Annals of Case Reports and Clinical Studies

Salient Visionary Publications

Research Article (ISSN: 2832-5788)

# Investigating the Role of Epigenetics in Disease Development Diagnosis and Progression

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**Citation:** *Kotha R. Investigating the Role of Epigenetics in Disease Development Diagnosis and Progression. Ann Case Rep Clin Stud. 2024;3(2):1-8.*

**Received Date:** 22 March, 2024**; Accepted Date:** 26 March, 2024**; Published Date:** 29 March, 2024

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## ABSTRACT

Epigenetics entails studying the mechanisms through which cells regulate and control gene activity without altering the sequence and structure of the DNA. It involves studying factors beyond the genetic code, such as an individual's behavior, exercise, and the environment. These factors result in DNA changes and modifications that determine whether genes are turned on or off. Epigenetic modification is composed of three main processes: DNA methylation and demethylation, histone alteration and non-modification, and coding RNA silencing. Epigenetic modifications also result in the growth and advancement of various illnesses in multicellular organisms, such as cancers, autoimmune diseases, diabetes, and neurological disorders such as Fragile X syndrome, Huntington's, Alzheimer's, Parkinson's disease, and schizophrenia. Since reversible genetic modifications cause these disorders, epigenetic treatments can counter them. These treatments mainly alter DNA methylation and Histone acetylation. Though coding DNA was only two percentage, the majority of the DNA was regulatory DNA, which changed the genetic code due to environmental pressures. These changes are very useful, particularly the regularization of organ-specific functions by suppressing other functions in specific organs. But in certain situations, these changes may be harmful. For example, stress due to urbanization may transfer to future generations. In the descendants of Holocaust survivors that result in a marked increase of post-traumatic stress disorder, depression, and obesity, all resulting from differential methylation of the FKBP5 gene. The majority of preterm deliveries, which were pushed by nature, will have obesity and hypertension, which will trnsver in the form of epigenitics to future generation to decrease the lifespan of human. This may be a single step in the future evaluation process.

**Keywords:** Epigenetics; Environment; Disease progression; DNA methylation; Histones; RNA interference

Research Article (ISSN: 2832-5788)

## INTRODUCTION

Epigenetics is an essential aspect of today's world. It entails studying the mechanisms through which cells regulate and control gene activity without altering the sequence and structure of the DNA. “Epi” is a Greek term meaning above or beyond. “Epigenetic” involves studying factors beyond the genetic code, such as an individual's behavior, exercise, and environment[1]. These factors result in DNA changes and modifications determining whether genes are switched on or of[2]. While these genetic changes are attached to the DNA, they are reversible and do not alter the structure and sequence of the DNA or its building blocks. However, they can change how DNA sequences are read within the body. For example, the font will change, but not the words in the textbook. On the other hand, the epigenome is the set of changes that control gene expression within a complete DNA set or genome. Epigenetic modifications, as mentioned earlier, impact the switching on or off of genes; thus, they significantly impact the production of proteins within the cells through gene expression. They ensure that the proteins functional for the cell are produced. If only the environment alone is responsible for evaluation, as per Darwin, it may take much more time. The environment, through epigenetics, will change the species as per necessity. Stochastic epigenetic variation, also known as spontaneous epimutations, can maintain phenotypic variety. Sickl e cell anemia is more fortunate in areas where malaria is predicted, but after human intervention in malaria control, sickle cell anemia turns into a curse[3]. This is because nature is more intelligent and will protect its offspring. In many situations, though we are much more advanced, we are unable to overcome nature. We should respect nature.

The fact that epigenetic gene regulation in disease states is a nonmutational and reversible process makes it, at le ast in theory, amenable to therapy, which is another clear practical reason to investigate it. In this article, we briefly explain how epigenetics will cause disease and how we will investigate them to counteract it.

