# The Effect of DNA Hypomethylation on the Process of Breast Cancer

Mehrnaz Ajorloo and Saeed Soroush

## Introduction:

Cancer is a disease that ranks first in the world in terms of mortality and morbidity, and regardingly breast cancer that can be caused by environmental and genetic factors. Therefore, more detailed studies and studies on the effect of epigenetic factors in cancer. Breasts can lead to practical results in preventing and treating them. As we know, the set of controlled processes that cause hereditary changes in gene expression and mark the gene independent of a change in the nucleotide sequence of DNA is epigenetic. The direct or indirect factors in this process are the expression of microRNAs. They change in the cell, and amputation in these mechanisms certainly leads to the activation or inhibition of various messenger pathways and the development of cancer. Hypermethylation of epigenetic mechanisms in specific promoters can activate the expression of inappropriate oncogenes and act as a tumoral suppressor gene in breast cells in the hypermethylated form. More than 100 hypermethylene genes have been identified in breast tumors with breast cancer cell lines in recent research. Most of these methylated genes play an important role in the cell cycle of the apoptotic cell cycle. It is a cell, and its increasing expression inhibits the transition from G1 to S cell cycle. This gene is often found in breast cancer and is the first event in the development of this cancer.

## Results:

We found a progressive decrease in global DNA methylation from healthy tissues to the primary tumors and, in turn, to their associated metastases, suggesting a successive loss of DNA methylation during tumorigenesis. This phenomenon was further underlined by primary component analysis, which revealed growing distances as cancer progressed. The reduction in the level of DNA methylation caused a more heterogeneously methylated genome, illustrated by the loss of the association between methylation levels of neighbouring CpG sites, demonstrating that hypomethylation happened randomly rather than at discrete consecutive CpG sites. The oncogenic progression in the colon triplet could also be discovered at locus points that gain DNA methylation, such as differentially methylated sections hyper methylated in the primary cancer compared with the in line healthy tissue, which then gained methylation strengths in the metastasis. Despite the increase in DNA methylation intensity, the number of hypermethylated differentially methylated regions increased only marginally taken from the primary colon tumor or the matched liver metastases. Considering that the number of hypomethylated differentially methylated regions more than doubled from the primary colon tumor to the metastasis, resulting in global DNA hypomethylation, we hypothesize that DNA methylation is progressively lost during tumorigenesis, whereas DNA hypermethylation may underlie positive clonal selection in the metastatic process.

Functional modifications of DNA methylation in human tumour overlap with regulatory vital sections, such as the transcription start site or enhancers. Given the impact of DNA methylation on transcriptional activity and hence cellular phenotypes, we aimed to comprehensively profile the DNA methylation landscape for regions actively contributing to gene regulation in normal tissues and to determine their variation among cancers. Although genome wide, the majority of CpGs are greatly methylated, discrete sections show strikingly lesser methylation levels at successive CpG sites. These hypo methylated sections are related with the availability of the transcriptional machinery and transcription elements, and mark epigenetically active sites within the DNA methylome. Promoters of transcribed genes constantly harbor HMRs, and past the promoter context HMRs are supposed to mark cis-regulatory elements. Hence, we suggest that the DNA methylation landscape is an informative genomic feature that facilitates the interpretation of the genetic code and the identification of functional alterations in human cancers.

## Conclusion:

The variation in DNA methylation was very much greater in tumor samples in which two-thirds of the genome was affected by potential consequences for gene expression and tumor cell heterogeneity. DNA methylation is altered in cancer, we have so far only been able to speculate about its magnitude. Therefore, we comprehensively profiled the DNA methylation landscape at base-pair resolution of numerous normal samples and cancer samples representing the most frequent cancer types. In line with previous studies using equivalent technologies, we observed a general consistency of DNA methylation levels in a large proportion of normal somatic cells

From a functional perspective, we identified distinct HMRs with common and tissue-specific characteristics, which are probably essential for cell maintenance and cell-type-specific functions, respectively. Both types were greatly altered in the cancer context, with probable consequences for cell integrity and identity. In particular, DNA hypermethylation proved to be a very frequent event in all cancer types, and is probably involved in neoplastic transformation as a disease-driving event. Genetically defined cancer genes were epigenetically silenced in an unselective or cancer-type-specific manner. Potentially positively selected alterations were consistently mutually exclusive, suggesting that they actively contribute to neoplastic transformation and progression.

*Name: Mehrnaz Ajorloo[1] and Saeed Soroush[2]*

*Afiliation: [1]Avicenna research Center, Shahid Beheshti University of medical science, Shiraz University of medical science, Iran [2]Guilan University of medical science, Iran*
*Email: mehrnazajorloo@yahoo.com*