

UNDERSTANDING CANCER: Epigenetics 101

This PIP Digest provides an overview of epigenetics and its importance in understanding cancer causation and prevention.

Key Concepts

- Epigenetics definition
- Epigenetic mechanisms: DNA methylation and histone modification
- Social epigenomics

Related PIP Digest

- Understanding Cancer: Genetics 101

Epigenetics are what makes us unique – and the reason why one identical twin is taller than another, or one develops cancer and the other does not. “Epi” is Greek for above, over, on, or in addition to, so epigenetics refers to changes in gene behaviour that do not involve changes to the genetic code itself but are over and above our underlying DNA. Environmental factors can turn genes off or on without changing the code. Sometimes these changes make the difference between being sick or healthy. Epigenetic changes can be influenced by factors including fetal environment, age, lifestyle, drug use, stress levels, socioeconomic factors and much more.

Epigenetics focuses on processes that regulate how and when certain genes are turned on and turned off, while epigenomics pertains to the analysis of epigenetic changes across many genes in a cell or entire organism.¹

Epigenetic Mechanisms

The approximately two metres of DNA in a human cell wraps tightly around proteins called “histones.” Both DNA and histones are covered with chemical “tags” which make up the “epigenome.” The epigenome shapes the physical structure of the genome. It can cover certain genes making them “unreadable,” and therefore inactive. It can also expose genes, allowing them to activate.

Epigeneticists and epigenomicists study these chemical tags to understand how they regulate gene activation. When epigenomic compounds attach to DNA and modify its function, they are said to have ‘marked’ the genome.

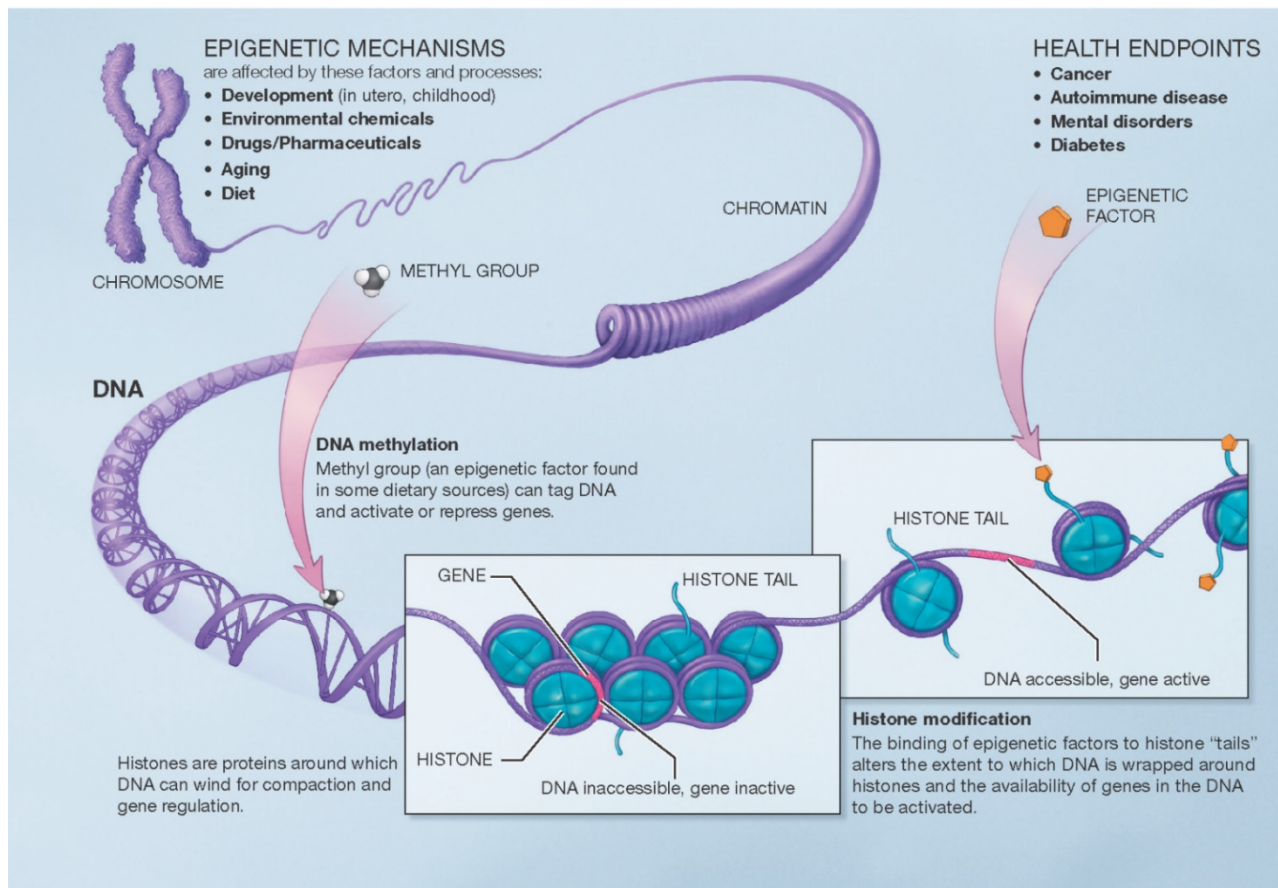
¹From: <https://epi.grants.cancer.gov/epigen.html>.

