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# A Review on Epigenetics

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**ABSTRACT:** The epigenetics field is growing fast, and it is the study of elements controlling gene transcription. However, one extent that has not achieved adequate contemplation is the impact of epigenetic elements on various aspects of an individual's life. This topic has been examined by studying how transcriptional control modulates the human brain's growth and continuous functioning, environmental factors affecting the genome, and might add to the expansion of consciousness. Epigenetics plays an imperative role in an individual's consciousness across the lifetime. The goal is to present a relationship between epigenetics and the human brain and behavior. So in this review paper, we have also discussed epigenetics in bacteria and the future of epigenetic drugs supported with techniques used to study epigenetics.

**KEYWORDS:** Gene transcription, Human brain, Human consciousness, DNA, Epigenetic techniques, Epigenetic drugs

## I. INTRODUCTION

The study in which cells regulate gene activity (expression) without switching the sequence of DNA is known as epigenetics (Cavalli, & Heard, 2019). In Greek, "epi" means on or above. So epigenetics refers to on top of or beyond genetics. The epigenome (Feinberg, 2018) is a collection of chemical tags that alter DNA and its related structures. It also includes any genetic activity modifier free of a gene's DNA sequence. The genome is the complete set of genetic facts presented in the DNA of each individual's cells. On the other hand, the epigenome is created of complex modifications to genomic DNA (Dai, Ramesh, & Locasale, 2020) that confer developmental and cellular and identity. The epigenome (Mahajan, Taliun, Thurner, Robertson, Torres, Rayner, & McCarthy, 2018) combines the data encoded in the genome with cellular, extracellular, environmental molecular and chemical cues. The epigenome and the genome instruct each cell type's unique gene expression program to describe its fully functioning identity throughout development or disease.

In some ways, the epigenome exemplifies an organism's ability to adapt and develop during the interpretation of various attributes or physical characteristics of an organism developed in response to an external stimulus. Compared to the genome's consistency (Jin, Yu, Yang, Song, DePamphilis, Yi, & Li, 2020), the epigenome is categorized by a flexible and dynamic response to intracellular and extracellular stimulation, via cell to cell contact, by adjacent cells, physiology, or wholly by the environment an organism is laid bare. Cytokines, growth regulators, hormonal levels changes, and the discharge of stress-response and neurotropic elements are instances of molecules that the environment modulates and fall under the category of epigenome modifiers. Finally, the environs offer all such aspects to the person that impact the epigenome, and each individual's genetic profile and unique epigenetic regulate the particular response to such aspects.

Enzyme activity in reaction to environmental cues encourages the inclusion or disposal of epigenetic tags on DNA or chromatin or both, resulting in a cascade of modification that temporarily, permanently, either with a genetically inherited change, influences cellular memory.

## II. EPIGENETICS IN BACTERIA

Epigenetics is pivotal in eukaryotes (Antonova, Boeren, Timmers, & Snel, 2019), particularly metazoans. It has a unique role in bacteria (Ghosh, Veeraraghavan, Elangovan, & Vivekanandan, 2020). The former primarily utilize epigenetic mechanisms to control gene activity. The latter hardly ever does and extensively uses postreplicative DNA methylation to control epigenetics for DNA-protein interactions. Bacteria even employ DNA adenine methylation like an epigenetic signal (instead of DNA cytosine methylation). It is significant in the infectivity of bacteria such as Salmonella, Escherichia coli, Vibrio, Haemophilus, Yersinia, as well as Brucella. It controls the cell cycle and is responsible for gene transcription and DNA replication in Alphaproteobacteria. Adenine methylation in



Gammaproteobacteria signalizes for DNA replica, incompatible maintenance, chromosome separation, bacteriophage packaging, transposase function, and gene activity control in Gammaproteobacteria. In the pneumococcus, the genetic (*Streptococcus pneumoniae*) switch enables the bacterium to arbitrarily change its features in six different states, which could lay the foundations for better vaccines. A phase variable methylation system randomly generates each form. In Firmicutes, for example, *Clostridioides difficile*, adenine methylation controls biofilm formation, sporulation, as well as host adaptation.

### III. EPIGENETICCHANGES

Epigenetic changes (Kumar, Gonzalez, Rameshwar, & Etchegaray, 2020) are DNA modifications that control genes turning on or off. These adjustments are appended to DNA and do not affect the sequential manner of the basic components of DNA. The epigenome refers to all the adjustments that govern the genes expression within a cell's full set of DNA (genome).