## LITERATURE REVIEW

### Examples of Epigenetic Modifications

Epigenetic modification ensues in patterns that are unique to each individual. These patterns also differ within various tissues in the same individual and cells in the same tissue. These modifications in multicellular organisms enable different cells to express specific genes. These genes are not only necessary in each cell type but also enable the spread of data to the offspring[4]. Numerous epigenetic changes in multicellular organisms involve epigenetic processes such as paramutations, bookmarking, gene silencing, X chromosome inactivation, cloning, and heterochromatin states. Epigenetic modification is composed of three main mechanisms: DNA methylation and demethylation, histone modification and non-modification, and RNA silencing coding.

### DNA Methylation and Demethylation

DNA Methylation ensues at the CpG sites by mediating DNA methyltransferase enzymes. These enzymes consist of DNMT1, DNMT3a, and DNMT3b. It entails adding methyl groups to the building blocks of DNA. Methyl

groups are small chemical groups consisting of one carbon atom and three hydrogen atoms, and they are donated by S-adenosyl methionine in the cells[5]. Upon attachment to the gene, these methyl groups silence or switch it "off" since they reduce gene expression by blocking transcription elements from binding to enhance protein formation. They also prevent protein production from the gene by enhancing the binding of methyl-CpG-binding proteins. DNA Methylation can be reversed through demethylation, thus turning the gene. Loss of methylation can cause abnormally high gene activation by altering chromatin arrangement, while too much methylation can undo the work of protective tumor suppressor genes. Fragile X syndrome is the most common inherited mental disability, especially in males, affecting around 1 in 4,000 males and 1 in 8,000 females. It is caused by an abnormality in the FMR1 gene, which causes CpG islands in the promoter region to become methylated. This methylation stops the FMR1 gene from producing the fragile X mental retardation protein, which is essential for the disorder[6].

## Histone Modification and Non-Modification

Histones are structural proteins found in the cell's nucleus, forming an essential component of DNA structure. The DNA wraps around them to assume their shape. Histone modification is a mechanism of gene regulation through a process termed chromatin remodeling. It entails mechanisms such as methylation, acetylation, phosphorylation, and ribosylation[7]. Methylation and acetylation entail adding methyl or acetyl elements to histones, while phosphorylation and ribosylation involve adding phosphate and ribose groups. Acetylation, for instance, is mediated by acetyltransferase enzymes in the histones. Acetyl groups have two carbons, three hydrogens, and an oxygen atom in their structure. Adding these chemical groups results in the tight packing of DNA, preventing the proteins that "read" genetic codes during protein formation from accessing the DNA, thus switching it "off." On the contrary, when not added, DNA is loosely packed, thus exposing the proteins that read the genetic codes during protein formation, which turns the gene "on."The methylation of a specific lysine on histone H3 (K9) is found throughout heterochromatin, marking silent DNA[7]. This kind of epigenetic change is responsible for the inactivation of one X chromosome in females[8].

## Non-Coding RNA

Both coding and non-coding RNA are manufactured through orders given by the DNA. Coding RNA is helpful in protein synthesis, while non-coding RNA regulates gene expression. It attaches to the coding RNA alongside other chemical groups, thus breaking it and preventing protein synthesis[9]. It also recruits other proteins, thus modifying histones and turning the gene "on" or "off." Epigenetic modifications are maintained as the cells multiply, and some are inherited from generation to generation. However, they can be altered by various factors, such as environmental influences, an individual's diet, and exposure to pollutants such as ultraviolet rays, impacting the epigenome.

## Testing for These DNA Modifications

Research Article (ISSN: 2832-5788)

Epigenetic modifications can be assessed using various methods that primarily investigate the effects of these modifications on the gene, such as locus-specific and genome-wide alterations for the various codes. These epigenetic methodologies utilize different strategies, such as advanced antibody assays, chromatin functional tests, imaging methodologies, advanced sequencing techniques, and combined bioinformatics pipelines. Of the numerous assays utilized in epigenetic modification studies, two of them are more commonly used: chromatin immunoprecipitation (CHIP) and the bisulfite modification test.

