

Review

Transforming antimicrobial resistance mitigation: the genomic revolution in one health and public health

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Abstract

The integration of genomics into the One Health framework presents a transformative opportunity to address antimicrobial resistance (AMR), a critical global health challenge impacting human, animal, and environmental well-being. This review explores the intersection of genomics, AMR, and public health, with a focus on cutting-edge tools such as whole-genome sequencing (WGS), metagenomics, and CRISPR-based diagnostics. These technologies enhance our ability to identify resistance mechanisms, track pathogen transmission, and develop targeted interventions. However, significant barriers, including limited bioinformatics capacity, economic constraints, and fragmented governance, hinder the widespread adoption of these tools, particularly in low- and middle-income countries (LMICs). Emerging advancements, such as big data analytics, machine learning, and personalized antimicrobial therapies, offer new pathways to overcome these challenges. This review underscores the urgency of international collaboration and capacity-building initiatives to ensure equitable access to genomic technologies and strengthen AMR mitigation efforts. By harnessing the potential of genomics, the One Health framework can drive innovative solutions to safeguard global health and combat AMR effectively.

Article Highlights

- Application of genomic technologies improve AMR detection, tracking, and intervention within the One Health framework.
- Bioinformatics gaps, costs, and poor governance limit widespread adoption of genomic technologies, especially in LMICs.
- Advances in AI, big data, and global collaboration offer solutions to strengthen AMR control effort

Keywords One health · Genomics · Antimicrobial resistance · Public health · Epidemiology · CRISPR · Metagenomics · Whole genome sequencing · AI · Machine learning

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1 Introduction

1.1 Background

The escalating threat of antimicrobial resistance (AMR) poses a significant challenge to global health, necessitating urgent and coordinated efforts to mitigate its impact. AMR affects human, animal, and environmental health through interconnected pathways that require integrated strategies for effective management. The One Health framework, which emphasizes the interdependence of these domains, provides a robust and holistic approach to addressing AMR. This transdisciplinary strategy promotes collaboration across sectors to address health issues that arise at the nexus of human, animal, and environmental systems, recognizing the ecological roots of AMR and zoonotic diseases [1].

The concept of One Health emerged from earlier ideas, such as "One Medicine," introduced by Calvin Schwabe in the 1960s, which highlighted the intrinsic link between human and veterinary medicine [2]. Over the decades, this framework has evolved to include environmental health, reflecting the growing recognition of the complex dynamics underlying global health threats. Today, One Health serves as a cornerstone for addressing challenges such as emerging infectious diseases, food security, and AMR.

AMR, a critical focus within the One Health framework, is fueled by factors such as the overuse of antimicrobials in healthcare and agriculture, the release of pharmaceutical residues into the environment, and the horizontal transfer of resistance genes between microbial populations. These drivers have facilitated the rapid spread of resistance across species and ecosystems, underscoring the necessity of integrated surveillance and intervention strategies [3].

The One Health initiative has gained international traction, particularly through collaborative efforts by the World Health Organization (WHO), the Food and Agriculture Organization (FAO), and the World Organization for Animal Health (OIE). This tripartite partnership has spearheaded policies and programs aimed at mitigating AMR, including coordinated surveillance of antimicrobial use and resistance patterns across human, animal, and environmental domains [3]. The increasing frequency of zoonotic disease outbreaks, such as the H1N1 influenza pandemic and the West African Ebola outbreak, highlights the critical importance of adopting a One Health approach to enhance preparedness and response capabilities [4, 5].

1.2 Importance of incorporating genomics into one health

The advent of genomic technologies has revolutionized our ability to study infectious diseases and AMR. Within the One Health framework, genomics offers powerful tools to trace the evolution of pathogens, identify transmission pathways, and detect genetic determinants of resistance across diverse ecosystems [6]. Technologies such as whole-genome sequencing (WGS), metagenomics, and CRISPR-based diagnostics provide high-resolution data that enhances our understanding of pathogen diversity, evolution, and resistance mechanisms [7].

The COVID-19 pandemic demonstrated the transformative potential of genomic surveillance. By enabling real-time tracking of viral mutations, genomic sequencing facilitated the identification of new variants of concern and informed public health interventions globally [8, 9]. Similarly, genomic tools have been instrumental in mapping the spread of resistant bacteria, such as methicillin-resistant *Staphylococcus aureus* (MRSA), across healthcare and agricultural settings [10, 11].

Integrating genomics into One Health enhances our capacity to address AMR in human, animal, and environmental health. For instance, genomic epidemiology combines traditional epidemiological methods with genomic data to provide detailed insights into the origins and spread of resistant pathogens [12]. Surveillance programs that incorporate WGS and metagenomics can identify hotspots of resistance development, particularly in regions where antimicrobial misuse is prevalent [13, 14].

1.3 Objectives and scope

This review aims to explore the role of genomics in mitigating AMR through the One Health framework, with a focus on the following objectives:

- 1 To analyze the application of genomic tools in understanding AMR mechanisms and improving pathogen surveillance.
- 2 To identify the challenges hindering the integration of genomics into AMR management, particularly in low- and middle-income countries (LMICs).
- 3 To examine emerging innovations, such as machine learning, big data analytics, and microbiome-based interventions, in advancing AMR control.

By addressing these objectives, this review seeks to highlight the transformative potential of genomics in combating AMR while emphasizing the need for international collaboration and capacity-building initiatives. The integration of genomic technologies into the One Health framework represents a critical step toward achieving sustainable solutions for AMR management and safeguarding global health.

2 Understanding antimicrobial resistance (AMR)

2.1 Mechanisms of AMR development

Antimicrobial resistance (AMR) develops when microorganisms such as bacteria, viruses, fungi, or parasites evolve in ways that render medications ineffective via the possession of antimicrobial resistant genes (ARGs) through varying routes, (see Fig. 1). This complex process is driven by both natural and anthropogenic factors. As tabulated in Table 1, two primary genetic mechanisms contribute to AMR: *mutation* and *horizontal gene transfer (HGT)*.

2.1.1 Mutations

Spontaneous mutations in the microbial genome can lead to alterations in drug targets or metabolic pathways, providing resistance against certain antimicrobials. For instance, mutations in the *gyrA* gene of *Escherichia coli* confer

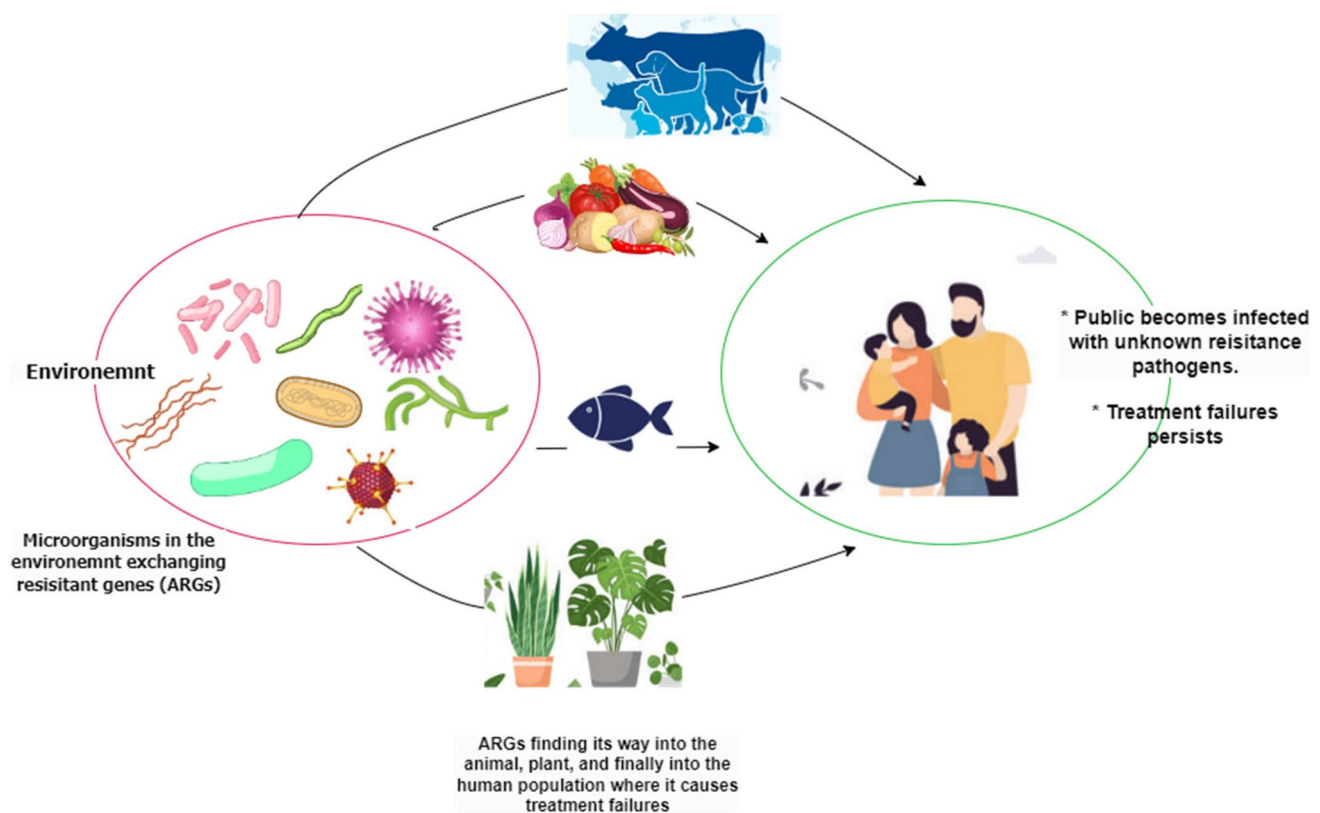


Fig. 1 Routes of Spread of ARGs in the environment

Table 1 Genetic mechanisms of AMR

Mechanism	Description	Example	References
Mutation	Spontaneous genetic changes that affect antimicrobial target sites	Mutations in <i>gyrA</i> leading to fluoroquinolone resistance	[15]
Horizontal Gene Transfer (HGT)	Acquisition of resistance genes via plasmids, transposons, or bacteriophages	Spread of <i>bla</i> NDM-1 gene leading to carbapenem resistance	[16]

resistance to fluoroquinolones by altering the drug’s target, DNA gyrase [17–19]. These mutations can occur naturally but are often accelerated by selective pressures exerted through overuse or misuse of antimicrobials in both clinical and agricultural settings [20, 21].

