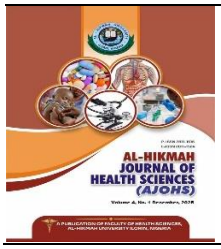
P-ISSN: 2811-1516
E-ISSN: 2811-1524



AL-HIKMAH JOURNAL OF HEALTH SCIENCES (AJOHS)

Official Publication of Faculty of Basic Medical Sciences

Al-Hikmah University Ilorin, Nigeria

https://alhikmahuniversity.edu.ng/AJOHS/index.php/journal

Review Article

Environmental Epigenetics and Its Clinical Relevance to Healthcare Delivery in Nigeria: A Narrative Review of Evidence

Imam-Fulani A.Y.[1], Yusuf A.O.[1*], Buhari A. O.[2], Lawal A. Y.[1], Mahmmud Z.A.[1], Abdulkabir A.A.[1], Ibrahim R.M.[1], Ibrahim Z.J.[1], Yakubu U.R.[1], Kolapo R.O.[1], Abdulraheem I.S.[1]

[1]Department of Community Medicine and Public Health, Faculty of Basic Medical Sciences, Al-Hikmah University, Ilorin, Nigeria

[2]Department of Nursing Sciences, Faculty of Allied Health Sciences, University of Abuja

ARTICLE INFO

Article History
Received: 19th September, 2026
Accepted: 10th October, 2026
Available online: 15th November, 2026

Keywords:
Environmental epigenetics
DNA methylation
Non-communicable diseases
Precision medicine
Nigeria

Corresponding Author:

Yusuf A. O.
Department of Community Medicine and Public Health, Faculty of Basic Medical Sciences, Al-Hikmah University, Ilorin, Nigeria.

Email: olayiwolakakarash@gmail.com

ABSTRACT

Introduction: Environmental epigenetics examines how environmental exposures influence gene regulation without altering the DNA sequence, providing a mechanistic link between pollution, nutrition, toxic metals, psychosocial stress and chronic disease.

Objective: To review current evidence on environmentally induced epigenetic changes and their clinical and public health relevance to healthcare delivery in Nigeria.

Methods: A narrative review with a structured literature search was conducted, prioritising peer-reviewed and authoritative sources published from 2020 to September 2026.

Results: Environmental exposures are associated with changes in DNA methylation, chromatin regulation and non-coding RNA activity, with reported links to cancer, cardiovascular, metabolic and respiratory diseases, biological ageing and mental-health outcomes.

Conclusion: Environmental epigenetics provides a useful framework linking modifiable exposures with disease and may strengthen prevention, research and future precision healthcare in Nigeria.

Please cite this article as: Imam-Fulani, A. Y., Yusuf, A. O., Buhari, A. O., Lawal, A.Y., Mahmmud, Z. A., Abdulkabir, A. A., Ibrahim, R. M., Ibrahim, Z. J., Yakubu, U.R., Kolapo, R.O. & Abdulraheem, I.S. (2026). Environmental Epigenetics and Its Clinical Relevance to Healthcare Delivery in Nigeria: A Narrative Review of Evidence. *Al-Hikmah Journal of Health Sciences, 5*(3), 287-292.

Introduction

Traditionally, environmental health has focused on the effects of physical, chemical, biological and social exposure on disease. Environmental epigenetics is another layer of this relationship, which involves the study of how epigenetic changes to the regulation of genes are caused by environmental exposures, but not by changes in the nucleotide sequence of DNA. Recent studies have proposed the epigenome to be a dynamic regulatory system that is sensitive to the environment throughout life, such as air pollution, diet, toxic chemicals, psychosocial stress and lifestyle factors. The most extensively studied mechanisms are DNA methylation, post-translational modification of histone proteins and regulation by non-coding RNAs, but with the advancement of modern research, the roles of chromatin remodelling, mitochondrial function, and extracellular vesicles and the epitranscriptome are being added to this list of mechanisms (Wu et al., 2023; Faraji & Metz, 2026).

