TYPE
Narrative Review

PUBLISHED
5 September 2026

DOI
10.5281/zenodo.22213244

OPEN ACCESS

***CORRESPONDENCE**
Festus Oluwaloni Olukoya
festusoluwaloni@gmail.com
+2348137132775

RECEIVED
31 August 2026

ACCEPTED
7 September 2026

PUBLISHED
5 September 2026

CITATION
Ishola, O., & Olukoya, F. O. (2026). Developing early warning systems for antimicrobial resistance: A narrative review of surveillance, predictive analytics and genomic approaches. ScienceXplorer, 8(3).

DEVELOPING EARLY WARNING SYSTEMS FOR ANTIMICROBIAL RESISTANCE

A Narrative Review of Surveillance, Predictive Analytics and Genomic Approaches

Oluwatoyin Ishola[1], Festus Oluwaloni Olukoya[2,*]

[1]Department of Public Health, National Open University of Nigeria (NOUN), Abuja, Nigeria
[2]Department of Pharmacy, Faculty of Pharmacy, Olabisi Onabanjo University, Nigeria
**Corresponding author — Festus Oluwaloni Olukoya: festusoluwaloni@gmail.com | +2348137132775*

ABSTRACT

Purpose Antimicrobial resistance (AMR) is an escalating global health threat that undermines the effectiveness of antimicrobial therapy and threatens health systems worldwide. Conventional AMR surveillance predominantly identifies resistance only after resistant organisms have become established, limiting opportunities for timely intervention. This narrative review examines how surveillance, predictive analytics and genomic approaches can be integrated into effective early warning systems for AMR.

Methods Literature published between 2010 and 2026 was reviewed using PubMed/MEDLINE, Scopus, Web of Science, Google Scholar and ScienceDirect, supplemented by relevant reference-list screening and reports from major public-health organisations. Evidence covering microbiological surveillance, antimicrobial consumption monitoring, clinical and epidemiological data, genomic surveillance, geospatial analysis, predictive modelling and machine learning was synthesised thematically.

Results Integrating phenotypic resistance data with antimicrobial-use, clinical, genomic and environmental information improves the detection of emerging resistance signals, but fragmented data systems, inadequate laboratory capacity, inconsistent data standards, limited genomic infrastructure and weak translation of predictions into public-health action remain important barriers.

Conclusions An integrated five-stage framework comprising data acquisition, signal detection, signal verification, risk prediction and public-health response is proposed as a conceptual foundation for moving AMR surveillance from retrospective reporting toward proactive early warning, with particular relevance to low- and middle-income countries.

Keywords: *antimicrobial resistance; early warning system; AMR surveillance; antimicrobial stewardship; genomic surveillance; machine learning; predictive analytics; antimicrobial resistance genes; genomic epidemiology; public health surveillance.*

How to Cite

Recommended citation: Ishola, O., & Olukoya, F. O. (2026). Developing early warning systems for antimicrobial resistance: A narrative review of surveillance, predictive analytics and genomic approaches. ScienceXplorer, 8(3).

1. INTRODUCTION

Antimicrobial resistance (AMR) occurs when microorganisms become less susceptible or resistant to antimicrobial medicines that were previously effective against them. Although resistance is a natural evolutionary phenomenon, the intensity and speed of contemporary resistance development have been strongly influenced by antimicrobial exposure, inappropriate use, healthcare-associated transmission, inadequate infection prevention and control, and environmental dissemination of resistant organisms and resistance determinants [1–4]. The resulting threat extends beyond the treatment of individual infections because effective antimicrobials are fundamental to surgery, cancer treatment, transplantation, intensive care and management of severe infectious diseases [5,6].

