REVIEW ARTICLE

ENVIRONMENTAL CARCINOGENS AND THE FUTURE OF CANCER PREVENTION: LEVERAGING GENOMIC SURVEILLANCE AND ARTIFICIAL INTELLIGENCE IN PERSONALIZED PREVENTION OF CANCER.

Abstract

Air pollutants, industrial chemicals, and contaminated water are all sources of environmental carcinogens and have been identified as top contributors to the rise in global cancer burden. There is an inequality that exists between developed and developing countries when it comes to the risk of exposure to environmental carcinogens. Lack of regulatory oversight, environmental monitoring, and health care infrastructures are top contributors to the risk of exposures in developing countries. This paper employs a narrative review methodology, drawing on interdisciplinary literature from environmental health, cancer genomics, and artificial intelligence to explore innovative approaches to cancer prevention. AI technologies have made it possible to interpret complex data sets such as genomic profiles, environmental exposure records, and clinical histories, especially with machine learning and deep learning. This paper carefully analyzed the challenges that exist which include, including data privacy, genetic discrimination, algorithm bias, limited funding, and infrastructure gaps in low-resource settings, and this collectively calls for policy reforms, international cooperation, interdisciplinary collaborations, and engagement in community activities. In conclusion, integrating genomic surveillance and AI is a game changer to cancer prevention, changing its scope from reactive care to tailored, personalized treatment interventions.

KEYWORDS: Environmental Carcinogen, Genomic Surveillance, Artificial Intelligence, Cancer Prevention.

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Introduction

Cancer is one of the leading causes of death globally, with an estimated 19.3 million cases and 10 million deaths as reported in the year 2020 by the World Health Organization (WHO) (Deo et al., 2022). With the aging population, lifestyle changes, and continuous exposure to environmental carcinogens, it has been projected that the burden of this disease will increase significantly in the coming decade (De Guzman & Schiller, 2025; Mbemi et al., 2020). Lifestyle factors such as smoking, diet, and physical inactivity are known to be potential risk factors, but environmental exposures to agents like industrial chemicals, heavy metals, radiation, and contaminated water or soil play a huge role in cancer development (Iwasaki et al., 2023). Environmental agents have been classified by the International Agency for Research on Cancer (IARC) into different groups, with asbestos, benzene, formaldehyde, arsenic, and fine particulate matter (PM2.5) as group 1 carcinogens because of the strong evidence of their carcinogenicity in humans (Blanco et al., 2023). It is worth noting that exposure to carcinogenic materials is unbalanced in the populations: those living in low-income countries are at higher risk of being exposed to high levels of environmental toxins due to bad regulatory frameworks, industrialization without safety equipment, and limited access to proper health care. This inequality has led to a form of environmental bias where the weight of environmentally induced cancers affects the most vulnerable. Despite the growth in cancer treatment and identification of risk factors, preventing this disease remains a huge burden (Larsen et al., 2023). Recent cancer prevention strategies only focus on behavioral modification and screening, with little focus on detection and environmental hazards. Systems for monitoring environmental carcinogens are disorganised and even nonexistent in many regions (Klein et al., 2021). Notwithstanding, conventional epidemiological approaches take time to capture new risk trends, and they cannot combine complex data sets that involve genetics, environmental exposures, and social determinants of health (Zhao et al., 2024). The introduction of genomic surveillance and artificial intelligence (AI) has brought about a game-changing opportunity to change the course of cancer prevention from a reactive to a predictive, precision-based model. Genomic surveillance enables the identification of molecular signatures and mutations associated with carcinogen exposure long before the commencement of the disease. In the same vein, AI technologies can process large environmental, genomic, and clinical data to recognize patterns, predict risk trajectories, and support public health decision-making at scale (O’Connor & McVeigh, 2025a). This paper aims to examine the scope and impact of environmental carcinogens on global cancer incidence, explore the role of genomic surveillance in identifying cancer risks linked to environmental exposures, and investigate how AI technologies can enhance public health responses by integrating environmental and genomic data.