Since epigenetic modifications affect genes mode, they impact protein production in cells. This act makes sure that every cell generates only the required proteins for its functioning. Proteins responsible for promoting bone growth, for example, are not created in muscle cells. Modifications in epigenetic patterns differ between individuals, tissues in a human, and cells inside a tissue. Environmental factors, for example, a person's diet and exposure to toxins, can affect the epigenome. Epigenetic changes can be passed down from cell to cell as cells divide and, in certain instances, passed down through generations.

DNA methylation (Greenberg, & Bourc'his, 2019) is a popular type of epigenetic modification. It is the process by which tiny chemical groups known as methyl groups (comprising three hydrogen atoms and one carbon atom ) are attached to DNA's key components. The presence of methyl groups on a gene is on silent or off mode and produces no protein.

Histone modification is yet another common epigenetic change. Histones are structural proteins located in the cell nucleus. The shape of chromosomes is determined by the way DNA wraps around histones. However, how tightly DNA wraps around histones is affected by chemical groups. Therefore, histones can be altered by adding or removing chemical groups, for example, methyl, which determines a gene turning on or off.

Discrepancies in the epigenetic method, for example, incorrect gene modification or inability to incorporate a chemical group to a specific histone, can lead to inappropriate gene inactivity or activity. Gene activity changes, incorporating those induced by epigenetic inconsistencies, are a prevalent trigger of genetic problems.

### IV. TYPES OF EPIGENETICCHANGES

Epigenetic changes influence gene expression in a variety of ways. The following are the types of epigenetic changes:

- ***DNAMethylation***

DNA methylation (Luo, Hajkova, & Ecker, 2018) involves adding a chemical group to DNA. This group is usually added to particular areas on the DNA, where it inhibits proteins that append to DNA to "read" the gene. The removal of this group is via a process called demethylation. In most cases, methylation tends to turn genes on "off" mode, while demethylation puts them on "on" mode.

- ***Histonemodification***

Histone proteins (Wang, Gao, Zheng, Liu, Dong, Li, & Li, 2019) are proteins that wrap around DNA. Proteins that "read" the gene cannot access tightly wrapped DNA around histones. Some genes on "off" mode are wrapped around histones, whereas others on "on" mode are not wrapped around them. Addition or removal of chemical groups and alters whether a gene is on "on" mode or "off" mode (i.e., wrapped or unwrapped).

- ***Non-codingRNA***

DNA serves as a blueprint for producing coding and non-coding RNA (Ransohoff, Wei, & Khavari, 2018). Coding RNA is utilized to prepare proteins. On the other hand, non-coding RNA regulates gene activity by linking coding RNA with specific proteins to break it down so that it cannot make proteins. It may even attract and retain proteins to alter histones, allowing genes to be turned "on" or "off."





## V. HOW DO EPIGENETICS CHANGE?

Epigenetics keep changing as you get older due to normal development and age and behavior patterns and surroundings.

- **Development and Epigenetics**

Changes in epigenetics occur before birth (Lickliter, & Witherington, 2017). Cells contain uniform genes, but they all act and look diversely. Epigenetics help define which feature a cell will possess as you grow and mature, such as will it become a heart, nerve, or skin cell.

**Example: Muscle cell vs. Nerve cell**

Although muscle cells and nerve cells share the same DNA, they function differently. A muscle cell has an arrangement that aids in the body's movement. A nerve cell is a type of cell that transmits information to other cells in the body. Epigenetics enables a muscle cell to turn "on" genes that make proteins necessary for its function and turn "off" genes that make proteins necessary for a nerve cell's function.

- **Age and Epigenetics**

Throughout the lifespan of a human, epigenetics alter (Chen, & Kerr, 2019). That is why epigenetics at birth are not anything like epigenetics during childhood or youth.

**Example: Study of newly born vs. at 20-years of age vs. at 100-years of age**

With age, the DNA methylation level decreases. A newly born baby had the most DNA methylation, a 100-year-old had the least, and a 20-year-old had DNA methylation levels in between both of them.

- **Reversibility and Epigenetics**

All epigenetic changes are not irreversible (Zhang, Zhao, Hambly, Bao, & Wang, 2017). Some can be added or deleted in response to behavioral or environmental changes.

**Example: Former smokers vs. present smokers vs. nonsmokers**

Smoking is another factor that can lead to epigenetic changes. For instance, Tobacco use can cause epigenetic changes. For example, present smokers have less DNA methylation than nonsmokers at certain parts of the AHRH gene. The gap is larger for heavy and long-term smokers. Former smokers may experience increased DNA methylation at this gene after quitting smoking. They can eventually reach levels comparable to nonsmokers. That can happen in as little as a year in some cases, but the time duration is based on how long and how much a former smoker has smoked before quitting.

