

Review Article

# Bridging the Gap Between Genomic Surveillance of Antimicrobial Resistance and Public Health Decision-Making: A Review

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## Abstract:

Antimicrobial resistance (AMR) poses an escalating threat to global public health, undermining the effectiveness of infectious disease prevention and treatment and placing sustained pressure on health systems worldwide. Advances in genomic technologies, including whole-genome sequencing and metagenomic analyses, have substantially enhanced the resolution and scope of AMR surveillance. However, despite growing investments in genomic surveillance, the routine translation of genomic data into public health policy and action remains limited. This review examines the persistent data-to-decision (D2D) gap that constrains the public health impact of genomic AMR surveillance. Using a narrative review approach, the literature on genomic AMR surveillance, public health surveillance systems, and decision-making frameworks was synthesized to assess how genomic data are generated, interpreted, and operationalized within public health systems. The review integrates evidence from international and national surveillance initiatives, policy analyses, and implementation studies, with particular attention to organizational, analytical, and governance factors influencing data use. Findings indicate that while genomic surveillance offers high potential for early detection of resistance, transmission tracking, and proactive intervention, its public health utility is frequently limited by insufficient integration with decision-making structures, lack of standardized reporting and interpretation frameworks, and unclear action thresholds. The review highlights emerging best practices, including standardized translational reporting, decision-support tools, predefined genomic action triggers, and multidisciplinary collaboration, as critical mechanisms for closing the D2D gap. Persistent inequities in access to genomic surveillance capacity, particularly in low- and middle-income countries, further underscore the need for governance models that prioritize sustainability, local ownership, and equitable capacity building. Overall, this review argues that realizing the full public health value of genomic AMR surveillance requires moving beyond technological advancement toward intentional systems-level integration that aligns genomic intelligence with timely, evidence-informed public health decision-making.

**Keywords:** Antimicrobial Resistance; Genomic Epidemiology; Public Health Policy; Surveillance Systems; Translational Genomics; Data-To-Decision Gap; Genomic Surveillance Systems

## Introduction

### Background on Antimicrobial Resistance

Antimicrobial resistance (AMR) represents a major and escalating threat to global public health, undermining the effectiveness of antimicrobial therapies and complicating the prevention and control of infectious diseases. The increasing prevalence of resistant pathogens contributes to prolonged illness, higher mortality, and rising healthcare costs, placing substantial strain on health systems worldwide [1, 2]. Beyond its clinical consequences, AMR poses a systemic challenge to public health by reducing the reliability of infection control, antimicrobial stewardship, and outbreak response strategies.

Effective surveillance is central to mitigating the impact of AMR, as it enables the detection of emerging resistance patterns, monitoring of temporal and geographic trends, and prioritization of public health interventions. However, the rapid evolution and dissemination of resistant organisms increasingly expose limitations in traditional surveillance systems, particularly in their ability to generate timely and actionable intelligence for population-level decision-making.

### Limitations of Conventional Phenotypic Surveillance

Historically, AMR surveillance has relied on phenotypic antimicrobial susceptibility testing (AST) conducted in clinical microbiology laboratories. These methods remain essential for guiding patient-level treatment decisions and for producing standardized resistance profiles used in national and international surveillance frameworks [3, 4]. Phenotypic surveillance has supported the identification of priority pathogens and long-term resistance trends, particularly within hospital settings.

Despite these strengths, phenotypic surveillance has notable limitations when applied to public health decision-making. Culture-based workflows are inherently time-consuming, often delaying the availability of results beyond windows in which early intervention would be most effective. In addition, phenotypic data provide limited insight into the genetic mechanisms underlying resistance, the relatedness of circulating strains, or the pathways of transmission that sustain outbreaks and regional spread. As a result, phenotypic surveillance alone is poorly suited to early warning, transmission tracking, and anticipatory public health action [5, 6].