2.1.2 Horizontal gene transfer (HGT)

HGT enables bacteria to acquire resistance genes from other bacteria via mobile genetic elements such as plasmids, transposons, or bacteriophages [22, 23]. This mechanism allows the rapid spread of resistance across bacterial populations, even between different species. A notable example is the spread of the *bla*NDM-1 gene, which confers resistance to carbapenems and has spread globally among various bacterial species, posing a significant challenge in clinical settings (Mohan et al., 2015; [24, 25].

2.2 Global Burden of AMR across human, animal, and environmental health

The global burden of AMR has reached alarming levels, threatening to undermine decades of progress in medical treatment. AMR is responsible for an estimated 1.27 million deaths annually, with many more deaths linked to complications arising from resistant infections (Kim et al., 2023; [26]). The situation is especially dire in low- and middle-income countries (LMICs), where access to effective antimicrobials and robust healthcare systems is limited, exacerbating the spread and impact of resistant infections [27–29]. Regions such as sub-Saharan Africa and Southeast Asia bear a disproportionate burden of AMR-related deaths due to factors including poor regulation of antibiotic use, insufficient access to healthcare, and widespread use of antibiotics in agriculture [30, 31]. In these regions, infections caused by multidrug-resistant (MDR) organisms, such as MDR *Mycobacterium tuberculosis*, have become significant public health concerns [32]. The economic cost of AMR is also substantial. By 2050, AMR is projected to result in a cumulative economic loss of up to \$100 trillion globally, primarily due to increased healthcare costs, reduced productivity, and the loss of effective treatments for life-threatening infections [33].

2.3 AMR as a multisectoral issue: human, animal, and environmental health

AMR is a classic example of a One Health issue, as it affects human, animal, and environmental health in interconnected ways (See Table 2). Antibiotic use in livestock and aquaculture contributes significantly to the emergence of resistance, as antimicrobials are often used not only to treat infections but also to promote growth and prevent disease in crowded farming conditions [33, 34]. This practice exerts selective pressure on bacteria, encouraging the development of resistance genes that can be transmitted to humans through direct contact with animals, contaminated food, or environmental pathways [35], Landers et al., 2022; [14]. For example, the overuse of colistin in livestock in some countries has led to the emergence of *mcr-1*, a gene that confers resistance to colistin, a last-resort antibiotic used to treat infections caused by multidrug-resistant Gram-negative bacteria (Liu et al., 2018; [36]). The *mcr-1* gene has since been detected in human clinical isolates, highlighting the transmission of resistance from animals to humans. The environmental dimension of AMR is increasingly recognized as critical (Martino et al., 2024). Waste from farms, hospitals, and pharmaceutical factories often contains high concentrations of antibiotics, which enter water sources and create environments conducive to the spread of resistant bacteria (Mahmud et al., 2023). Wastewater treatment plants, particularly in LMICs, are frequently unable to fully remove antibiotics and resistant bacteria, thereby contributing to the environmental reservoir of resistance [37].

Table 2 The one health component of AMR

Sector	Contribution to AMR	Examples	References
Human health	Overuse of antibiotics in medicine	Overprescribing antibiotics for viral infections	[38]
Animal health	Use of antibiotics for growth promotion and disease prevention	Use of colistin in livestock leading to <i>mcr-1</i> gene emergence	[39]
Environmental health	Antibiotic residues in wastewater and soil	Detection of resistant bacteria in water systems near farms and hospitals	[40]

Table 3 Challenges in AMR Surveillance

Challenge	Description	Example	References
Lack of standardization	Inconsistent reporting and detection methods between countries	Inconsistent AMR reporting in different regions, especially in LMICs	[38]
Limited infrastructure	Inadequate access to genomic sequencing technologies in resource-poor settings	Lack of WGS facilities in rural hospitals in sub-Saharan Africa	[42]
Reliance on phenotypic methods	Traditional culture-based methods may miss emerging resistance genes	Failure to detect the <i>mcr-1</i> gene via culture methods	[43]
Cost and resource limitations	High cost of genomic surveillance and shortage of trained personnel in low-income settings	Limited implementation of genomic AMR surveillance in Southeast Asia	[44]

2.4 Challenges in AMR surveillance and detection

Accurate surveillance of AMR is vital to understanding its spread and informing public health interventions. However, several challenges hinder effective AMR surveillance globally. As shown in the Table 3, one of the primary obstacles is the lack of standardized methods for detecting and reporting resistance patterns, particularly in LMICs [27], Hassall et al., 2024). While high-income countries have established networks and protocols for AMR surveillance, such systems are often fragmented or absent in resource-limited settings [41].

Another major challenge is the reliance on *phenotypic methods* for detecting resistance, which are labor-intensive, slow, and may not detect all resistance mechanisms. Traditional methods of AMR detection, such as culture-based sensitivity testing, often miss emerging resistance genes that are not well characterized or cannot be expressed phenotypically in certain conditions [45–47]. Genomic methods, such as whole-genome sequencing (WGS), provide a more comprehensive approach to detecting resistance, but they are costly and require significant infrastructure and expertise [48, 49].

The development and global spread of antimicrobial resistance are driven by genetic mechanisms such as mutations and horizontal gene transfer. The One Health framework provides a valuable perspective on the interconnectedness of AMR across human, animal, and environmental health. However, substantial challenges remain in surveillance and detection, particularly in LMICs where infrastructure and resources for advanced genomic techniques are limited. Addressing these gaps is essential to curbing the global burden of AMR and preventing the emergence of untreatable infections.

While surveillance gaps in low- and middle-income countries (LMICs) are well-documented, it is equally important to acknowledge that antimicrobial resistance (AMR) surveillance remains fragmented even within high-income countries (HICs) [27, 50]. Despite having more established healthcare infrastructures and technological resources, many HICs continue to operate sector-specific surveillance systems with limited integration between human, veterinary, and environmental health domains [51–53].

For instance, AMR data from clinical settings are often not systematically linked with resistance trends in livestock farming or wastewater monitoring, leading to missed opportunities for early detection of emerging resistance patterns [54–56]. In many HICs, regulatory and institutional barriers further hinder cross-sectoral data sharing, with public health agencies, agricultural regulators, and environmental authorities working in parallel rather than collaboratively [57, 58]. Additionally, differences in surveillance methodologies and reporting standards between sectors create inconsistencies that complicate comparative analyses and coordinated interventions [59].

This siloed approach not only limits our understanding of AMR transmission dynamics across One Health compartments but also undermines the effectiveness of comprehensive mitigation strategies [60]. Strengthening interdisciplinary collaboration, standardizing data-sharing frameworks, and adopting unified surveillance platforms will be essential in maximizing the impact of a One Health approach in both HICs and LMICs alike.

3 The role of genomics in AMR mitigation

Genomic technologies have revolutionized antimicrobial resistance (AMR) research and mitigation strategies by providing detailed insights into resistance mechanisms, tracking the spread of resistant pathogens, and enabling targeted interventions. Several key genomic techniques (as shown in Table 4), such as whole-genome sequencing (WGS), metagenomics, and CRISPR-based methods, have emerged as pivotal in addressing the growing threat of AMR. By integrating genomics into AMR surveillance and detection, researchers can improve our understanding of the genetic determinants of resistance and enhance the efficacy of public health responses.

3.1 Applications of genomics in AMR detection, surveillance, public health response and evolutionary studies

Genomics facilitates the precise identification of resistance genes, the tracking of resistant pathogens, and the prediction of emerging resistance threats, public health response and evolutionary studies (See Table 4). Surveillance programs that employ whole-genome sequencing (WGS) and metagenomics allow real-time monitoring of resistance patterns across human, animal, and environmental domains. For instance, WGS has been used to identify resistance genes in

Table 4 Key Applications of Genomics within the One Health Framework

Application	Human Health	Animal Health	Environmental Health	References
Pathogen Surveillance	Identifying sources of outbreaks	Zoonotic disease tracking	Monitoring environmental reservoirs	[61]
AMR Detection	WGS of clinical isolates	Detection of resistant bacteria in livestock	Tracking AMR genes in water/soil samples	[62]
Public Health Response	Guiding infection control measures	Limiting spread in animal populations	Preventing contamination from waste	[63]
Evolutionary Studies	Tracking pathogen evolution over time	Identifying cross-species transmission	Analyzing genetic exchange in microbial populations	[64]

healthcare-associated pathogens, such as methicillin-resistant *Staphylococcus aureus* (MRSA), and track their dissemination across geographic regions [6].

Metagenomics further enhances surveillance by analyzing the genetic material of entire microbial communities without requiring culture-based methods. This approach is particularly valuable for identifying resistance genes in complex environments such as wastewater and agricultural soils, where unculturable bacteria harboring resistance genes can act as reservoirs for transmission [65].

Genomic tools also improve public health interventions by enabling early detection of outbreaks and targeted control measures. For example, genomic surveillance of *Escherichia coli* isolates in food production chains has helped identify the emergence of resistance genes linked to agricultural antibiotic misuse [66]. Integrating these technologies into routine surveillance systems strengthens global efforts to mitigate AMR.

