters and proteins that interact with DNA. During cell division or from one generation to the next, certain epigenetic alterations may be transferred from parent cell to daughter cell. The term "epigenome" refers to the collection of all epigenetic alterations in a genome (Yang et al., 2005).

Both the proteins that interact with a particular gene and the DNA letters in a gene are present. Both have a chemical alteration that control the ways, places, and times the gene is switched on and off. The field of epigenetics, also known as epigenomics, investigates the potential genetic transmission of certain epigenetic alterations. The term "epigenome" refers to the collection of all epigenetic alterations in a genome (Carel et al., 2009).

Epigenetic modifications affect the synthesis of proteins in cells by influencing the decision of which genes are activated

or inactive. Each cell only generates the proteins required for it to operate thanks to this control. For instance, muscle cells do not create the proteins that support bone formation. Epigenetic alteration patterns range across people, between tissues within a person, and even between individual cells within a tissue. The epigenome can be impacted by environmental factors including a person's nutrition and exposure to contaminants. When cells divide, epigenetic alterations can be preserved from cell to cell and, in certain situations, passed down through the generations (Konforte et al., 2013).

The study of epigenetics, a branch of biology that is expanding quickly, focuses on changes in gene expression that don't result from changes in DNA sequence but rather from chemical alterations of DNA and the proteins that bind to it. Gene expression, cell differentiation, tissue development, and disease susceptibility can all be significantly influenced by epigenetic pathways. To clarify the processes underpinning the increasingly acknowledged significance of environmental and lifestyle variables in health and disease as well as the intergenerational transfer of phenotypes, understanding an epigenetic alteration is crucial (Davis et al., 2006). Epigenetics may play a key role in a number of illnesses, including cancer, cardiovascular disease, and problems of neurodevelopment and neurodegeneration, according to recent research. Epigenetic alterations have the potential to be reversible and might open up new therapeutic paths for employing epigenetic modulators to treat various disorders. Additionally, epigenetics offers information on the pathophysiology of diseases as well as biomarkers for

illness diagnosis and risk assessment (Zec et al., 2012). However, epigenetic treatments may have unintended repercussions and raise the chance of unanticipated events, such as cancer, unfavourable medication responses, and developmental abnormalities. Thus, thorough research is necessary to reduce the hazards connected with epigenetic treatments and to provide secure and efficient interventions for enhancing human health (Elmlinger et al., 2005).

Epigenetics and human diseases

Methylation is a frequent and popular method for altering the epigenetic state of cells. Numerous human diseases have been linked to it, including various malignancies, immunological conditions, neurological disorders (including schizophrenia and the Fragile X syndrome as well as Huntington, Alzheimer, and Parkinson diseases), and tumours. Additionally, it has been proposed that methylation may be taken into account for complex disorders affected by various tertiary variables, such as sex differences and age, which may alter the severity of the ailment (Soldin et al., 2005).

Cancer is significantly impacted by epigenetic changes. Many tumour suppressor activities can be rendered inactive by hyper methylation of promoter regions of tumour suppressor genes. Aside from cell division, DNA repair, differentiation, apoptosis, angiogenesis, metastasis, growth factor response, detoxification, and drug resistance, methylation levels also play a significant role in these processes. These characteristics have greatly advanced the use of methylation levels in the early identification of cancer (Owen et al., 2010). For instance, promoter hyper methylation in the APC and RASSF1A genes is regarded as a typical epigenetic marker for cancer early detection. Additionally, it has been shown that hyper methylation of the TP53 promoter area is a frequent sign for assessing the progression of cancer. Additionally, there are several other epigenetic modifications in cancer. The deregulation of miRNAs, which has the potential to be utilised as diagnostic biomarkers, has been established in recent years in breast cancer. Multiple genes' hyper- and hypo-methylation in breast cancer has also been confirmed (Elmlinger et al., 2002).

A complicated inflammatory disease of the airways and alveoli, COPD is influenced by both hereditary and environmental variables in its aetiology. Additionally, COPD serves as a potent illustration of how environmental factors, such as cigarette smoke, affect the (de)regulation of gene expression in people. The first study on the impact of cigarette smoke on chromatin remodelling in airways was published in the early 2000s, and it showed that smoking reduced HDAC2's ability to suppress the production of cytokines that are pro-inflammatory. After then, a slew of publications were released that gave additional information regarding the epigenetic process causing COPD inflammation and discussed how an imbalance in histone acetylation/de-acetylation played a significant role. Smokers had higher NF-

kB expression levels while having lower HDAC2 expression levels. Additionally, smoking reduces SIRT1 expression, which is a key regulator of NF-kB activity. SIRT1 activation has been suggested as a possible COPD therapy method. In this case, HATs and NF-kB collaborate to promote histone acetylation. Collectively, these occurrences cause inflammatory genes to express themselves in an unchecked manner (Chan et al., 2009).

CONCLUSION

The epigenetic landscape is only slightly explored in this essay. However, it encapsulates the key ideas in the area: the beginning, how DNA is arranged in chromatin, how DNA and proteins linked with it undergo secondary and regulatory changes, which enzymes control chromatin activity, and how these alterations affect gene expression. Finally, we emphasised the idea that epigenetics may be a useful source for creating new medications for the treatment of chronic diseases and gave a few instances. The epigenetic modification of non-histone proteins, the involvement of metabolites in the activity of epigenetic enzymes, and the epigenetic role of RNA, which includes miRNAs and long-non-coding RNAs, are just a few of the many pertinent features that were discovered. We do think that this article could provide practitioners a taste of epigenetics and its potential to advance medicine, though. With the promise of new strategies for healthy ageing soon arriving, much more is anticipated in the upcoming years where epigenetics is viewed as the key source of information in the study area on ageing and aging-associated disorders.

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