### Emergence of Genomic Surveillance in AMR

Advances in genomic technologies, particularly whole-genome sequencing (WGS) and metagenomic approaches, have expanded the analytical capacity of

AMR surveillance. Genomic surveillance enables high-resolution characterization of resistance determinants, mobile genetic elements, and phylogenetic relationships among pathogens. When integrated with epidemiological metadata, genomic data can distinguish sporadic cases from outbreaks, identify transmission networks, and detect emerging resistance before it becomes widespread [7, 8].

In several high-income countries, genomic surveillance has been incorporated into reference laboratories and national surveillance systems, demonstrating its value for outbreak investigation, infection prevention, and antimicrobial stewardship [8, 9]. Compared with earlier molecular methods, genomic approaches provide greater resolution and flexibility, allowing simultaneous analysis of resistance, virulence, and pathogen evolution. These capabilities position genomic surveillance as a potentially transformative component of public health intelligence rather than a purely research-oriented tool.

### The Data-to-Decision Gap and Objectives of This Review

Despite the growing availability of genomic AMR data, its routine use in public health decision-making remains limited. In many settings, genomic surveillance outputs are generated within research or reference laboratory environments but are not systematically translated into information that informs policy, planning, or intervention. This disconnect, commonly described as a data-to-decision (D2D) gap, reflects challenges that extend beyond technological capacity, including limited genomic and bioinformatics expertise among public health practitioners, fragmented surveillance infrastructures, unclear governance arrangements, and the absence of predefined pathways linking genomic signals to public health action. [7, 10].

While existing reviews have primarily focused on the technical performance and feasibility of genomic tools, fewer have examined how genomic surveillance can be operationally integrated into public health systems in ways that directly support decision-making. The central contribution of this review is to synthesize the literature using the D2D gap as an explicit analytical lens, examining how genomic AMR surveillance interfaces with organizational structures, governance mechanisms, and decision thresholds within public health systems.

Specifically, this review aims to: (i) examine the evolution and current applications of genomic surveillance for AMR; (ii) identify analytical, organizational,

and governance barriers that impede translation of genomic data into public health action; and (iii) synthesize emerging frameworks and best practices that support

the systematic integration of genomic surveillance into routine public health decision-making, with particular attention to global equity and sustainability.

## Literature Review

### Evolution of AMR Surveillance Systems

The World Health Organization and the Centers for Disease Control and Prevention both outline the global and national public health impacts of antimicrobial resistance (AMR). Continuous systematic surveillance of AMR is fundamental in shaping relevant public health responses. AMR surveillance systems have traditionally relied on clinical microbiology laboratory testing for antimicrobial susceptibility (AST) at the phenotypic level [4, 11]. These surveillance systems isolate and test a sample for the presence of a pathogen and develop a susceptibility profile (e.g., resistant, intermediate, susceptible, or not tested). From a national and global perspective, this surveillance approach provides sample-based treatment options, identifies emergent resistance patterns, and contributes to customized national and international reporting obligations. Large-scale surveillance in hospital settings and for prioritized pathogens has been the basis of reporting on the prevalence and temporal trends of resistance [12, 13]. Reporting on the prevalence and temporal trends of resistance has relied on prioritized pathogens and hospital settings.

Nonetheless, there are significant drawbacks to relying solely on phenotypic surveillance. Because of the reliance on culture-based methods, the testing and reporting processes are time-consuming and can take several days just to produce actionable results after a test is administered. Because of this, speciation cannot be completed promptly, and response actions to a public health (or epidemiologic) threat may be delayed. The evolutionary mechanisms driving resistance may go unexamined or unexplained, and closely associated strains that may be of public health concern can go unexamined. Because of this, there may not be a reliable means of identifying the routes of transmission, and the early stages of an outbreak may go unrecognized, which may impede the understanding of the resistance and the public health response [13, 14].

As a response to some of the limitations, the initial design of the surveillance of AMR systems included some of the early molecular methods. The initial methods of molecular testing included the polymerase chain reaction (PCR), the pulse field gel electrophoresis, and the multilocus sequence typing methods, which, along with testing for the phenotypic expression of resistance, improve strain differentiation. These methods im-

proved testing for the phenotypic expression of resistance and gave greater detail to the analysis of the resistance gene(s); however, the methods were still limited by the presence of some genes and the resistance determinants [15].

