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Letter to the Editor

Epigenetics, Epigenomics, and Personalized Medicine

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Dear Editors,

The field of epigenetics is transforming our understanding of gene regulation by providing insights into how exposure to pathogens, environmental factors, and lifestyle choices can impact gene expression without changing the sequence of genomic DNA.[1] Epigenetics involves alterations in gene activity that do not modify the genetic code itself but can be inherited by future generations.[2] These changes play a critical role in controlling gene expression during development and in response to environmental cues. Epigenomic research expands this focus to a genome-wide level, documenting the complete set of epigenetic modifications throughout the genome.[3] Recent progress in epigenetic research has shown that mechanisms, including DNA methylation, histone modifications, and interactions with non-coding RNAs (ncRNAs), play significant roles in normal physiology as well as in disease development. For example, abnormal patterns of DNA methylation have been associated with cancer, as excessive methylation leads to the suppression of tumor suppressor genes, thereby contributing to tumor formation.[4,5]

ncRNAs, such as microRNAs (miRNAs), long non-coding RNAs (lncRNAs), small interfering RNAs (hereinafter referred to as siRNAs), and PIWI-interacting RNAs, are crucial in regulating gene expression through various mechanisms at both the transcriptional and post-transcriptional levels. These regulatory processes are vital for maintaining cellular balance and are frequently disrupted in diseases, especially cancer and neurodegenerative disorders.

ncRNAs are pivotal in controlling gene expression through epigenetic regulation, particularly in human development and disease. These ncRNAs significantly impact chromatin structure, transcription, and post-transcriptional gene expression. Among the most well-known ncRNAs involved in epigenetic regulation are miRNAs, lncRNAs, and siRNAs. For example, lncRNAs can recruit chromatin-modifying complexes to specific genomic sites, altering the chromatin state and either activating or suppressing the transcription of target genes. Research shows that ncRNA epigenetics influences nearly all aspects of RNA metabolism, controlling the stability of ncRNAs, the processing of miRNAs, the competing endogenous RNA network, and the interaction between lncRNAs and RNA-binding proteins.

The potential of epigenetic therapies is significant, as they provide the opportunity to reverse harmful epigenetic changes. Medications targeting specific epigenetic modifications, such as histone deacetylase inhibitors, are currently under investigation for their therapeutic potential in cancer and other illnesses.[6] The fields of epigenetics and epigenomics are unveiling new possibilities in medical research, offering hope for innovative treatments and improved health outcomes (Fig. 1).[7] To discover epigenetic mechanisms that impact complex traits and diseases, it is crucial for medical researchers to combine animal models with human clinical and population-based approaches. This includes investigating key periods of vulnerability, assessing environmental and dietary influences, and exploring cell type-specific epigenetic patterns. Highlighting the significance of this research for public health is essential as we further explore the epigenome.[8] Understanding how lifestyle factors such as diet, exercise, and stress affect the epigenome can lead to new preventive strategies and personalized medicine approaches. The regulation of gene expression in a cell is controlled by epigenetic modifications. The fields of epigenetics and epigenomics are opening up fresh opportunities in medical research, providing optimism for innovative therapies and enhanced health outcomes. The emerging field of epigenomics is reshaping the healthcare landscape by offering profound insights into disease mechanisms.[9–11] This knowledge is paving the way for personalized treatments, driving the development of novel therapies, and offering strategies for disease prevention and overall health promotion.

Epigenetic data holds the promise of guiding the development of targeted therapies that directly combat abnormal epigenetic alterations associated with various diseases. This is particularly evident in cancer, where therapies can be tailored to reactivate inactive tumor suppressor genes or inhibit hyperactive oncogenes.[12,13] Drugs that alter epigenetic states, such as DNA methyltransferase inhibitors or histone deacetylase inhibitors, aim to treat conditions, such as cancers and neurodegenerative diseases.[14] These treatments have the potential to be customized based on the individual epigenetic changes present in a patient's illness. Epigenetics investigates heritable changes in gene expression without altering the DNA sequence, playing a crucial role in precision medicine. Epigenetic modifications such as DNA methylation, histone modification, and regulation by ncRNAs are pivotal in controlling gene expression.[15,16] Despite the potential of epigenetics in precision medicine, challenges remain. Current epigenetic therapies, such