## VI. IMPACT OF EPIGENETICS ON HEALTH

Epigenetic changes can have a variety of effects on human health:

- **Infections**

Germs can alter your epigenetics (Cardoso, Lobo, Miranda-Gonçalves, Henrique, & Jerónimo, 2021) to destroy your immune system and aid the germ's survival.

**For instance: Mycobacterium tuberculosis**

It is the underlying cause of tuberculosis. Infections bearing germs can induce histone changes in some immune cells, resulting in the IL-12B gene "turn off." This deteriorates our immune system and increases Mycobacterium tuberculosis's survival.

- **Cancer**

Specific mutations increase the chances of developing cancer (Park, & Han, 2019). Similarly, some epigenetic changes enhance the risk of suffering from cancer. For example, possessing a mutation in the BRCA1 gene prevents it from proper function and increases the risk of developing breast and other cancers. Likewise, enhanced DNA methylation increases such cancer types by reducing BRCA1 gene activity. Though cancer cells increase DNA methylation at specific genes, cumulative DNA methylation levels in cancer cells are lesser than that in normal cells. In addition, various cancer types with similar appearances may have varied DNA methylation patterns. Epigenetics can help determine a person's cancer type or detect difficult-to-find cancers previously. However, epigenetics solely can't diagnose cancer, so additional screening tests are required to confirm them.

**For instance: Colorectal Cancer**

The SEPT9 gene is methylated more frequently in this cancer. Some commercial epigenetic-based colorectal cancer tests, and when combined with some other diagnostic screening tests, these epigenetic-based tests can aid in early



cancer detection.

- **Nutritional Needs During Pregnancy**

The environment and behavior of a pregnant woman during pregnancy, such as whether she eats healthy food, can influence the baby's epigenetics (Caffrey, Irwin, McNulty, Strain, Lees-Murdock, McNulty, & Pentieva, 2018). In addition, some epigenetic changes can last for even a hundred years and make that child prone to certain diseases. **For instance: Dutch Hunger Winter Famine (1944-1945)**

Children whose mothers were pregnant in the famine were at a higher risk of developing certain diseases like schizophrenia, heart disease, and type 2 diabetes. Compared to their siblings who were not exposed to famine before birth, they had more methylation at certain genes and reduced methylation at others. This methylation gap could suggest why they were more likely to develop particular diseases later in their lifespan.

## VII. TECHNIQUES FOR STUDYING EPIGENETICS

Epigenetic research uses many molecular biological techniques to comprehend epigenetic phenomena. These techniques incorporate:

- **Chromatin Immunoprecipitation**

This technique has aided in bridging the epigenetic interactions and DNA gap (Nicolglou, & Merlin, 2017). Experimenters can learn about ascertaining chromatin structure, transcription mechanisms, and gene regulation using this technique.

- **Fluorescent in situ hybridization (FISH)**

This technique is critical for understanding epigenetic mechanisms (Rozitis, Johnson, Cheng, & Lee, 2020). It is used to locate genes that are there on chromosomes and to identify non-coding RNAs. It is used primarily in humans to detect chromosomal irregularities.

- **Methylation-sensitive restriction enzymes**

When combined with PCR (KANOOSH, ALFALAH, JANO, & ALAWADI, 2021), this technique can be used to assess DNA methylation, specifically at CpG sites. If it is methylated, restriction enzymes cannot separate the strand. If not, the enzymes will break it, and PCR will augment it.

- **Bisulfite sequencing**

This technique is one of the other ways to assess DNA methylation (Heer, Ullrich, Hiss, Liepelt, Schulze Brüning, Zhou, & Rensing, 2018) apart from methylation-sensitive restriction enzymes. When cytosine is exposed to sodium bisulfite, it gets converted to uracil, whereas methylated cytosines are unaffected.

## VIII. THE FUTURE OF EPIGENETIC DRUGS

Epigenetic therapeutic approaches have displayed capability in treating various diseases that epigenetic changes influence. Azanucleosides (Morel, Jeffery, Aspeslagh, Almouzni, & Postel-Vinay, 2020), which are pyrimidine analogs, are regarded as the first true epigenetic drugs created in the 1960s.

