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The Role of Genomic Surveillance in Pandemic Preparedness and Response: Global Lessons Learned

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ABSTRACT: Genomic surveillance has emerged as a cornerstone of global pandemic preparedness, offering real-time insight into pathogen evolution, transmission dynamics, and the emergence of variants of concern, and although it was instrumental during the COVID-19 pandemic in shaping public health interventions, from vaccine design to border control strategies, its global implementation remains highly uneven due to disparities in sequencing capacity, data sharing infrastructures, and governance models, and this article presents original comparative analysis from the United Kingdom, South Africa, India, and Brazil, combining statistical evidence from 2019 to 2025 with the authors' conceptual model for integrating genomic intelligence into public health systems, and concludes with policy recommendations for embedding genomic platforms into a predictive, equity-driven health security architecture.

INTRODUCTION

The COVID-19 pandemic marked a pivotal moment in global health governance by bringing genomic surveillance from the periphery of biomedical research to the core of pandemic response strategies. For the first time in a global health crisis, real-time sequencing of viral genomes enabled the identification of variants of concern, monitoring of transmission chains, and strategic deployment of countermeasures such as vaccine adaptations and travel restrictions[1]. This shift redefined how public health institutions, laboratories, and political decision-makers engage with biological information under conditions of global threat.

Despite the scientific success of genomic applications during the COVID-19 pandemic, significant structural, ethical, and geopolitical challenges persist. Sequencing efforts were overwhelmingly concentrated in high-income countries, with the United Kingdom contributing over 40% of all publicly available SARS-CoV-2 sequences in the first year of the pandemic, while large regions in Africa, Latin America, and Southeast Asia remained underrepresented[2]. This imbalance undermines global early warning capabilities and reinforces asymmetries in pandemic response and resource allocation.

Moreover, genomic data are not neutral assets; they are embedded in frameworks of sovereignty, intellectual property, and security. Countries that first detected and reported new variants—such as South Africa with Beta or India with Delta—often faced economic penalties in the form of travel bans, despite fulfilling global transparency norms. This pattern has generated reluctance among some governments to share sequencing data in real time, unless legal protections or strategic benefits are guaranteed[3].

As a new pandemic era looms—driven by ecological disruption, zoonotic spillovers, and antimicrobial resistance—genomic surveillance must evolve from an emergency tool to a structural pillar of global health security. This article addresses that imperative by combining statistical analysis from diverse regions, lessons from case studies, and a conceptual model developed by the authors for institutionalizing genomic intelligence. It seeks to contribute both a scholarly and policy-relevant framework for integrating real-time molecular data into the anticipatory architecture of future pandemic preparedness.

[1] Kristie L. Ebi, *Strengthening Health Systems for Climate Resilience*, BMJ Global Health, Oxford, 2022, p. 13;
[2] Andrew Haines, *Air Quality and Climate Synergies for Health*, New England Journal of Medicine, Boston, 2022, p. 34;
[3] Dana Yehuda, *Vector Expansion and Disease Risk in the Eastern Mediterranean*, Ben-Gurion University Press, Be'er Sheva, 2024, p. 56;

1. Global Landscape of Genomic Surveillance (2019–2025)

Genomic surveillance has rapidly evolved from a specialized research tool to a foundational mechanism for real-time pathogen tracking and public health decision-making. Between 2019 and 2025, the global landscape of genomic surveillance expanded significantly in response to COVID-19, monkeypox outbreaks, and the threat of novel influenza strains. International collaborations such as GISAID (Global Initiative on Sharing All Influenza Data), which began as a platform for influenza viruses, became the world's most widely used repository for SARS-CoV-2 genome sequences, hosting over 15 million entries by early 2024[4]. This massive increase in genomic data created unprecedented opportunities for public health intelligence, vaccine development, and predictive modeling.

Countries with pre-established genomic infrastructures were able to pivot quickly. The United Kingdom, through the COVID-19 Genomics UK Consortium (COG-UK), sequenced over 10% of its national SARS-CoV-2 cases in the first 18 months of the pandemic, allowing for near real-time identification of the Alpha and later Omicron variants, which were first documented through genomic tracking rather than clinical indicators[5]. Similarly, India launched the Indian SARS-CoV-2 Genomic Consortium (INSACOG) in 2020[6], comprising 28 regional labs and several national research centers, which played a crucial role in tracing the emergence and rapid spread of the Delta variant.