P-ISSN: 2811-1516
E-ISSN: 2811-1524

DNA methylation commonly involves the addition of methyl groups to cytosine residues, particularly at CpG sites. The effect of DNA methylation on transcriptional activity depends on its genomic context. These epigenetic changes may be tissue-specific, reversible or adaptive and do not necessarily represent permanent or harmful changes or establish a causal relationship with disease. These processes offer plausible pathways by which environmental exposures might give rise to long-lasting alterations in cell function (Wu et al., 2023; Faraji & Metz, 2026).

Methods

This narrative review used a structured literature search to examine recent evidence on environmental epigenetics and its relevance to healthcare in Nigeria. We focused mainly on peer-reviewed studies and credible reports published between January 2020 and September 2026. The search covered environmental exposures, DNA methylation, histone modification, non-coding RNA, epigenetic ageing, biomarkers, precision medicine and related health outcomes. Relevant studies were selected based on their contribution to understanding epigenetic mechanisms, clinical applications and public-health implications. The findings were then organised around key themes, including major environmental exposures, molecular pathways, clinical translation and their relevance to the Nigerian healthcare setting.

Results and Thematic Synthesis

Core epigenetic mechanisms linking environmental exposure to disease

The recent literature consistently identifies DNA methylation, histone modification and non-coding RNA regulation as principal epigenetic pathways linking environmental exposures with altered cellular behaviour. DNA methylation is the most extensively investigated mechanism in human environmental epidemiology. Histone modifications change chromatin accessibility, while microRNAs and long non-coding RNAs influence gene expression after transcription. Contemporary environmental-health research increasingly places these mechanisms within broader networks involving oxidative stress, inflammatory signalling, mitochondrial function and metabolic regulation rather than treating each mechanism in isolation (Wu et al., 2023; Faraji & Metz, 2026).

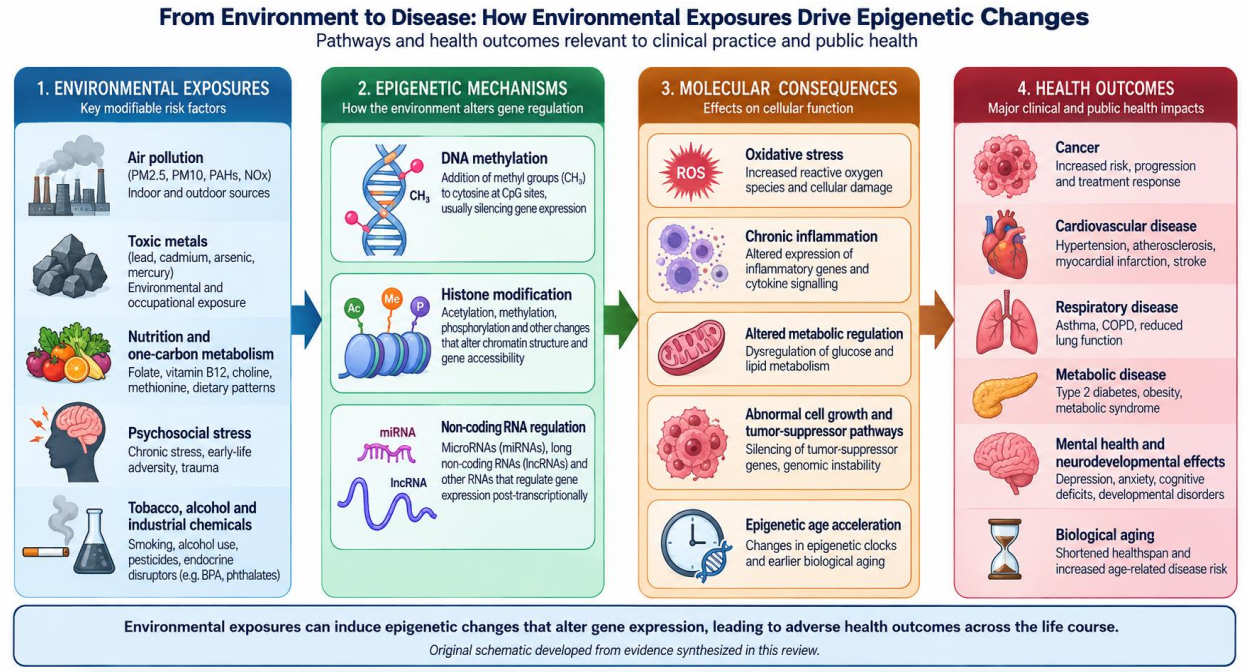


Figure 1. Integrated pathway from environmental exposure to epigenetic change and health outcomes. The figure summarises major exposures, core epigenetic mechanisms, downstream molecular effects and representative disease outcomes. Original schematic developed by the authors from evidence synthesised in this review (Source: Prepared by the author, 2026).