Amongst modes of action recognized for such drugs, hypomethylation is typically caused by hindering the liable methyltransferase enzymes. Also, it is believed that the drugs hinder RNA-based methylation and can induce specific immune responses to cure some cancer types primarily by (Villanueva, Álvarez-Errico, & Esteller, 2020) up-regulating endogenous retroviruses after methylation inhibitory activity, thereby boosting interferon manufacturing.

Histone deacetylase drugs, which help eliminate acetyl groups from DNA for maintaining gene activity, are also growing (Agrawal, Das, Vyas, & Hajdúch, 2018) - histone deacetylase inhibitors. The history of these medications indicates their use as mood stabilizers and anti-epileptics. Still, they are presently being studied as an anticancer therapy in place of or when combined with several conventional chemotherapeutic drugs.

Such drugs can probably reinstate silent tumor-specific and stimulating genes in the coming time. However, the particularity toward the intended cancer cells is minor in the present time, and causing epigenetic modifications in non-intended cells (Sessions, Sánchez-Cruz, Prieto-Martínez, Alves, Santos Jr, Muratov, & Medina-Franco, 2020) increases many security concerns. Also, enzymes fastly degrade them in vivo and have a brief retention time (RT) in a body.

Nanoparticle drug delivery systems, which have good bioavailability, a prolonged RT, and have active and passive targeting approaches for inflammation sites like tumor parenchyma, might be the solution to the poor pharmacokinetic profile of these drugs.

These sites of inflammation often show fenestrated and disorganized blood vasculature where nanoparticles collect if passive targeting, in a method called the enhanced permeability and retention (EPR) effect. This method is deemed to target nanoparticles in a passive aspect.



But the EPR effect relies extremely on the particular tumor type and differs significantly from individual to individual. The active targeting approach for inflammation sites seeks to integrate a ligand, i.e., complementary to a receptor commonly known as over-expressive, ideally predominately expressed, on the target cancer cell's surface. This enables the nanoparticles to engage with the cell, which frequently enters through endocytosis and releases the drug payload straight to the cytoplasm.

Nanoparticles likewise allow for the concurrent synergistic drug co-delivery in properly balanced drug payloads, greatly enhancing each drug payloads' effectiveness. Drug carriers produced with polymers, lipids, carbon, silica, and metals have been studied while no clinical trial has started.

Specific and advanced epigenetic drugs will even permit adequate management of the animal models' epigenome in the study, permitting epigenetic disorders to be more nearly customized and drugs to be tested better. The genes' responsibility could probably be explored in the coming time utilizing typical epigenetic promoters or silencers, enabling the study to turn genes on quickly "on" and "off" mode in a regulated and clear manner.

### IX. CONCLUSION

Epigenetics is an amalgamation of two words and is concerned with gene activity. Epigenome and genome are two relevant terms. The former is formulated with complex modifications to genomic DNA, conferring developmental and cellular and identity. The latter means a set comprising of genetic facts located in the DNA of every individual's cells. Any change in epigenetics puts genes in 'on' or 'off' mode. Also, epigenetics is present in humans to even bacteria.