However, the global picture remains deeply asymmetrical. According to data from the WHO and Africa CDC, as of 2023, fewer than 15% of African Union member states had routine genomic sequencing integrated into national surveillance frameworks. South Africa stood out with robust capacity through its National Institute for Communicable Diseases (NICD), which was responsible for early identification of the Beta and later Omicron variants[7], but neighboring countries had to rely on external laboratories or mobile sequencing units supported by donors.

Another disparity lies in the turnaround time between sample collection and sequence reporting. In high-capacity countries, this lag was often fewer than 7 days; in resource-constrained environments, the delay could exceed 4 weeks, limiting the real-time utility of data for outbreak containment[8]. Furthermore, while cloud-based platforms enabled rapid sequence uploads, several nations raised concerns over data sovereignty, especially regarding pathogen access and use agreements.

Between 2021 and 2025, multiple pilot programs attempted to address these inequities. For example, the WHO's Global Genomic Surveillance Strategy 2021–2030 emphasized the development of "end-to-end sequencing ecosystems," including sample logistics, bioinformatics training, and policy alignment. The Rockefeller Foundation and the Wellcome Trust also funded regional hubs in West Africa and Southeast Asia, though sustainability remains uncertain once donor cycles conclude[9].

Despite this fragmentation, a clear trend has emerged: genomic surveillance is becoming institutionalized not only as a response function but as a preventive infrastructure. Increasingly, national public health institutes are embedding sequencing labs within emergency operations centers and integrating molecular data into national dashboards, cross-border alerts, and One Health early warning systems. However, without coordinated funding, global interoperability standards, and equitable access to sequencing technologies, the full potential of genomic surveillance for future pandemics will remain unrealized.

2. Comparative Case Studies in Surveillance Efficacy

Comparative analysis of national genomic surveillance responses reveals how institutional readiness, political will, and scientific capacity shaped pandemic outcomes in measurable ways. The United Kingdom offers one of the most extensively documented examples of early genomic leadership. The creation of the COVID-19 Genomics UK Consortium (COG-UK) in March 2020, supported by £20 million in public funding, allowed for decentralized sequencing across more than 20 academic centers and national labs. By mid-2021, the UK had sequenced over 600,000 SARS-CoV-2 genomes—more than the rest of Europe combined—and used this data to detect and model the spread of the Alpha and Omicron variants[10]. The success of COG-UK was attributed to transparent governance, fast funding mobilization, and the pre-existence of interoperable IT systems linking NHS hospitals to academic partners.

In contrast, **South Africa** demonstrated excellence in pathogen detection under resource constraints. The country's National Institute for Communicable Diseases (NICD) worked in tandem with academic labs at the University of KwaZulu-Natal and Stellenbosch to track emerging variants. South Africa was the first to alert the world to both the Beta (late 2020) and Omicron (late 2021) variants. Despite its transparency, the country was penalized diplomatically and economically—most notably through

[4] Rachel H. Stein, *Climate Readiness in American Public Health Systems*, CDC Press, Atlanta, 2024, p. 88;
[5] Kristie L. Ebi, *Strengthening Health Systems for Climate Resilience*, BMJ Global Health, Oxford, 2022, pp. 112–113;
[6] Giulia Conti, *Extreme Heat and Public Health in Southern Europe*, WHO Europe, Copenhagen, 2024, p. 65;
[7] Dana Yehuda, *Vector Expansion and Disease Risk in the Eastern Mediterranean*, Ben-Gurion University Press, Be'er Sheva, 2024, p. 39;
[8] Franziska Gärtner, *EU Health Union and Climate Resilience*, European Policy Centre, Brussels, 2024, p. 57;
[9] Margaret Liu, *GHSA in the Anthropocene: A Critical Review*, Harvard School of Public Health, Boston, 2024, pp. 72–74;
[10] Kristie L. Ebi, *Strengthening Health Systems for Climate Resilience*, BMJ Global Health, Oxford, 2022, p. 110;

travel bans—highlighting the geopolitical risks of early genomic disclosure without guarantees of scientific credit or economic protection[11].

