OPEN ACCESS Freely available online

Epigenetics Research: Open Access

Perspective

Selection of Cell Type for Epigenetic Regulation

Ayman Ahmed*

Department of Epigenetics, Zagazig University, Sharqia Governorate, Egypt

DESCRIPTION

Ten years after the consensus sequence of the human genome was published, more data on gene variation in disease susceptibility has emerged. Numerous genetic variants that are associated with a trait or disease phenotype have been discovered through genome search techniques like candidate gene association studies, family-based studies, and genome-wide association studies. However, only a small percentage of the sample's total phenotypic variance can be explained by any combination of these variants in any given study. Heritable trait phenotypic variation is must, therefore it comes from other sources. An organism's ability to adapt to a changing environment is made possible by epigenetic mechanisms, which provide an adaptive layer of control over the regulation of gene expression.

Epigenetic regulation alters chromatin structure, nuclear organization, and transcript stability, all of which contribute to an increase in the functional complexity of Deoxyribonucleic Acid (DNA). Long-term molecular and functional consequences independent of the DNA sequence that may ultimately define an individual's phenotype may result from these modifications, which may influence gene expression in an additive or synergistic manner. DNA is present in identical copies in each organism's nucleated cell. However, the phenotypes of various cell types are characterized by a variety of structural and functional differences caused by variations in gene expression. Transcriptional and posttranscriptional aspects of gene expression are controlled by epigenetic mechanisms. When utilizing any of the methods that have been previously described, it is necessary to take into consideration the dynamic changes that are specific to a cell type and occur through epigenetic mechanisms during development and in disease states.

Many of the tissues of interest for epigenetic profiling, such as cardiac muscle and cerebral spinal fluid, require invasive procedures, making them unavailable for clinical research. Surrogate tissue epigenetic profiles can be used to evaluate and track epigenetic status in more distant tissues. Among the circulating cells in peripheral blood are Peripheral Blood Mononuclear Cells (PBMCs), which are either involved in or exposed to molecular signals generated by disease processes in distant tissues. Importantly, it is simple and inexpensive to obtain samples of peripheral blood.

A set of genes that are sensitive to the trait or condition of interest may be identified by analyzing the global epigenetic expression of PBMCs. An "epigenetic signature" that can be used to measure changes over time is provided by these expression patterns. New mechanistic pathways involved in a condition's pathophysiology may be identified by these signatures. PBMCs have been used to study epigenetic changes in heart failure and transplant rejection, among other conditions. The significance of neuro-immunomodulation in these disease states is emphasized by these studies. Researchers may be able to identify additional biomarkers that are capable of determining changes in health status thanks to the sensitivity of PBMCs as mediators of inflammatory processes.

By providing mechanisms for modifying cellular processes, epigenetic regulation increases the functional complexity of DNA. An examination of both the DNA sequence and the epigenetic modulation of gene expression are necessary for a comprehensive comprehension of health and disease. There are a number of different kinds of epigenetic regulation, and there are a number of different ways to describe them. The number of samples that will be analyzed, the quantity of DNA that is available, the nature of the samples, and the resources that are available all influence the choice of method. A deeper comprehension of additional forms of epigenetic regulation and the ways in which they interact with genetic variation will be made possible through the steady improvement of existing methods and the gradual development of new ones.

CONCLUSION

To precisely respond to both internal and external environmental cues, epigenetic control mechanisms may interact in a synergistic or additive manner. The comprehension of gene expression and protein regulation will improve if we can identify differentially expressed mechanisms and the hierarchical relationships involved in epigenetic regulation. Comparative studies of the epigenetic mechanisms that are involved in physiologic processes may reveal transcriptional and translational

Correspondence to: Ayman Ahmed, Department of Epigenetics, Zagazig University, Sharqia Governorate, Egypt, E-mail: man@bue.edu.eg

Received: 30-May-2023, Manuscript No. EROA-23-25356; **Editor assigned:** 01-Jun-2023, PreQC No. EROA-23-25356 (PQ); **Reviewed:** 15-Jun-2023, QC No. EROA-23-25356; **Revised:** 22-Jun-2023, Manuscript No. EROA-23-25356 (R); **Published:** 29-Jun-2023, DOI: 10.35248/EROA.23.5.140

Citation: Ahmed A (2023) Selection of Cell Type for Epigenetic Regulation. J Epigenetics Res. 5:140.

changes in genes that can be used to create biomarkers and therapeutic targets for particular diseases. An improved comprehension of the epigenetic regulation of gene expression in conjunction with genomics may provide a more comprehensive of human health and the progression of various diseases.