

Genomic surveillance in public health: contributions of biotechnology and molecular biology to epidemic monitoring

Vigilância genômica na saúde pública: contribuições da biotecnologia e da biologia molecular para o monitoramento de epidemias

Vigilancia genómica en salud pública: aportaciones de la biotecnología y la biología molecular al seguimiento de las epidemias

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ABSTRACT

Introduction: Genomic surveillance has become a cornerstone of modern public health by integrating biotechnology, molecular biology, and bioinformatics to enhance the detection and monitoring of infectious threats. Objective: To analyze the contributions of biotechnology and molecular biology to genomic surveillance and their applications in epidemic monitoring and preparedness for public health emergencies. Methods: An integrative literature review was conducted in PubMed/MEDLINE, Scopus, Web of Science, SciELO, and Google Scholar.

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Studies published in English, Portuguese, or Spanish between 2016 and 2026 were considered. Search terms addressed biotechnology, genomics, molecular biology, genomic surveillance, epidemiological surveillance, and epidemic monitoring. From 546 identified records, 10 studies met the eligibility criteria and were included after duplicate removal, screening, and full-text assessment. Results: The evidence indicates that genomic surveillance improves early pathogen detection, genomic characterization, outbreak investigation, antimicrobial resistance monitoring, and the development of vaccines and diagnostic tools. Integrating genomic with epidemiological, clinical, and digital health data strengthens predictive capacity and enables more timely public health responses. Nevertheless, significant barriers persist, including inadequate laboratory infrastructure, limited bioinformatics expertise, shortages of trained personnel, ethical issues related to genomic data governance, and unequal access to sequencing technologies, particularly in low- and middle-income countries. Conclusion: Genomic surveillance is a transformative component of contemporary public health systems, enhancing preparedness and response to infectious disease emergencies. Expanding equitable access to sequencing, strengthening scientific and technological capacity, and integrating genomic approaches with digital health, artificial intelligence, and One Health strategies are essential for building resilient and globally connected surveillance systems.

Keywords: genomic surveillance; bioinformatics; biotechnology; public health surveillance; public health emergencies.

1 INTRODUCTION

Contemporary health surveillance has been profoundly transformed by advances in biotechnology, especially through the integration of genomics and molecular biology, which offer unprecedented tools for monitoring and controlling epidemics (Ogunlaja, 2025).

These approaches allow not only the early identification of pathogens but also a detailed understanding of their evolution, transmission patterns, and the detection of new variants, which are essential for rapid and effective responses to health crises (Molina; Arias, 2021).

The 21st century has already witnessed the emergence of four viral pandemics, highlighting the ongoing need for epidemiological surveillance and real-time monitoring of infectious diseases (Anekpo *et al.*, 2024).

In this context, the bioeconomy and biotechnology play a crucial role by providing innovations for the diagnosis, prevention, and treatment of pandemics, as well as supporting public health control (Molina; Arias, 2021).

The COVID-19 pandemic, in particular, catalyzed a significant increase in pathogen genomic surveillance capacity, driving the integration of large datasets to inform policy decisions and strengthen surveillance infrastructure (Westhuizen *et al.*, 2024).

This experience underscored the importance of updated and integrated information systems, as well as the need for trained health teams capable of interpreting indicators and implementing rapid actions in the event of outbreaks (Barcellos; Villela, 2021).

Genomic surveillance, in particular, uses DNA sequencing and computational analyses to identify and characterize pathogens, providing in-depth insight into their presence in clinical or environmental samples (Santos *et al.*, 2021).

This modern methodology enables tracking the spread of infectious diseases and identifying new lineages or genetic variants, as demonstrated during the COVID-19 pandemic, when rapid sequencing of the SARS-CoV-2 genome was crucial for understanding and combating the disease (Geantă *et al.*, 2023; Silva *et al.*, 2023).