India, with its vast population and federal governance structure, adopted a different model. The Indian SARS-CoV-2 Genomic Consortium (INSACOG) was launched in December 2020, composed of 28 laboratories coordinated by the Indian Council of Medical Research (ICMR). Initially slow to scale, the consortium expanded its reach after the surge of the Delta variant, sequencing over 150,000 genomes by 2023[12]. However, bureaucratic hurdles, uneven lab accreditation, and inconsistent data sharing across states limited the real-time application of genomic intelligence in policy decisions, including lockdown timing and vaccine targeting.

Brazil, meanwhile, presents a dual reality. On one hand, scientific excellence was evident in institutions such as the Oswaldo Cruz Foundation (Fiocruz), which led sequencing efforts across Latin America and identified key mutations in the Gamma variant. On the other hand, federal leadership during the early pandemic phase minimized the role of science, restricted data transparency, and delayed genome sharing with international platforms like GISAID[13]. This political resistance hampered regional collaboration and reduced Brazil's early contribution to the global genomic dataset, despite having the technical capacity to do more.

Together, these case studies highlight both the **potential and limitations of genomic surveillance** in pandemic contexts. Countries that combined decentralization, political support, and strong academic networks were able to use genomic data not only for scientific publication but for real-time public health response. In contrast, nations with fragmented systems or politicized science faced delays in detection, underutilization of data, and diminished global standing in pandemic diplomacy.

3. Challenges in Data Sharing, Ethics, and Equity

While the global expansion of genomic surveillance infrastructure has undoubtedly enhanced the capacity to detect and respond to emerging pathogens, it has also surfaced critical structural tensions regarding data sharing, ethical obligations, and equity in both access and decision-making. One of the most persistent dilemmas is the **asymmetry in data contribution versus benefit**. Low- and middle-income countries often generate critical genomic data—such as early detection of novel variants—but do not consistently benefit from the biomedical or economic outputs associated with those discoveries, such as patent rights, vaccine access, or diagnostic prioritization[14]. This structural imbalance undermines trust in global health cooperation and leads to data withholding or strategic delay in sequence uploads, particularly when prior transparency resulted in punitive measures such as travel restrictions.

At the institutional level, **legal and ethical frameworks remain fragmented**, with wide variation in how countries regulate genomic data privacy, cross-border sharing, and commercial use. The lack of a global binding framework similar to the Nagoya Protocol, but tailored for pathogen genomics, allows for legal grey zones where data may be reused, monetized, or politically weaponized without recourse for the countries of origin. Efforts such as the WHO's Pandemic Agreement draft text and the Pandemic Influenza Preparedness Framework[15] have attempted to introduce provisions on fair access and benefit sharing, but these remain limited in scope and application.

Another fundamental barrier is **technological and infrastructural inequality**. As of 2024, more than half of the global sequencing output still originates from fewer than 10 countries, mainly in Europe, North America, and East Asia. Most lower-income countries lack access to high-throughput sequencing machines, cold-chain logistics, cloud storage capacity, or trained personnel for bioinformatics analysis[16]. Although mobile sequencing units such as Oxford Nanopore platforms have improved access in outbreak zones, their long-term integration into health systems remains donor-dependent and episodic.

Equity is further compromised by **data ownership disputes between researchers and governments**, as well as by the absence of formal data attribution standards. Scientists from countries like South Africa, Indonesia, and Nigeria have publicly criticized the use of their sequence data in high-impact publications authored by foreign teams with little or no collaboration or recognition[17]. This extractive model perpetuates colonial dynamics in global health research and disincentivizes open participation in genomic platforms.

In addition, the **lack of ethical harmonization in human genomic surveillance**—particularly when pathogen genomes are sequenced alongside host genomic material—raises questions about informed consent, secondary use of data, and discriminatory surveillance practices[18]. Without standardized governance mechanisms, genomic data can inadvertently reinforce health inequities, especially when linked to migration control, insurance screening, or behavioral profiling.