3.2 Key tools in genomics for AMR mitigation

3.2.1 Whole-genome sequencing (WGS)

Whole-Genome Sequencing (WGS) is a transformative tool in antimicrobial resistance (AMR) surveillance, offering comprehensive insights into the genetic makeup of pathogens. It enables the identification of both known and novel resistance genes (It has been instrumental in mapping the spread of carbapenem-resistant *Enterobacteriaceae* (CRE)), facilitates outbreak investigations, and informs infection control strategies [67, 68] (See Fig. 2). By identifying both known and novel resistance genes, WGS allows for the rapid detection of emerging resistance threats, depicted in Fig. 2, which is essential for effective public health interventions [69–71]. WGS has been instrumental in identifying the spread of multidrug-resistant *Klebsiella pneumoniae* and *Escherichia coli* in clinical settings, allowing healthcare systems to monitor transmission and control outbreaks [72, 73].

Additionally, WGS is used in outbreak investigations to determine whether resistance genes are spreading horizontally via plasmids or vertically through bacterial lineages [74]. However, its implementation presents various challenges that need to be addressed to optimize its utility across different settings.

Whole Genome Sequencing (WGS) offers several notable advantages over traditional phenotypic methods, with one of its primary strengths being its high resolution and accuracy. Unlike conventional techniques, WGS enables the precise identification of antimicrobial resistance (AMR) genes, including those found on mobile genetic elements like plasmids

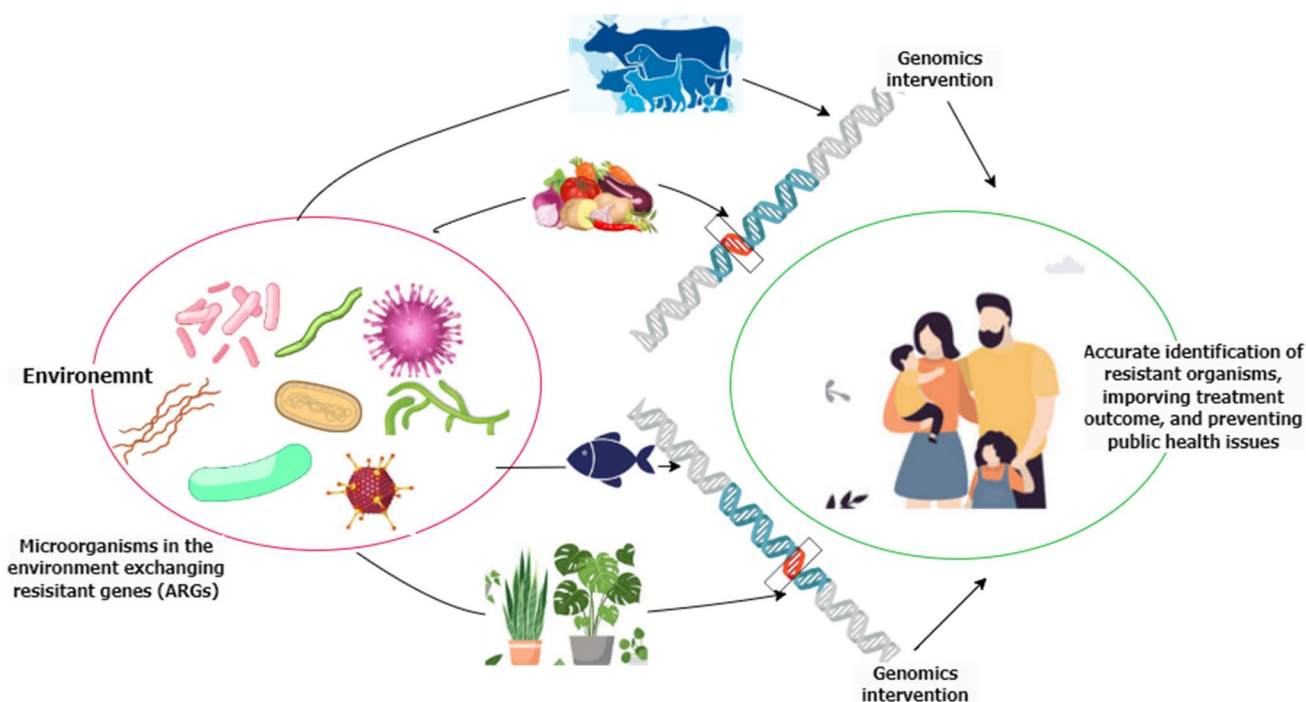


Fig. 2 Genomic intervention in tackling AMR

[69]. This level of detail significantly enhances the ability to detect and monitor resistance patterns. Furthermore, WGS supports phylogenetic analysis, making it an invaluable tool for tracking the evolution and transmission of resistant strains. This capability is particularly useful in healthcare environments and across geographical boundaries, offering insights into how resistance spreads over time [70]. Another strength of WGS lies in its versatility. The technology can be applied across a broad spectrum of pathogens—bacteria, fungi, and viruses—making it suitable for comprehensive One Health surveillance strategies [71]. Moreover, WGS can detect resistance-conferring mutations in housekeeping genes, many of which go undetected by conventional PCR-based assays. This comprehensive surveillance potential makes WGS a powerful resource for public health and epidemiological studies focused on antimicrobial resistance.

Despite its strengths, WGS is not without limitations. One of the most significant barriers to widespread adoption is the high cost associated with sequencing, infrastructure, and the need for skilled personnel. This is especially problematic in low- and middle-income countries (LMICs), where financial and technical resources are often limited [73]. Additionally, the massive volume of data generated by WGS requires sophisticated bioinformatics tools and expertise, which are not always available in resource-constrained settings [72]. Another challenge is the turnaround time. Although faster than many traditional methods, WGS is still slower than PCR-based diagnostics, which can be critical in acute clinical scenarios where timely decision-making is essential. Moreover, the lack of standardized sequencing protocols and analysis pipelines across institutions and countries impedes consistent data interpretation and comparability [74]. These issues highlight the need for systemic improvements to make WGS more accessible and practical in diverse settings.

The feasibility of implementing WGS varies significantly across different contexts. In high-income countries (HICs), the integration of WGS into public health surveillance is increasingly common due to the presence of robust infrastructure and established data-sharing frameworks. These settings benefit from economies of scale and the ability to rapidly process and analyze genomic data. Conversely, in LMICs, the adoption of WGS remains limited due to persistent cost barriers, a shortage of technical expertise, and inconsistent bioinformatics support. Nonetheless, international collaborations and cost-sharing initiatives are beginning to bridge these gaps, offering a pathway to more equitable access [71]. In veterinary and environmental health contexts, WGS has proven valuable for monitoring resistance genes in animal and environmental reservoirs. However, the complexity of sample processing from non-clinical sources presents additional technical challenges that must be addressed to fully leverage its potential in these areas.

Several strategies have been proposed to overcome the limitations of WGS. One promising approach involves reducing costs through international collaboration. Global initiatives such as the WHO's Global AMR Surveillance System (GLASS) and the African Pathogen Genomics Initiative aim to subsidize sequencing efforts in LMICs. Additionally, the use of open-source bioinformatics platforms like Galaxy and Nextstrain offers cost-effective alternatives for data analysis. Building capacity and training the workforce are also critical steps. Enhancing bioinformatics education through online courses and in-country training programs can help close the skills gap. Establishing regional sequencing hubs can further streamline operations and optimize resource use. Another promising avenue is the integration of WGS with rapid diagnostic methods such as PCR and CRISPR-based assays. This hybrid approach can provide both quick results and comprehensive resistance profiling. Finally, efforts toward standardization and improved data sharing are vital. Harmonizing sequencing protocols and interpretation criteria will facilitate better comparability across institutions and borders. Platforms such as the European Nucleotide Archive (ENA) and the National Center for Biotechnology Information (NCBI) support open-access genomic data sharing, which is crucial for collaborative research and global surveillance efforts.

3.2.2 Metagenomics

Metagenomics is a powerful genomic tool that enables the sequencing of genetic material from entire microbial communities without the need for culturing individual organisms. This approach is particularly valuable in antimicrobial resistance (AMR) surveillance, as it allows for the identification of resistance genes within complex environments such as the human gut, wastewater, and agricultural soils [65]. Metagenomics has provided critical insights into the environmental reservoirs of AMR, revealing that water bodies, hospital effluents, and livestock farming areas harbor a diverse array of resistance genes, some of which have the potential to be transferred to human and animal pathogens [75]. However, despite its potential, the practical application of metagenomics in AMR mitigation varies across different settings and presents distinct challenges that need to be addressed.

Metagenomics offers a number of advantages over traditional culture-based and targeted sequencing methods, particularly in the field of antimicrobial resistance (AMR) surveillance. Unlike whole-genome sequencing (WGS), which focuses on individual isolates, metagenomics captures the entire pool of microbial DNA in a sample. This allows for a more comprehensive assessment of microbial diversity and the prevalence of resistance genes. One of the most notable

benefits is the ability to identify unculturable organisms, a significant limitation in conventional laboratory methods. This is especially useful in environmental studies where many bacterial species cannot be cultured, enabling the discovery of novel and cryptic resistance genes. Additionally, metagenomics proves highly valuable in One Health contexts, allowing researchers to simultaneously assess AMR genes across human, animal, and environmental ecosystems. Despite these strengths, metagenomics presents several challenges that limit its widespread application. The method demands significant computational resources and advanced bioinformatics expertise, which can be a major barrier for institutions with limited technical infrastructure. Another limitation is its inability to reliably distinguish between functional and non-functional resistance genes, making it difficult to determine the clinical relevance of some findings. Furthermore, metagenomics typically relies on high-throughput sequencing, which incurs substantial costs and may not be feasible for routine surveillance in low-resource settings. These constraints highlight the need for strategic investments and technical support to make metagenomics more accessible and actionable in AMR research.