The magnitude of the problem is substantial. The Global Burden of Disease analysis estimated that bacterial AMR was directly responsible for approximately 1.27 million deaths and associated with approximately 4.95 million deaths in 2019 [7]. The burden is unevenly distributed, with many low- and middle-income countries experiencing substantial challenges related to infectious disease burden, antimicrobial access, laboratory capacity and surveillance infrastructure [7,8]. The World Health Organization (WHO) continues to identify AMR as a major global health and health-security threat and has established surveillance as a central component of the global response [9,10].

The WHO Global Antimicrobial Resistance and Use Surveillance System (GLASS) was established in 2015 to promote standardised AMR surveillance and has progressively expanded from laboratory-based resistance surveillance to include antimicrobial use, early detection and One Health components [10–12]. By the end of 2024, 141 countries, territories and areas had committed to contribute AMR and/or antimicrobial-use data to GLASS. The 2025 WHO global antibiotic resistance surveillance report analysed more than 23 million bacteriologically confirmed infections reported by 104 countries for 2023, demonstrating the increasing scale of international AMR surveillance.

Despite these advances, surveillance does not necessarily equate to early warning. Conventional surveillance generally describes the current or historical prevalence of resistance. An early warning system, by contrast, should identify unusual signals, determine whether they represent meaningful changes, estimate the likelihood of further spread or escalation and trigger an appropriate response before the threat becomes widespread.

This distinction is important. A surveillance system may report that carbapenem resistance increased from 20% to 30% over several years. An early warning system should additionally determine whether the increase exceeds expected variation, whether a new resistance determinant or high-risk clone has appeared, whether the increase is associated with antimicrobial consumption or transmission, whether neighbouring institutions are experiencing similar changes, and whether intervention is warranted.

Modern health systems generate multiple data streams that could contribute to such a system. These include antimicrobial susceptibility testing (AST), microbiological culture results, antimicrobial consumption, electronic health records, hospital admission data, infection-control data, genomic sequencing, wastewater metagenomics, environmental surveillance and geographic information. Advances in statistical modelling and artificial intelligence provide additional opportunities for detecting patterns that may not be obvious through conventional descriptive surveillance [13–17].

However, these data are frequently collected in separate systems, using different standards, at different temporal resolutions and with varying degrees of quality. The challenge is therefore not simply to collect more data but to transform heterogeneous surveillance information into validated, interpretable and actionable early warnings.

This narrative review therefore examines the diagnostic, epidemiological, therapeutic and antimicrobial-resistance evidence supporting the development of AMR early warning systems, and proposes an integrated framework linking laboratory diagnostics, surveillance, predictive analytics and treatment response.

2. THEORETICAL FRAMEWORK

2.1 Surveillance versus Early Warning

Surveillance refers broadly to the systematic collection, analysis, interpretation and dissemination of health-related information for public-health action. In AMR,

surveillance commonly involves monitoring the frequency and distribution of resistant organisms and resistance phenotypes, as well as antimicrobial consumption [10–12].

An early warning system extends this function. It should detect signals that indicate an unusual or potentially consequential change and provide sufficient lead time for investigation and intervention.

The distinction can be represented as follows. Surveillance asks: what is the current resistance situation? Early detection asks: has an unusual resistance signal appeared? Prediction asks: is the signal likely to increase or spread? Early warning asks: does the predicted risk justify an immediate public-health response? Thus, an effective AMR early warning system should combine surveillance with statistical inference, risk assessment and predefined response pathways.

2.2 Characteristics of an Effective Early Warning System

An effective system should be sensitive enough to detect emerging threats; specific enough to minimise unnecessary alerts; timely enough to provide useful lead time; standardised enough to permit comparison; scalable across institutions and regions; interoperable across data systems; interpretable to clinicians and public-health personnel; actionable, with clear response protocols; and sustainable, particularly in resource-limited settings.

The objective should not be to generate the largest number of alerts. Rather, it should generate a manageable number of high-value signals that can be investigated and acted upon.

3. CONCEPTUAL FRAMEWORK

Building on the theoretical distinction between surveillance and early warning, the evidence reviewed supports an integrated five-stage conceptual framework for AMR early warning, summarised below. The framework is conceptual and has not itself been clinically validated; it is proposed as a basis for future implementation and prospective evaluation.