Whole genome sequencing was the first major development in the surveillance of AMR systems. The first significant development in surveillance systems based on genomics was the ability to do analysis on the complete genome of the organism's pathogens and simultaneously determine the presence of resistance gene(s), virulence factors, and the organism's phylogenetic lineage(s) [16]. Additionally, on the basis of sequencing cost and the development of bioinformatics systems, converting sequence-based molecular methods into comprehensive routine genomic surveillance systems has been possible for the majority of high-income countries. This has been a major step in the use of genomic technologies for public health surveillance systems.

### Applications of Genomic Surveillance in AMR

Documented applications of the use of genomics in antimicrobial resistance (AMR) include surveillance of the genomics of the resistance mechanisms, tracking, and the detection of outbreaks. In the analysis of the whole genomes of the pathogenic microorganisms (isolates), relatedness of the isolates can be determined with a high degree of precision to differentiate between sporadic cases and true outbreaks. This feature has been particularly useful in the case of infections that are healthcare-associated; thus, genomics has been able to identify chains of transmission that were hidden, clarify the source of the outbreaks, and assess the effectiveness of the infection control strategies. Genomics can provide analysis of outbreak dynamics accurately and promptly when compared to traditional typing methods [7, 17].

Genomic surveillance aids in the detection and characterization of resistance mechanisms. With the use of whole genomes, it is possible to identify resistance genes that are known and new ones that may be emerging. Genomics can describe the genetic elements that resistance is associated with, including transposons, plasmids, and integrons that provide horizontal gene transfer.[8]. This information is useful to understand the mechanism of spread of resistance throughout populations of bacteria and even across species, which can assist in clinical management and public health strategies [18].

Outside of specific healthcare contexts, genomic surveillance has also been used to examine transmission dynamics in other community and environmental settings. Resistant pathogens have been tracked through genomic data analysis in and out of hospitals and across borders, including omcs. These research exemplars reinforce the AMR dissemination problem and the need for multi-level and cross-sector surveillance systems. The combination of genomic, epidemiological, and other types of metadata has also improved the understanding of the factors that maintain and drive resistance [8, 19].

Acknowledged technical difficulties aside, the literature documenting the disparate impacts of genomic surveillance is extensive. A lack of uniformity in sequencing tech and analytics, as well as report generation, has created a disparity in outcomes that has limited the genomic surveillance effort's comparability across areas, as well as the scalability of these efforts.

#### **Public Health Decision-Making Frameworks**

Decision-making in public health relies on evidence from various scientific fields, as well as social, ethical, and resource-based considerations. Integrative frameworks use evidence to create priorities among interventions, optimize the use of available resources, and achieve the highest possible health gain at the population level. In the context of the control of antimicrobial resistance (AMR), activities that involve this kind of decision-making include formulating antimicrobial stewardship policies, planning for infection control, and planning for emergency response to infection outbreaks [20].

Decision-making in public health includes a systematic and structured assessment of risk, which involves identifying and analyzing potential threats in terms of their probability and their impact. In the realm of AMR, this involves evaluating the levels of certain resistant pathogens, the gravity of the infections they cause, and the risk of transmitting those infections. To perform effective prioritization, decision-makers need data that is reliable and available within a reasonable time frame, and is easy to interpret and translate, so that the decision-making process can be related to the risk context of AMR [2].

The design and implementation of interventions are contingent on the surveillance activities being linked to actionable outcomes. Health authorities and policy makers prefer synthesized information to raw data, and even more so, they tend to prefer simple and straightforward metrics that facilitate the construction of estimates of the indicators, so that they can choose among different paths of potential outcomes for strategic planning. It is widely accepted that the technical

outputs of surveillance and the policy demands related to them are bridged through effective communication and the proper mechanisms for the translation of the knowledge accumulated [21].

Though surveillance technology has advanced, the data needs identified by policymakers continue to go largely unaddressed. Data from genomics is detailed and extensive, but is not always presented in ways that facilitate decision-making. This discrepancy leads to underutilization of the outputs from genomic surveillance and reduces their potential impact on the development of policy and the practice of public health [22].