The ability to reconstruct genetic variability in real time through genomic epidemiology has been fundamental in identifying new pathogen lineages, as observed in outbreaks of H1N1 influenza, MERS, and SARS (Álvarez-Díaz *et al.*, 2020).

However, the widespread implementation of genomic surveillance in public health faces significant challenges, such as the need for robust laboratory infrastructure, personnel training, and the development of efficient bioinformatics platforms for analyzing and interpreting large volumes of genomic data (Álvarez-Díaz *et al.*, 2020).

Despite the evident potential of these technologies, a central research problem remains: how can genomic surveillance be equitably integrated into global public health systems, particularly in resource-constrained settings, to ensure a proactive rather than reactive response to emerging infectious diseases? The justification for this review lies in the urgent need to map these biotechnological advances and clearly identify the infrastructural and ethical bottlenecks that prevent their universal application. The guiding hypothesis is that while molecular biology provides the necessary analytical precision, the true effectiveness of epidemic monitoring depends intrinsically on overcoming technological disparities and integrating these tools with classical epidemiological data.

Given this context, the present study aims to analyze the evolution of biotechnology and molecular biology in health surveillance, highlighting their impact on epidemic monitoring and responses to health emergencies, with special attention to the democratization of access to these technologies in developing countries (Santos *et al.*, 2023; Silva *et al.*, 2023).

2 THEORETICAL FRAMEWORKS

The theoretical foundations of genomic surveillance in public health emerge from the intersection of molecular biology, biotechnology, bioinformatics, and classical epidemiology, reflecting a paradigm shift in the way infectious threats are detected, monitored, and controlled.

Traditionally, surveillance systems relied predominantly on syndromic reporting, clinical notification, and retrospective epidemiological analyses, approaches that frequently limited the capacity for early outbreak detection and timely intervention. The advent of next-generation sequencing (NGS) technologies transformed this landscape by enabling direct characterization of pathogen genomes in near real time, thereby introducing a new era of genomic-enhanced surveillance and precision public health.

Within this framework, health interventions are no longer guided solely by population averages but increasingly informed by pathogen-specific evolutionary dynamics, transmission patterns, and geographically localized risks (Khoury *et al.*, 2017).

Consequently, pathogen genomics has become an essential instrument for identifying emerging variants, reconstructing transmission chains, and monitoring antimicrobial resistance determinants with unprecedented temporal and spatial resolution (Engelthaler, 2024).

Complementing this perspective, the concept of "Pathogen Intelligence" proposes that genomic information acquires epidemiological value only when integrated with clinical, demographic, environmental, and behavioral datasets. This theoretical approach transforms genomic sequences from isolated molecular observations into actionable public health intelligence capable of informing surveillance strategies and policy responses.

Such integration aligns closely with the One Health paradigm, which recognizes the interdependence between human, animal, and environmental health systems in the emergence and dissemination of infectious diseases. From this perspective, genomic surveillance transcends its traditional diagnostic function and assumes a predictive and preventive role, enabling the identification of zoonotic spillover events, the monitoring of pathogen evolution across ecosystems, and the anticipation of epidemic risks before widespread community transmission occurs. Thus, biotechnology and molecular epidemiology increasingly function not merely as instruments for outbreak response, but as strategic pillars of global health security and pandemic preparedness in an interconnected world (Wang *et al.*, 2023).

3 METHODS

This study is an integrative literature review conducted to synthesize and critically analyze the scientific evidence on the contributions of biotechnology and molecular biology to genomic surveillance in epidemic monitoring and public health emergency preparedness.

The review was initiated in February 2026 through a structured search of the electronic databases PubMed/MEDLINE, Scopus, SciELO, and Google Scholar, selected because they provide broad coverage of biomedical, epidemiological, and public health literature, as well as relevant scientific publications from both international and Latin American contexts.

Studies published from January 2016 to February 2026 were considered eligible. This ten-year time frame was established to provide an up-to-date overview of advances in biotechnology, molecular biology, and genomic surveillance, particularly following the rapid technological developments and global public health challenges observed during recent epidemics and pandemics.