The feasibility of implementing metagenomics for AMR surveillance varies considerably depending on the socio-economic context. In high-income countries (HICs), the necessary infrastructure—such as high-throughput sequencing platforms and skilled bioinformatics personnel—is generally available. As a result, metagenomics is increasingly being adopted for both clinical and environmental surveillance of resistance genes. These settings can also support comprehensive data analysis and integration with existing public health frameworks. In contrast, low- and middle-income countries (LMICs) face significant challenges in adopting metagenomics. Cost constraints, limited access to sequencing technology, and a shortage of trained bioinformatics professionals hinder its implementation. Nonetheless, there is growing potential for progress through regional collaborations and international partnerships. The use of cloud-based analytical tools and shared data platforms can also help LMICs overcome infrastructure limitations, making metagenomic surveillance more attainable and effective.

To realize the full potential of metagenomics in AMR surveillance, several key challenges must be addressed with practical, targeted solutions. One major barrier is the high cost of sequencing. A viable solution is the adoption of targeted metagenomics approaches—such as shotgun sequencing focused on specific resistance gene families—which can reduce costs while still delivering critical insights. Another pressing issue is the lack of standardization in data analysis. Developing globally accepted bioinformatics pipelines and reference databases will enhance consistency and comparability of results across different studies and regions. A third challenge lies in the limited expertise in data analysis, particularly in LMICs. Investing in bioinformatics training programs and fostering collaborations with institutions that already possess metagenomics expertise can help bridge this skills gap. Additionally, metagenomics is often conducted in isolation from clinical and epidemiological data, reducing its impact on public health decision-making. Integrating metagenomic findings with patient records and epidemiological information can strengthen our understanding of the links between resistance genes, disease outcomes, and transmission dynamics.

Valuable insights for overcoming metagenomics challenges can be drawn from other areas of genomic research. For instance, the global response to the COVID-19 pandemic demonstrated the effectiveness of rapid genomic sequencing and international data sharing. The large-scale sequencing of SARS-CoV-2 and the establishment of open-access repositories showed that real-time genomic surveillance is feasible with sufficient collaboration and infrastructure. Applying similar models to metagenomic AMR monitoring could significantly enhance its implementation and impact. Furthermore, research in the human microbiome has successfully used metagenomics to explore microbial community composition and function. These studies offer a blueprint for understanding the dynamics of resistance gene spread within and between microbiomes. By adopting methodologies from microbiome science and combining them with One Health principles, metagenomics can offer a powerful, holistic approach to AMR surveillance.

Metagenomics presents a transformative opportunity for AMR surveillance, offering culture-independent, high-resolution insights into resistance gene prevalence across diverse environments. However, realizing its full potential requires overcoming significant challenges related to cost, bioinformatics capability, and data integration. By addressing these barriers and drawing on successful strategies from other genomic disciplines, metagenomics can be firmly established as a cornerstone of AMR mitigation within the One Health framework. Global cooperation and sustained investment will be essential in making this vision a reality.

3.2.3 CRISPR-based diagnostics

The CRISPR-Cas9 system, initially developed as a revolutionary genome-editing tool, has been repurposed for rapid and precise identification of antimicrobial resistance (AMR) genes in microbial populations. This adaptation has led to the development of several CRISPR-based diagnostic methods, including SHERLOCK (Specific High-sensitivity Enzymatic

Reporter unLOCKing) and DETECTR (DNA Endonuclease-Targeted CRISPR Trans Reporter), which have demonstrated high sensitivity and specificity in detecting resistance determinants. These tools represent a significant advancement in AMR surveillance, particularly in settings where rapid, accurate detection is critical for treatment decisions and infection control [76].

Traditional molecular diagnostics such as polymerase chain reaction (PCR) and whole-genome sequencing (WGS) have long served as the benchmarks for antimicrobial resistance (AMR) detection. However, CRISPR-based diagnostics are emerging as a powerful alternative, offering several key advantages. Unlike PCR, which relies on thermal cycling and sophisticated laboratory setups, CRISPR diagnostics function under isothermal conditions. This makes them more suitable for field applications and settings with limited infrastructure (See Table 5). Additionally, CRISPR technologies provide single-molecule detection sensitivity, outperforming the detection limits of standard PCR methods [76]. While WGS remains a valuable tool for comprehensive genomic analysis, it is time-intensive and costly. In contrast, CRISPR-based diagnostics offer a rapid, cost-effective solution for point-of-care testing, especially when speed and accessibility are critical.

Despite the promise of CRISPR-based diagnostics, their feasibility and scalability vary across healthcare systems, largely due to differences in infrastructure and resources. In high-income countries (HICs), CRISPR technologies can be seamlessly integrated into existing surveillance frameworks, offering decentralized, rapid AMR detection and alleviating pressure on central laboratories. However, implementation in low- and middle-income countries (LMICs) presents several notable challenges. One major obstacle is the stability and storage of reagents, as many CRISPR components require cold-chain logistics, which are difficult to maintain in resource-poor regions. Additionally, while traditional diagnostics like PCR and culture methods are supported by established regulatory frameworks, CRISPR-based tools are still undergoing validation, creating hurdles for routine clinical or environmental use. Cost and accessibility are also significant barriers. Though less expensive than WGS, CRISPR-based diagnostics still entail substantial upfront costs related to reagent procurement and assay development, limiting their affordability in LMICs. Furthermore, technical expertise is essential for accurate implementation, from assay preparation to data interpretation. Many healthcare facilities in LMICs may lack the skilled personnel needed to operate these advanced tools effectively, compounding the implementation challenges.

Several strategies are being explored to promote the broader adoption of CRISPR-based diagnostics, particularly in resource-limited settings. One promising development is the formulation of lyophilized (freeze-dried) CRISPR reagents, which eliminate the need for cold-chain storage and significantly improve feasibility in LMIC contexts [77]. Another innovative approach involves integrating CRISPR diagnostics with mobile health technologies. For instance, smartphone-based readouts allow for field-level AMR testing without requiring specialized equipment, making the technology more accessible [78]. Policy and funding support will also be essential to scaling up CRISPR deployment. Public-private partnerships and financial backing from global health organizations like the World Health Organization (WHO) and the Bill & Melinda Gates Foundation can help subsidize implementation costs. Equally important is the development of training and capacity-building programs to equip healthcare workers and laboratory personnel with the necessary skills to use CRISPR tools effectively. By combining these efforts, it becomes more feasible to integrate CRISPR-based diagnostics into routine AMR surveillance across both high-resource and low-resource settings.

CRISPR technology continues to evolve, with new innovations enhancing its capabilities in AMR detection. Emerging variants such as Cas12 and Cas13 enable RNA-based detection, expanding the range of resistance genes that can be identified beyond just DNA targets. Additionally, researchers are developing multiplexed CRISPR assays capable of detecting multiple resistance genes simultaneously, which would significantly improve the efficiency of surveillance efforts [79]. These advancements signal a promising future for CRISPR diagnostics, making them not only more powerful but also more adaptable to different public health needs. Ultimately, by addressing current limitations and leveraging technological progress, CRISPR-based diagnostics are poised to revolutionize AMR detection. They offer a scalable,

Table 5 Comparative Analysis of CRISPR-Based Diagnostics and other genomic methods

Feature	CRISPR-Based Diagnostics	PCR-Based Methods	Whole-Genome Sequencing
Sensitivity	High	Moderate	High
Specificity	High	High	High
Time to Results	Minutes to hours	Hours	Days
Equipment Needed	Minimal	Extensive	High-throughput
Cost	Low to moderate	Moderate	High
Feasibility in LMICs	High	Moderate	Low

cost-effective solution that is both accessible and adaptable, making them a valuable asset for AMR surveillance in both high-income and resource-constrained environments.

4 The role of genomics in public health

4.1 Genomics in infectious disease surveillance

The application of genomics in public health has significantly enhanced the capacity to monitor, detect, and respond to infectious diseases (See Table 4 above). Genomic sequencing technologies, particularly whole-genome sequencing (WGS), have revolutionized disease surveillance by enabling the detailed characterization of pathogens, including their transmission dynamics, evolution, and resistance mechanisms. This capability is vital for controlling infectious diseases, especially in the context of emerging and re-emerging pathogens, where rapid identification of new strains or variants can inform timely public health interventions [80, 81].

Genomic surveillance has been particularly impactful in tracking the spread of zoonotic diseases and antimicrobial-resistant pathogens. For example, the widespread use of WGS in public health laboratories has facilitated the early detection of resistant strains such as carbapenem-resistant *Enterobacteriaceae* (CRE) and methicillin-resistant *Staphylococcus aureus* (MRSA), allowing for more targeted infection control strategies in both healthcare settings and the community [80, 82]. In the One Health framework, genomics enables the tracing of pathogens and resistant strains across human, animal, and environmental interfaces, providing a holistic view of disease spread [83, 84].

The ability to link epidemiological data with genomic information, as depicted in Figs. 3, is a key advancement in modern public health surveillance. This combined approach allows for the identification of transmission clusters and the source of outbreaks, as well as the assessment of intervention effectiveness. Genomic epidemiology, which

Fig. 3 One Health Intersection
Genomics



integrates genomic data with traditional epidemiological information, has become a cornerstone of public health efforts to control infectious diseases and mitigate the spread of AMR [84].

By retrieving simultaneously, the genomic information of environmental samples, plant and animal species, we can capture their immune response genes and microbiomes together with their antimicrobial resistances, as well as (zoonotic) pathogens that can influence animal and human health. Retrieving genomic data from the three subsystems (environment, human, animal) and including biodiversity conservation, health management and other actions, can generate a sustainable change in One Health outcomes.

4.2 Applications of genomics in outbreak response

The use of genomics in outbreak response has transformed how public health authorities detect and contain infectious disease outbreaks. WGS allows for the real-time monitoring of pathogen evolution and transmission, enabling rapid identification of sources of infection and tracking the spread of disease. This capability has proven critical in multiple recent outbreaks, including the COVID-19 pandemic, where genomics was essential for tracking the emergence and spread of new variants [8, 85].