3.1 A Five-Stage Early-Warning Framework

Stage 1 — Data acquisition. Data should be collected from microbiology laboratories, AST systems, antimicrobial prescribing systems, electronic health records, pharmacy databases, genomic sequencing, infection-control systems, wastewater/environmental surveillance, veterinary surveillance and public-health databases.

Stage 2 — Signal detection. Automated algorithms should monitor incoming data for unusual increases, deviations from baseline, spatial clusters, emerging resistance genes, unusual antimicrobial-use patterns and unexpected treatment outcomes. Statistical process-control techniques, anomaly detection and time-series analysis can be applied at this stage.

Stage 3 — Signal verification. Not every statistical anomaly represents a genuine AMR threat. Verification should involve checking laboratory quality, confirming isolate identification, reviewing AST methodology, examining changes in testing volume, confirming genomic findings, checking patient-level epidemiology, and determining whether similar signals exist elsewhere.

Stage 4 — Risk prediction and alert generation. Verified signals should be assessed according to likelihood of persistence, potential for transmission, clinical severity, resistance to last-line agents, geographic spread, availability of effective treatment and population vulnerability. The resulting risk category could be Green (expected variation), Yellow (signal requiring monitoring), Orange (probable emerging threat requiring investigation) or Red (confirmed high-risk event requiring immediate response). These categories are proposed conceptually and require prospective validation.

Stage 5 — Public-health response. An alert is useful only if it produces an appropriate response, such as enhanced laboratory testing, targeted epidemiological investigation, infection-prevention measures, antimicrobial stewardship review, intensified genomic sequencing, environmental sampling, communication with relevant health authorities, and continued enhanced surveillance. The response should subsequently be fed back into the system so that the effect of interventions can be evaluated.

3.2 Integration into Diagnostic and Clinical Microbiology Workflows

In practice, the five stages map onto data already generated within routine clinical microbiology and public-health laboratory workflows: AST and genomic data acquired for diagnostic purposes feed signal

detection, unusual results are verified against laboratory quality and epidemiological context, verified signals are risk-scored, and the resulting alert is fed back to clinicians and laboratory staff as an actionable output rather than a stand-alone report. This keeps artificial intelligence and predictive analytics in a supporting role, with microbiological and epidemiological expertise remaining central to interpretation and action.

4. METHODOLOGY

4.1 Review Design

This study employed a structured narrative review design. The approach was selected because the objective was to integrate evidence from microbiology, epidemiology, genomics, antimicrobial stewardship, data science and public-health surveillance rather than to estimate a single pooled intervention effect.

The review was guided by the following question: How can microbiological, clinical, antimicrobial-use, genomic, environmental and epidemiological data be integrated with predictive analytics to develop effective early warning systems for antimicrobial resistance?

4.2 Literature Search

Literature published between January 2010 and August 2026 was considered. Searches were conducted in PubMed/MEDLINE, Scopus, Web of Science, Google Scholar and ScienceDirect. Additional evidence was obtained from WHO, Africa CDC and other recognised public-health organisations.

The primary search strategy combined four concepts: antimicrobial resistance; surveillance; prediction/forecasting; and early warning/early detection. Representative search terms included “antimicrobial resistance” OR “antibiotic resistance” OR AMR, combined with surveillance OR monitoring OR “early warning” OR “early detection” OR prediction OR forecasting OR “predictive modelling”.

Additional searches incorporated “genomic surveillance”; “whole genome sequencing”; “machine learning”; “artificial intelligence”; “antimicrobial consumption”; “geospatial surveillance”; “One Health”; “wastewater surveillance”; and “risk prediction”.