1. Environmental Carcinogens

1.1 Definitions and Classifications of Environmental Carcinogens

Environmental carcinogens are agents present in the air, water, or soil that can bring about the development of cancer in humans. They may be naturally occurring or artificial, and the hazardous nature depends on different factors such as exposure levels, duration, and individual susceptibility (Wogan et al., 2004; Manisalidis et al., 2020). Carcinogens have been classified into five groups based on their ability to induce cancer by the International Agency for Research on Cancer (IARC). A specialized agency of the World Health Organization (WHO)

Group 1: carcinogenic to humans (e.g., asbestos, benzene, formaldehyde, arsenic, ultraviolet radiation, outdoor AIr pollution)

Group 2a: probably carcinogenic to humans (e.g., glyphosate, emissions from high-temperature frying)

Group 2b: possibly carcinogenic to humans (e.g., lead compounds, chloroform)

Group 3: not classifiable as to its carcinogenicity to humans

Group 4: probably not carcinogenic to humans

Group 1 agents are of the highest public health concern due to robust human evidence of carcinogenicity.

1.2. Epigenetic Changes from Pollutants

Environmental pollutants can induce epigenetic alterations, which are heritable changes in gene expression that do not involve alterations in the DNA sequence. These include DNA methylation, histone modification, and non-coding RNA regulation. Persistent exposure to AIr pollutants like PM2.5, diesel exhaust, and heavy metals (e.g., cadmium, arsenic) can dysregulate these epigenetic mechanisms. For example, arsenic exposure has been associated with global DNA hypomethylation, which can activate oncogenes, as well as hypermethylation of tumor suppressor gene promoters like p16INK4a, leading to their silencing. Histone modifications, such as altered acetylation and methylation patterns, can also disrupt chromatin structure, promoting a shift in gene expression that favors uncontrolled cell division. Moreover, exposure to environmental toxins can affect the expression of microRNAs (miRNAs), which regulate the translation of mRNAs involved in cell proliferation, apoptosis, and DNA repair. Dysregulated miRNA profiles have been identified in populations exposed to high levels of AIr pollution, linking environmental exposure to post-transcriptional gene regulation in cancer pathways. These epigenetic changes are reversible but can persist long enough to contribute significantly to cancer initiation and progression.

1.3 Sources of Environmental Carcinogens

Environmental carcinogens are from different sources, and they are often related to industrialization, urbanization, and agricultural practices

• Air pollutants particulate matter (PM2.5), nitrogen dioxide (NO₂), and polycyclic aromatic hydrocarbons (PAHS) from vehicular emissions, industrial processes, and biomass burning are known to cause lung and bladder cancers. Ambient AIr pollution is now identified as a group 1 carcinogen by IARC.

• Arsenic contamination, most especially from groundwater, has been a serious burden in regions like South Asia and sub-Saharan Africa.

• Industrial chemicals: Continuous exposure to chemicals such as benzene, formaldehyde, and vinyl chloride, frequently used in manufacturing and construction, may cause hematologic malignancies and liver cancers (Poynter et al.,2017).

• Pesticides: Some insecticides and herbicides, like organophosphates and glyphosate, have been associated with increased risks of non-Hodgkin lymphoma and other cancers, most especially in populations with high occupational exposure (Roos et al., 2021).

• Occupational exposures: individuals who work in mining, construction, agriculture, and chemical industries are occupationally exposed to carcinogenic materials such as asbestos, silica dust, PAHs, and solvents. This puts them at risk of cancer development. (Manisalidis et al., 2020)

 2. Global Cancer Trends Due to Environmental Carcinogenesis

Environmental carcinogenesis has contributed to shaping the pattern of global cancer, leading to an increase in the cancer burden. Exposure to environmental carcinogens such as AIr pollutants, heavy metals, pesticides, and radiation has increased due to industrialization, urbanization, and climate change, especially in underdeveloped countries (Ochieng et al., 2015). The World Health Organization stated that nearly one in five cancer deaths can be linked to environmental and occupational exposures worldwide. Studies have shown that there is an increase in the incidence of environmentally induced cancers in developing regions, where industrial growth is greater than the available regulatory control policies. For instance, sub-Saharan Africa and South Asia have experienced increased rates of liver and bladder cancers linked with aflatoxin-contaminated food and arsenic-laden drinking water, respectively (Hashim & Boffetta, 2014). Meanwhile, in developed countries, there is a decline in the incidence of cancer mortality due to timely detection and environmental regulation. This inequality underscores the interface between environmental injustice and cancer epidemiology. Underprivileged populations face a dual burden: increased exposure to carcinogens and a lack of healthcare infrastructure for prevention and treatment. To reduce the effect, global cancer control strategies must integrate environmental monitoring, public health interventions, and policies to combat pollution and occupational hazards(Arnold et al., 2016). Without a strategic initiative, cancers driven by environmental factors will continue to rise and increase the gap in cancer outcomes in vulnerable regions (Omotoso et al., 2023).

