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The Epigenetic Landscape of Colorectal Cancer: Unveiling Mechanisms and Therapeutic Potentials

Tango Akinsanpe*

Department of Public Health, Obafemi Awolowo University, Ile Ife 220103, Osun State, Nigeria

Introduction

Colorectal Cancer (CRC) remains a significant health burden worldwide, with its etiology often involving complex interplay between genetic and environmental factors. However, recent research has shed light on the critical role of epigenetic alterations in driving CRC development and progression. Epigenetic modifications, including DNA methylation, histone modifications and non-coding RNA regulation, contribute to the dysregulation of gene expression patterns, ultimately leading to tumorigenesis. This article aims to delve into the intricate mechanisms of epigenetic alterations in CRC, their clinical implications and the emerging therapeutic strategies targeting epigenetic dysregulation [1].

Aberrant DNA methylation patterns, particularly CpG island hypermethylation and global hypomethylation, are hallmark features of CRC. Hypermethylation-mediated silencing of tumor suppressor genes, such as MLH1, CDKN2A and APC, promotes CRC initiation and progression. Global hypomethylation leads to genomic instability and activation of oncogenes, exacerbating CRC aggressiveness. DNA methylation signatures serve as diagnostic, prognostic and predictive biomarkers in CRC management [2].

Description

Histone modifications, including acetylation, methylation, phosphorylation and ubiquitination, regulate chromatin structure and gene expression in CRC. Dysregulation of histone modifying enzymes, such as HDACs, HATs and HMTs, contributes to CRC pathogenesis. Histone modification patterns are associated with CRC subtypes, stage and patient outcomes, offering insights into disease heterogeneity and progression. MicroRNAs long non-coding RNAs and circular RNAs exert regulatory effects on gene expression networks in CRC. Dysregulated miRNAs, such as miR-21, miR-34a and miR-200 family members, modulate CRC proliferation, invasion and metastasis. lncRNAs, such as HOTAIR and MALAT1, participate in CRC Epithelial-Mesenchymal Transition (EMT) and chemoresistance. CircRNAs, like circHIPK3 and circRNA_100290, serve as diagnostic biomarkers and therapeutic targets in CRC management.

Epigenetic signatures offer promising biomarkers for CRC detection, risk stratification and early diagnosis. DNA methylation panels, histone modification profiles and non-coding RNA signatures enhance the accuracy of CRC screening and surveillance programs. Epigenetic alterations provide valuable prognostic indicators and predictive markers for CRC patient outcomes and treatment responses. Integrating epigenetic biomarkers into clinical decision-making improves personalized treatment strategies and long-term survival rates in CRC. Targeting epigenetic modifiers, such as DNA methyltransferases histone deacetylases and non-coding RNAs, represents a promising therapeutic approach in CRC. Epigenetic inhibitors, including DNMT inhibitors and HDAC inhibitors demonstrate efficacy in preclinical models and clinical trials for CRC treatment. Combination therapies incorporating epigenetic agents with conventional chemotherapy, immunotherapy, or targeted therapies hold potential for overcoming drug resistance and improving CRC patient outcomes [3].

Further elucidation of the dynamic interplay between genetic and epigenetic alterations in CRC is warranted to unravel novel therapeutic targets and predictive biomarkers. Precision medicine approaches integrating multi-omics data, including genomics, epigenomics, transcriptomics and proteomics, offer personalized treatment strategies tailored to individual CRC patients. Overcoming challenges related to epigenetic heterogeneity, tumor microenvironment interactions and drug resistance mechanisms remains critical for optimizing epigenetic-based therapies in CRC [4,5].

Conclusion

Epigenetic alterations play a pivotal role in CRC pathogenesis, offering invaluable insights into disease biology, diagnosis, prognosis and therapeutic interventions. Harnessing the therapeutic potential of epigenetic modifiers holds promise for improving CRC patient outcomes and advancing precision oncology strategies in the era of personalized medicine. Continued research efforts aimed at deciphering the epigenetic landscape of CRC are essential for translating scientific discoveries into clinical benefits for patients afflicted by this deadly disease.

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Conflict of Interest

There are no conflicts of interest by author.

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***Address for Correspondence:** Tango Akinsanpe, Department of Public Health, Obafemi Awolowo University, Ile Ife 220103, Osun State, Nigeria; E-mail: Tan.ankinsa89@gmail.com*

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