

## **International Journal of Research Publication and Reviews**

Journal homepage: www.ijrpr.com ISSN 2582-7421

# **Exploring the Role of Epigenetics in Drug Development**

Twinkle J. Bhatt<sup>1</sup>, Zainab H. Zaveri<sup>2</sup>, Urjita R. Sanghavi<sup>3</sup>.

<sup>1</sup>Assistant professor, pharmacognosy, Gyanmanjari Pharmacy College, Bhavnagar 364001, Gujarat, India

<sup>2</sup> Student, Gyanmanjari Pharmacy College, Bhavnagar 364001, Gujarat, India

<sup>3</sup>Student, Gyanmanjari Pharmacy College, Bhavnagar 364001, Gujarat, India

#### ABSTRACT:

Scientists have long attempted to characterize illnesses only in terms of hereditary or environmental variables. Nonetheless, research on the function of epigenetics in human illnesses began to be conducted fifty years ago. Over the past ten years, there has been a lot of interest in this topic, particularly in relation to complex disorders like addiction, cancer, autoimmune diseases, behavior plasticity, memory, and neurodegenerative and psychological disorders. This overview first discusses the taxonomy and history of epigenetic changes. It then goes on to discuss the function of epigenetics in biology and the relationship between epigenetics and environment. Additionally, the function of epigenetics in human diseases is examined by concentrating on a few diseases with a few complex traits, and we conclude by outlining the field's future prospects. Disease is known to be influenced by epigenetics, which are heritable variations in gene expression without alterations in DNA sequence. Aberrant methylation patterns of DNA and chromatin modifications involving histones are two significant epigenetic alterations that are known to be associated with disease. This article discusses a recent advancement in pharmacology called "epigenetic therapy," which aims to reverse these modifications. Two categories of medications are being developed at this time. One suppresses DNA methylation of tumor suppressor genes silences those genes. | Normal cellular phenotypes are established by the dynamic and reversible process of epigenetic control of gene expression, which also plays a role in human illnesses. Histones and other DNA-packaging proteins, as well as DNA itself, undergo hierarchical covalent alteration as part of the molecular process of epigenetic control.

Keywords: DNA methylation, Demethylation, Histone modification, molecular aspects of epigenetic, non-histone modification.

#### Introduction:

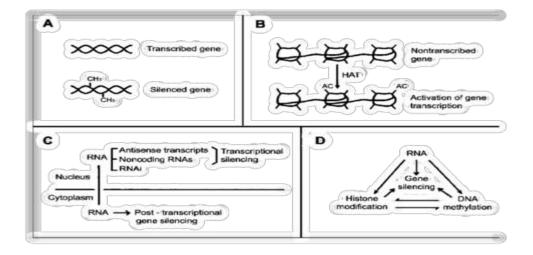
Epigenetics is like a control panel for our genes. It is about how certain factors can switch genes on or off without changing the actual genetic code. These changes can affect properties of cell but without causing change in the DNA sequence<sup>1.</sup> Also, epigenetics impacts on areas which includes developmental biology, somatic gene therapy, cloning and genomic imprinting<sup>2</sup> Epigenetics was first detected in humans in 1983 by Feinberg and Vogelstein<sup>3</sup>. It plays major role in pathogenesis and multifactorial disorders<sup>4</sup>. The mechanism of epigenetic impact the gene activity at transcriptional and post-transcriptional level. Such mechanism results in varieties of cell differentiations, morphogenesis and adaptability of an organism which is affected by genetic and environmental factors<sup>5</sup>. Also, this mechanism is important, they play role in diseases related to lifestyle, early life experience, and exposure to toxins<sup>6</sup>. Other mechanism contributes to chromatin remodelling via ATP-dependent processes and they exchange the histones variants, covalent modification of histones, DNA is regulated by non-coding RNAs, methylation and other modifications related to it<sup>7</sup>. Nucleosome is the basic building block of chromatin which is octamer of histone proteins contains around 147 base pairs of DNA<sup>8</sup>. Multicellular organisms have different mechanism that each type of cell in body has unique pattern of gene activity and specific expression of gene<sup>9</sup>. The epigenetic state of the cell is dynamic and its response to environmental factors both during the development of foetal and adults<sup>10</sup>. The overall state of the cell's genome is called as epigenome<sup>11</sup>. Epigenetic alterations can be caused by nutritional change as well as oxidative stress level which lead to change in internal and external environment of biological system<sup>12</sup>. A genotype of organism is capable to convert into phenotype due to majority of environmental factors this is called as plasticity<sup>13</sup>. The history of epigenetics in 1879 by Thomas hunt morgan described

#### Molecular aspects of epigenetics:

Epimutations is heritable defect in expression of genes, this does not involve changes in DNA sequence<sup>15</sup>. Epigenetics changes occur due to environmental factors so this change lead to inheritance of daughter cells during cell division which also influence the germline<sup>16</sup>. Epigenetics is rapidly evolving based on molecular aspects , three molecular mechanism like DNA methylation, histone modification, and RNA associated silencing which interact with each other<sup>17</sup>. This therapy is very useful form because this is easily reversible with pharmacological intervention when compared to genetic defects<sup>18</sup>.