## Bisulfite Modification Test

DNA methylation is among the most studied epigenetic alterations, and there are numerous methodologies used to establish the exact methylation patterns and content of DNA. However, the bisulfite modification acts as a foundation for most of these techniques. According to the American Association for Cancer Research Human Epigenome Task Force (2008, these assay methods convert the non-methylated cytosines to uracils, which are then subsequently changed to thymines upon multiplication by the polymerase chain reaction (PCR). On the other hand, the methylated cytosines are shielded from bisulfite modifications[10].

When analyzing bisulfite-treated DNA, methylation-sensitive primers (MSPs), single nucleotide primer extension (SNuPE), and DNA sequencing are employed. DNA sequencing enables the determination of the methylation status of specific cytosines, while on the other hand, MSPs are useful when rapidly assessing a collection of CpG islands (American Association for Cancer Research Human Epigenome Task Force, 2008)[10]. SnuPEs entail the extension of the oligonucleotide at the 5’ side of the CpG island. The extension is mediated by deoxycytidine and followed by quantitative analysis of the methylation patterns using real-time PCR. The PCR enables the application of this method to multiple sites at the same time.

## Digestion Using Endonucleases

Digestion of genomic DNA using endonucleases does not require bisulfite-treated DNA. It enables the effective mapping of methylation modifications on a genomic scale. The method involves using DNA endonucleases with different methylation sensitives, thus enabling one to get a whole picture of the totality of methylation[11]. One example of these methods is restriction landmapping genomic scanning, which entails the utilization of methylation-sensitive restriction enzymes. These enzymes target non-methylated sequences, thus breaking them.

### Chromatin Immunoprecipitation Test (CHIP)

While there are numerous methods for assessing and studying histone alterations, most of them are based on the chromatin immunoprecipitation technology. This method is semi-quantitative, and it assesses modifications in the chromatin structure by monitoring DNA-protein interactions[11]. It enables the analysis of chromatin structures surrounding specific DNA sequences. Conventional CHIP utilizes formaldehyde, which crosslinks the DNA and

the protein. Consequently, this is followed by the immunoprecipitation of the DNA-protein structures. Upon reversing the crosslinks, the DNA acquired is analyzed using PCR.

Another modification of this method is the native CHIP, which employs micrococcal nuclease. These enzymes digest the chromatin, thus preparing it for analysis. It enables the assessment of histone alterations such as methylation and acetylation more precisely than when fixing using formaldehyde[11]. However, it is not effective when analyzing proteins that have a weak binding affinity for DNA. Lastly, the specific antibody-directed CHIP assay is also essential in the analysis of DNA-protein crosslinking. Like the other techniques, it permits the chromatin structure surrounding certain DNA sequences to be assessed.

## Epigenetics and Huma Disorders

Epigenetic modifications also result in the advancement and progression of various diseases in multicellular organisms[12]. For instance, methylation, a commonly used mechanism for epigenetic modifications in cells, is connected to several disorders such as cancer, autoimmune diseases, diabetes, and neurological disorders such as Fragile X syndrome, Huntington's, Alzheimer's, Parkinson's disease, and schizophrenia. Additionally, histone modifications can lead to infections such as tuberculosis and carcinogenesis.

## Infections, Obesity, Carcinogenesis, and Cardiovascular Disease.

Epigenetic changes are significantly impacted by various environmental factors, such as germs, stress, nutrition, arsenic exposure, drugs, and exercise. These changes result in the modification of epigenetics, thus resulting in various infections. For instance, germs play an instrumental role in influencing an individual's epigenetics, thus weakening the immune system and subsequently resulting in various infections[5]. Mycobacterium tuberculosis, which causes tuberculosis, causes significant changes to histones in a person's immune cells, which switches "off" the IL-12B gene. It weakens the immune system, thus ensuring the bacterium's survival, resulting in severe tuberculosis[13].

