ISSN: 2157-2518
Journal of Carcinogenesis & Mutagenesis

OPEN ACCESS Freely available online

Commentary

Gene Expression Modulation by Epigenetic alterations in Cancer

Paula Argente*

Department of Oncology, The Affiliated Cancer Hospital of Nanjing Medical University, Nanjing, China

DESCRIPTON

Gene expression is a fundamental biological process through which genetic information encoded in DNA is transcribed into RNA and then translated into proteins that perform essential cellular functions. Proper regulation of gene expression ensures normal cell growth, differentiation, and response to environmental signals. Dysregulation of this process, however, can lead to uncontrolled cell proliferation, evasion of apoptosis, and other hallmarks of cancer. Understanding the mechanisms governing gene expression has therefore become central to the study of carcinogenesis and the development of targeted therapies.

Gene expression is controlled at multiple levels, including transcription, RNA processing, translation, and post-translational modifications. Transcriptional regulation is mediated by promoters, enhancers, silencers, and transcription factors that interact with DNA to either initiate or suppress RNA synthesis. Epigenetic modifications, such as DNA methylation and histone modification, further modulate accessibility of transcriptional machinery to specific genes. In cancer, hypermethylation of tumor suppressor gene promoters often silences protective pathways, while hypomethylation can activate oncogenes, contributing to tumor initiation and progression.

Post-transcriptional regulation also plays a significant role in gene expression. Alternative splicing allows a single gene to produce multiple protein isoforms with diverse functions, and aberrant splicing patterns are frequently observed in malignancies. Non-coding RNAs, particularly microRNAs (miRNAs) and long non-coding RNAs (lncRNAs), can influence gene expression by degrading messenger RNAs or inhibiting their translation. Dysregulation of these molecules has been linked to cancer cell survival, metastasis, and resistance to chemotherapy.

Translation, the process of synthesizing proteins from messenger RNA, is another critical control point. Alterations in translation initiation factors, ribosomal proteins, or signaling pathways such as the mTOR pathway can lead to enhanced production of proteins that support cancer growth. Additionally, post-translational modifications such as phosphorylation, acetylation, and ubiquitination further fine-tune protein activity, localization, and stability, ultimately influencing cellular behavior.

The study of gene expression in cancer has been revolutionized by high-throughput technologies such as RNA sequencing, microarrays, and single-cell transcriptomics. These tools enable comprehensive profiling of gene expression patterns across different tumor types and stages, revealing distinct molecular signatures associated with prognosis, treatment response, and metastatic potential. Identification of such signatures has facilitated the development of personalized medicine approaches, allowing clinicians to tailor therapies based on the gene expression profiles of individual tumors.

Targeting aberrant gene expression has become a promising therapeutic strategy. Small molecules, antisense oligonucleotides, and RNA interference technologies can specifically modulate the expression of oncogenes or restore tumor suppressor activity. Additionally, drugs targeting epigenetic regulators indirectly influence gene expression, reversing aberrant silencing or activation of critical genes in cancer cells. Combining gene expression based therapies with conventional chemotherapy, immunotherapy, or targeted agents offers potential for enhanced efficacy and reduced resistance.

In conclusion, gene expression is a tightly regulated process essential for normal cellular function and organismal health. Its dysregulation plays a central role in the initiation and progression of cancer, affecting multiple molecular pathways and cellular behaviors. Advances in genomic and transcriptomic technologies have expanded our understanding of gene expression patterns in tumors, providing novel biomarkers and therapeutic targets. Continued exploration of gene expression regulation will not only deepen our insight into carcinogenesis but also guide the development of precision medicine strategies, ultimately improving cancer diagnosis, treatment, and patient outcomes.

Correspondence to: Paula Argente, Department of Oncology, The Affiliated Cancer Hospital of Nanjing Medical University, Nanjing, China, E-mail: paula@argente.cn

Received: 01-Jul-2025, Manuscript No. JCM-25-30113; **Editor assigned:** 03-Jul-2025, PreQC No. JCM-25-30113; **Reviewed:** 17-Jul-2025, QC No. JCM-25-30113; **Revised:** 24-Jul-2025, Manuscript No. JCM-25-30113; **Published:** 31-Jul-2025, DOI: 10.35248/2157-2518.25.16.002

Citation: Argente P (2025). Gene Expression Modulation by Epigenetic alterations in Cancer. J Carcinog Mutagen. 16:002.