#### DNA methylation and demethylation:

DNA methylation has much high stability which throughout the periods of cell cycle serves as a special epigenetic memory of cells<sup>19</sup>. Throughout the entire human lifecycle epigenetic events occurs from embryogenesis to adulthood. As there is division of zygote the embryo undergoes de-Novo methylation, and again new level of DNA methylation occurs<sup>20</sup>. The existence of DNA methylation primarily occurs with cytosine-phosphate-guanine(CpG) dinucleotide <sup>21</sup>. For the formation and maintaining the DNA methylation patterns three catalytic active enzyme are required like DNMT3a, DNMT3b, DNMT3c,<sup>22</sup>.



Methylation of DNA occurs at site of cytosine by adding a methyl group, using S-adenosylmethionine as a source of methyl group<sup>23</sup>. DNMT1 is considered to be maintenance methyltransferase that copies DNA methylation patterns of parenteral strand to newly replicated strand during cell division and DNMT3a and DNMT3b as De-novo methyltransferases<sup>24</sup>. DNA methylation has many functions such as silencing of transposable elements against viral sequence and repression of certain gene<sup>25</sup>. Histones can be modified by number of ways like acetylation, methylation and phosphorylation<sup>26</sup>. Acetylation of histones occurs at lysine and catalysed by HATs associated with activation of gene transcription. Histones is decatalysed by HDACs<sup>27</sup>.

#### Histone and non-histone modifications:

Gene regulation is way through which histone modification occur through including acetylation, methylation, phosphorylation, ribosylation, sumoylation and citrullination<sup>28</sup>. Non-histone is the another mechanism of structural inheritance<sup>29</sup>.

#### Mitotic gene bookmarking:

The mitosis gene bookmarking is the important issue in epigenetic interpreting<sup>30</sup>. Transcription agents and RNA polymerase are the most excluded from mitotic chromatin and is transcriptionally inactive<sup>31</sup>.

### **Types of Diseases Involve Epigenetic Changes:**

<u>Cardiovascular diseases</u>: these genes occur in normal vascular smooth muscle cells, due the age there is decrease in expression level which lead to vascular damage<sup>32</sup>.

<u>Neurological disorders</u>: epigenetic play a vast role in nervous system. During neuronal differentiation CpG is lost in methylation and H3K4 demethylation is gained<sup>33</sup>. Hence it is important to bind CpG protein in methyl regulation. Mutations and duplication of CpG methyl binding protein gene cause Rett syndrome which lead to mental retardation<sup>34</sup>.

<u>Metabolic disorders</u>: epigenetic changes occurs due to temporary changes in diet, though it serves as invaluable tool in prevention and treatment of disorders which are metabolically linked<sup>35</sup>.

<u>Cancer</u>: it is the uncontrolled growth of cell with metastatic potential<sup>36</sup>. This involve changes in both DNA methylation and histone modification at residues of CpG. Oncogenes like ras and src becomes active by methylation<sup>37</sup>. In upstream regions methylation is caused by regulation of DNMT1 and is mostly observed in cancer cells apart from normal <sup>38</sup>.

<u>Autoimmune diseases</u>: it include studies in both monozygotic and dizygotic twins as have role for epigenetics<sup>39</sup>. The frequency of occurrence is more in females due to female sex hormones<sup>40</sup>.

<u>Addiction</u>: opioids estimation of people in worldwide is about 13.5 out of which 9.2 is heroin<sup>41</sup>. The responses of organism for environmental condition is changed through alterations and epigenetic changes which are corelated with learning and memory<sup>42</sup>.

<u>Regenerative medicine</u>: it play a role in embryonic stem cell and differentiation and reprograming. The epigenetic proteins shows utility in regenerative medicine particularly in embryonic stem and formation of pluripotent stem cells<sup>43</sup>.