Other germs that affect a person’s well-being through modifications in the epigenome include Listeria monocytogenes, Clostridium perfringes, and Streptococcus pneumonia. The toxins they produce result in modifications in histone acetylation, thus resulting in weak immune systems and infections[14]. Nutrition also results in the development of diseases through epigenetic alterations. Folate, which plays a significant role in methylation, also influences methionine production through the remethylation of homocysteine[15]. Alhamwe et al. 2020 also assert that defects or shortages of folate result in colorectal carcinogenesis due to the hypomethylation of genomic DNA[16]. Arsenic exposure also leads to carcinogenesis. It results in DNA alterations, gene promoters' methylation levels, histone acetylation, and phosphorylation, which results in carcinogenesis and epigenetic dysregulation[17]. Lastly, exposure to stress and stressful situations such as childhood abuse causes alterations in DNA methylation; hence, they are more susceptible to obesity in their adult lives[18].

Gharipour M et al. found that histone modifications in carotid atherosclerotic plaques in patients with carotid artery stenosis contribute to plaque development. Methylation in H3K9 and H3K27 decreases in CVD patients, while H3K4 and H3K9ac increase in atherosclerotic MSCs and macrophages. Acetylation in H3K9ac increases in atherosclerotic plaque endothelial cells[19].

## CANCER

While cancer is primarily associated with mutations, it also results from epigenetic changes. Epigenetic modifications result in hypermethylation in the promoter areas of tumor suppressor genes, thus inactivating them. These genes can then not adequately perform their tumor suppressor functions[20]. For instance, if a mutation happens in the BRCA 1 gene, thus hindering its proper functioning, it exposes a person to breast cancer. The same is also true when increased DNA methylation prevents or reduces the expression of the BRCA 1 gene. While some cancer cells display increased DNA methylation, most malignant ones have lower DNA methylation than normal cells. Additionally, the dysregulation of miRNA is also another measure used to diagnose breast cancer. The methylation patterns differ significantly across different cancers, though they exhibit reductions in methylation levels[21].

Other cancers have also been associated with epigenetic causes, such as gastric cancer, caused by the hypermethylation of RUNX3 genes due to the increased demethylation of H3K9 genes and decreased H3 acetylation[22]. According to Chen and Yan (2021), lung cancer is associated with hypermethylation of the RASSF1A, RARB2, and CHFR genes. It is also associated with increased histone acetylation due to the up-regulation of alpha-2 glycoprotein[23]. Lastly, liver cancer is associated with the hypermethylation of CDKN2A cells in the liver[24]. Methylation is also essential in the early detection of cancer. Physicians screen for levels of methylation in cancer-suspected cells and tissues. For instance, excessive methylation of the promoter regions of the APC gene is used for early detection of cancer. It is an epigenetic marker of cancer in human beings . It can also be used to evaluate the development of cancer-for instance, the hypermethylation of the TP53 gene promoter region. Renal cell cancer is a focus area of the Epigenetic Etiology of Human Disease Laboratory, primarily involving epigenetic regulator gene mutations like SETD2, PBRM1, and BAP1. SETD2 trimethylates the H3K36 position, promoting DNA methylation and antagonizing the PRC2 complex's function[25].

## Autoimmune Diseases

The normal functioning of the immune system heavily relies on self-tolerance; a deficiency of self-tolerance results in autoimmune diseases in individuals[25]. Epigenetic aspects also enhance the advancement of these illnesses in mono- and dizygotic individuals. Ecological features alter normal epigenetic functioning, resulting in changes in gene expression in specific differentiated cells. Subsequently, this results in the dysregulation of self-tolerance in the immune system. Epigenetics controls certain essential immune functions, such as inducible

immune responses; thus, any alteration in epigenetic mechanisms results in the development of autoimmune disorders. For instance, in rheumatoid arthritis individuals, there is a hypomethylation of HDAC1 and HDAC2 cells coupled with the hyperacetylation of histones H3 and H4 and hypomethylation of H3 at Lysine 9 in the synovial areas[26].