#### **Gaps Identified in Existing Literature**

The implementation of genomic surveillance and routine decision-making processes in public health has been discussed in the literature multiple times. Even though there have been multiple examples demonstrating the feasibility and power of genomics in the area of public health, there have been few examples of operationalizing genomics within health systems. Genomic surveillance functions in most cases as a separate, tandem, or temporary project and not as an integral component of the surveillance infrastructure, a situation that occurs all too often in the literature [7, 8].

The literature has also pointed out the issues of data standardization and interoperability. Even though there have been attempts at interoperability between different platforms (analytical pipelines and databases), they have not been universally successful. The lack of a unified approach still results in different (and often suboptimal) public health responses to the genomic data. This is most often the case in the critical closure of the gap between public health and laboratory structures (responding to public health issues).

Public health literature has pointed out the equity of access issues within the field (high, low, and middle-income) and the economic barriers of low and middle-income countries. While genomic surveillance has been a public health benefit for most high-income countries, the lack of adequate infrastructure, trained health care workers, and an inability to attain sustainable funding principles has created barriers to the implementation of genomic surveillance in most low and middle-income countries.

Taken together, these gaps illustrate a focus for more integrated frameworks beyond simply technological innovation. Increasingly, the literature highlights the need to align genomic surveillance frameworks with decision-making, governance, and capacity-building frameworks. To fully address the public health challenges of genomic surveillance in the fight against antimicrobial resistance, these gaps must be addressed.

## Methodology

### Review Design

This study was conducted as a narrative review aimed at critically examining the integration of genomic antimicrobial resistance (AMR) surveillance into public health decision-making frameworks. A narrative review approach was selected because the objectives of this study extend beyond the synthesis of empirical outcomes to include conceptual, organizational, and policy-oriented dimensions of surveillance systems. This approach is particularly appropriate for interdisciplinary topics that span genomics, epidemiology, public health practice, and governance structures.

Unlike systematic reviews, which are designed to answer narrowly defined research questions, a narrative review allows for the integration of heterogeneous evidence, including empirical studies, surveillance reports, policy analyses, and conceptual frameworks. This flexibility was essential for examining the data-to-decision (D2D) gap in genomic AMR surveillance, which is shaped by technical capacity, institutional design, and decision-making processes rather than by a single intervention or outcome.

### Data Sources and Search Strategy

A structured literature search was conducted across three major electronic databases: PubMed, Scopus, and Web of Science. These databases were selected for their comprehensive coverage of biomedical research, public health surveillance, and interdisciplinary policy literature. Additional relevant sources were identified through manual screening of reference lists from key articles and prior reviews to ensure adequate coverage of foundational and emerging work.

The search strategy combined controlled vocabulary terms and free-text keywords related to antimicrobial resistance, genomic surveillance, and public health decision-making. Representative search terms included combinations of: “antimicrobial resistance,” “genomic surveillance,” “whole-genome sequencing,” “metagenomics,” “public health surveillance,” “decision-making,” “policy,” and “governance.” Boolean operators were used to refine searches and capture variations in terminology across disciplines.

The search focused on literature published between 2010 and 2024, reflecting the period during which genomic technologies became increasingly integrated into AMR surveillance systems. Only articles

published in English were included, due to resource constraints and to ensure consistency in interpretation.

### Inclusion and Exclusion Criteria

Studies were eligible for inclusion if they addressed genomic or molecular surveillance of AMR in human health contexts, examined public health surveillance systems, or discussed mechanisms for translating surveillance data into policy or practice. Included sources comprised original research articles, national and international surveillance reports, policy analyses, and conceptual or methodological frameworks relevant to AMR decision-making.

Studies were excluded if they focused exclusively on non-human sectors, such as agriculture or environmental surveillance, without clear relevance to human public health decision-making. Articles limited to purely technical bioinformatics methods without discussion of surveillance application or policy relevance were also excluded. Editorials, opinion pieces, and conference abstracts lacking sufficient methodological or conceptual detail were not considered.