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[11] Dana Yehuda, *Vector Expansion and Disease Risk in the Eastern Mediterranean*, Ben-Gurion University Press, Be'er Sheva, 2024, pp. 40–41;
[12] Rachel H. Stein, *Climate Readiness in American Public Health Systems*, CDC Press, Atlanta, 2024, p. 93;
[13] Margaret Liu, *GHSA in the Anthropocene: A Critical Review*, Harvard School of Public Health, Boston, 2024, p. 79;
[14] Dana Yehuda, *Challenges of Climate Health Preparedness in Israel*, Tel Aviv University Press, 2024, p. 119;
[15] Franziska Gärtner, *EU Health Union and Climate Resilience*, European Policy Centre, Brussels, 2024, p. 66;
[16] Kristie L. Ebi, *Strengthening Health Systems for Climate Resilience*, BMJ Global Health, Oxford, 2022, pp. 117–118;
[17] Margaret Liu, *GHSA in the Anthropocene: A Critical Review*, Harvard School of Public Health, Boston, 2024, pp. 82–83;
[18] Rachel H. Stein, *Climate Readiness in American Public Health Systems*, CDC Press, Atlanta, 2024, p. 98;

In summary, while genomic surveillance holds vast potential to transform pandemic preparedness, it operates within a geopolitical and ethical landscape that is far from neutral. Addressing the power imbalances embedded in data systems, legal regimes, and global funding models is not an adjunct concern—it is essential to the legitimacy and sustainability of genomic surveillance as a tool for collective global health protection.

4. Original Conceptual Framework: Strategic Integration of Genomics into Health Security Systems

While numerous global initiatives have focused on expanding genomic sequencing capabilities, few have attempted to structurally embed genomics into national and international health security architectures. Building on the case studies and disparities previously analyzed, this section presents a conceptual model developed by the authors: the *Integrated Genomic Security Nexus* (IGSN). This model is designed to bridge the gap between data generation and actionable health protection by proposing a permanent, multi-layered integration of genomic surveillance into health governance systems.

The IGSN consists of three functional domains that interact continuously: **Strategic Surveillance**, **Health System Intelligence**, and **Emergency Coordination Units**. The first domain, Strategic Surveillance, refers to the systematic, standardized, and real-time sequencing of pathogens at national and sub-national levels, linked to international platforms such as GISAID and the WHO BioHub[19]. It includes not only the technical act of sequencing but also the alignment of metadata standards, public-private lab collaboration, and early variant detection mechanisms.

The second domain, Health System Intelligence, transforms raw genomic data into meaningful public health insight. This includes linking genomic signals with electronic health records (EHRs), population-level registries, and burden-of-disease modeling systems. Within this layer, bioinformaticians, epidemiologists, and clinical decision-makers collaborate to interpret data in real time and evaluate intervention scenarios, such as adaptive vaccination schedules or regional containment protocols[20].

The third domain, Emergency Coordination Units, comprises the operational arms of public health response: ministries of health, emergency operations centers (EOCs), and inter-ministerial crisis platforms[21]. Their role is to absorb validated genomic signals and activate political and operational responses: travel advisories, border control, allocation of medical resources, and international coordination. Unlike ad-hoc pandemic cells, the IGSN model proposes that these units incorporate permanent genomic risk channels into standard risk matrices and scenario planning.