The search strategy integrated controlled vocabulary terms obtained from Medical Subject Headings (MeSH) and Health Sciences Descriptors (DeCS) with relevant free-text keywords related to biotechnology and genomic surveillance. Search terms included *Biotechnology*, *Genomics*, *Molecular Biology*, *Genomic Surveillance*, *Public Health Surveillance*, *Epidemiological Surveillance*, and *Epidemic Monitoring*. Boolean operators (**AND** and **OR**) were employed to combine descriptors and optimize retrieval sensitivity and specificity, with adaptations according to the indexing characteristics and search syntax of each database.

Studies published in English, Portuguese, and Spanish were considered for inclusion.

The inclusion criteria comprised original articles, review studies, and official institutional publications addressing the application of biotechnology, genomics, or molecular biology in epidemiological surveillance and public health. Eligible studies included those investigating pathogen detection, genomic surveillance, molecular epidemiology, antimicrobial resistance monitoring, outbreak investigation, emerging infectious diseases, and technological innovations applicable to health surveillance systems.

The exclusion criteria consisted of duplicate publications, editorials, letters to the editor, conference abstracts, dissertations, theses, studies without full-text availability, and publications exclusively focused on laboratory or experimental techniques without discussing their application to epidemiological surveillance or public health decision-making. Studies that did not directly address the research objective were also excluded.

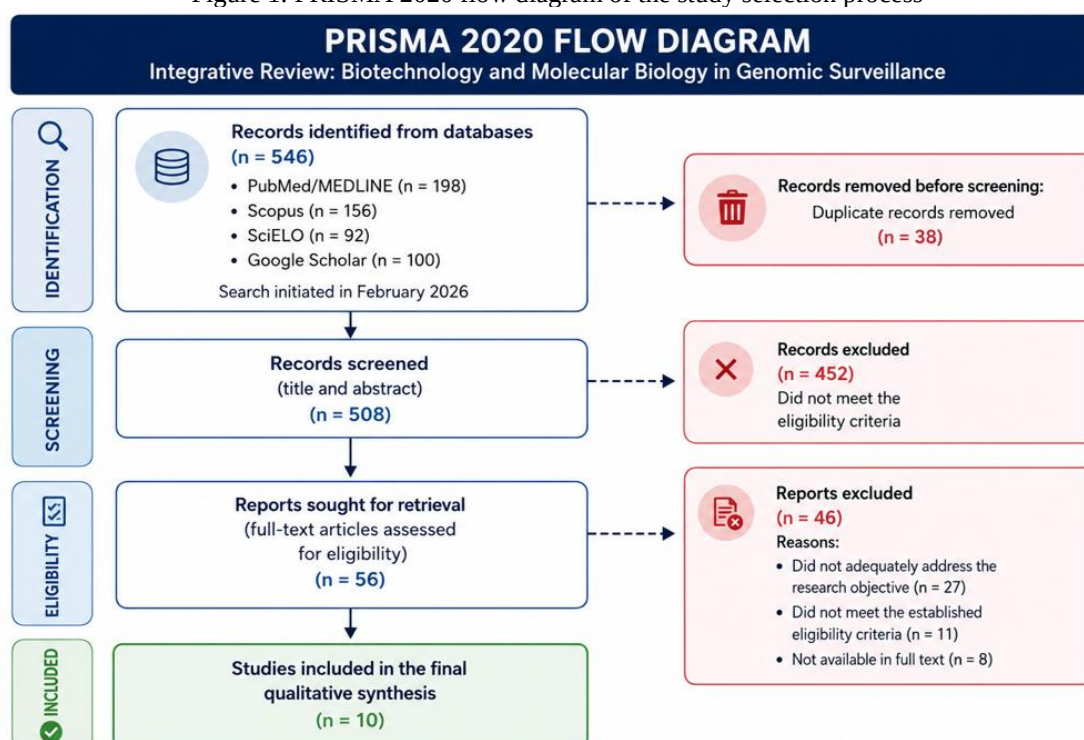
The study selection process consisted of four sequential stages: identification of records in the selected databases; removal of duplicate publications; screening of titles and abstracts according to the predefined eligibility criteria; and full-text assessment of potentially eligible studies.