4.2.1 Case studies of genomic use in disease outbreaks

COVID-19 Pandemic: The COVID-19 pandemic underscored the importance of genomics in public health surveillance and outbreak response. From the identification of SARS-CoV-2 to the global monitoring of viral variants, genomic sequencing played a crucial role in informing public health decisions. As shown in Table 6, Genomic data allowed researchers to track mutations in the virus, leading to the identification of variants of concern such as Alpha, Delta, and Omicron [86]. This information was used to guide vaccination strategies, assess vaccine effectiveness, and inform public health measures such as travel restrictions and lockdowns. In countries with robust genomic surveillance programs, such as the United Kingdom and South Africa, sequencing data provided early warnings of new variants, allowing for timely public health responses [8, 87].

Tuberculosis (TB): WGS has also been applied in the surveillance and control of tuberculosis (TB), particularly in monitoring the spread of multidrug-resistant (MDR) and extensively drug-resistant (XDR) TB strains. By analyzing the genomes of TB bacteria, public health authorities can identify mutations that confer resistance to first- and second-line antibiotics, enabling more effective treatment regimens [88]. Genomic data has been used to track the transmission of drug-resistant TB in high-burden areas, informing targeted interventions aimed at reducing the spread of resistant strains as shown in Table 6 [89]. In some settings, genomic epidemiology has been instrumental in identifying outbreaks of MDR-TB within communities and healthcare facilities, leading to improved infection control practices.

Methicillin—Resistant Staphylococcus aureus (MRSA): Genomic tools have also played a significant role in controlling the spread of MRSA, a major cause of healthcare-associated infections. WGS has enabled the detailed tracking of MRSA transmission within and between hospitals, identifying transmission chains and sources of infection that would otherwise remain undetected using traditional epidemiological methods [90]. By understanding the genomic diversity of MRSA strains, public health authorities have been able to implement targeted infection control measures, such as enhanced screening protocols and isolation strategies, to reduce the spread of the pathogen in healthcare settings ss shown in Table 6 below.

Table 6 Case studies of genomics in public health outbreak response

Outbreak	Genomic Application	Impact
COVID-19	Tracking variants of concern (e.g., Delta, Omicron)	Informed vaccination strategies and public health measures
Tuberculosis (MDR-TB)	WGS to identify resistance mutations and transmission chains	Improved treatment regimens and targeted infection control
MRSA	WGS to trace transmission in healthcare settings	Reduced healthcare-associated infections through enhanced control measures

4.2.2 Case studies of genomic applications in AMR surveillance

Several case studies illustrate the impact of genomic technologies on AMR surveillance and public health.

4.2.3 Tracking Carbapenem-resistant Enterobacteriaceae (CRE)

Carbapenem-resistant *Enterobacteriaceae* (CRE), including strains of *Klebsiella pneumoniae* and *Escherichia coli*, are among the most critical AMR threats globally [91]. WGS has been used extensively to track the global spread of the *blaKPC* and *blaNDM* resistance genes, which confer resistance to carbapenems. In a landmark study, researchers used WGS to identify the cross-border transmission of CRE between healthcare facilities in Europe and the Middle East, highlighting the need for international collaboration in AMR surveillance (ECDC, 2011). Tracking Carbapenem-Resistant Enterobacteriaceae (CRE): WGS has been pivotal in monitoring the spread of the *blaKPC* gene, which confers resistance to carbapenems. In a landmark study, genomic data revealed cross-border transmission of CRE strains, emphasizing the need for international collaboration in AMR surveillance [92].

Metagenomic Surveillance in Wastewater: Metagenomic studies have shown that untreated wastewater contains diverse resistance genes, including those conferring resistance to last-resort antibiotics like colistin. These findings have informed policies to improve wastewater treatment processes, reducing environmental AMR reservoirs [93].

CRISPR-Based Detection of Colistin Resistance: A recent study employed CRISPR-based diagnostics to detect the *mcr-1* gene in livestock samples, linking resistance to the overuse of colistin in agriculture. This rapid diagnostic approach has supported interventions to reduce colistin use and monitor its impact on resistance trends [94].

5 Role of genomics in AMR prediction models

In addition to its role in surveillance and outbreak response, genomics is increasingly being integrated into AMR prediction models, which combine genomic data with epidemiological, clinical, and environmental information to forecast the emergence and spread of resistant pathogens. These models enable public health authorities to anticipate AMR trends and implement preemptive measures, such as optimizing antibiotic stewardship programs and adjusting treatment guidelines based on the predicted prevalence of resistance [95, 96].

Machine learning algorithms, trained on large genomic datasets, have been developed to predict resistance phenotypes from pathogen genomes. These algorithms can identify patterns in genetic data that are associated with resistance to specific antibiotics, allowing for the early detection of resistance even before it is observed in clinical settings [95, 97]. By incorporating additional factors such as antibiotic usage patterns and patient demographics, these models provide a more comprehensive picture of AMR dynamics, enabling more effective public health planning and resource allocation.

For instance, genomic data has been used to predict the spread of carbapenem-resistant *Enterobacteriaceae* (CRE) in healthcare settings, allowing hospitals to implement targeted interventions such as enhanced screening and isolation procedures for high-risk patients [98]. In agricultural settings, AMR prediction models have been used to assess the risk of resistance transmission from livestock to humans, informing policies on antibiotic use in food production [99], Yunxiao et al., 2022; [100].

5.1 Ethical considerations in the use of genomics in public health

The application of genomics in public health offers numerous benefits. Also, its application in public health and AMR surveillance presents critical ethical considerations as summarized in Table 4, particularly in low- and middle-income countries (LMICs) where data governance structures, regulatory frameworks, and equitable access to genomic technologies remain underdeveloped. These challenges involve data privacy, genomic sovereignty, and equitable benefit-sharing, all of which have implications for global health equity and AMR mitigation efforts. To strengthen ethical practices in genomics, various global frameworks, regional policies, and case studies highlight both challenges and potential solutions.

5.2 Data privacy and confidentiality in genomic surveillance

One of the foremost ethical concerns in genomic AMR surveillance is the protection of sensitive genetic information (Table 7). Genomic data—particularly human sequencing data—can reveal personal health risks, ancestry information, and susceptibility to infections, raising concerns about patient confidentiality, misuse, and unauthorized access [101].

Table 7 Ethical considerations in genomic public health

Ethical Concern	Description	Potential Solutions	Reference
Data privacy	Ensuring the confidentiality of genomic data	Implementing robust data protection frameworks	[102]
Equity in access	Unequal access to genomic technologies between high- and low-income countries	Capacity-building initiatives and international collaborations	[103]
Data Sharing	Balancing the need for global data sharing with the protection of individual rights	Development of global data-sharing frameworks and ethical guidelines	[104]

5.3 Case study: data privacy challenges in South Africa

In South Africa, the Protection of Personal Information Act (POPIA) imposes strict regulations on genomic data-sharing to protect individuals' genetic privacy. However, these stringent laws limit South Africa's participation in global AMR genomic surveillance networks, slowing down international collaboration on emerging AMR threats [105].

Ethical Dilemma—While privacy protection is crucial, overly restrictive policies can hinder global AMR mitigation efforts by preventing real-time genomic data exchange across borders.

Proposed Solution—International genomic data-sharing frameworks, such as the Global Pathogen Surveillance Network (GPSN), advocate for secure, anonymized data-sharing models, ensuring both privacy and public health benefits [106].

5.4 Genomic sovereignty: the right to control genetic data

Genomic sovereignty refers to a nation's right to control the collection, storage, and use of genomic data generated within its borders. While this principle aims to protect LMICs from exploitation by foreign researchers and commercial entities, it can also create barriers to AMR collaboration and innovation.

5.5 Case study: genomic sovereignty and biopiracy concerns in Brazil

Brazil has enacted strict genomic sovereignty laws through its Genetic Heritage Management Council (CGEN), which requires government approval before genetic data collected in Brazil can be exported or shared internationally.

Ethical Dilemma: While Brazil's policies prevent foreign exploitation of genetic resources, they also restrict the ability of Brazilian researchers to collaborate on AMR genomic studies with international partners [107].

Proposed Solution: Initiatives such as the Nagoya Protocol promote fair and equitable benefit-sharing agreements, ensuring that LMICs retain ownership of their genomic data while still participating in global AMR research.

5.6 Equitable benefit-sharing in global genomic research

Genomic surveillance is often funded and led by high-income countries (HICs), raising concerns about data exploitation, research equity, and the fair distribution of benefits (Table 7). LMICs contribute valuable genomic data to global AMR monitoring but frequently lack access to the resulting diagnostic tools, technologies, and public health interventions.

5.7 Case Study: The Ebola Genomics Debate in West Africa

During the 2014–2016 Ebola outbreak in West Africa, genomic samples from infected patients were rapidly sequenced by HIC-funded research groups to track viral evolution. However, much of this genomic data was not shared with African scientists or public health agencies in real-time, delaying local outbreak response efforts [108].

Ethical Dilemma—While global research efforts helped characterize the Ebola virus, local researchers in Guinea, Sierra Leone, and Liberia had limited access to the sequencing data and were not involved in key decision-making.

Proposed Solution—Ethical frameworks such as the WHO Genomic Data Sharing Guidelines advocate for mandatory benefit-sharing mechanisms, ensuring that LMICs receive equal access to sequencing data, training, and technological resources.

5.8 Ethical Frameworks for Genomic Data Governance in LMICs

To address ethical concerns, several international organizations have developed frameworks to promote ethical, equitable, and responsible genomic data use.

The Global Antimicrobial Resistance Surveillance System (GLASS)—Launched by WHO in 2015, GLASS promotes transparent and equitable access to AMR genomic data, particularly for resource-limited countries [51–53]. Provides technical support and funding to ensure LMICs can contribute to and benefit from global AMR monitoring. The Nagoya Protocol on Access and Benefit-Sharing (ABS)—Ensures that countries contributing genomic data receive a

fair share of research benefits. Protects LMICs from biopiracy while still promoting collaborative genomic research (Convention on Biological Diversity, 2014). The African Union Data Policy Framework—Developed in 2022, this framework guides genomic data-sharing policies in African countries, ensuring both data protection and international collaboration (Africa CDC, 2022).