On the other hand, individuals with multiple sclerosis exhibit hypomethylation of their DNA in the CNS white matter. Similar observations are also seen in individuals with systemic lupus erythematosus who have hypomethylated apoptotic DNA and modified histones[4]. These altered cells are the primary targets for autoantibodies produced by the immune system. Epigenetics also impacts allergic conditions such as asthma. Environmental factors such as smoking result in allergens that change the epigenetic marks of asthma.

### Neurodegenerative and Psychological Disorders

Imprinting control regions (ICRs) are parental allele-specific gene expressions resulting from specialized sequence elements[27]. They are situated in a single copy of the parental DNA, and their primary role is to control gene expression in an allele-unique fashion. DNA methylation and histone modifications have been reported in these regions, thus affecting them. These alterations have been recognized in Alzheimer's disease and schizophrenia. These modifications have also been identified in psychiatric disorders, Huntington's disease, and Fragile X syndrome.

For instance, Fragile X syndrome is among the most congenital mental disorders. It is mainly found in men who have solitary X chromosomes. Persons with this disorder exhibit extreme intellectual incapacities and deferred oral development. The hypermethylation of the CpG islands at the promoter area of the FMR1 gene causes it. According to Rasmi et al[27], the gene is turned off by methylation, thus stopping the FMR1 gene from manufacturing the Fragile X protein mental retardation protein. The lack of this protein results in Fragile X syndrome. Huntington's disorder is triggered by histone modifications in the HDACs genes and the KDM5D histone, while schizophrenia is caused by the hypomethylation of the MB-COMT promoter in the brain[28].

## DISCUSSION

Epigenetics involves regulating cell expression in genes without altering DNA sequence. It results in modifications called epigenetic modifications. Epigenetic modifications also occur in coding and non-coding RNA involved in protein synthesis[29]. DNA methylation involves accumulating methyl elements in promoter groups and switching off genes, thus preventing gene expression and protein synthesis. Histone modifications involve several modifications, such as acetylation, which entails adding acetyl groups; phosphorylation, which entails adding phosphate groups; and ribosylation, which involves adding ribose sugars.

In some situations, epigenetics overshadows phenotypes, as these arise from genotypes through programmed changes and interaction with the environment. Two monogenetic twins have a similar genetic code but different susceptibilities due to exposure to different blood flow and environments.

These changes can be assessed using different methods, such as DNA methylation, which can be assessed using a bisulfite modification test. It detects the methylation patterns and the composition of DNA. Additionally, one can also use digestion through the use of endonucleases, which enable the effective mapping of methylation modifications on a genomic scale. Histone alteration is investigated using the Chromatin Immunoprecipitation Test (CHIP). CHIP consists of three main branches: conventional, native, and specific antibody-directed. These methods enhance the analysis of the chromatin structures surrounding certain DNA sequences[11].

DNA methylation analysis aids researchers in understanding gene regulation and biomarkers affecting diseases like cancer, obesity, and addiction. High-throughput technologies like NGS and microarrays enable genome-wide methylation profiling, providing insights into variations's functional consequences. These technologies reveal DNA methylation significance and functional consequences.

Researchers can gain insight into regulatory events that are crucial for many biological processes and disease states by analyzing DNA-protein interactions. DNA sequencing, genotyping, gene expression, and other types of genomic analysis are complemented by this epigenetic data.

ChIP-Seq is a powerful method for identifying genome-wide DNA binding sites for transcription factors and proteins. It involves immunoprecipitation, coprecipitation, purification, and sequencing. Next-generation sequencing (NGS) enhances understanding of gene regulation events in diseases and biological pathways.