The initial search identified 546 records. After removing 38 duplicate publications, 508 records remained for title and abstract screening. Of these, 452 studies were excluded because they did not meet the eligibility criteria. The remaining 56 articles underwent full-text assessment, and 46 were excluded because they did not adequately address the research objective or failed to meet the established eligibility criteria. Consequently, 10 studies were included in the final qualitative synthesis.

Data extraction was performed systematically using a standardized data collection form. The following information was recorded for each study: authorship, year of publication, study objective, methodological characteristics, biotechnology or molecular approach employed, field of application, principal findings, and reported limitations.

The findings were synthesized through thematic analysis, allowing the identification of recurrent themes and convergent evidence across the selected studies. The analysis was organized into five thematic domains: (i) genomic surveillance in epidemic monitoring; (ii) integration of genomic, epidemiological, and clinical information; (iii) ethical, legal, and governance challenges; (iv) infrastructure and capacity building for genomic surveillance, particularly in low- and middle-income countries; and (v) applications of biotechnology in diagnosis, prevention, vaccine development, and preparedness for future public health emergencies.

Figure 1. PRISMA 2020 flow diagram of the study selection process



Source: Adapted by the authors from Page et al. (2021)

4 RESULTS AND DISCUSSION

The main characteristics of the studies included in this integrative review are summarized in Table 1. Overall, the selected studies demonstrate the growing importance of biotechnology, genomics, and molecular biology in strengthening public health surveillance, particularly in epidemic monitoring, antimicrobial resistance surveillance, and preparedness for emerging infectious diseases.

Table 1. Characteristics of the studies included in the review

Author	Year	Study focus	Biotechnology/Method	Main contribution
Álvarez-Díaz <i>et al.</i>	2020	SARS-CoV-2 surveillance in Latin America	Genomic sequencing	Strengthened early warning systems and regional genomic surveillance.
Khoury <i>et al.</i>	2017	Precision public health	Public health genomics	Transition from public health genomics to precision public health.
Brito <i>et al.</i>	2022	Global genomic surveillance	SARS-CoV-2 genome sequencing	Identified inequalities in genomic

				surveillance capacity.
Akande <i>et al.</i>	2023	WHO regional initiatives	Pathogen genomic surveillance	Highlighted capacity building and regional cooperation.
Hill <i>et al.</i>	2023	Global surveillance networks	Viral genomics	Proposed strengthening international genomic surveillance.
Struelens <i>et al.</i>	2024	Real-time surveillance	Genomic surveillance	Enhanced control of infectious diseases and antimicrobial resistance.
Engelthaler	2024	Pathogen intelligence	Bioinformatics and genomics	Emphasized integration of genomic and epidemiological intelligence.
Webb <i>et al.</i>	2024	National genomic program	Pathogen genomics	Implementation of a nationwide genomic surveillance program.
Getchell <i>et al.</i>	2024	Low-resource settings	Genomic surveillance	Identified infrastructural barriers in resource-limited countries.
Marklewitz <i>et al.</i>	2025	Cost-effectiveness	Next-generation sequencing	Discussed economic aspects of genomic surveillance.

Source: prepared/adapted by the authors.

The literature analysis reveals that genomics has played a fundamental role in pathogen identification and characterization, offering a detailed understanding of genetic diversity and transmission patterns (Wang *et al.*, 2023).

This approach has been particularly relevant in detecting new outbreaks, monitoring antimicrobial resistance, and tracking emerging viral lineages, as demonstrated in arbovirus and zoonosis surveillance (Nürmberger *et al.*, 2024).