3.0 Mechanism of carcinogenesis

1. Genotoxic vs. Non-genotoxic Carcinogens

Based on the mechanism of carcinogenesis, carcinogens are broadly classified into genotoxic and non-genotoxic. Genotoxic carcinogens cause direct damage to DNA, which would ultimately lead to mutations interfering with normal cell cycle regulation. Benzene, aflatoxins B1, and polycyclic aromatic hydrocarbons (PAHs) bind with DNA to form adducts, leading to point mutations, insertions, or chromosomal aberrations (Hartwig et al., 2020). Based on the mechanism of carcinogenesis, carcinogens are broadly classified into genotoxic and non-genotoxic. Genotoxic carcinogens cause direct damage to DNA, which would ultimately lead to mutations interfering with normal cell cycle regulation (Hartwig et al., 2020). Benzene, aflatoxins B1, and polycyclic aromatic hydrocarbons (PAHs) bind with DNA to form adducts, leading to point mutations, insertions, or chromosomal aberrationsCell signaling pathways may be altered by these agents and they may also promote epigenetic reprogramming or increase their susceptibility to other genotoxic agents(Chatterjee & Walker, 2017). Even though they do not cause direct damage like the genotoxic agents, they contribute to tumorigenesis by making the tissue microenvironment conducive for malignant transformation(Correia & Bissell, 2012). Fig. 1 shows how carcinogens can cause cancer through two main pathways. Genotoxic pathways directly damage DNA, while non-genotoxic pathways disrupt cell signaling, cause inflammation, and suppress the immune system. Both mechanisms lead to genomic instability, uncontrolled cell growth, and cancer development



Fig 1. Overview of genotoxic and non-genotoxic effects of carcinogens: Carcinogens follow two primary pathways: genotoxic and non-genotoxic. Genotoxic effects include DNA adduct formation, chromosome aberrations, and mis-segregation, leading to direct genomic damage. Non-genotoxic effects involve inflammation, oxidative stress, receptor-mediated signaling, immunosuppression, and epigenetic silencing. Both mechanisms result in genomic instability, altered cell signaling, resistance to apoptosis, and uncontrolled cell growth—hallmarks of cancer progression. (Anetor et al., 2012) Chemical Carcinogenesis: Risk Factors, Early Detection and Biomedical Engineering." *Biomedical Science, Engineering and Technology* 69–90.<https://doi.org/10.5772/20209>

2. Oxidative Stress and Inflammation Pathways

Oxidative stress is a common feature of many environmental carcinogens. It is a condition where reactive oxygen species (ROS) are produced rapidly, overpowering the cell’s antioxidant defense. DNA damage, lipid peroxidation, and protein oxidation are consequences of chronic oxidative stress, all of which can disrupt cellular functions and encourage carcinogenesis. For example, nucleotide bases and DNA strands are damaged by tobacco smoke, and Airborne particulate matter generates ROS. In the same vein, chronic inflammation, a known driver of cancer, is often induced by oxidative stress(Pizzino et al., 2017). Inflammatory cytokines such as IL-6, TNF-α, and NF-κB are overexpressed in response to tissue damage and ROS, bringing about a pro-tumorigenic environment. These cytokines induce angiogenesis, suppress apoptosis, and promote cell proliferation, which are distinguishing features of cancer. Immune cells are recruited as a result of inflammation, leading to the release of additional ROS and reactive nitrogen species (RNS), further increasing the cycle of tissue damage and accumulation of mutations (Yu et al., 2022). Oxidative stress and inflammation create a good environment for the development and progression of cancer, thereby improving genetic instability, interfering with the cellular repair mechanisms, and changing the tumor microenvironment (Reuter et al., 2010).