#### Drugging the epigenome:

HDACs: HDACs, this are divided into five different phylogenetic types<sup>44</sup>.

Class 1 include- HDAC1, HDAC2, HDAC3 and HDAC8

Class 2 include-HDAC4, HDAC5, HDAC7 and HDAC9

Class 2(b) include- HDAC6 and HDAC10

Class 3 include- sirtuins SIRT1-SIRT7

Class 4 include- HDAC11.

This all the classes from 1-4 requires a divalent metal ion for catalysis<sup>45</sup>.

Sirtuines are the enzymes dependent on NAD<sup>+</sup> which deacetylase the protein and ADP include ribosylase activity. This are structurally and biochemically unrelated to other classes<sup>46</sup>. Substrate like histone and non-histone deacetylase by HDACs <sup>47</sup>. Increased acetylation of histone and non-histone substrates mediated by drugs are linked to arrest tumour cell growth, apoptosis and anti-angiogenesis<sup>48</sup>.

#### **Epigenetic regulation of ADME genes:**

There are approximately 300 genes involved in absorption, distribution, metabolism and excretion. Approximately 60 genes participate in regulation of DNA methylation and histone modification<sup>49</sup>. CYP1A2, is an enzyme abundant in liver which is involved in metabolism of several drugs<sup>50</sup>. CpG island of exon2 consist of 17 CpG dinucleotides which is in corelation with differences in CYP1A2 mRNA levels<sup>51</sup>. In the cancer cell lines , there is promoter of ABCB1 gene which codes for MDR1 transporter<sup>52</sup>. Irinotecan is a first line treatment for metastatic corectal cancer. SN-38 is an active metabolite which is inactivated by glucuronidation mediated by UGT1A1 enzyme<sup>53</sup>. The gene which codes for folate carrier is SLC19A1. This is responsible for uptake of reduces folate and for antifolate drugs which include methotrexate<sup>54</sup>.

#### **References:**

- 1. Lewin B., Genes VIII, upper saddle river, NJ: Pearson Prentice Hall; 2004.
- 2. Wolffe AP, Matzke MA. Epigenetics: regulation through repression. Science 1999: 286: 481-6.
- 3. Issa J-PJ, Baylin SB. Epigenetics and human disease. Nat Med 1996; 2: 281-2.
- 4. Egger G, Liang G, Aparicio A, Jones PA. Epigenetics in human disease and prospects for epigenetic therapy. Nature 2004; 429: 457-63.
- 5. Holliday R. Epigenetics: A historical overview. Epigenetics 2006; 1(2); 76-80.
- 6. Meaney, M.J. Epigenetics and the biological definition of gene and environmental interactions. Child Dev. 81, 2010, 41-79.
- 7. Allis, C.D., jenuwein, T.\$ Reinberg, D. Epigenetics (Cold Spring Harbour Laboratory Press, New York, 2007).
- 8. Bernstein BE, Meissner A, Lander ES. The Mammalian Epigenome. Cell 2007; 128:699-81.
- 9. Berger SL, kouzarides T, Shiekhattar R, Shilatrifard A. An operational definition of epigenetics. Genes Dev 2009; 23:781-3.
- 10. Sim, S.C.\$ Ingelman-sundberg, M.pharmacogenomic biomarks: new tools in current and future drug therapy. Trends pharmacol. Sci.32, 72-81(2011).
- 11. Szyf, M. The dynamic epigenome and its implication in toxicology. Toxicol. Sci. 100,7-23(2007).
- 12. Heijmans BT, Tobi EW, Stein AD, Putter H, Blauw GJ, Susser ES, Slagboom PE, Lumey LH: Persistent epigenetic diffrences associated with prenatal exposure to famine in humans. Proc Natl Acad Sci 2008, 105:17046-49.

McGowan PO, Sasaki A, D'Alessio AC, Dymov S, Labonte B, Szyf M, Turecki G, Meaney MU: Epigenetic regulation of the glucocorticoid receptor in human brain associates with childhood abuse. Nat Neurosci 2009, 12;342-348.

- 13. Jirtle RL, Skinner MK: Enviormental epigenomics and disease susceptibility. Nat Rev Genet 2007, 8:253-262.
- 14. Felsenfeld G. A brief history of epigenetics. Cold spring harbor perspectives in biology 2014; 6(1): doi: 10.1101/cshperspect.a018200.

Holliday R. Epigenetics: a historical overview. Epigenetics 2006; 1(2): 76-80.

Choudhuri S. From Waddington's epigenetic landscape to small noncoding RNA: some important milestones in the history of epigenetics research. Toxicology mechanisms and methods 2011; 21(4): 252-274.