### Data Extraction and Analytical Approach

Data extraction was conducted through iterative and structured reading of included sources. Key information was identified and summarized across four analytical domains: (i) surveillance system design and data generation, (ii) genomic and analytical methods, (iii) mechanisms of data interpretation and reporting, and (iv) pathways linking surveillance outputs to public health decisions.

A thematic synthesis approach was employed to identify recurring patterns, barriers, and enabling factors across the literature. Themes were refined iteratively as additional sources were reviewed, and thematic saturation was considered achieved when no substantively new concepts emerged within the analytical domains. The synthesis was explicitly guided by the data-to-decision framework, enabling comparative analysis of how genomic surveillance outputs are generated, interpreted, and translated into public health action across different settings.

This approach facilitated identification of gaps between technical capacity and operational use, as well as opportunities for improving alignment between genomic surveillance systems and public health decision-making processes.

## Results and Discussion

### Current Models of Genomic AMR Surveillance

The reviewed literature describes a growing number of

national and international initiatives that have incorporated genomic approaches into antimicrobial resistance

(AMR) surveillance. In high-income settings, whole-genome sequencing (WGS) has increasingly been integrated into reference laboratory workflows to support surveillance of priority pathogens, outbreak investigation, and infection prevention efforts [7, 23, 24]. These systems typically combine genomic data with epidemiological metadata to enhance resolution of transmission pathways and resistance dynamics.

As summarized in Table 1, genomic surveillance consistently demonstrates superior resolution for transmission analysis, improved capacity to detect novel resistance determinants, and greater potential for proactive public health decision-making when compared with conventional methods [8, 26]. These features enable more precise characterization of resistance evolution and dissemination at the population level.

**Table 1. Comparative Evaluation of Antimicrobial Resistance Surveillance Approaches for Public Health Decision-Making**

Dimension	Phenotypic Surveillance	Targeted Molecular Methods	Genomic Surveillance (WGS/Metagenomics)
<b>Turnaround Time</b>	Moderate to slow due to culture-based testing and incubation requirements	Faster than phenotypic methods, but dependent on predefined targets	Rapid once sequencing workflows are established, near-real-time analysis is possible
<b>Resolution for Transmission Analysis</b>	Low; limited ability to distinguish closely related strains	Moderate; improved strain discrimination but limited genomic context	High; enables precise phylogenetic analysis and transmission mapping
<b>Ability to Detect Novel Resistance</b>	Limited to phenotypically expressed resistance	Limited to known resistance targets	High; capable of identifying novel or emerging resistance determinants
<b>Insight into Resistance Mechanisms</b>	Indirect; does not reveal the genetic basis of resistance	Partial; identifies specific genes but lacks contextual information	Comprehensive; characterizes genes, mutations, and mobile genetic elements
<b>Data Complexity</b>	Low; standardized and widely understood	Moderate; requires molecular interpretation	High; requires bioinformatics expertise and advanced data management
<b>Infrastructure and Expertise Requirements</b>	Widely available laboratory infrastructure	Moderate laboratory and molecular expertise required	High infrastructure, computational capacity, and a specialized workforce are needed
<b>Actionability for Policy Decisions</b>	Well-established for clinical guidelines, but limited for proactive public health action	Useful for targeted interventions but constrained in scope	High potential for proactive, data-driven decision-making when effectively translated
<b>Scalability Across Health Systems</b>	High; feasible in most resource settings	Variable; dependent on laboratory capacity	Uneven; currently concentrated in high-resource settings

*Source: Synthesized from reviewed literature.*

Despite these advantages, the public health impact of genomic surveillance remains uneven. In many documented systems, genomic data are generated and analyzed within laboratory or research environments, but are not systematically integrated into routine public health surveillance workflows. This

misalignment contributes to delays in interpretation and response, limiting the operational value of genomic surveillance despite its analytical strength [25]. These findings reinforce the existence of a persistent data-to-decision (D2D) gap, wherein advanced surveillance capacity does not reliably translate into timely public

health action. Figure 1 conceptualizes the integrated pathway from genomic AMR surveillance to public health action, explicitly highlighting points at which

data interpretation, communication, and governance breakdowns contribute to the D2D gap.