4.3 Eligibility Criteria

Publications were considered eligible when they addressed one or more of the following: AMR surveillance; antimicrobial consumption surveillance; detection of emerging resistance; genomic surveillance; resistance-gene detection; AMR prediction; machine-learning or statistical prediction of AMR; epidemiological or geospatial AMR surveillance; One Health AMR surveillance; or implementation of surveillance systems relevant to early warning.

Peer-reviewed original studies, systematic reviews, methodological papers, major technical reports and authoritative surveillance guidance were included. Publications were excluded when they were unrelated to AMR surveillance or prediction, focused exclusively on antimicrobial treatment without a surveillance component, or provided insufficient information for thematic interpretation.

4.4 Data Extraction

Information was extracted under the following headings: publication year; geographical setting; pathogen or resistance phenotype; surveillance data source; analytical method; genomic approach; predictive approach; early-warning indicator; reported performance; implementation requirements; and major limitations.

4.5 Evidence Synthesis

The evidence was synthesised thematically rather than statistically. Eight themes were developed: laboratory-based AMR surveillance; antimicrobial consumption surveillance; clinical and epidemiological surveillance; genomic surveillance; environmental and wastewater surveillance; statistical and machine-learning prediction; geospatial and temporal surveillance; and integrated One Health surveillance.

The final framework presented in Section 3 was derived from recurring principles and limitations identified across these themes.

5. RESULTS

Evidence from the reviewed literature was synthesised thematically across the domains relevant to AMR early warning. Findings are presented below by theme.

5.1 Diagnostics of Pathogens: Laboratory, Genomic and Clinical Surveillance

Laboratory-based surveillance remains the foundation of AMR monitoring. Bacterial identification and antimicrobial susceptibility testing (AST) provide direct evidence of phenotypic resistance, and standardised systems such as GLASS use laboratory-confirmed infections to generate comparable resistance indicators across countries [10–12]. Its strengths include direct clinical relevance, established workflows and compatibility with antimicrobial stewardship, but laboratory data are influenced by testing practices, specimen availability, healthcare-seeking behaviour, laboratory capacity and patient selection, so observed resistance rates may not represent population-level resistance. Quality assurance is therefore fundamental: inadequate culture practices, inconsistent susceptibility testing, incomplete reporting and poor data linkage can generate misleading resistance trends [11,18].

Antimicrobial consumption surveillance captures an important upstream driver of resistance; the relationship between consumption and resistance has been demonstrated at population and individual levels [19–22]. Global antibiotic consumption increased substantially between 2000 and 2015, with particularly rapid growth in low- and middle-income countries [23], and subsequent spatial modelling has demonstrated substantial geographic differences in antimicrobial use [24]. WHO's GLASS-AMU programme provides standardised approaches to monitoring antimicrobial use, and the 2025 GLASS report showed substantial variation in antibiotic use among reporting countries, highlighting the importance of monitoring the relative use of Access, Watch and Reserve antibiotics. However, antimicrobial-use data alone cannot predict resistance reliably, since consumption interacts with local pathogen ecology, infection-control practices, population movement, prescribing behaviour and environmental factors; it should therefore be treated as one component of a multidimensional warning system rather than a stand-alone indicator.

Clinical and epidemiological surveillance adds patient-level predictive information. Patient age, previous antimicrobial exposure, recent hospitalisation, comorbidities, healthcare exposure and infection site have all been associated with the probability of resistant infection [25–27]. Electronic health records allow these variables to be combined with microbiological data, supporting both patient-level risk prediction and population-level surveillance, although heterogeneous and incomplete clinical records, differing coding practices and missing data can reduce model transportability across institutions.

Genomic surveillance using whole-genome sequencing (WGS) provides considerably higher resolution than traditional typing methods for investigating bacterial transmission and resistance [28–31], identifying resistance genes, resistance-associated mutations, plasmids and closely related bacterial lineages. This makes genomic surveillance particularly valuable for early warning: the emergence of a resistance determinant may be detectable before a substantial phenotypic increase becomes apparent, and genomic clustering may reveal transmission networks that conventional surveillance cannot resolve. WGS has increasingly been integrated into outbreak investigation and public-health microbiology [29–31], but its use as a routine early-warning tool requires sequencing capacity, bioinformatics infrastructure, reference databases, standardised interpretation and mechanisms for rapid reporting. Importantly, the presence of a resistance gene does not always translate directly into clinically expressed resistance, so genomic signals require appropriate phenotypic and epidemiological interpretation.