### REFERENCES

1. Agrawal, K., Das, V., Vyas, P., & Hajdúch, M. (2018). Nucleosidic DNA demethylating epigenetic drugs—a comprehensive review from discovery to clinic. *Pharmacology & therapeutics*, 188,45-79.
2. Antonova, S. V., Boeren, J., Timmers, H. M., & Snel, B. (2019). Epigenetics and transcription regulation during eukaryotic diversification: the saga of TFIID. *Genes & development*, 33(15-16),888-902.
3. Cavalli, G., & Heard, E. (2019). Advances in epigenetics link genetics to the environment and disease. *Nature*, 571(7766),489-499.
4. Caffrey, A., Irwin, R. E., McNulty, H., Strain, J. J., Lees-Murdock, D. J., McNulty, B. A., ... & Pentieva, K. (2018). Gene-specific DNA methylation in newborns in response to folic acid supplementation during the second and third trimesters of pregnancy: epigenetic analysis from a randomized controlled trial. *The American journal of clinical nutrition*, 107(4),566-575.
5. Cardoso, A. R., Lobo, J., Miranda-Gonçalves, V., Henrique, R., & Jerónimo, C. (2021). Epigenetic alterations as therapeutic targets in testicular germ cell tumours: current and future application of 'epidrugs'. *Epigenetics*, 16(4), 353-372.
7. Chen, D., & Kerr, C. (2019). The epigenetics of stem cell aging comes of age. *Trends in cell biology*, 29(7), 563-568.
8. Dai, Z., Ramesh, V., & Locasale, J. W. (2020). The evolving metabolic landscape of chromatin biology and epigenetics. *Nature Reviews Genetics*, 21(12),737-753.
9. Feinberg, A. P. (2018). The key role of epigenetics in human disease prevention and mitigation. *New England Journal of Medicine*, 378(14),1323-1334.
10. Ghosh, D., Veeraraghavan, B., Elangovan, R., & Vivekanandan, P. (2020). Antibiotic resistance and epigenetics: more to it than meets the eye. *Antimicrobial agents and chemotherapy*, 64(2),e02225-19.
11. Greenberg, M. V., & Bourc'his, D. (2019). The diverse roles of DNA methylation in mammalian development and disease. *Nature reviews Molecular cell biology*, 20(10), 590-607.
12. Heer, K., Ullrich, K. K., Hiss, M., Liepelt, S., Schulze Brüning, R., Zhou, J., ... & Rensing, S. A. (2018). Detection of somatic epigenetic variation in Norway spruce via targeted bisulfite sequencing. *Ecology and evolution*, 8(19),9672-9682.
13. Jin, J. J., Yu, W. B., Yang, J. B., Song, Y., DePamphilis, C. W., Yi, T. S., & Li, D. Z. (2020). GetOrganelle: a fast and versatile toolkit for accurate de novo assembly of organelle genomes. *Genome biology*, 21(1),1-31.
14. KANOOSH, O. A., ALFALAH, A. O., JANO, F. O., & ALAWADI, H. F. N. (2021). Epigenetic role of dna methylation in hybrid vigor of cytoplasmic male sterility in sunflower. *Pak. J. Bot*, 53(1),191-196.
15. Kumar, S., Gonzalez, E. A., Rameshwar, P., & Etchegaray, J. P. (2020). Non-coding RNAs as mediators of epigenetic changes in malignancies. *Cancers*, 12(12),3657.



16. Lickliter, R., & Witherington, D. C. (2017). Towards a truly developmental epigenetics. *Human Development*, 60(2-3),124-138.
17. Luo, C., Hajkova, P., & Ecker, J. R. (2018). Dynamic DNA methylation: In the right place at the right time. *Science*, 361(6409),1336-1340.
18. Mahajan, A., Taliun, D., Thurner, M., Robertson, N. R., Torres, J. M., Rayner, N. W., ... & McCarthy, M. I. (2018). Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. *Nature genetics*, 50(11),1505-1513.
19. Morel, D., Jeffery, D., Aspeslagh, S., Almouzni, G., & Postel-Vinay, S. (2020). Combining epigenetic drugs with other therapies for solid tumours—past lessons and future promise. *Nature Reviews Clinical Oncology*, 17(2), 91-107.
21. Nicoglou, A., & Merlin, F. (2017). Epigenetics: A way to bridge the gap between biological fields. *Studies in History and Philosophy of Science Part C: Studies in History and Philosophy of Biological and Biomedical Sciences*, 66,73-82.
22. Park, J. W., & Han, J. W. (2019). Targeting epigenetics for cancer therapy. *Archives of pharmacal research*, 42(2),159-170.
23. Ransohoff, J. D., Wei, Y., & Khavari, P. A. (2018). The functions and unique features of long intergenic non-coding RNA. *Nature reviews Molecular cell biology*, 19(3),143-157.
24. Rozitis, E., Johnson, B., Cheng, Y. Y., & Lee, K. (2020). The use of immunohistochemistry, fluorescence in situ hybridization, and emerging epigenetic markers in the diagnosis of malignant pleural mesothelioma (MPM): a review. *Frontiers in Oncology*, 10, 1742.
25. Sessions, Z., Sánchez-Cruz, N., Prieto-Martínez, F. D., Alves, V. M., Santos Jr, H. P., Muratov, E., ... & Medina-Franco, J. L. (2020). Recent progress on cheminformatics approaches to epigenetic drug discovery. *Drug Discovery Today*.
26. Villanueva, L., Álvarez-Erriço, D., & Esteller, M. (2020). The contribution of epigenetics to cancer immunotherapy. *Trends in immunology*.
27. Wang, L., Gao, Y., Zheng, X., Liu, C., Dong, S., Li, R., ... & Li, P. (2019). Histone modifications regulate chromatin compartmentalization by contributing to a phase separation mechanism. *Molecular cell*, 76(4), 646- 659.
28. Zhang, X., Zhao, L., Hambly, B., Bao, S., & Wang, K. (2017). Diabetic retinopathy: reversibility of epigenetic modifications and new therapeutic targets. *Cell & bioscience*, 7(1),1-8.





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