5.9 Ethical best practices for AMR genomic surveillance

- Strengthen LMIC Participation in Genomic Research – Policies should require that LMIC researchers and institutions be involved as equal partners in AMR genomic studies.
- Develop Open-Source Genomic Data Platforms – Platforms like Pathogen.watch and EnteroBase should prioritize open-access models, ensuring that all countries can use and analyze AMR data.
- Implement Equitable Technology Transfer Programs – Public–private partnerships should invest in genomic infrastructure and workforce training in resource-limited settings.
- Enforce Transparent Data Governance Agreements – Ethical frameworks should mandate data-sharing reciprocity, where LMICs contributing genomic data also receive diagnostic and surveillance benefits.

The use of genomics in public health and AMR surveillance raises significant ethical challenges, particularly in LMICs where issues related to data privacy, genomic sovereignty, and benefit-sharing remain contentious. Addressing these challenges requires globally coordinated frameworks, inclusive research partnerships, and equitable data-sharing policies. By promoting ethical governance models and ensuring LMICs receive equal benefits from genomic advancements, the global AMR response can become more just, effective, and sustainable.

6 Advances in genomics for AMR surveillance

Genomics has transformed AMR surveillance, offering new avenues for tracking the spread of resistance across human, animal, and environmental health (See Table 6). Traditionally, AMR surveillance relied on phenotypic testing, which involved culturing organisms and testing their response to antibiotics. However, these methods are time-consuming and may fail to detect low-frequency resistance mechanisms [109, 110]. Genomic approaches, particularly WGS, provide a more comprehensive solution by identifying the entire resistance gene repertoire of a pathogen, allowing for more accurate and timely surveillance (David et al., 2021).

One of the major advancements in genomic surveillance is the ability to *track the global dissemination of resistance genes*. For example, WGS has been used to map the spread of the *blaKPC* gene, which confers resistance to carbapenems, across different regions and healthcare settings [92, 111, 112]. By comparing the genetic sequences of resistant pathogens isolated from different geographical areas, researchers can identify transmission pathways and implement targeted interventions to control the spread of AMR.

Metagenomics-based surveillance has also advanced our understanding of environmental reservoirs of resistance. A key finding from metagenomics studies is that human and animal waste, often containing residual antibiotics, creates environments that select resistant bacteria (David et al., 2016; [113]). For instance, metagenomic studies in wastewater treatment plants have revealed the presence of AMR genes, including those conferring resistance to last-resort antibiotics like colistin [93]. This highlights the importance of environmental surveillance in identifying and mitigating AMR at the source before resistant bacteria enter clinical settings.

6.1 Colistin resistance and the spread of *mcr-1*

Colistin, a last-resort antibiotic, has become less effective due to the emergence of the *mcr-1* gene, which confers resistance to this vital drug. WGS and metagenomics have been used to trace the origin of *mcr-1* from livestock to humans, revealing that the overuse of colistin in agriculture played a key role in spreading this resistance mechanism [94]. Genomic surveillance has since been expanded to monitor the presence of *mcr-1* in food products and environmental samples, providing early warnings for public health interventions [114].

6.2 Genomic tracking of multidrug-resistant tuberculosis (MDR-TB)

Genomics has also been crucial in the surveillance and control of multidrug-resistant tuberculosis (MDR-TB). WGS has been used to identify resistance mutations in the *rpoB* and *katG* genes, which confer resistance to rifampicin and isoniazid, respectively [115]. By analyzing the genomes of MDR-TB isolates, researchers can track the spread of resistance across regions and predict the effectiveness of different treatment regimens. In some cases, genomic data has led to identifying resistance hotspots, where targeted public health interventions can be implemented to prevent further transmission [8].

The integration of genomic techniques such as whole-genome sequencing, metagenomics, and CRISPR-based diagnostics has revolutionized the field of AMR detection and surveillance. These tools enable the rapid identification of resistance genes and provide valuable insights into the transmission dynamics of resistant pathogens (See Table 8). Genomic data, when integrated into predictive models, also enhances the ability to forecast the emergence and spread of resistance, guiding public health interventions and antibiotic stewardship programs. As the application of genomics continues to expand, it will play an increasingly critical role in mitigating the global AMR crisis [71].

6.3 Online tools for genomic surveillance

The integration of genomic technologies into antimicrobial resistance (AMR) mitigation requires not only advanced sequencing platforms but also accessible bioinformatics tools that facilitate genomic data analysis, pathogen tracking, and epidemiological investigations. Online genomic surveillance platforms provide user-friendly, cloud-based solutions that lower computational barriers, particularly for researchers and public health agencies in low- and middle-income countries (LMICs) with limited bioinformatics infrastructure. These tools complement large-scale sequencing efforts by enabling real-time data interpretation, strain characterization, and outbreak detection across human, animal, and environmental health sectors. This section highlights three widely used online platforms—PubMLST, EnteroBase, and Pathogen.watch—that have significantly contributed to AMR genomic surveillance, particularly in resource-limited settings.

6.4 PubMLST: A global platform for multi-locus sequence typing (MLST)

PubMLST (Public Multi-Locus Sequence Typing Database) is a widely used open-access genomic platform that supports the standardized classification of bacterial pathogens through multi-locus sequence typing (MLST) [120]. Developed at the University of Oxford, PubMLST is particularly valuable for tracking the evolutionary relationships and global spread of AMR pathogens across different sectors.

Key Features and Benefits: *Standardized Typing Schemes* – Enables researchers to classify bacterial strains based on stable genetic markers, allowing global comparability of AMR isolates. *Cloud-Based Accessibility* – No requirement for local bioinformatics expertise or high-performance computing, making it ideal for LMICs with limited infrastructure. *AMR Surveillance Applications* – Used extensively for tracking *Neisseria meningitidis*, *Streptococcus pneumoniae*, and *Klebsiella pneumoniae*, among other AMR-prone pathogens. *Integration with Genomic Epidemiology* – Helps public health agencies monitor AMR emergence and assess the effectiveness of intervention strategies.

6.5 Case study: PubMLST in meningococcal AMR surveillance

In South Africa, PubMLST has been instrumental in genomic surveillance of *Neisseria meningitidis*. By leveraging this online platform, researchers identified the introduction of ciprofloxacin-resistant strains, prompting policy changes in national vaccination and antibiotic use strategies [120].

6.6 EnteroBase: tracking enteric pathogens in one health surveillance

EnteroBase is a specialized genomic surveillance platform designed for tracking enteric bacteria, including *Salmonella*, *Escherichia coli*, *Shigella*, *Vibrio*, and *Yersinia* [121]. Developed at the University of Warwick, EnteroBase provides an integrated system for analyzing whole-genome sequencing (WGS) data, making it a powerful tool for foodborne AMR outbreak investigations and cross-border pathogen tracking [122].

Table 8 Genomic techniques in AMR surveillance

Genomic Technique	Application	Example	Reference
Whole-genome sequencing (WGS)	Sequencing the entire genome of pathogens to identify resistance genes and trace transmission	Tracking the global spread of <i>blaKPC</i> and <i>mcr-1</i> resistance genes	[116]
Metagenomics	Sequencing all genetic material in a sample to detect AMR genes in microbial communities	Identifying resistance genes in wastewater and agricultural soils	[117]
CRISPR-based Diagnostics	Rapid identification of specific AMR genes using CRISPR-Cas systems	Detecting <i>blaNDM-1</i> in clinical and environmental samples	[118] [119]

Key Features and Benefits: *Comprehensive Global Database* – Contains thousands of curated bacterial genomes, enabling real-time comparison of isolates from clinical, veterinary, and environmental sources. *Automated MLST & Phylogenetic Analysis* – Facilitates rapid strain typing and evolutionary relationship mapping. *High-Resolution AMR Detection* – Identifies resistance genes and plasmids associated with foodborne outbreaks and zoonotic transmission. *Supports One Health AMR Surveillance* – Widely used in food safety monitoring, agricultural biosecurity, and hospital infection control programs.

6.7 Case study: enterobase in global salmonella surveillance

In Brazil, Enterobase was used to trace the source of a multi-country outbreak of *Salmonella* Heidelberg, which was linked to contaminated poultry exports [123]. By comparing genomic sequences from human infections, retail chicken, and farm environments, researchers identified antibiotic-resistant clones, leading to stricter regulations on antimicrobial use in food production.

6.8 Pathogen.watch: AI-powered real-time genomic surveillance

Pathogen.watch is an artificial intelligence (AI)-driven online genomic analysis platform, developed by the Centre for Genomic Pathogen Surveillance (CGPS). Designed to support real-time AMR surveillance, Pathogen.watch integrates whole-genome sequencing data with geospatial mapping, enabling health authorities to detect AMR hotspots and emerging resistant strains.

Key Features and Benefit: *Real-Time Pathogen Monitoring* – Allows users to upload WGS data and receive instant reports on resistance genes, virulence factors, and outbreak clusters. *Geospatial Tracking of AMR Strains* – AI-driven mapping of AMR spread across different countries and regions, improving cross-border outbreak responses. *Low-Cost Bioinformatics Solution* – Removes the need for advanced computing infrastructure, making it highly suitable for LMIC public health programs. *Direct Integration with Public Health Systems* – Used by national disease control centers to inform infection control policies and antimicrobial stewardship programs.

6.9 Case study: pathogen.watch in AMR hotspot detection

In Bangladesh, Pathogen.watch was implemented by the International Centre for Diarrhoeal Disease Research, Bangladesh (ICDDR, B) to track carbapenem-resistant *Klebsiella pneumoniae* in hospital settings [124]. The tool identified hospital-acquired resistance clusters, leading to targeted infection control measures and improved antibiotic prescribing guidelines [125].