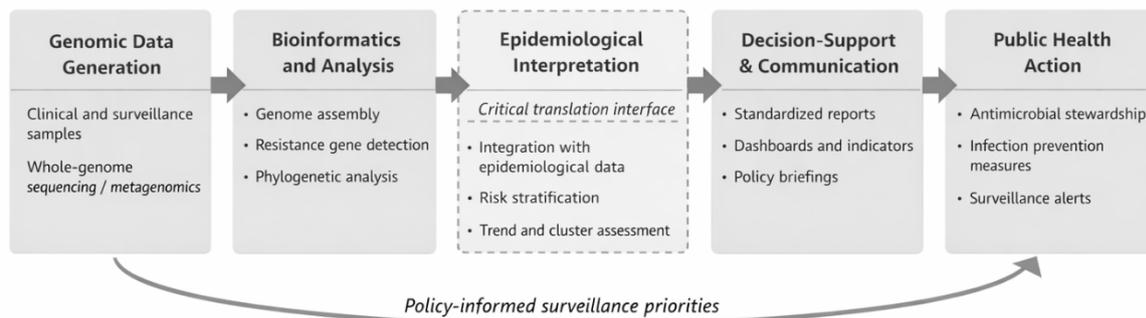


Figure 1. From Genomic AMR Surveillance to Public Health Decision-Making: An Integrated Pathway. This figure visually demonstrates how genomic AMR data should move from laboratories to policy action, while explicitly highlighting the “translation gap” that currently limits impact. It integrates the technical, analytical, and governance dimensions discussed in Sections 4.1–4.4.

**Barriers to Translating Genomic Data into Public Health Action**

Across the reviewed literature, multiple interrelated barriers impede the translation of genomic AMR data into actionable public health measures. Technical barriers remain significant, particularly in relation to data volume, analytical complexity, and computational infrastructure. Whole-genome sequencing generates large datasets that require specialized bioinformatics expertise and sustained computational resources, which are often limited outside specialized centers [7, 10].

Organizational barriers further constrain translation. Public health agencies frequently lack personnel

with the training required to interpret genomic outputs or contextualize them within epidemiological risk assessments. Communication between laboratories, surveillance units, and policy-making bodies is often fragmented, resulting in unclear accountability for translating genomic findings into action. In several documented cases, substantial investment in genomic data generation yielded limited public health benefit due to the absence of predefined pathways for data utilization [26].

Governance-related challenges compound these barriers. The lack of standardized reporting formats and agreed-upon interpretive guidelines creates uncertainty regarding how genomic signals should inform decision-making. Data-sharing restrictions, ethical considerations, and concerns regarding data ownership can delay reporting and limit cross-jurisdictional coordination [27].

These barriers and corresponding enabling strategies across the genomic data-to-decision continuum are systematically summarized in Table 2.

**Table 2. Barriers and Enablers Across the Genomic AMR Data-to-Decision Continuum**

Continuum Stage	Key Barriers	Enabling Strategies	Implications for Public Health Decision-Making
Data Generation	Uneven access to sequencing platforms; inconsistent sampling strategies; high operational costs	Investment in shared sequencing infrastructure; harmonized sampling protocols	Determines representativeness and timeliness of resistance signals
Data Analysis	Limited bioinformatics capacity; lack of standardized analytical pipelines; computational resource constraints	Centralized or cloud-based analysis platforms; workforce training	Affects the accuracy and comparability of genomic outputs

Continuum Stage	Key Barriers	Enabling Strategies	Implications for Public Health Decision-Making
<b>Interpretation</b>	Complexity of genomic outputs; limited genomic literacy among public health practitioners	Multidisciplinary interpretation teams; translational summaries	Influences confidence in using genomic evidence for action
<b>Reporting and Communication</b>	Non-standardized reporting formats; delayed dissemination of findings	Standardized reporting templates; real-time dashboards	Shapes the usability and responsiveness of decision-makers
<b>Policy Translation and Action</b>	Absence of predefined action thresholds; governance and data-sharing restrictions	Decision-support tools; clear governance frameworks	Determines whether genomic data lead to timely interventions

*Source: Synthesized from reviewed literature.*

*Addressing these barriers through targeted enabling strategies is essential for embedding genomic surveillance within routine public health decision-making processes.*

### From Genomic Signals to Decisions: Translation Mechanisms and Enablers

The literature identifies several mechanisms that facilitate the translation of genomic surveillance into public health decision-making. Standardized reporting frameworks are consistently highlighted as a critical enabler, particularly when complex genomic outputs are distilled into concise, policy-relevant summaries emphasizing risk, uncertainty, and trend [8].