- 15. Peedicavil J. The importance of cultural inheritance in psychiatric genetics. Med Hypotheses 2002; 58 : 164-6.
- 16. Holliday R. The inheritance of epigenetic defects. Science1987; 238 : 163-70.
- 17. Jones PA, Takai D. The role of DNA methylation in mammalian epigenetics. Science 2001; 293 : 1068-70.
- 18. Issa J-P. Epigenetic variation and human disease. J Nutr 2002; 132 (Suppl 8) : 2388-92S.

Zelent A, Waxman S, Carducci M, Wright J, Zweibel J, Gore SD. State of the translational science: summary of Baltimore workshop on gene re-expression as a therapeutic target in cancer January 2003. Clin Cancer Res 2004;10 : 4622-9.

Miyamoto K, Ushijima T. Diagnostic and therapeutic applications of epigenitics. Jpn J Clin Oncol 2005; 35:293-301.

 Abdolmaleky HM, Zhou JR, Thiagalingam S, Smith CL. Epigenetic and pharmacoepigenomic studies of major psychoses and potentials for therapeutics. Pharmacogenomics 2008; 9(12): 1809-1823.

Kim YI. Nutritional epigenetics: impact of folate deficiency on DNA methylation and colon cancer susceptibility. The journal of nutrition 2005; 135(11): 2703-2709.

- 20. Li E. Chromatin modification and epigenetic reprogramming in mammalian development. Nat Rev Genet. 2002;3:662-673.
- 21. Bird AP. CpG-rich islands and the function of DNA methylation. Nature. 1986;321:209-213.
- 22. Bird A. DNA methylation patterns and epigenetic memory. Genes Dev. 2002;16: 6–21.
- 23. Costello JF, Plass C. Methylation matters. J Med Genet 2001; 38 : 285-303.
- 24. Brueckner B, Lyko F. DNA methyltransferase inhibitors: old and new drugs for an epigenetic cancer therapy. Trends Pharmacol Sci 2004; 25 : 551-4.
- 25. Egger G, Liang G, Aparicio A, Jones PA. Epigenetics in human disease and prospects for epigenetic therapy. Nature 2004; 429 : 457-63.
- 26. Jenuwein T, Allis CD. Translating the histone code. Science 2001; 293 : 1074-80.
- Hake SB, Xiao A, Allis CD. Linking the epigenetic 'language' of covalent histone modifications to cancer. Br J Cancer 2004; 90 : 761-9.
  Herman JG, Baylin SB. Gene silencing in cancer in association with promoter hypermethylation. N Engl J Med 2003; 349 : 2042-54.
- 28. Lu C, Thompson CB. Metabolic regulation of epigenetics. Cell metabolism 2012; 16(1): 9-17.
- 29. Sapp J. Concepts of Organization the Leverage of Ciliate Protozoa. A Conceptual History of Modern Embryology. Germany: Springer; 1991.
- 30. Kadauke S, Blobel GA. Mitotic bookmarking by transcription factors. Epigenetics and chromatin 2013; 6(6): DOI: 10.1186/1756-8935-6-6.
- 31. Lodhi N, Kossenkov AV, Tulin AV. Bookmarking promoters in mitotic chromatin: poly (ADP-ribose) polymerase-1 as an epigenetic mark. Nucleic acids research 2014; 42(11): 7028-7038.
- Beedle AS, Buklijas T, Gluckman PD, Hanson MA, Low FM. Epigenetic mechanisms that underpin metabolic and cardiovascular diseases. Nat Rev Endocrinol. 2009;5:401.

Mattson MP, Kruman II, Duan W. Folic acid and homocysteine in age-related disease. Ageing Res Rev. 2002;1:95-111.

- Hirabayashi Y, Gotoh Y. Epigenetic control of neural precursor cell fate during development. Nat Rev Neurosci. 2010;11:377–388.
  Meissner A, Mikkelsen TS, Gu H, et al. Genome-scale DNA methylation maps of pluripotent and differentiated cells. Nature. 2008;454:766–770.
- Amir RE, Van den Veyver IB, Wan M, Tran CQ, Francke U, Zoghbi HY. Rett syndrome is caused by mutations in X-linked MECP2, encoding methyl-CpGbinding protein 2. Nat Genet. 1999;23:185–188.