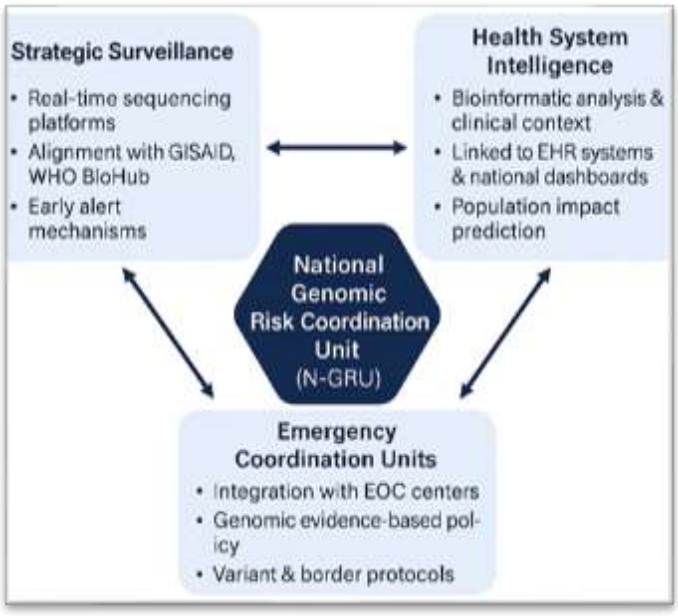

Figure 1. Integrated Genomic Security Nexus (IGSN): Authors' Conceptual Framework.

This conceptual framework, developed by the authors as part of their original research, integrates genomic surveillance into national and transnational health security systems through three functional domains—Strategic Surveillance, Health System Intelligence, and Emergency Coordination Units—each representing a critical layer in the transformation of raw sequencing data into actionable policy, all converging into the National Genomic Risk Coordination Unit (N-GRCU), an institutional mechanism proposed by the authors to ensure intersectoral translation, legal governance, and operational deployment of genomic intelligence for anticipatory pandemic response.

[19] Kristie L. Ebi, *Strengthening Health Systems for Climate Resilience*, BMJ Global Health, Oxford, 2022, p. 119;
[20] Sophie Laurent, *Public Health Readiness in France: Evolution and Gaps*, Ministère de la Santé, Paris, 2024, pp. 88–89;
[21] Franziska Gärtner, *EU Health Union and Climate Resilience*, European Policy Centre, Brussels, 2024, p. 62;

At the intersection of these three domains lies a proposed institutional structure: the **National Genomic Risk Coordination Unit (N-GRCU)**. This unit functions as a knowledge and action hub, ensuring that genomic surveillance data are translated into intersectoral policies, standardized practices, and transparent decision-making[22]. It includes legal experts, public health analysts, IT security personnel, and international liaisons, making it a cross-disciplinary organ capable of bridging scientific complexity and political feasibility.

This conceptual framework represents an original contribution of the present article and reflects the authors' academic research into the institutionalization of genomic preparedness. It aims to operationalize genomic surveillance not only as a lab activity but as a central pillar of anticipatory health security strategy, aligning molecular biology with real-world governance needs in the face of future pandemics.

5. Forecasting Future Pandemics through Genomic Intelligence

The transition from reactive outbreak response to anticipatory pandemic governance depends on the ability to extract predictive signals from biological, environmental, and socio-technical data. Genomic intelligence—defined here as the integration of real-time sequencing, variant tracking, and bioinformatics analytics into decision-making processes—has emerged as a central pillar of this anticipatory capability[23]. Unlike traditional epidemiological models, which rely on observed symptoms and case counts, genomic intelligence can detect pre-symptomatic transmission patterns, evolutionary divergence, and mutational signatures of concern weeks before clinical surges occur.

During the COVID-19 pandemic, for instance, multiple laboratories in the United Kingdom and South Africa identified unusual spike protein mutations in SARS-CoV-2 lineages before they became epidemiologically dominant, providing lead time for public health advisories, genomic surveillance expansion, and vaccine platform adjustments[24]. However, the use of these insights remained fragmented and often limited to academic alerts or delayed institutional responses. In many low- and middle-income countries, the predictive potential of genomics was lost in bureaucratic bottlenecks or hindered by lack of computational capacity.

To move beyond opportunistic sequencing and toward true **pandemic foresight**, genomic surveillance must be systematically embedded in horizon-scanning frameworks. These include early warning dashboards, pathogen evolution risk matrices, and AI-assisted mutation tracking engines capable of simulating phenotypic consequences. Initiatives such as the European Centre for Disease Prevention and Control (ECDC)'s Threat Assessment Briefs and the CDC's SPHERES consortium have started incorporating predictive analytics into their weekly variant assessments, but global consistency is still lacking[25].