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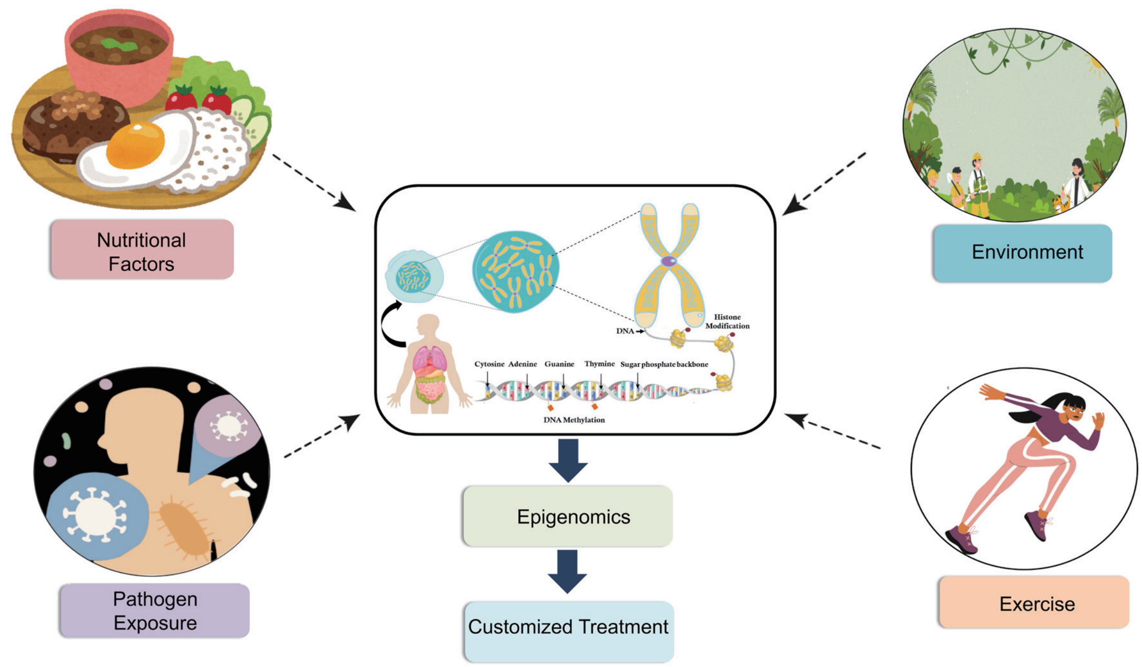

Fig. 1. Impact of various factors on the expression of genome.

as DNA methyltransferase inhibitors and histone deacetylase inhibitors, lack specificity, leading to off-target effects. This lack of specificity increases the risk of toxicity and limits drug effectiveness, especially in cancer, where distinguishing between normal and malignant cells is essential. Additionally, the reversibility of epigenetic changes presents a dual challenge for therapy: while it allows for the correction of harmful modifications, it also means the therapeutic effects may be temporary. To address these challenges, researchers are developing more efficient delivery systems, such as nanoparticles or targeted delivery vectors. Epigenetic changes are dynamic and reversible, influenced by factors such as age, environment, and disease state, making it difficult to identify stable and reliable biomarkers.[17,18] However, epigenetics is poised to revolutionize precision medicine by offering insights into disease mechanisms. As the field advances, integrating epigenetic data into precision medicine will lead to more effective personalized healthcare solutions, ultimately improving patient outcomes.[9,19] By gaining deeper insights into the epigenome, medical professionals can offer personalized interventions that account for an individual's unique genetic makeup, environmental influences, and lifestyle, leading to improved health outcomes and more effective healthcare systems.[20] The timing of environmental influences and genetic factors significantly impacts disease onset. A primary objective would be to investigate and establish connections between alterations in DNA methylation patterns and the development of diseases.[21] In epigenetics, a comprehensive research approach could involve closely monitoring individuals exposed to environmental factors over extended periods. Such studies aimed to provide conclusive evidence of whether exposure directly triggers these epigenetic modifications, rather than merely coinciding with them. The integration of various omics approaches (genomics, epigenomics, transcriptomics, proteomics, metabolomics) with data on environmental exposures allows researchers to better understand how genetic and environmental factors interact through epigenetic mechanisms to drive disease development.[22] This approach offers more thorough insights into disease mechanisms, facilitating the identification of biomarkers, therapeutic targets, and personalized interventions. The field of epigenomics holds the potential to revolutionize precision medicine and healthcare by enabling personalized prediction, prevention, and treatment of diseases, promising significant improvements in individualized patient care and outcomes.

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Conflict of interest

The authors declare no conflict of interest.

Author contributions

All the authors made substantial contributions to the preparation of the manuscript. Conceptualizing and conceiving the idea, formal analysis, project administration, supervision, validation, and writing - reviewing and editing (GKP, KBS), data curation, formal analysis, investigation, methodology, and writing - original draft (SM, RD, AS). All the authors have read and approved the final manuscript before submission.

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