Epidemiological surveillance, strengthened by biotechnology, facilitates rapid and effective identification of cases and disease outbreaks, as well as monitoring disease evolution and evaluating the effectiveness of implemented actions (Silveira *et al.*, 2023).

Digital technologies, such as applications and social networks integrated with genomic data, enable enhanced disease monitoring, allowing targeted metagenomic testing in specific

populations based on indirect indicators, such as school absenteeism or online search patterns (Santos *et al.*, 2021).

4.1 Integration of Genomic and Epidemiological Data and Health Information Systems

Harmonizing these data sources is crucial for truly predictive and proactive public health surveillance, enabling faster and more targeted responses to emerging health threats (Matos *et al.*, 2024).

However, implementing standardized protocols for genomic data processing is essential to optimize comparisons across studies and facilitate interoperability among surveillance systems.

Rigorous data curation, combined with advanced bioinformatics algorithms, allows identification of complex epidemiological patterns that would be imperceptible using traditional methods (Matos *et al.*, 2024).

Interinstitutional collaboration emerges not merely as an operational facilitator but as a structural requirement for reducing inequalities in genomic surveillance capacity, particularly between high-income and low- and middle-income countries. According to Struelens *et al.* (2024), collaborative networks enable harmonization of sequencing protocols, bioinformatics pipelines, and data-sharing mechanisms, thereby increasing comparability and accelerating public health responses.

Nevertheless, validating genomic tests requires rigorous criteria, including differentiation between pathogens and commensals, adequate sensitivity and specificity, consistent reproducibility, and clear correlation between pathogen presence and disease manifestation (Akande *et al.*, 2023; Struelens *et al.*, 2024).

These criteria are complemented by the need to consider the cost of genomic technology and ethical implications arising from massive use of genetic data, especially in outbreak scenarios such as the COVID-19 pandemic, where the use of unvalidated or newly implemented approaches may generate significant challenges (Santos *et al.*, 2021).

Despite progress, expanding the application of genomics in public health remains hindered by a lack of adequate infrastructure, both in terms of equipment and specialized professionals in bioinformatics and genomics

4.2 Ethical and Infrastructural Challenges and the Democratization of Genomic Surveillance in Developing Countries

This gap is particularly pronounced in developing countries, where implementation costs, reagent availability, and technical training represent considerable barriers to routine adoption of these technologies (Zeghibib *et al.*, 2023).

The shortage of a qualified workforce, ranging from molecular biologists for data generation to bioinformaticians and molecular epidemiologists for analysis and interpretation, poses a significant obstacle to effective genomic surveillance implementation (Zeghibib *et al.*, 2023).

Weak integration of genomic data with epidemiological and clinical information represents an additional barrier, hindering holistic and real-time analysis for public health decision-making (Akande *et al.*, 2023; Struelens *et al.*, 2024).

Overcoming these challenges requires robust investment in technological infrastructure and training of qualified human resources, along with data governance that ensures interoperability and security of genomic information (Struelens *et al.*, 2024).

To this end, establishing public–private partnerships is essential to drive research and development of new tools, ensuring that the benefits of genomic sequencing are equitably shared among individuals, communities, and nations (Johnson; Parker, 2019).

This implies formulating public policies that encourage innovation and equitable access to genomic technologies, overcoming regional and socioeconomic disparities that still persist globally (Struelens *et al.*, 2024).

The creation of collaborative networks and sentinel laboratories, for example, can mitigate costs associated with equipment acquisition and maintenance, as well as specialized personnel training for genomic data analysis (Brandão, 2022).

Limited access to resources and imports restrictions can delay sequencing, while the use of outdated technology may lead to capacity issues and higher per-sample costs (Khan *et al.*, 2023).

4.3 Applications of Genomic Surveillance in Vaccine Development, Diagnostics, and Prevention Strategies

Genomic surveillance is crucial for understanding pathogen evolution, enabling development of more effective vaccines and more accurate diagnostics through identification of conserved genetic targets or hypervariable regions (Galarza *et al.*, 2023).