P-ISSN: 2811-1516
E-ISSN: 2811-1524

Table 1. Major environmental exposures, epigenetic mechanisms and health relevance.

Environmental exposure	Principal epigenetic pathway	Recent evidence	Health relevance	Nigerian relevance	References
Air pollution, PM2.5, PAHs and combustion products	Differential DNA methylation; histone changes; altered ncRNA expression	Systematic and mechanistic studies report exposure-associated methylation changes and inflammatory/oxidative-stress pathways, with substantial heterogeneity.	Respiratory and cardiovascular disease, cancer, inflammation and biological aging.	Household biomass use, traffic emissions, generators and industrial pollution create important exposure pathways.	Wu et al. (2021); Wu et al. (2023)
Lead, cadmium, arsenic and other metals	Global and locus-specific DNA methylation; histone and miRNA dysregulation	Recent reviews find the largest human evidence base for lead, cadmium and arsenic, including prenatal exposure studies.	Neurodevelopmental, carcinogenic, cardiovascular and metabolic effects.	Mining, contaminated soil/water, informal recycling and occupational exposure are relevant concerns.	Elkin et al. (2022)
Nutrition and one-carbon metabolism	Availability of methyl donors influences DNA and histone methylation	Folate, vitamin B12, choline and related one-carbon nutrients are associated with methylation patterns, although effects vary by tissue, timing and baseline status.	Development, metabolism and disease susceptibility.	Maternal nutrition, micronutrient deficiency and food insecurity may affect sensitive developmental periods.	Amenyah et al. (2020)
Combined exposures / exposome	Interactions among epigenetic and multi-omic pathways	Current research increasingly integrates epigenomics with transcriptomics, metabolomics and lifetime exposure assessment.	May better explain cumulative risk and complex chronic disease than single-exposure models.	Highly relevant where pollution, poor nutrition, stress and chemical exposure occur together.	Faraji and Metz (2026).

Source: (Authors' synthesis, 2026).

Air Pollution and Household Energy Exposure

Air pollution is a major environmental exposure of relevance to public health in Nigeria. The biological effects are not just on the lungs. Fine particles induce oxidative stress and inflammatory signalling in the lungs which may have systemic effects. The epigenetic changes reported in the literature encompass DNA methylation changes, as well as changes in expression of non-coding RNAs affecting inflammation, oxidative stress and vascular regulation (Wu et al., 2021; Wu et al., 2023).

Heavy metals and environmental toxicants

Environmental metals may affect the epigenome by regulating DNA methylation, histone modifications, oxidative stress and microRNA pathways. In recent years, with increasing focus on early life exposures to lead, cadmium, and arsenic, these have been the most widely studied metals according to a recent review of human and toxicological evidence (Elkin et al., 2022). The best evidence relates to methylation differences observed in tissues in contact with the exposure, but may differ depending on the dose, timing, tissue and analytical method.

P-ISSN: 2811-1516
E-ISSN: 2811-1524

Nutrition, One-Carbon Metabolism and Developmental Epigenetics

Nutrition is closely linked to epigenetic regulation through one-carbon metabolism. Nutrients such as folate, vitamin B12, choline and methionine contribute to the production of S-adenosylmethionine, an important methyl donor. In adults, a 2020 systematic review and meta-analysis reported that there were significant associations between one-carbon nutrients and DNA methylation, with high methodological variation (Amenyah et al., 2020).

Psychosocial stress and biological embedding

Psychosocial conditions can be transmitted biologically via epigenetic mechanisms. More recent epigenome-wide studies have investigated how maternal depression and anxiety and early life adversity and trauma are associated with DNA methylation. Drzymalla et al. (2023) conducted a systematic review of prenatal maternal mental health and infant epigenetic profiles and identified several differentially methylated regions with biological plausibility, although replication of individual CpG findings across studies remained limited.