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Fig 2: Oxidative Stress–Mediated Inflammatory Pathways in Cancer Progression. Oxidative stress activates key transcription factors such as NF-κB, AP-1, HIF-1α, Nrf-2, and the NLRP3 inflammasome complex. This activation promotes the release of inflammatory mediators, including TNF-α, TGF-β, and various interleukins. These mediators, in turn, generate further oxidative stress and sustain a chronic inflammatory response. The resulting inflammation facilitates cancer progression and metastasis, creating a self-perpetuating cycle between oxidative stress, inflammation, and tumor development Vaidya et al., 2020 Oxidative Stress and Inflammation Can Fuel Cancer. In: Maurya, P., Dua, K. (eds) *Role of Oxidative Stress in Pathophysiology of Diseases. Springer, Singapore.* https://doi.org/10.1007/978-981-15-1568-2\_14.

4. Disproportionate Impacts on Vulnerable Populations and Low-Resource Regions

The unequal distribution of exposures to environmental carcinogens between first-world countries and third-world countries is a huge burden. The underdeveloped countries are often without regulatory systems, monitoring infrastructures, and public awareness mechanisms. In that vein, individuals live near industrial cones, waste sites, or contaminated water sources without adequate protection or health monitoring (Hashim & Boffetta, 2014). In rural areas, exposure to pollutants from indoor cooking with biomass, pesticides, or water from uncontrolled sources is inevitable due to a lack of enforcement of regulatory policies. Occupational safety standards are not adhered by workers, and they are inherently exposed to high levels of carcinogens (Okafor et al., 2025). These disparities, combined with limited access to good health care facilities, will eventually lead to late diagnosis, advanced disease at presentation, and lower chances of survival (Rumchev et al., 2007).

5. Genomic Surveillances in Cancer Prevention

5.1 Understanding Genomic Surveillance

Genomic surveillance has to do with the step-by-step collection, sequencing, and analysis of genetic data to monitor changes in the genome, detect mutations, and recognize patterns that are in correlation with a certain disease risk or progression (Bianconi et al., 2023). In the scope of cancer prevention, genomic surveillance allows for the early detection of somatic mutations, DNA damage, and epigenetic alterations that may arise from continuous exposure to environmental carcinogens (Bianconi et al., 2023). Researchers can trace molecular signatures associated with carcinogen exposure, such as TP53 mutations from aflatoxin exposure or DNA adducts formed by polycyclic aromatic hydrocarbons (PAHs), by analyzing DNA from the population. Individuals at higher risk of developing cancers are identified by these genomic markers, and they serve as early warning signals. This timely approach can change the face of public health by taking cancer prevention from population-level screening towards personalized, risk-based intervention (Hollstein et al., 2013).



Fig 3: Molecular Surveillance Pipeline. The pipeline outlines the main concept of each process (sample collection, genotyping, clinical and metadata linkage, reporting, and public health response), and illustrates the solutions and roadblocks present at each stage of the pipeline. Asterisks in the genotyping section are representative of identified mutations in variant X (Ling-Hu et al., 2022). Challenges and Opportunities for Global Genomic Surveillance Strategies in the COVID-19 Era. *Viruses*, *14*(11), 2532. https://doi.org/10.3390/v14112532

5.2 Genomic Surveillance Tools in Cancer Prevention from Environmental Carcinogens

Tobacco smoke, ultraviolet (UV) radiation, and industrial chemicals are environmental carcinogens that lead to the development of cancer by inducing genetic and epigenetic alterations. Genomic surveillance, the continuous monitoring of these molecular changes, is necessary for the timely detection and prevention of cancer (Lawal, Taiye, et al., 2025). So many technologies are available, but a few tools have made an impact in reducing the risk of cancer caused by environmental exposures (Shehata et al., 2023)

A. Next-Generation Sequencing (NGS): The Cornerstone of Genomic Surveillance

Next-Generation Sequencing (NGS) has changed the scope of genomic surveillance by ensuring that comprehensive and rapid sequencing of DNA and RNA is done at an unprecedented scale. This technology is necessary for identifying mutations and structural variations induced by environmental carcinogens (Satam et al., 2023a). Researchers have been able to detect mutational patterns using these methods, and novel mutations and mutational signatures have also been discovered by NGS. This has improved our understanding of the progression of cancer induced by environmental carcinogens. (Satam et al., 2023b)