6.10 The role of online genomic tools in overcoming computational barriers

For many LMICs, the lack of bioinformatics expertise, local sequencing infrastructure, and high-performance computing resources hinders the widespread use of genomics for AMR surveillance. Online platforms like PubMLST, Enterobase, and Pathogen.watch help overcome these barriers by: *Providing Free Cloud-Based Solutions* – No need for expensive hardware or software licenses, making genomics more accessible to LMIC researchers. *Automating Data Analysis* – Reducing reliance on highly specialized bioinformaticians by offering pre-configured genomic pipelines. *Enabling Cross-Sectoral and International Collaboration* – Allowing scientists to share and compare AMR genomic data globally, strengthening the One Health response to AMR. *Enhancing Surveillance in Resource-Limited Settings* – Supporting low-cost sequencing projects that can rapidly identify resistant pathogens in hospitals, farms, and the environment.

To strengthen the role of online genomic surveillance in AMR monitoring, several key actions are essential. Enhancing platforms like Pathogen.watch with AI and machine learning can enable automated outbreak prediction, improving early detection and response. Expanding global data-sharing networks is also critical—open-access databases should be inclusive of LMICs to ensure broad participation and benefit-sharing in genomic AMR research. Building local capacity is another priority. Training programs in LMICs should equip healthcare professionals, veterinarians, and environmental scientists with the skills to effectively use genomic tools. This includes not just technical training but also guidance on data interpretation and application. Lastly, governments should formally integrate genomic surveillance platforms such as PubMLST, Enterobase, and Pathogen.watch into national AMR action plans. Institutionalizing these tools ensures consistent use and aligns genomic surveillance with broader public health strategies.

Online genomic surveillance tools such as PubMLST, EnteroBase, and Pathogen.watch have revolutionized AMR monitoring by providing scalable, cloud-based bioinformatics solutions that overcome computational and infrastructure limitations, particularly in LMICs. These tools enhance real-time AMR tracking, outbreak detection, and One Health surveillance, making genomic data more actionable for policymakers and public health agencies. By expanding accessibility, strengthening international data-sharing networks, and integrating AI-driven analytics, these platforms will continue to play a pivotal role in global AMR mitigation efforts.

7 Challenges in integrating genomics into one health

7.1 Technical challenges: data sharing, standardization, and analysis

One of the most significant challenges in integrating genomics into the One Health framework is the technical complexity involved in managing, analyzing, and sharing large volumes of genomic data across sectors (See summary in Table 9). The rapid generation of data from genomic sequencing technologies, such as whole-genome sequencing (WGS) and metagenomics, necessitates advanced bioinformatics tools and computing infrastructure. However, there are substantial gaps in the capacity for data analysis and interpretation, particularly in low- and middle-income countries (LMICs), where bioinformatics expertise and resources are limited [84, 126].

7.1.1 Case study: Europe's COMPARE initiative vs. AMR surveillance in India

In Europe, the COMPARE Initiative represents a major success in standardizing AMR genomic data-sharing across countries [130]. Launched in 2015 and funded by the European Union (EU) Horizon 2020 program, COMPARE integrates human, veterinary, and environmental genomic data to create a harmonized bioinformatics platform for outbreak detection and AMR surveillance. Through this initiative, the European Centre for Disease Prevention and Control (ECDC) [131] and the European Food Safety Authority (EFSA) have established common data-sharing protocols, making it easier for countries to integrate genomic AMR data into decision-making. This approach has allowed the EU to trace resistant strains across food chains, enhancing early warning systems for emerging AMR threats [8].

In contrast, in India, AMR genomic surveillance remains largely fragmented across sectors. The Indian Council of Medical Research (ICMR) and the National Centre for Disease Control (NCDC) oversee human AMR surveillance, while the Indian Veterinary Research Institute (IVRI) is responsible for monitoring resistance in livestock. However, there is no unified genomic database that integrates AMR data across these sectors. Data is often stored in different formats and analyzed using sector-specific methodologies, making cross-sectoral comparisons difficult [132]. Additionally, legal and institutional barriers restrict data sharing between agencies, slowing responses to zoonotic AMR outbreaks. This fragmentation highlights the urgent need for standardization in genomic AMR data-sharing policies to improve One Health surveillance systems.

7.2 Economic barriers: cost of genomic technologies

The high cost of implementing genomic technologies poses a significant barrier to their integration into One Health, particularly in LMICs. Technologies such as WGS, metagenomics, and bioinformatics platforms are expensive to acquire, operate, and maintain. For instance, the cost of sequencing a bacterial genome using WGS has decreased significantly in recent years but remains prohibitive for routine use in many settings, particularly where public health budgets are limited [133].

7.3 Case study: the united kingdom vs. Kenya – economic disparities in AMR genomic surveillance

In the United Kingdom, the National Health Service (NHS) and the UK Health Security Agency (UKHSA) have integrated WGS into routine AMR surveillance, with government funding supporting sequencing infrastructure and bioinformatics capacity. Programs like the Pathogen Genomics Service (PGS) provide real-time genomic insights to guide antimicrobial stewardship efforts, demonstrating the feasibility of national-scale genomic integration in a well-funded healthcare system [134].

Table 9 Key challenges in integrating genomics into one health

Challenge	Description	Example	Reference
Data Sharing	Lack of standardized frameworks for sharing genomic data across sectors	Differences in data collection/storage between human, animal, and environmental health	[127]
Cost of Technologies	High costs of sequencing technologies and bioinformatics infrastructure	Limited implementation of WGS and metagenomics in LMICs due to financial constraints	[128]
Policy and Governance Barriers	Fragmented policies across sectors and countries	Lack of coordinated antibiotic stewardship policies between agriculture and human health	[129]
Data Governance and Ethics	Concerns over privacy, intellectual property, and exploitation of genomic data	Restrictions on sharing AMR genomic data due to economic and political concerns	[58]

In contrast, Kenya faces substantial financial constraints in implementing genomic AMR surveillance. The Kenya Medical Research Institute (KEMRI) and the African Centre for Disease Control (Africa CDC) have initiated genomic sequencing projects, but reliance on international donors (e.g., Wellcome Trust, Bill & Melinda Gates Foundation) highlights the financial vulnerability of AMR genomic surveillance programs in LMICs. A lack of sustained national funding and high operational costs mean genomic AMR surveillance is not yet a routine practice but rather limited to research-based projects [105]. These examples emphasize the need for innovative financing models, such as public–private partnerships and international funding mechanisms, to ensure the sustainable expansion of genomic surveillance in LMICs.

7.4 Policy and governance barriers

Integrating genomics into One Health also presents significant policy and governance challenges. One Health inherently requires collaboration across sectors—human health, animal health, and environmental health—that have traditionally operated independently, each with its regulatory frameworks, priorities, and stakeholders. Aligning these sectors under a unified governance structure for genomic surveillance and AMR management is difficult due to the differing interests and regulatory environments that govern each sector [84, 135].

7.4.1 Case study: the United States vs. Brazil – policy coordination in one health genomics

In the United States, GenomeTrakr, managed by the US Food and Drug Administration (FDA), represents a successful example of federal-level policy coordination for genomic AMR surveillance. This initiative links public health agencies, veterinary departments, and environmental monitoring programs, ensuring seamless data integration across One Health sectors. Federal regulations enforce standardized genomic reporting, and collaborations with academic institutions have strengthened national AMR response strategies [135].

In contrast, in Brazil, the lack of a centralized One Health AMR governance framework hinders genomic data integration. Human AMR surveillance is managed by the Ministry of Health, while animal and environmental health fall under different ministries, creating policy fragmentation. This disjointed regulatory landscape may have led to inconsistent surveillance practices and difficulties in developing a unified AMR action plan [136]. The US example highlights the importance of strong governance frameworks and centralized policy coordination, whereas Brazil's experience underscores the need for cross-sectoral policy alignment to improve One Health AMR surveillance.

7.5 Ethical and data governance challenges

The sharing of genomic data between countries is often restricted due to concerns over data sovereignty, privacy, and intellectual property. Countries may be hesitant to share genomic data related to AMR pathogens due to concerns that the data could be misused or result in negative economic consequences, such as trade restrictions related to antimicrobial use in agriculture [107].

7.5.1 Case study: South Africa's data sovereignty vs. Europe's open science model

In South Africa, the government restricts the sharing of genomic data on infectious disease pathogens, including AMR strains, due to data sovereignty concerns. The Protection of Personal Information Act (POPIA) places strict regulations on genomic data sharing, limiting international research collaborations. While this policy protects national interests, it reduces participation in global AMR genomic databases, hindering early detection of cross-border resistance threats [105].

Conversely, in Europe, the European Nucleotide Archive (ENA) and Pathogen Genomics Initiative embrace open data-sharing principles, facilitating rapid AMR surveillance and cross-border collaboration. Countries within the EU benefit from harmonized data-sharing agreements, ensuring timely access to genomic data while maintaining ethical research standards [137–139]. This contrast demonstrates the delicate balance between national data sovereignty and global

scientific collaboration, highlighting the need for equitable data-sharing agreements that respect national interests while supporting global AMR mitigation efforts.

8 Bridging the gap: exploring potential solution

8.1 Enhancing capacity building and infrastructure development

One of the most significant barriers to integrating genomics into One Health AMR surveillance is the lack of bioinformatics expertise, sequencing infrastructure, and data management systems, particularly in low- and middle-income countries (LMICs). To address this, we now recommend:

Efforts to enhance genomic capacity in LMICs are advancing through initiatives like the WHO's GHSA and the Africa Pathogen Genomics Initiative. These programs focus on training local professionals in sequencing, bioinformatics, and data analysis, aiming to build sustainable expertise for effective pathogen surveillance and response [43, 44, 53]). Collaborations with high-income countries and private companies such as Illumina and Oxford Nanopore Technologies are helping LMICs access vital genomic tools and infrastructure. These partnerships support the deployment of sequencing platforms, data-sharing systems, and technical training, enabling countries to operate and maintain genomic technologies independently. That Africa CDC spearhead the development of regional genomic hubs that consolidate resources and expertise across multiple countries. These hubs facilitate shared facilities, centralized data analysis, and joint training initiatives, enhancing the efficiency and scope of genomic surveillance across the region. Together, these initiatives are building the foundation for self-reliant genomic surveillance in LMICs. Improved local capacity and infrastructure will reduce dependency on external labs and support real-time tracking of antimicrobial resistance (AMR) and other public health threats, promoting coordinated responses across One Health sectors.