This approach is also vital for continuous adaptation of prevention and control strategies, as it allows monitoring the emergence of variants with greater transmissibility or virulence (Webb *et al.*, 2024).

Advances in next-generation sequencing are therefore essential for pathogen surveillance and outbreak investigation, contributing to evidence-based decision-making and appropriate public health actions (Marklewitz *et al.*, 2025).

Genomic advances are instrumental in identifying, characterizing, and monitoring pathogen evolution and transmission patterns, as well as supporting the development of diagnostics, therapies, and vaccines (Marklewitz *et al.*, 2025).

Implementing metagenomic approaches for virus discovery, followed by targeted viral genome sequencing, can help overcome current limitations of molecular and syndromic surveillance strategies (Brito *et al.*, 2022).

This capacity for early and detailed detection is fundamental for anticipating the spread of new threats and refining public health interventions, as demonstrated by real-time monitoring of SARS-CoV-2 variants during the COVID-19 pandemic (Hill *et al.*, 2023; Struelens *et al.*, 2024).

Although the expansion of sequencing capacity after COVID-19 represented an unprecedented advance in global health preparedness, this progress occurred unevenly across regions. Brito *et al.* (2022) demonstrated that high-income countries generated approximately ten times more genomic sequences per reported COVID-19 case than low- and middle-income countries, while Getchell *et al.* (2024) identified persistent shortages of trained personnel and unstable supply chains in Asia. Similarly, Álvarez-Díaz *et al.* (2020) observed that genomic surveillance initiatives in Latin America remained largely dependent on academic research groups rather than institutionalized public health programs, highlighting structural vulnerabilities that threaten long-term sustainability.

Despite this, the implementation of a Global Genomic Surveillance Strategy for Pathogens with Epidemic and Pandemic Potential (2022–2032) by the World Health

Organization seeks to strengthen these capacities by fostering collaboration and technical support to optimize public health response at a global scale (Akande *et al.*, 2024).

Ultimately, genomic surveillance is progressively shifting public health practice from reactive outbreak response toward predictive and precision-oriented prevention strategies, representing one of the most transformative developments in infectious disease control since the emergence of molecular epidemiology.

5 FINAL CONSIDERATIONS

The findings of this review suggest that genomic surveillance has emerged as an indispensable pillar of contemporary public health, enabling rapid pathogen identification, real-time monitoring of evolutionary dynamics, and the implementation of timely and effective responses to epidemics and pandemics.

Despite advances, democratizing access to these technologies and overcoming infrastructural and capacity-building barriers remain critical challenges for consolidating a truly equitable and robust global genomic surveillance system.

Continuous efforts are necessary to level global access to genomic surveillance capacity, especially in low- and middle-income countries, where current infrastructure is inadequate to confront future pandemic threats.

It is imperative that pathogen surveillance systems be strengthened and become more accessible worldwide to ensure collective public health resilience.

Furthermore, future advances in public health surveillance will increasingly depend on the integration of genomic surveillance with One Health strategies, recognizing the interconnectedness of human, animal, and environmental health.

The incorporation of artificial intelligence, real-time data analytics, and interoperable digital platforms is expected to enhance the early detection of emerging pathogens, support predictive epidemiology, and optimize evidence-based decision-making. Strengthening these integrated surveillance systems will be essential to improve global preparedness and resilience against future epidemics and pandemics.

Ultimately, the hypothesis that integrating advanced biotechnology into public health systems enhances epidemic monitoring is robustly confirmed by recent literature. However, this review demonstrates that the maturation of genomic surveillance transcends mere molecular innovation; it is deeply entrenched in overcoming systemic global inequalities.

Establishing robust ethical governance, democratizing bioinformatics infrastructure, and ensuring that pathogen intelligence translates into tangible public policies are the definitive challenges of this decade. Future research must, therefore, pivot from demonstrating the efficacy of genomic tools to optimizing their implementation in the resource-limited settings that stand on the frontlines of emerging infectious diseases.

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