1. Liquid Biopsy: A Non-Invasive Window into Early Carcinogenesis

Traditional tissue biopsies are helpful, but they are quite invasive, and using them for regular surveillance is not feasible. Liquid biopsy, which can examine circulating tumor DNA (ctDNA) or other tumor-derived nucleic acids in blood, is the gold standard for non-invasive genomic surveillance (Cheng et al., 2016). It offers real snapshots of genetic alterations caused by carcinogens before tumors are even detected by capturing fragments of DNA shed from damaged or precancerous cells. This is helpful to individuals exposed to high-risk environmental agents, making it easier for frequent monitoring without invasive procedures. It is also used to track the progression of tumors and residual disease after intervention, supporting early adjustments in prevention and treatment strategies. It's highly sensitive and can detect low-frequency mutations, making it an appropriate tool in personalized cancer prevention (Cheng et al., 2016).

1. Mutation Signature Analysis: Linking Mutations to Environmental Causes

Mutation signature analysis is very useful for genomic data applications. It identifies distinct patterns of mutations caused by specific environmental carcinogens. Environmental agents are known to cause unique mutations, and they always leave a unique fingerprint. An example is tobacco smoke, which shows predominant C>A transversions and UV radiation inducing C>T transitions at dipyrimidine sites (Lawal, Egwuatu, et al., 2025). Examining these mutation signatures in patient samples using bioinformatic tools can identify the cause of cancer to its specific environmental exposure (Riva et al., 2020a). This information is a game-changing outcome in the prevention of cancer. It assists public health policies by detecting widespread carcinogenic sources in the population. It brings about a personalized prevention scheme by integrating individual genetic changes to specific exposures. Therefore, mutation signature analysis closes the gap between environmental epidemiology and molecular biology, ensuring targeted intervention(Riva et al., 2020b).

1. Epigenetic Profiling: Understanding the Hidden Impact of Carcinogens

Genetic mutations occur as a result of carcinogen exposure, but then epigenetic changes play a crucial role in carcinogenesis by altering gene expression without changing the DNA sequence. DNA methylation changes caused by carcinogens are detected using tools like bisulfite, providing early signs of altered cellular function preceding cancer development (Manić et al., 2022). Since epigenetic modifications can be changed, their recognition using genomic surveillance provides potential for preventive therapies that restore normal gene regulation. Genetic analysis is enhanced by Epigenetic profiling by adding another dimension to cancer risk assessment, making it an important part of comprehensive genomic surveillance (Baylin & Jones, 2016).

6. Opportunities and Limitations in Low-Resource Settings

Despite its prospects, the far-reaching integration of genomic surveillance in cancer prevention shows notable challenges, especially in underdeveloped countries. Limitations in infrastructures, such lack of sequencing facilities, biobanks, and data analytics capabilities, impede its fusion in routine public health practice (Ochola, 2025). Ethical concerns like data privacy, informed consent, and potential misuse of genetic information exist. Community engagement and public trust should be built, especially when working with populations historically marginalized or exploited in research. Notwithstanding, sequencing technologies and mobile health platforms are now more accessible, providing new opportunities for decentralized genomic data collection (Lee et al., 2025). With the right investment, underdeveloped countries can move from using traditional models to integrating genomic surveillance with digital health records, mobile diagnostics, and AI-powered analysis, creating a better and equitable cancer prevention infrastructure (Yeung et al., 2023).