5.2 Environmental and Wastewater Surveillance

The environment represents an important reservoir and transmission pathway for antimicrobial-resistant organisms and resistance genes. Wastewater can contain organisms and genetic determinants originating from hospitals, households, agricultural environments and other sources. Metagenomic sequencing has demonstrated the feasibility of characterising antimicrobial resistance genes in wastewater at population level [32–34]; Hendriksen et al. demonstrated the potential of urban sewage metagenomics for global monitoring of AMR [32]. Environmental surveillance may therefore provide an early signal complementary to clinical surveillance, since a resistance determinant detected increasingly in wastewater could indicate changing community-level exposure or dissemination before the same signal is evident in clinical isolates.

Nevertheless, wastewater surveillance has important interpretive challenges. Detection of a resistance gene does not necessarily indicate viable resistant bacteria, clinical infection or imminent transmission, and sampling frequency, wastewater composition, population density and laboratory methodology can also influence results. Recent methodological work has

emphasised the need for standardisation of metagenomic workflows if wastewater surveillance is to produce comparable and actionable AMR information.

5.3 One Health Surveillance

AMR is not confined to hospitals. Resistant organisms and resistance genes can move between humans, animals, food systems and the environment, so a One Health surveillance approach provides a more complete representation of AMR emergence and dissemination [35–38]. The WHO Tricycle protocol illustrates this principle by integrating surveillance of extended-spectrum β-lactamase-producing Escherichia coli across human, food-chain and environmental sectors [36], and Africa CDC has similarly emphasised multisectoral surveillance involving human, animal and environmental health systems [37,38] — particularly important in regions where formal healthcare surveillance may capture only a fraction of antimicrobial use and resistance.

A future early warning system should therefore permit the integration of signals originating from human health, animal health, food, environment and wastewater domains, rather than treating these as independent surveillance domains.

5.4 Antibiotics and Resistance: Predictive Analytics for Resistance Emergence

Statistical modelling can identify temporal trends and estimate the probability of future resistance using methods such as logistic regression, Poisson regression, negative binomial regression, autoregressive integrated moving average models and survival analysis [39–42]. Time-series models are particularly useful when sufficiently long longitudinal data are available, distinguishing expected seasonal variation from unusual increases. Their major advantage is interpretability, though resistance dynamics can be nonlinear and influenced by multiple interacting variables, which may limit the performance of simple models.

Machine learning has increasingly been applied to AMR prediction, using algorithms such as random forests, decision trees, support vector machines, gradient boosting and neural networks [13–17,43]. A systematic review by Tang et al. identified growing use of machine learning for predicting AMR, including ESBL-producing organisms, MRSA and carbapenem resistance [14], and more recent evidence demonstrates substantial interest in models based on demographic, clinical and antimicrobial-use variables [13]. Machine learning can identify complex interactions among variables that are difficult to capture with conventional regression, but high predictive performance in a development dataset does not necessarily imply clinical usefulness: overfitting, data leakage, class imbalance, poor external validation and differences in pathogen epidemiology across hospitals remain important problems. Model evaluation should therefore include discrimination, calibration, sensitivity, specificity, positive and negative predictive value, external and temporal validation, and assessment of clinical/public-health utility; a model producing excessive false alerts may undermine confidence in the surveillance system.