ATAC-Seq enables chromatin accessibility analysis, providing insights into genome regulatory landscapes for various applications, including nucleosome mapping, transcription factor binding, novel enhancer identification, disease-relevant mechanisms, and evolutionary studies. Subsequent experiments often include ChIP-Seq, Methyl-Seq, or Hi-C-Seq to further characterize forms of epigenetic regulation[11].

Given the relative specificity of epigenetic modifications in neoplasms, epigenetics is likely a major factor in early cancer detection and the differentiation of premalignant from malignant lesions. A tissue biopsy is not always easy to obtain, so using serum, plasma, or even other body fluids like bronchoalveolar lavage could be an alternative (Table 1). Hypermethylation of the SHOX1 gene in bronchial lavages is an extremely sensitive epigenetic biomarker that is found in 96% of patients with lung cancer, even in samples that are cytologically negative[30]. It was discovered that patients with Alzheimer's disease had significantly lower levels of peripheral blood DNA methylation in the NCAPH2/LMF2 promoter region, two genes involved in mitosis and lipoprotein lipase maturation, respectively[31]. Heavy methylation of the promoter HSD11B2 is

observed in essential hypertension or hypertension induced by glucocorticoids[32]. In a human placental cell line, it was discovered that DNA methylation controls the expression of CYP17A1, an enzyme essential to steroidogenesis. Antigen-1 (LFA-1; CD11a/CD18) linked to lymphocyte function is linked to ageing and the onset of autoimmunity[33].

**Table 1.** Different epigenitic markers for diagnosis and respected Investigating tools[2]

| Commercial kits designed for miRNA isolation and purification from biofluids | | |
|---|---|---|
| **Kit name** | **Phenol/chloroform extraction step** | **Advantages** |
| miRCURY™ RNA isolation kit biofluids | No | Carrier MS2 RNA or yeast tRNA that increases the miRNA concentration Duration 2-3h. |
| NucleoSpin® miRNA plasma | No | Allows isolating both small and large RNAs in one or two fractions. Duration 1.5-2.5h. |
| Commercial kits for cfDNA isolation and purification from biofluids | | |
| **Kit name** | **Additional and optional steps** | **Advantages** |
| NucleoSpin® Plasma XS kit | Proteinase K digestion treatment | This device can purify and concentrate nucleic acids from serum, plasma, and bronchial lavage (up to 240 µl), as well as DNA from buccal swabs and dried blood spots. The purification column is uniquely engineered to allow for elution quantities as low as 5 µl. Duration 30mn-1h |
| QIAamp DNA blood mini kit | Protease or proteinase K digestion treatment | Allows for nucleic acid purification from serum, plasma, and urine (from 200 µl), as well as DNA purification from buccal swabs and dried blood spots in DSP format for IVD. Duration 2-3 h |
| Commercial kits detect whole chromatin or core histones isolation and purification from different biological sources. | | |
| **Biological source** | **Protein to be tested** | **Downstream uses** |

| | | |
|---|---|---|
| FFPE tissue | Histone/Whole chromatin | qPCR, sequencing |
| Cultured cells, fresh, and frozen tissue | Histone/Whole chromatin | *in vitro* protein-DNA binding assays and nuclear enzyme assays |
| n RT-qPCR assays for detecting circulating miRNAs in liquid biopsy | | |
| **Gene** | **Biological fluid** | **Disease** |
| *miR-16* and *miR-93* | Serum | *Gastric cancer* |
| *miR-16* | Plasma | *Friedreich*'s *ataxia* |