A key finding across multiple studies is the importance of predefined decision thresholds that link specific genomic signals to public health actions. For example, the detection of novel resistance genes, the identification of sustained genomic clustering suggestive of transmission, or the rapid expansion of high-risk lineages can be explicitly tied to actions such as intensified infection control, targeted antimicrobial stewardship interventions, or expanded surveillance [28]. These trigger-based mechanisms reduce reliance on ad hoc interpretation and improve the timeliness and consistency of responses.

Real-time analytics and visualization tools further enhance translation by integrating genomic, epidemiological, and clinical data into dashboards accessible to public health practitioners. These tools support situational awareness and enable proactive rather than reactive decision-making during outbreaks or periods of rapid resistance emergence [29]

### Integrating Genomic Surveillance Within Public Health Systems

Several conceptual and operational models propose systematic integration of genomic surveillance within public health decision-making frameworks. These models emphasize alignment between genomic outputs and existing risk assessment, response, and

governance structures, ensuring that genomic data complement rather than duplicate other surveillance inputs [25, 30].

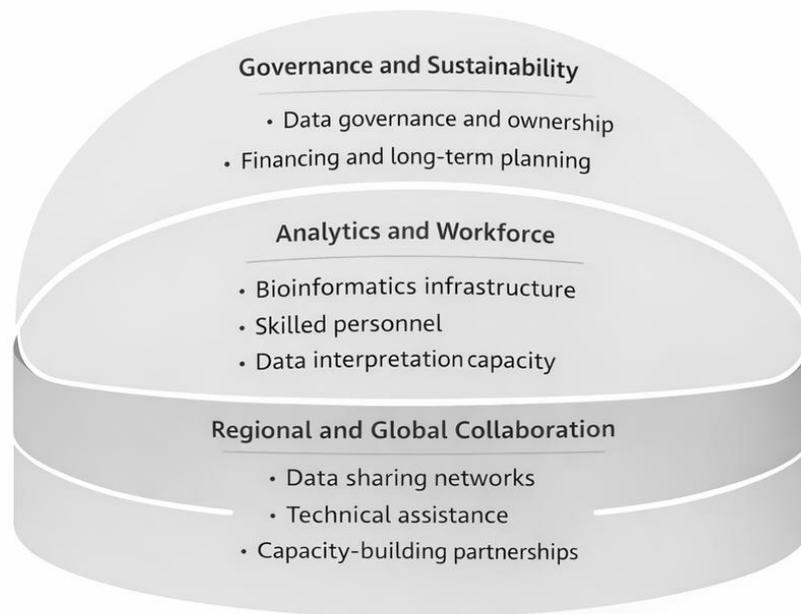
Decision-support systems represent a particularly promising approach. When genomic surveillance outputs are embedded within formal decision-support tools, they can be translated into actionable recommendations based on predefined criteria and escalation protocols. Such systems strengthen accountability and reduce delays between detection and intervention.

### Implications for Global Health Equity

The literature highlights substantial inequities in access to genomic AMR surveillance capacity. While high-income countries have made significant progress, many low- and middle-income countries (LMICs) continue to rely primarily on phenotypic methods due to constraints in infrastructure, workforce capacity, and sustainable funding [28]

An equity-oriented framework for implementing genomic AMR surveillance is illustrated in Figure 2, which depicts the interdependent layers of sequencing capacity, analytics, workforce development, and governance required for sustainable implementation. This framework emphasizes the importance of regional and global partnerships in supporting equitable surveillance systems.