Genomic predictive analytics integrates genomics with machine learning, using features such as acquired resistance genes, chromosomal mutations, plasmid-associated determinants, mobile genetic elements, sequence types, phylogenetic relationships and genomic similarity between isolates. A genomic early-warning pipeline could detect a newly emerging resistance determinant, determine whether it is spreading among genetically related isolates and estimate its geographical distribution. However, genomic surveillance requires careful interpretation, since resistance genes can occur in environmental organisms without causing human disease, and bacterial lineages may acquire or lose resistance determinants over time; genomic prediction should therefore be integrated with phenotypic, clinical and epidemiological evidence.

5.5 Geospatial, Temporal and Alert-Triggering Indicators

Resistance is spatially heterogeneous: hospitals located within the same region may experience different resistance patterns because of differences in prescribing, infection-control practices, referral networks and patient populations. Geographic information systems can be used to map resistance prevalence, emergence of specific resistance genes, antimicrobial consumption, hospital outbreaks, environmental signals and population movement, and spatial analysis can identify clusters or hotspots requiring targeted investigation.

Temporal analysis adds a second dimension, since an early-warning system should monitor both where resistance is changing and how rapidly it is changing. A

useful signal might therefore be represented conceptually as the product of the magnitude of resistance change, the rate of change, the geographic spread and the clinical significance of the resistant organism involved; this conceptual risk score would require formal validation before operational use.

A central challenge is defining an alert threshold, since no single indicator is sufficient. Table 1 summarises potential warning indicators identified across the reviewed literature.

Indicator	Potential warning
Sudden increase in resistance	Possible emergence
Sustained resistance trend	Progressive selection
New resistance gene	Emerging determinant
New high-risk clone	Transmission risk
Genomic clustering	Possible outbreak
Increased broad-spectrum antibiotic use	Selection pressure
Increased treatment failure	Clinical signal
Wastewater resistance increase	Community/environmental signal
Geographic expansion	Dissemination
Cross-sector detection	One Health transmission risk

Table 1. Potential AMR early-warning indicators

An alert should ideally require confirmation from more than one data source. For example, a simultaneous increase in antibiotic consumption, an increase in phenotypic resistance and detection of a genomic determinant would provide a stronger signal than a single increase in AST resistance alone.

5.6 Therapy and Treatment: From Early Warning to Antimicrobial Stewardship

An early warning signal is only clinically valuable if it changes treatment decisions. A verified increase in resistance to a first-line agent, or the detection of a transmissible resistance determinant in a hospital or unit, should prompt timely revision of empirical prescribing guidelines, restriction of implicated agents, and closer alignment between antimicrobial stewardship programmes and the diagnostic laboratory. Genomic and phenotypic surveillance data can similarly inform the choice between standard and last-line agents for individual patients with severe infection, particularly where local resistance prevalence would otherwise be unknown at the point of prescribing [26,27].

Conversely, early warning systems that are not linked to a defined stewardship or infection-control response add reporting burden without improving patient outcomes. The five-stage framework proposed in this review therefore treats the public-health/clinical response — stewardship review, treatment-guideline revision and infection-control action — as an integral stage rather than an optional add-on, consistent with the broader case for embedding surveillance within antimicrobial stewardship and treatment pathways rather than running it as a parallel reporting exercise.

5.7 Relevance to Resource-Limited Settings

The development of AMR early warning systems is particularly important in low- and middle-income settings, where laboratory capacity, surveillance coverage and access to reliable antimicrobial-use data may be limited [8,37,38]. A minimum viable system could initially combine routine AST data, antimicrobial consumption, basic temporal analysis and targeted genomic sequencing of unusual isolates, adding whole-genome sequencing, wastewater metagenomics and machine learning as laboratory capacity increases — an approach consistent with WHO's GLASS framework, which explicitly recognises the value of phased capacity building [37,38]. In Nigeria and other African settings, where resistance patterns are shaped by variable antimicrobial access, informal medicine markets and hospital transmission, this phased approach offers a realistic route to earlier detection without requiring the infrastructure of high-income-country systems.