“Accumulated” changes describe marks that persist through rounds of cell division. “Inherited” changes are those passed down from one generation to the next.

The epigenome can mark DNA in two ways. The first is called **DNA methylation**, which occurs when certain chemical tags called “methyl groups” attach to the backbone of a DNA molecule. DNA methylation can activate or repress gene expression. When this process goes awry, it can cause diseases like cancer. For example, DNA hypomethylation can activate cancer-causing “oncogenes” and lead to chromosome instability. Entire or partial chromosomes can be duplicated or deleted. DNA hypomethylation is frequently found in the genes of colorectal cancer cells.

The second way that the epigenome can mark the DNA is called “**histone modification.**” This occurs when chemical tags attach to the tails of histones. Histone modifications alter the ability of a gene to be transcribed (copied into RNA) and expressed. Global histone modification patterns have been connected to prostate, breast, and pancreas cancers.

Importantly, cancer cells leave a distinct epigenetic signature, which means epigenetic changes can be used as useful biomarkers for the prevention, early diagnosis, and treatment of cancers. The diagram below illustrates the epigenetic mechanisms.



Graphic from the U.S. National Institutes of Health (<https://commonfund.nih.gov/epigenomics/figure>).



The Canadian Epigenetics, Environment and Health Research Consortium (CEEHRC) (<http://www.epigenomes.ca/>) is a national network of epigenetic researchers focused on building research capacity, developing software, expanding tools and resources, and facilitating access to epigenomic data. It is funded by the Canadian Institutes of Health Research and Genome Canada.

It includes Epigenomics Mapping and Data Coordination Centres in Vancouver (BC Cancer in partnership with Genome BC) and Montréal (McGill University in partnership with Genome Quebec). The CEEHRC Network is also part of the International Human Epigenome Consortium (IHEC) (<http://ihc-epigenomes.org/>) a global consortium that provides high-resolution reference human epigenome maps, both for normal and disease cell types, to help the research community reduce redundancy.

Social Epigenomics

Social epigenomics is an emerging area of cancer research. It is the study of how social experiences affect genes and biology. This research area may provide important insights and answers to reduce health disparities among different socioeconomic groups.

“Health disparities may arise not only because of higher exposure to environmental hazards among certain population groups, but also as a result of the synergistic effect of exposure to multiple environmental hazards and social stressors. Operating through epigenomic changes, adverse social and environmental experiences early in life may predispose an individual to dysfunctional physiological response and to future stressors in adulthood.”²

References:

- U.S. National Human Genome Research Institute. *Epigenomics Fact Sheet*. <https://www.genome.gov/about-genomics/fact-sheets/Epigenomics-Fact-Sheet>
- Genetic Science Learning Center, University of Utah. "Epigenetics." <https://learn.genetics.utah.edu/content/epigenetics/> July 15, 2013. Accessed July 9, 2019.

² From <https://epi.grants.cancer.gov/epigen.html>.

These videos will help to expand your understanding of epigenetics:

- MinuteEarth. *Why Inheritance Is Weirder Than We Thought: Epigenetics*. (YouTube) November 18, 2015 [2:47 minutes]
<https://www.youtube.com/watch?v=AvB0q3mg4sQ>
- University of Utah. *The Epigenome at a Glance* (Learn.Genetics) [1:47 minutes]
<https://learn.genetics.utah.edu/content/epigenetics/intro/>
- The Royal Institution. *What is Epigenetics? with Nessa Carey*. (YouTube) April 8, 2015 [39:25 minutes]
https://www.youtube.com/watch?v=9DAcJSAM_BA
- KidCareCanada. *Epigenetics Explained*. (YouTube) October 26, 2011 [1:22 minutes]
https://www.youtube.com/watch?time_continue=82&v=L-_53c-Gzg8

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