Epigenetic ageing and cumulative exposure to the environment

Epigenetic clocks use DNA methylation patterns to estimate biological or epigenetic age. Epigenetic clocks are more commonly used to estimate morbidity, mortality, or physiological decline than chronological age. Kusters and Horvath (2025) describe these measures as promising public-health biomarkers, and remind that interpretation needs to take into account the differences between race, sex, lifestyle, environment, and population.

Fadadu et al. (2025) reviewed 102 studies involving over 180,000 participants and reported greater epigenetic age acceleration with exposure to air pollution and cigarette smoke, with less consistent findings for metals.

Clinical translation: Biomarker, liquid biopsy and epigenetic therapy

The best example of clinical translation is cancer. Epigenetic dysregulation has been observed in tumors and often plays a role in tumour initiation, progression, immune escape and resistance to therapeutic interventions. This understanding has supported the development of diagnostic and prognostic biomarkers, as well as therapies targeting epigenetic enzymes (Suraweera et al., 2025).

Analysis of methylation patterns of cell-free DNA (cfDNA) is one of the most promising developments in the realm of diagnostics. Tissue- and disease-associated methylation signals can be carried by DNA in plasma (Pan et al., 2025).

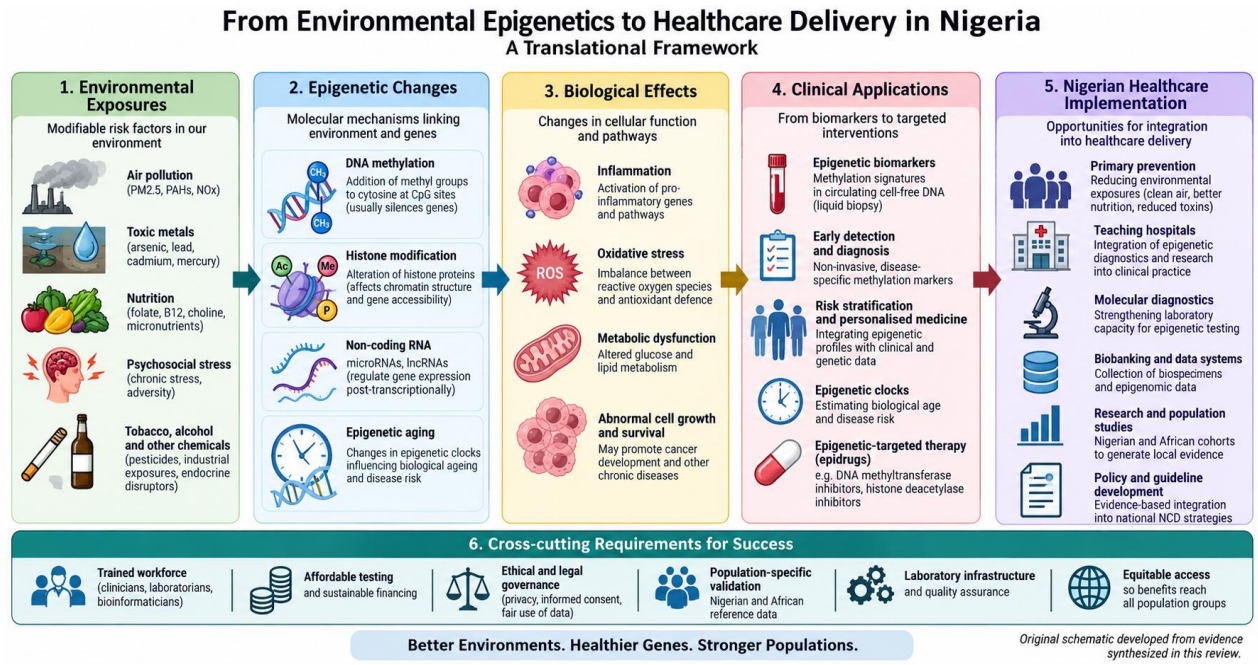


Figure 2. Translational framework from environmental epigenetics to healthcare delivery in Nigeria. The figure links exposure, epigenetic change, biological effects and clinical applications with implementation requirements including workforce, laboratory infrastructure, governance, affordability, population-specific validation and equitable access. Original schematic developed by the authors from evidence synthesised in this review (Source: Prepared by the author, 2026).