7. Artificial Intelligence in Cancer Genomics

7.1 Role of Artificial Intelligence in Cancer Genomics

Artificial intelligence has transformed the terrain of public health genomics by the analysis of large and complex datasets within a short time with high accuracy. When used in cancer prevention, it can be linked to genomic, environmental, and clinical data to detect patterns, project disease risk, and bring about targeted solutions (Bajwa et al., 2021). AI models like machine learning and deep learning models have been developed to detect subtle genomic mutations and epigenetic changes that are related to environmental exposures long before they become symptomatic. They can stratify populations into risk levels, aiding in the timely detection of individuals who take advantage of the screening or preventative care (Jamialahmadi et al., 2024). An example is the IBM Watson Genomics project, which is used in oncology settings to compare patients’ genomic profiles with potential cancer therapies and determine carcinogenic exposures based on mutational patterns (Zhou et al., 2019). In China, AI-based genomic surveillance is used during a public health program to examine the effects of AIr pollution on the risk of lung cancer. They made use of satellite data on AIr quality, genetic sequencing from exposed populations, and cancer incidence registries to identify mutation hotspots induced by PM2.5 exposure (Xing et al., 2019). Pilot studies were carried out in sub-Saharan Africa to examine genetic susceptibility to aflatoxin-induced liver cancer. AI has enhanced genomic analysis, real-time risk modeling, automated biomarker recovery, and the improvement of healthcare delivery. Its integration with genomic surveillance tools has changed the course of cancer prevention (Amaeshi et al., 2025). Merging artificial intelligence (AI), genomic surveillance, and environmental monitoring is a game changer in cancer prevention, ensuring the early detection of carcinogenic exposures and personalized interventions (Lawal, Egwuatu, et al., 2025). This integrative framework connects continuous environmental data with molecular insights from genomic analysis, using AI to produce complex information and guide timely public health actions (Chapla et al., 2024). In genomic surveillance, DNA samples from exposed populations are analyzed to detect genetic mutations associated with cancer. By integrating this data with AI-powered analytics, gene-environment interactions can be recognized together with population-specific cancer risk that may go unnoticed. By combining data from different sources like remote sensing, health records, and genomic banks, algorithms can recognize cancer risk patterns and project the trajectory of disease. This method allows the early detection, risk stratification and targeted interventions which will ultimately lead to a reduction in environmentally induced cancers (O’Connor & McVeigh, 2025b).



FIG 4: Clinical applications of AI in early cancer diagnosis. Abbreviations: GP: general practitioner, NLP: natural language processing, EHR: electronic healthcare record, ML: machine learning, DL: deep learning, NGS: next-generation sequencing. Hunter et al., 2022. The Role of Artificial Intelligence in Early Cancer Diagnosis*. Cancers*. 14. 10.3390/cancers14061524.

7.2 Application of AI in Cancer Prevention

A. AI for Predictive Risk Modeling

Predictive risk assessment is one of the powerful applications of AI. Large volumes of genomic data, lifestyle factors, environmental exposures, and social determinants can be analyzed by AI algorithms to predict the probability of developing cancer. Polygenic risk scores can be used by machine learning models together with environmental data to determine individuals who are at risk of developing cancers such as lung, bladder, and even liver cancer (Khanna et al., 2023). AI has been used in breast cancer prevention to link BRCA mutation status, reproductive history, and hormone exposure to project future risk and suggest personalized screening schedules. These models enhance the accuracy of risk stratification, ensuring that timely and more personalized interventions are carried out (Ahn et al., 2023)

1. Early Detection through Biomarker and Imaging Analysis

AI is necessary for early detection, which is an important element in cancer prevention. In the detection of tumors and precancerous lesions that may be missed by human interpretation, deep learning algorithms can be used in mammograms, CT scans, and MRIs (Ayomide et al., 2024). Early detection of biomarkers is improved by the use of radigenomic models by integrating imaging findings with underlying genetic mutations (Bi et al., 2019). Furthermore, AI plays an important role in examining biomolecular data from minimally invasive samples. AI models can detect circulating tumor DNA (ctDNA), epigenetic changes, and abnormal protein expressions in blood through liquid biopsy analysis. These biomarkers are often present during asymptomatic periods, allowing for early and potentially life-saving intervention (Ginghina et al., 2022).

1. Environmental and Population-Level Surveillance

The integration of environmental and genomic data to detect cancer hotspots and vulnerable populations is being made possible by AI. Large datasets from environmental monitoring systems to hospital records can be scanned using natural language processing (NLP) tools to identify areas where cancer is prevalent (Maleki Varnosfaderani & Forouzanfar, 2024). For instance, AI has been used to lay out lung cancer trends in polluted urban areas by examining satellite AIr quality data together with local cancer registries. This is most valuable in developing countries, where traditional surveillance systems may be weak or disjointed (Lei, 2024).

1. AI for Public Education and Behavioral Interventions

AI is changing the course of health communication beyond diagnostics and surveillance. Personalized cancer prevention counsel based on an individual’s health profile and exposure history can be accessed using AI-powered apps and chatbots. Health literacy is promoted by these tools because complex genomic and environmental risks are translated into understandable messages (Goumas et al., 2024).