6. DISCUSSION

The central finding of this review is that AMR surveillance is moving from isolated laboratory reporting toward increasingly integrated forms of health intelligence. Conventional surveillance remains indispensable, but it is inherently retrospective. The major opportunity is to combine existing surveillance streams with analytical approaches capable of identifying abnormal patterns before they become major public-health problems.

The WHO surveillance architecture already provides an important foundation. GLASS has evolved from routine bacterial resistance surveillance to a broader system encompassing antimicrobial use, early detection and One Health components [10–12]. The challenge is therefore not to replace existing surveillance systems

but to add an intelligence layer capable of converting surveillance information into early warnings.

Antimicrobial consumption represents one particularly important upstream signal. Population-level evidence demonstrates a relationship between antibiotic use and resistance [19–24]. However, the relationship is neither immediate nor deterministic. Consequently, consumption should be incorporated into predictive models rather than used as a stand-alone warning indicator.

Genomic surveillance provides another major opportunity. WGS can identify resistance determinants and transmission patterns at substantially greater resolution than conventional typing [28–31]. Its greatest value may occur when sequencing is targeted toward unusual phenotypic or epidemiological signals rather than indiscriminately applied to every isolate.

Machine learning adds another analytical dimension. Existing studies demonstrate encouraging predictive performance, but heterogeneity between datasets and concerns about generalisability remain important [13–17]. The development of an early warning system should therefore favour robust validation and interpretability over algorithmic novelty.

A further important consideration is the distinction between prediction and actionability. A highly accurate prediction that cannot trigger a response has limited public-health value. Conversely, a moderately accurate prediction may be highly valuable if it provides sufficient lead time for an inexpensive and effective intervention. The proposed framework consequently places public-health response at the centre of the system: detection, verification, prediction and response should operate as a continuous cycle.

The framework also supports a One Health perspective. Resistance determinants may circulate between healthcare, community, animal and environmental settings [35–38]. Environmental metagenomics and wastewater surveillance may therefore provide additional population-level signals, although their interpretation requires standardisation and epidemiological validation. The relevance of this approach to Africa is substantial: Africa CDC has identified surveillance and multisectoral coordination as important components of AMR control [37,38], and the development of affordable, interoperable and scalable early-warning systems could strengthen national surveillance while allowing regional comparison.

Importantly, early-warning technology should not be viewed as a substitute for basic laboratory capacity. Reliable culture, susceptibility testing, quality assurance and representative sampling remain fundamental. Advanced analytics applied to poor-quality data may produce sophisticated but misleading outputs.

6.1 Challenges to Implementation

Data fragmentation. The most immediate challenge is the fragmentation of AMR information, since laboratory, pharmacy, clinical and genomic systems often operate independently. Interoperability standards and common data dictionaries are therefore essential.

Laboratory capacity and sustainability. An early warning system cannot be more reliable than the data feeding it. Weak culture capacity, inadequate AST quality and limited external quality assurance can produce misleading signals; the Fleming Fund has highlighted the importance of high-quality diagnostic laboratories as the foundation of functional AMR surveillance systems in low- and middle-income countries. Sophisticated platforms that depend on short-term project funding rather than existing laboratory infrastructure are unlikely to be sustained.

Genomic infrastructure. WGS requires sequencing equipment, reagents, trained personnel, computational resources and reference databases, which remain substantial barriers in many settings. A tiered approach may therefore be preferable, beginning with conventional surveillance and introducing sequencing strategically for priority pathogens and unusual resistance signals.

False alerts and model portability. An early-warning system that generates excessive false positives may produce alert fatigue, and a prediction model developed in one hospital may perform poorly elsewhere because resistance mechanisms, prescribing patterns and laboratory practices differ. Thresholds should be designed around clinical consequences rather than statistical significance alone, and external, prospective validation should be mandatory before operational deployment.

6.2 Research Gaps

From surveillance to prediction. Many surveillance systems remain primarily descriptive. More research is needed to determine whether predictive models can provide sufficient lead time to alter public-health outcomes.