P-ISSN: 2811-1516
E-ISSN: 2811-1524

Table 2. Current and emerging clinical applications of epigenetics

Application	Epigenetics	Current evidence/status	Main limitations	Potential Nigerian relevance	References
Cancer liquid biopsy	Tumour-associated cfDNA methylation signatures	Rapidly developing; systematic reviews support diagnostic and prognostic potential.	Low ctDNA in early disease, cost, standardisation and bioinformatics.	Long-term potential for less-invasive diagnosis and monitoring in tertiary centres.	Pan et al. (2025)
Colorectal cancer methylation markers	SEPT9, SDC2, MYO1G, JAM3 and multi-marker methylation panels	Recent systematic review identifies promising blood-based markers for early detection.	Sensitivity varies by stage and assay; population validation remains necessary.	Could eventually complement, not automatically replace, established screening.	Khabbazpour et al. (2024)
Epigenetic clocks	Age-associated DNA methylation signatures	Useful research biomarkers of biological aging and exposure response.	Different clocks measure different constructs; limited clinical thresholds and African calibration.	Initially most useful for research on environmental exposure and NCD risk.	Kusters and Horvath (2025); Fadadu et al. (2025)
DNA methyltransferase inhibitors	Pharmacological reduction of abnormal DNA methylation	Established therapeutic principle in selected haematological malignancies.	Toxicity, resistance, cost and specialist monitoring.	Tertiary oncology/haematology relevance and professional education.	Suraweera et al. (2025)

Source: (Authors' synthesis, 2026).

Implications for healthcare delivery in Nigeria

The importance of environmental epigenetics to the Nigerian health care is more in the field of prevention, reduction of exposure and research capacity rather than in the field of universal epigenomic testing. Cleaner household energy, improvement of ventilation, pollution control, safe mining and waste disposal, occupational protection, proper nutrition for mothers, tobacco control and psychosocial support are interventions for which there is public-health value. Epigenetic evidence provides a biological basis for these interventions, but routine methylation testing is not necessary before established preventive measures are implemented.

Discussion

The findings of this review support the role of environmental epigenetics as a valuable framework for understanding how environmental exposures influence gene regulation and long-term health outcomes. Current evidence extends beyond a simple distinction between "genes" and "environment" and instead supports a dynamic interaction among environmental exposures, genomic background, epigenetic regulation and downstream cellular pathways throughout the life course (Wu et al., 2023; Faraji & Metz, 2026).

High-throughput methylation assays are more widely available than most other types of assays that have been developed in human environmental research, which is why the methylation process is the most commonly studied. But methylation data can be variable. Results may vary based on exposure dose, timing, tissue, age, sex, ancestry, nutrition, smoking and co-exposures. This is one of the main reasons why a 'statistically significant' methylation difference should not be viewed as a diagnostic biomarker or causal mediator.

Conclusion

P-ISSN: 2811-1516
E-ISSN: 2811-1524

Environmental epigenetics is increasingly important for understanding how environmental pollutants, toxic metals, nutrition, psychosocial stress, tobacco and other exposures influence molecular regulation and health. Evidence from 2020–2026 links environmental exposures with alterations in DNA methylation, chromatin regulation, non-coding RNA activity and epigenetic ageing, although the magnitude and direction of these associations vary by tissue, population, exposure and study design. The field is gradually moving from biological explanation toward clinical translation.

For Nigeria, the immediate value of environmental epigenetics may not yet be in routine testing for everyone, but in improving prevention, research and understanding of how environmental exposures contribute to disease. Strengthening local expertise, laboratory capacity and population-based research will be important in building evidence that reflects Nigerian communities. Over time, this can help move useful epigenetic discoveries from research into affordable and practical healthcare applications.

Recommendations

1. Nigerian health authorities should strengthen interventions that reduce modifiable environmental exposures, including household air pollution, unsafe occupational exposures, tobacco smoke, toxic metals and preventable nutritional deficiencies.
2. Universities should integrate core environmental epigenetics, molecular biomarkers, liquid biopsy and precision-health concepts into relevant medical and public-health curricula.
3. Teaching hospitals and research institutions should expand molecular diagnostics, biobanking, bioinformatics and quality-assurance capacity through sustainable local investment and equitable research partnerships.

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