Importantly, equity-oriented genomic surveillance must prioritize local ownership of data and analytical capacity. Initiatives that do not align with national decision-making structures risk reinforcing dependency rather than strengthening public health systems. Governance frameworks that support ethical data sharing and national priorities are therefore essential for sustainable and equitable genomic AMR surveillance.



*Barriers at any layer limit the public health impact of genomic AMR surveillance*

Figure 2. An equity-oriented framework for implementing genomic antimicrobial resistance (AMR) surveillance globally.

The network captures the critical and interrelated layers necessary for the sequencing capacity, analytics, workforce, and governance for fair and effective genomic AMR surveillance. As pertaining to all layers, and especially for sustainable implementation in the lowest and middle-income countries, regional and global partnerships are crucial.

There are many approaches that have been found to be useful in the growing field of ADR prediction.

## Conclusion

Antimicrobial resistance (AMR) continues to pose a substantial and evolving threat to global public health, necessitating surveillance systems that are both scientifically robust and operationally actionable. This review has synthesized the existing literature on genomic AMR surveillance with a specific focus on the persistent gap between data generation and public health decision-making. While genomic technologies have significantly enhanced the resolution and scope of AMR surveillance, their public health impact remains constrained by limitations that extend beyond technical capacity alone.

The findings of this review demonstrate that the principal challenges in genomic AMR surveillance are increasingly organizational, analytical, and governance-related rather than purely technological. In many settings, genomic data are generated within advanced

laboratory environments but are insufficiently integrated into routine public health workflows. The absence of standardized reporting formats, limited genomic literacy among decision-makers, fragmented surveillance infrastructures, and unclear decision thresholds collectively contribute to the underutilization of genomic evidence in policy and practice.

Such as statistical modeling, machine learning, and deep learning approaches. Each is associated with different assumptions, strengths, and limitations. Whereas classical statistical modeling provides interpretability and simplicity, modern machine learning and deep networks seek to capture nonlinearities, interactions, and high-dimensional signals; hybrid models aim to harness both structured and unstructured data to optimize performance. We discussed these approaches in detail under the following headings:

laboratory environments but are insufficiently integrated into routine public health workflows. The absence of standardized reporting formats, limited genomic literacy among decision-makers, fragmented surveillance infrastructures, and unclear decision thresholds collectively contribute to the underutilization of genomic evidence in policy and practice.

By applying the data-to-decision (D2D) gap as an explicit analytical framework, this review highlights the importance of aligning genomic surveillance outputs with public health risk assessment and response structures. Surveillance systems that incorporate predefined action thresholds, decision-support tools, and multidisciplinary interpretation mechanisms are better positioned to translate genomic signals into timely and effective interventions. Importantly, genomic surveillance is most impactful when embedded within broader

surveillance and governance systems that support accountability, communication, and sustained use.

Equity considerations are central to the future of genomic AMR surveillance. Substantial disparities persist between high-income countries and low- and middle-income countries (LMICs) in access to sequencing infrastructure, analytical capacity, and trained personnel. Addressing these inequities requires coordinated investment across technical, workforce, and governance domains, supported by regional and global partnerships. Capacity-building initiatives must prioritize local data ownership and decision-making authority to ensure that genomic surveillance strengthens, rather than bypasses, national public health systems.

Several limitations of this review should be acknowledged. As a narrative review, the synthesis emphasizes conceptual integration rather than quantitative comparison, and some relevant literature from One

Health domains may not be fully captured. Additionally, genomic surveillance models and standards are evolving rapidly, and some operational frameworks discussed here may require refinement as technologies and policies advance.

In conclusion, genomic surveillance has the potential to serve as a cornerstone of modern AMR control, but its effectiveness depends on more than analytical sophistication. Closing the data-to-decision gap requires intentional integration of genomics into public health decision-making frameworks, supported by clear governance structures, standardized translation mechanisms, and sustained capacity building. Viewing genomic surveillance as an integral component of public health intelligence rather than as a standalone technical capability is essential for realizing its promise in strengthening equitable and responsive AMR surveillance systems.

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