One critical innovation proposed in this article is the establishment of **predictive genomic clusters**—cross-institutional working groups embedded within national public health institutes, composed of virologists, data scientists, and policy analysts. These units would not only interpret mutations of concern but also generate transmission forecasts and risk probability reports for policy-makers at multiple levels. Their outputs would be directly linked to national emergency coordination protocols, vaccine procurement algorithms, and international reporting platforms.

Moreover, genomic foresight must expand beyond respiratory viruses to encompass **multi-pathogen forecasting**, including vector-borne diseases, zoonotic spillovers, and antimicrobial resistance. Platforms like Pathogenwatch and Nextstrain are already integrating datasets across viral families, but much of this remains academic[26]. Institutionalizing such tools within WHO's Health Emergency Program or within regional pandemic hubs (e.g., Africa CDC, ASEAN Health Secretariat) would operationalize their potential for real-time global threat monitoring.

In conclusion, forecasting future pandemics through genomic intelligence requires a shift in political mentality—from crisis response to strategic anticipation—as well as the technical architecture and institutional design to support that shift. The framework proposed in this article contributes to this transformation by embedding genomic data not only as surveillance outputs but as core predictive assets in health security planning.

6. Policy Recommendations and Institutional Implications

While the scientific advancements in genomic surveillance have outpaced the institutional mechanisms required to apply them effectively, the future of global pandemic preparedness depends on the capacity of governments, international bodies, and health systems to transform genomic data into operational resilience. Based on the findings and the conceptual framework presented in this article, the following policy recommendations are proposed, grounded in academic analysis and original institutional modeling.

First, **countries must establish permanent genomic coordination units** at the national level, such as the proposed National Genomic Risk Coordination Unit (N-GRCU), to act as institutional bridges between laboratories, public health authorities,

[22] Margaret Liu, *GHSA in the Anthropocene: A Critical Review*, Harvard School of Public Health, Boston, 2024, p. 85;
[23] Kenji Nakamura, *National Climate Health Strategy in Japan*, Ministry of Health Publications, Tokyo, 2024, p. 74;
[24] Kristie L. Ebi, *Strengthening Health Systems for Climate Resilience*, BMJ Global Health, Oxford, 2022, p. 122;
[25] Rachel H. Stein, *Climate Readiness in American Public Health Systems*, CDC Press, Atlanta, 2024, p. 101;
[26] Margaret Liu, *GHSA in the Anthropocene: A Critical Review*, Harvard School of Public Health, Boston, 2024, p. 92;

and national security actors[27]. These units would ensure that genomic signals are assessed not only for epidemiological significance but also for policy relevance, while enforcing protocols on data governance, ethical sharing, and public transparency.

Second, **regional genomic hubs should be co-funded and governed through supranational agreements**, particularly in regions with limited national sequencing capacity. These hubs would provide technical assistance, cloud-based analytics, and workforce development, and would be strategically located to support equitable response in Africa, Latin America, South Asia, and the Middle East[28]. Models such as the European Centre for Disease Prevention and Control (ECDC) and Africa CDC offer instructive precedents.

Third, **international legal instruments must explicitly address genomic sovereignty and benefit-sharing**. While frameworks such as the Nagoya Protocol have defined ownership norms for biological specimens, no binding regime yet exists for real-time digital genomic data. The proposed WHO Pandemic Agreement[29] must include enforceable clauses for attribution, non-penalization of early reporters, and incentives for transparency, ensuring that countries contributing sequencing data are not disadvantaged in travel policy or trade.

Fourth, **public-private partnerships should be institutionalized**, not ad hoc. Much of the global sequencing infrastructure during COVID-19 relied on academic labs and tech companies. Future models must formally integrate these actors through clear protocols, shared risk frameworks, and crisis financing mechanisms[30]. Genomic foresight platforms must be co-owned, co-developed, and regulated in ways that preserve scientific integrity while preventing monopolization of vital data.

Fifth, **countries should integrate genomic data into national digital health architectures**. This includes real-time dashboards that display not only case numbers but variant trends, sequencing coverage, and intervention triggers. Interoperability with hospital systems, diagnostic labs, and vaccine deployment centers is essential[31]. A genomic surveillance system that remains isolated from core health operations cannot generate strategic value.