8. Real-World Implementations of Genomic Surveillance and AI in Cancer Screening

A. Genomic England’s 100,000 Genomes Project (United Kingdom)

The 100,000 Genomes Project, initiated by Genomic England, is one of the most transformative applications of genomic surveillance in cancer prevention. It was in collaboration with the UK’s National Health Service (NHS)(Oseghale et al., 2024). This ambitious initiative was aimed at sequencing 100,000 genomes from individuals with rare diseases and common cancers, by using genomic data with clinical records to enhance early diagnosis, treatment decisions, and public health strategies. Undetectable hereditary cancer syndromes were identified using standard diagnostic methods through this project. Whole-genome sequencing (WGS) was used, and researchers were able to reveal somatic mutations, gene fusions, and copy number variations in tumor DNA, which are necessary in understanding the behavior and aggressiveness of various cancers (Behrens et al., 2024). This project stood out with the integration of AI-driven analysis, which allowed the interpretation of a massive volume of sequencing data, signaling mutations with high clinical relevance(Caudai et al., 2021). The classification of variants was made possible by these AI tools, which can differentiate between benign polymorphisms and potentially harmful mutations, streamlining the process from sequencing to actionable clinical insights. Additionally, the project built the ground for population-wide screening models that consider genetic predisposition and environmental risk factors (Erfanian et al., 2023). The knowledge generated is being used in cancer screening programs across the NHS, focusing on high-risk individuals for frequent surveillance(Qurashi & Sharma, 2024).

B. Tempus Labs (United States)

For the advancement of cancer screening and treatment, personalization US-based precision medicine company, Tempus Labs, has been at the forefront of combining genomic surveillance with artificial intelligence. The next-generation sequencing (NGS) has been offered by this company, and it provides a comprehensive view of the molecular landscape of cancer patients. Its powerful AI platform makes it innovative as it draws a large, growing database of genomic, clinical, and therapeutic data AI algorithms compare unique molecular profiles of millions of anonymized records with a patient’s sequenced tumor gene to identify actionable mutations, potential drug targets, and relevant clinical trials (Ghoreyshi et al., 2025). Physicians are aided with this AI-enabled system, from general treatment protocols to personalized oncology care, especially in difficult cases like non-small cell lung cancer, breast cancer, and hematological malignancies. Notably, Tempus offers a liquid biopsy that can identify circulating tumor DNA (ctDNA) from blood samples, enhancing noninvasive cancer surveillance and early detection (Ladbury et al., 2023).

9. Challenges and ethical considerations

A. Data privacy and genetic discrimination: Genomic data is highly sensitive and should be confidential. When data is not protected, the software may be hacked, and patients may be at risk of genetic discrimination in employment, insurance, or society (Arshad et al., 2021).

B. Bias in AI algorithms and genomic datasets: Many AI models are trained on highly developed datasets, and this may lead to inaccurate predictions for underrepresented populations. This may worsen the health of the individual (Norori et al., 2021).

C. Infrastructure, capacity, and funding gaps in low- and middle-income countries (LMICS): The implementation of AI-driven surveillance in developing countries is a huge problem due to challenges in funding, thereby limiting their ability to participate in new development (Khan et al., 2024).

D. Need for regulatory oversight and public trust: Clear regulations should be established to ensure the ethical use of AI. Public trust can be developed through transparency, informed consent, and the participation of the community (Rossi & Lenzini, 2020).

9. Policy and implementation strategies

A. Building capacity in public health institutions: Building effective AI-enabled genomic surveillance for cancer prevention requires comprehensive policy frameworks and collaborative efforts across sectors. Developing public health infrastructure is crucial to genomic and AI surveillance. This can be made possible by investing in labs, professionals, data analytics, expertise, and training researchers to make use of these technologies efficiently (Akingbola et al., 2024).

B. International cooperation and data-sharing frameworks: In genomic surveillance, global collaboration and data-sharing frameworks are needed. International agreements from organizations like the Global Alliance for Genomics and health will ensure proper data sharing and promote transparency, equity and individual rights (Knoppers, 2014).

C. Community engagement and public education: Engaging in community activities and public education is necessary to build public trust and encourage individuals to participate in genomic surveillance. This can be made possible through awareness and culturally sensitive communication (Haga et al., 2013).