Epigenetic biomarkers like methylated DNA, histones, and miRNAs anatomized from multiple biospecimens like liquid vivisection, fresh towel, and FFPE towel may allow contemporaneous conduction of opinion and targeted remedy, thus contributing to theragnosis and perfection drug. Wang H. et al. reported that cases diagnosed with bone cancer whose primary excrescences displayed methylation of the NT5E CpG islet were less likely to develop metastatic conditions (P = 0.003) [34]. Pils et al. mentioned that the methylation status of the tumor suppressor gene TUCS3 has been suggested to be of prognostic significance in ovarian cancer[35]. Kato et al. observed that the methylation of the apoptosis-related genes TMS1 and DAPK was studied in 81 primary gastric cancers using methylation-specific PCR[36]. The chemosensitivity was lower in cases with methylation in either genos than in those without. In clear-cell renal cell melanoma (CCRCC), the methylation status of tumor suppressor RASSF1A was assessed about prognostic factors by Kawai Y et al., who noticed High situations of methylation in the RASSF1A protagonist were significantly more frequent in advanced grades and advanced stages, and cases with high methylation situations had a significantly less favorable prognostic compared with those with low methylation situations[37]. Fiaschetti et al. observed that in medulloblastoma, there's a significant correlation between a controller of neuronal development, miRNA-9, low expression, and the opinion of aggressive variants with poor outgrowth[38]. After posttransplantation of the pancreas in diabetismellitis causes elevation of Unmethylated insulin DNA, it will predict greater hyper-glycemia at 90 days. MikR-375 and miR-541 expression changes in type 2 diabetes patients will predict coronary artery disease[39].

These changes impact gene expression and result in several illnesses, such as cancer, autoimmune disorders, neurodegenerative and mental ailments, infections, obesity, and carcinogenesis. These disorders have devastating effects on individuals. For instance, infections result in weakened immune systems, cancers lead to death, and neurogenetic and psychological disorders result in mental retardation. As mentioned, reversible genetic modifications cause these disorders, they can be countered by epigenetic treatments. These treatments mainly alter DNA methylation and Histone acetylation. DNA methylation inhibitors, such as 5-azacytidine and 5-aza-2'-deoxycytidine, re-energize silenced genes[40]. They act like cytosine by incorporating into DNA during replication and blocking DNMT enzymes, thus preventing DNA methylation. On the other hand, histone deacetylase inhibitors such as phenyl butyric acid and depsipeptide prevent histone modifications by removing the acetyl molecules from DNA, which condense chromatin and stop transcription. They activate gene expression[41].

The influence of environmental factors in human evolution is a contentious issue that has been studied extensively in the field of epigenomics. This emerging field of study, which explores how environmental factors can affect gene expression without altering the underlying DNA sequence, has identified a correlation between different complexions and epigenetic modifications. This suggests a role for environmental factors in shaping human evolution. The universality of human developement across diverse parts of the world may be attributed to the biosphere's role as a shared ecological niche. However, it is important to acknowledge that humans possess exceptional cognitive abilities that set us apart from other animals. As such, it is paramount that we utilize our critical thinking skills to understand and respect the delicate balance of the natural world and all its inhabitants, both living and non-living. In line with the precautionary principle, which emphasizes the importance of preventing environmental degradation, it is imperative to prioritize the preservation of a healthy planet. This approach acknowledges that, despite our technological advancements, humans remain vulnerable to the profound power of nature. Events such as tsunamis serve as stark reminders of this fundamental truth.

## CONCLUSION

In conclusion, epigenetics entails studying the mechanisms through which cells regulate and control gene activity without altering the sequence and structure of the DNA. It involves studying factors beyond the genetic code, such as an individual's behavior, exercise, and environment. These factors result in DNA changes and modifications that determine whether genes are turned on or off. Epigenetic modification consists of three mechanisms: DNA methylation and demethylation, histone modification and non-modification, and coding RNA silencing. Epigenetic modifications also result in the development and advancement of various illnesses in multicellular organisms. They include cancers, autoimmune diseases, diabetes, and neurological disorders such as Fragile X syndrome, Huntington's, Alzheimer's, Parkinson's disease, and schizophrenia. The illnesses are the result of reversible genetic modifications; hence, epigenetic treatments can counter them. These treatments mainly alter DNA methylation and Histone acetylation.

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