- 35. Wren JD, Garner HR. Data-mining analysis suggests an epigenetic pathogenesis for type 2 diabetes. J Biomed Biotechnol. 2005;2005:104–112.
- 36. Hanahan D, Weinberg RA. Hallmarks of cancer: the next generation. Cell. 2011;144:646-674.
- 37. Mataga M, Rosenthal S, Heerboth S, et al. Anti-breast cancer effects of histone deacetylase inhibitors and calpain inhibitor. Anticancer Res. 2012;32:2523–2530.

Frew A, Lindemann R, Martin B, et al. Combination therapy of established cancer using a histone deacetylase inhibitor and a TRAIL receptor agonist. Proc Natl Acad Sci U S A. 2008;105(32):11317–11322.

Sarkar S, Faller DV. T-oligos inhibit growth and induce apoptosis in human ovarian cancer cells. Oligonucleotides. 2011;21(1):47–53.

Sarkar S, Horn G, Moulton K, et al. Cancer development, progression, and therapy: an epigenetic overview. Int J Mol Sci. 2013;14:21087–21113.

- 38. Byler S, Goldgar S, Heerboth S, et al. Genetic and epigenetic aspects of breast cancer progression and therapy. Anticancer Res. 2014;34:1071– 1077.
- 39. Hewagama A, Richardson B. The genetics and epigenetics of autoimmune diseases. Journal of autoimmunity 2009; 33(1): 3-11.
- 40. Greer JM, McCombe PA. The role of epigenetic mechanisms and processes in autoimmune disorders. Biologics 2012; 6: 307.
- 41. http://www.drugfreeworld.org/drugfacts/heroin/international-statistics.html.
- 42. Volkow ND, Baler RD. Addiction science: Uncovering neurobiological complexity. Neuropharmacology 2014; 76: 235-249.
- 43. Meissner, A. Epigenetic modifications in pluripotent and differentiated cells. Nature Biotech. 28, 1079–1088 (2010).
- de Ruijter, A. J., van Gennip, A. H., Caron, H. N., Kemp, S. & van Kuilenburg, A. B. Histone deacetylases (HDACs): characterization of the classical HDAC family. Biochem. J. 370, 737–749 (2003).
- 45. Finnin, M. S. et al. Structures of a histone deacetylase homologue bound to the TSA and SAHA inhibitors. Nature 401, 188–193 (1999).
- 46. Sauve, A. A. Sirtuin chemical mechanisms. Biochim. Biophys. Acta 1804, 1591–1603 (2010).

Sauve, A. A., Wolberger, C., Schramm, V. L. & Boeke, J. D. The biochemistry of sirtuins. Annu. Rev. Biochem. 75, 435-465 (2006).

- 47. Choudhary, C. et al. Lysine acetylation targets protein complexes and co-regulates major cellular functions. Science 325, 834–840 (2009).
- 48. Marks, P. A. The clinical development of histone deacetylase inhibitors as targeted anticancer drugs. Expert Opin. Investig. Drugs 19, 1049–1066 (2010).

Butler, L. M. et al. Suberoylanilide hydroxamic acid, an inhibitor of histone deacetylase, suppresses the growth of prostate cancer cells in vitro and in vivo. Cancer Res. 60, 5165–5170 (2000).

- 49. Chuang, J.C. & Jones, P.A. Epigenetics and microRNAs. Pediatr. Res. 61, 24R-29R (2007).
- Zhou, S.F., Wang, B., Yang, L.P. & Liu, J.P. Structure, function, regulation and polymorphism and the clinical significance of human cytochrome P450 1A2. Drug Metab. Rev. 42, 268–354 (2010).

Jiang, Z. et al. Search for an association between the human CYP1A2 genotype and CYP1A2 metabolic phenotype. Pharmacogenet. Genomics 16, 359–367 (2006).

- Ghotbi, R. et al. Allele-specific expression and gene methylation in the control of CYP1A2 mRNA level in human livers. Pharmacogenomics J. 9, 208–217 (2009).
- 52. Baker, E.K. & El-Osta, A. MDR1, chemotherapy and chromatin remodeling. Cancer Biol. Ther. 3, 819–824 (2004).
- Gagnon, J.F., Bernard, O., Villeneuve, L., Têtu, B. & Guillemette, C. Irinotecan inactivation is modulated by epigenetic silencing of UGT1A1 in colon cancer. Clin. Cancer Res. 12, 1850–1858 (2006).
- 54. Ferreri, A.J. et al. Aberrant methylation in the promoter region of the reduced folate carrier gene is a potential mechanism of resistance to methotrexate in primary central nervous system lymphomas. Br. J. Haematol. 126, 657–664 (2004).