D. Role of interdisciplinary partnerships: Collaboration across different disciplines. Genomics, environmental science, informatics, and public health collaboration will build innovative solutions, better data integration, and equitable interventions (Javaid et al., 2024)

10. Future directions and research needs

A. Exposomics and AI-driven toxicogenomics: Exposomics, which is the study of environmental exposures and their impact on health, can revolutionize cancer prevention. Researchers can analyze complex data to determine gene-environment driven by cancer, allowing predictive models to identify high risk individuals with the use of AI-driven toxic o genomics (Petit & Vuillerme, 2025).

B. Longitudinal studies for gene-environment-cancer pathways: Longitudinal studies are necessary for understanding the relationship between genetic predispositions, environmental exposures, and cancer development with time. By tracing the progression of individuals from childhood to adulthood, researchers can detect biomarkers of cancer risk and understand how environmental factors influence gene expression and tumor progression (Motsinger-Reif et al., 2024).

C. Evaluating outcomes and cost-effectiveness in real-world settings: Examining the effectiveness of AI-enabled genomic surveillance in real life is necessary for its adoption. Economic evaluation will assist in determining the value of these technologies in mitigating the incidence of cancer and improving health outcomes (Khanna et al., 2022).

D. Federated learning: Federated learning models are trained across multiple decentralized institutions without data sharing. This is very important in genomics because privacy concerns, data sensitivity, and ethical regulations are not in support of centralized data pooling. Hospitals, research centers, and countries can now train different AI models on diverse genomic and clinical data sets while keeping their existing data secure(Zwiers et al., 2024). This enables better model generalizability across populations, most especially marginalized groups, and calls for cooperation in cancer research without compromising on individuals’ confidentiality and data sovereignty.

E. Explainable AI (XAI): Making AI models transparent and trustworthy

The black box nature of many algorithms remains one of the biggest challenges in AI for cancer genomics. Explainable AI (XAI) intends to clarify this by making AI decisions more transparent, interpretable, and understandable to clinicians, researchers, and patients(S Band et al., 2023). In the context of genomics, XAI can underscore which genetic variants or environmental factors are more contributing to a specific cancer risk or treatment guidelines. This not only enhances clinical trust in AI systems but also facilitates regulatory validation and informed decision-making(Shifa et al., 2025).

F. Multi-omics integration: toward a holistic view of cancer:

The integration of multi-omics data, including proteomics (protein expression), metabolomics (metabolic changes), epigenomics (DNA methylation), and transcriptomics (RNA expression) into cancer genomics is the future of AI models (Subramanian et al., 2020). Cancer is a complex disease, and integration of these layers provides a more complete biological picture. AI models proficient enough in evaluating these complex, multidimensional datasets will provide a profound understanding of tumor biology, response to environmental carcinogens, and disease progression. It will help reveal new therapeutic targets or biomarkers that were missed during genomic evaluation (Alum, 2025).

G. AI-driven clinical decision support systems (CDSS):

AI-powered clinical decision support systems (CDSS) are set to transform cancer care by assisting clinicians in understanding genomic results in real-time and making informed treatment decisions. Targeted therapies are recommended based on an individual's mutational needs(Elhaddad & Hamam, 2024). For example, immunotherapies for patients with a particular mismatch gene deficiency could be recommended by a CDSS that is powered by AI. As AI models are becoming more powerful and compatible with electronic health records (EHRs), CDSS will play an important role in precision oncology (Karuppan Perumal et al., 2025).

H. Ethical frameworks for responsible AI in genomics:

Strong ethical frameworks are necessary to guide the development and use of cancer genomics as aa becomes more integrated. AI applications in genomics will continue to strengthen existing health inequalities, especially among marginalized populations, if these frameworks are not put into place(Abujaber & Nashwan, 2024). These frameworks are necessary to hinder AI models from exacerbating the disparity, especially in areas that are underrepresented communities. Participation in community activities, regulatory oversight, and compliance with principles such as the fair (findable, accessible, interoperable, reusable) and fair (fairness, accountability, transparency, explainability) guidelines will be necessary in facilitating equitable, human-centered AI in cancer prevention and care (Singhal et al., 2024).

11. Conclusion

In conclusion, the fusion of artificial intelligence (AI) and genomic surveillance into cancer prevention represents a transformative approach to public health by taking the focus from reactive treatment to proactive health management. The integration of advanced data analytics with molecular insights will enable the identification of environmental carcinogens and genetic susceptibilities, promoting early detection and personalized treatments.

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