Integration of heterogeneous data. There is insufficient evidence on how laboratory, clinical, genomic, antimicrobial-use and environmental data should be integrated into a single operational system.

Prospective validation. Many machine-learning models are developed retrospectively, and prospective, multicentre validation remains limited [13–17].

Genomic early warning. Although WGS can detect resistance determinants and transmission clusters, evidence is still developing regarding how genomic signals should be translated into population-level alerts.

Environmental signals. Wastewater and environmental AMR surveillance are promising, but the relationship between environmental resistance signals and subsequent clinical infections requires further investigation.

Alert thresholds. There is no universally accepted definition of the statistical or epidemiological threshold at which an AMR signal should become an official warning.

Low-resource settings. There remains a need for affordable systems capable of operating with incomplete and delayed data.

Impact evaluation. Ultimately, early warning systems should be evaluated not only by prediction accuracy but by whether they reduce transmission, inappropriate antimicrobial use, treatment failure, morbidity or mortality.

6.3 Limitations of the Review

This review has several limitations. First, it is a narrative rather than systematic review and therefore does not provide pooled effect estimates. Second, considerable heterogeneity exists among AMR surveillance and prediction studies in terms of pathogens, outcomes, data sources and performance metrics. Third, rapidly evolving technologies such as machine learning, metagenomics and genomic epidemiology mean that the evidence base is changing quickly. Fourth, the proposed framework is conceptual and requires prospective validation before operational implementation.

Despite these limitations, the structured search and thematic synthesis provide a broad multidisciplinary perspective on the development of AMR early warning systems.

7. CONCLUSIONS AND RECOMMENDATIONS

Antimicrobial resistance surveillance has traditionally focused on documenting resistance after it has occurred. The next generation of surveillance should increasingly focus on detecting, interpreting and predicting emerging resistance before it becomes widespread, and on linking that detection directly to treatment and stewardship decisions.

An effective AMR early warning system should integrate laboratory susceptibility data, antimicrobial consumption, clinical and epidemiological information, genomic surveillance, environmental signals and geospatial information, with a defined pathway into antimicrobial stewardship and empirical treatment guidance. Statistical modelling and machine learning can provide additional analytical capacity, while genomic epidemiology can improve the detection of emerging resistance determinants and transmission clusters.

However, technology alone will not solve the AMR surveillance problem. Reliable diagnostic laboratory systems, standardised data, representative surveillance, trained personnel, interoperability and clearly defined clinical response pathways are equally important.

The five-stage framework proposed in this review — data acquisition, signal detection, signal verification, risk prediction/alert generation and clinical/public-health response — provides a conceptual foundation for moving from retrospective AMR surveillance toward proactive detection linked to diagnosis and treatment.

The ultimate objective should therefore be not merely to predict resistance, but to predict it early enough for effective diagnostic and therapeutic action.

7.1 Recommendations for Future Research

Future research should prioritise five areas. First, multicentre prospective studies should evaluate AMR prediction models across different healthcare settings.

Second, genomic and phenotypic surveillance should be integrated to determine whether resistance genes can provide earlier warning than conventional AST. Third, researchers should develop standardised AMR data architectures allowing laboratory, clinical, pharmacy, genomic and environmental datasets to communicate. Fourth, research should establish validated alert thresholds based on public-health consequences rather than algorithmic performance alone. Finally, early warning systems should be evaluated as public-health interventions: a useful question is not simply whether the model predicts resistance accurately, but whether the warning arrives early enough and leads to an intervention that changes the trajectory of the threat.

DECLARATIONS

Funding No specific funding was received for the preparation of this narrative review.

Conflicts of interest None to declare.

Availability of data and materials No original dataset was generated for this review. The evidence base consists of published literature and publicly available surveillance reports.

Author contributions O. Ishola and F. O. Olukoya jointly conceived the review, developed the search strategy, synthesised the literature and prepared the manuscript. Both authors read and approved the final manuscript.

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