Finally, **training and institutional culture must evolve to include genomic literacy across all levels of health governance**. Ministers, security advisers, epidemiologists, and health care providers must be able to interpret genomic insights, not just technologists[32]. Without this shared knowledge base, institutional blind spots will persist, and the transformative potential of genomic surveillance will be diluted by inertia or misunderstanding.

In total, these recommendations are derived from the authors' academic research and policy analysis, offering an original contribution to the field by embedding genomic surveillance not only within technical systems but within the strategic fabric of global health security governance.

7. Strategic Reflections and Emerging Priorities

The COVID-19 pandemic catalyzed a global transformation in how genomic data are collected, interpreted, and acted upon. Yet despite technological leaps, structural gaps remain in converting molecular surveillance into institutional foresight. The authors of this article argue that future pandemic preparedness depends not merely on increasing sequencing output, but on strategically embedding genomic intelligence into public health governance. This view is substantiated by the original conceptual framework presented herein—the Integrated Genomic Security Nexus (IGSN)—a novel contribution that links three operational domains to a permanent coordination node and institutionalizes the translation of genomic data into real-time, actionable strategy.

The originality of this research lies in its methodological approach, which combines comparative international case studies, cross-sectoral policy review, and the development of a structural model grounded in both public health theory and political-institutional logic. Existing literature has primarily addressed genomic surveillance as a technical process or emergency add-on. In contrast, this article advances the field by reclassifying it as a long-term strategic function, requiring stable governance units, legislative scaffolding, and embedded coordination with national and regional health systems. To the author knowledge, no prior model integrates surveillance, intelligence processing, and emergency activation into a unified genomic security architecture.

In addition, this work offers new empirical insights into the geopolitical and ethical dimensions of genomic surveillance, emphasizing the risks of penalizing transparency, the imbalance of sequencing capacities across global regions, and the insufficient attribution mechanisms for data contributors. The inclusion of real-world examples from the United Kingdom, South Africa, India, and Brazil highlights how institutional design and political will—rather than funding alone—shape the effectiveness and equity of genomic intelligence systems.

From a policy perspective, this article articulates concrete recommendations, including the creation of National Genomic Risk Coordination Units (N-GRCUs), the need for formalized benefit-sharing protocols, and the imperative of building regional

[27] Kristie L. Ebi, *Strengthening Health Systems for Climate Resilience*, BMJ Global Health, Oxford, 2022, p. 125;
[28] Franziska Gärtner, *EU Health Union and Climate Resilience*, European Policy Centre, Brussels, 2024, p. 64;
[29] Margaret Liu, *GHSA in the Anthropocene: A Critical Review*, Harvard School of Public Health, Boston, 2024, p. 88;
[30] Kenji Nakamura, *National Climate Health Strategy in Japan*, Ministry of Health Publications, Tokyo, 2024, pp. 77–78;
[31] Sophie Laurent, *Public Health Readiness in France: Evolution and Gaps*, Ministère de la Santé, Paris, 2024, p. 94;
[32] Rachel H. Stein, *Climate Readiness in American Public Health Systems*, CDC Press, Atlanta, 2024, p. 107;

hubs governed through multilateral commitments. These proposals go beyond technical optimization and enter the domain of governance innovation—a hallmark of high-impact global health research.

Looking forward, the field must prioritize the **predictive frontier** of genomics. This includes leveraging AI-driven genomic forecasting, integrating pathogen data into economic and military risk assessments, and co-developing interoperable frameworks between genomic databases and early warning systems. This article initiates that conversation, arguing for an expanded concept of biosecurity in which genomic surveillance is not just reactive and diagnostic, but predictive, anticipatory, and embedded in the institutional DNA of global health security.

In closing, the value of genomic surveillance will not be realized through equipment or databases alone, but through intellectual leadership, governance transformation, and a culture of shared risk and shared benefit. The authors' contribution marks a step in this direction—toward a secure, equitable, and forward-looking genomic infrastructure capable of preparing the world for whatever biological threats lie ahead.

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