8.2 Standardizing data sharing and interoperability through global initiatives

To overcome inconsistencies in genomic data reporting across human, animal, and environmental health sectors, we recommend the following:

Global Antimicrobial Resistance Surveillance System (GLASS): The WHO's GLASS initiative provides standardized protocols for AMR data collection, reporting, and comparison across countries and sectors [137–139]. By ensuring consistency in metadata reporting, GLASS enhances the interoperability of genomic databases. **One Health AMR Surveillance Frameworks:** Multi-sectoral initiatives like the Quadripartite Collaboration (WHO, FAO, WOA, UNEP) are developing unified AMR surveillance platforms to integrate human, veterinary, and environmental data [140]. **Development of Common Data Repositories:** The Pathogen Genomics Initiative and Genomic Epidemiology Network facilitate global data-sharing platforms, ensuring AMR genomic data can be accessed, compared, and integrated across regions. These harmonized surveillance methodologies will enable researchers and policymakers to identify global AMR trends, predict emerging resistance hotspots, and develop coordinated mitigation strategies.

8.3 Innovative financing mechanisms for genomic AMR surveillance

The high cost of sequencing technologies, bioinformatics software, and data storage remains a major challenge, especially in LMICs. To address this, we have made the following suggestions:

International Funding Support: Organizations such as the Bill & Melinda Gates Foundation, the Global Fund, and the World Bank are providing targeted funding to improve genomic surveillance infrastructure in LMICs. **Public–Private Partnerships (PPPs):** Collaboration between governments, biotech companies, and research institutions can help subsidize the cost of sequencing technologies and make them more accessible [141, 142]. **Cost-Effective Sequencing Models:** Advances in portable sequencing technologies (e.g., Oxford Nanopore MinION) allow for low-cost, field-deployable sequencing, making genomic AMR surveillance feasible in remote areas. Ensuring financial sustainability for One Health genomic surveillance will help integrate sequencing technologies into routine AMR monitoring, even in resource-limited settings.

8.4 Strengthening governance and cross-sectoral policy coordination

Governance fragmentation remains a major obstacle, as human health, animal health, and environmental regulators often operate independently. To improve governance, we have suggested:

National and Regional One Health Committees: Countries such as the UK, Canada, and the Netherlands have established cross-sectoral AMR governance committees that bring together human, veterinary, and environmental health policymakers to create unified surveillance strategies. **Legislation and Policy Harmonization:** Efforts by the European Union (EU) to create legally binding regulations on antibiotic use and resistance reporting across human and veterinary sectors serve as a model for other regions [143]. **Data Governance and Ethical Frameworks:** International agreements are being developed to promote equitable access to genomic data while addressing privacy concerns, particularly regarding data sovereignty in LMICs [105]. Establishing unified governance frameworks will ensure AMR policies align across sectors, enabling more effective surveillance, intervention, and antibiotic stewardship.

8.5 Ethical and equitable data sharing practices

Ethical concerns surrounding genomic data access, ownership, and benefit-sharing can hinder global AMR collaborations. To address this, we now highlight:

FAIR Data Principles (Findable, Accessible, Interoperable, Reusable): These principles are being adopted in global genomic databases to facilitate ethical and responsible data sharing [144]. **Benefit-Sharing Frameworks:** Ethical policies are being developed to ensure LMICs and vulnerable populations benefit from genomic data they contribute, through capacity-building and equitable research collaborations [107]. **Open-Access vs. Controlled-Access Databases:** We discuss the trade-offs between fully open genomic databases (e.g., NCBI GenBank) and restricted-access platforms that protect sensitive patient and country-level data. Addressing data-sharing ethics will enhance international collaborations while safeguarding the rights of all stakeholders in the global AMR response.

9 Future directions in one health genomics

The field of genomics is rapidly evolving, and its integration into the One Health framework holds significant potential in combating antimicrobial resistance (AMR) and strengthening global health security (See Table 8). While several innovative approaches are emerging, their implementation—particularly in low- and middle-income countries (LMICs)—requires clear prioritization and feasible strategies. This section presents key next steps and actionable recommendations for advancing One Health genomics, focusing on: big data and machine learning for AMR surveillance, scaling genomic technologies in LMICs, strengthening international collaboration and governance.

Enhancing accessibility and capacity-building efforts.

9.1 Integration of big data and machine learning with genomics

The increasing availability of large-scale genomic datasets has enabled the integration of big data analytics and machine learning (ML) into One Health genomics. These technologies are transforming how AMR trends are predicted, how genomic data is analyzed, and how public health interventions are designed.

Big data & Big Data in Genomics:

Big data enables researchers to conduct large-scale analyses that provide insights into the genetic determinants of AMR, the transmission of resistant pathogens across different species, and the environmental factors contributing to the spread of resistance [145]. For example, global genomic surveillance networks are using big data approaches to monitor the spread of AMR genes across borders, enabling public health authorities to identify emerging threats in real-time [8].

Genomic data from whole-genome sequencing (WGS), metagenomics, and epidemiological studies has grown exponentially, requiring advanced computational tools for storage, management, and integration [146, 147]. Key Next Steps should include: establish open-access big data platforms to ensure LMICs have equitable access to genomic databases and analytics tools, expand cloud-based genomic surveillance networks, reducing reliance on local computing power.

Machine Learning in Genomic Data Analysis:

Machine learning (ML) algorithms, particularly those used in predictive analytics and pattern recognition, are revolutionizing the analysis of genomic data. These algorithms can process large-scale sequencing datasets, detect hidden patterns, and make accurate predictions about antimicrobial resistance (AMR) mechanisms that might not be evident through traditional analytical methods. In the context of AMR surveillance, ML models can:

- Predict Resistance Phenotypes** – ML-based models analyze whole-genome sequencing (WGS) data to predict phenotypic resistance even before laboratory confirmation, enabling early intervention strategies [97, 148].
- Identify Emerging Resistance Genes** – By analyzing vast genomic datasets from clinical, veterinary, and environmental sources, ML models can identify novel AMR genes and predict their potential for widespread resistance [149–151].
- Optimize Antibiotic Treatment Strategies** – Predictive ML models can forecast the evolution of resistance based on bacterial genetic profiles and previous antibiotic exposure histories, helping clinicians choose the most effective antimicrobial therapy [152].

To illustrate the transformative impact of ML in AMR surveillance, we highlight key case studies demonstrating its application in outbreak source attribution, resistance prediction, and One Health monitoring.

9.2 Case study 1: ML for source attribution of campylobacter infections in the United States

A study by Pascoe et al. [153] demonstrated the power of ML in AMR outbreak source attribution. The research used machine learning models to trace the origins of *Campylobacter* infections in the United States, a major cause of food-borne illness and antibiotic resistance transmission.

Key Findings include:

The ML model analyzed genomic data from *Campylobacter* isolates across human, animal, and environmental reservoirs. It accurately predicted the likely source of infections (e.g., poultry, cattle, or contaminated water), helping public health officials trace AMR outbreaks more efficiently. The tool provided data-driven insights to inform targeted mitigation strategies, such as reducing antibiotic use in poultry farming to prevent resistant strains from entering the food chain.

Impact on AMR Surveillance:

Enhanced AMR tracking – ML-based source attribution enables faster outbreak containment and reduces reliance on traditional epidemiological methods. **Supports One Health integration** – By linking human, animal, and environmental surveillance, ML strengthens cross-sectoral AMR mitigation efforts.

9.3 Case study 2: ML-driven resistance prediction in mycobacterium tuberculosis

ML models have been successfully applied to predict drug resistance in *Mycobacterium tuberculosis* (Mtb), the causative agent of tuberculosis (TB). A study by Chen et al. [154] trained ML algorithms on genomic sequences from over 10,000 Mtb isolates to predict resistance to first-line TB drugs.

Key Findings includes:

The ML models identified previously unrecognized genetic markers associated with multi-drug resistance (MDR). The predictions achieved > 90% accuracy, outperforming traditional culture-based resistance testing. The study demonstrated real-world applications of AI-powered diagnostics, which can be implemented in LMICs where TB remains a major public health challenge.

Impact on AMR Surveillance:

Accelerates resistance detection – ML models can replace slow, resource-intensive laboratory tests. **Improves treatment outcomes** – Clinicians can personalize TB therapy based on ML-predicted resistance profiles.

9.4 Case study 3: ML and AI for real-time AMR surveillance in hospital settings

ML is also being utilized to monitor hospital-acquired infections (HAIs) and optimize antibiotic stewardship. A study by Tran et al., [155] developed an AI-driven ML model to predict AMR outbreaks in intensive care units (ICUs) based on genomic and clinical metadata.

Key Findings are:

The ML algorithm analyzed real-time patient data (e.g., microbial isolates, antibiotic prescriptions, and patient outcomes). It also accurately predicted which patients were at risk of developing AMR infections before clinical symptoms appeared. The tool recommended targeted antibiotic regimens, reducing the use of broad-spectrum antibiotics and slowing resistance development.

Impact on AMR Surveillance:

Proactive infection control – Hospitals can preemptively isolate at-risk patients, preventing AMR spread. Antibiotic stewardship – Optimized treatment decisions help reduce unnecessary antibiotic exposure, minimizing selection pressure for resistance.

The integration of machine learning into AMR surveillance is redefining how we track, predict, and mitigate resistance at a global scale. By leveraging AI-driven analytics, ML models can: Improve outbreak source attribution [153] – *Campylobacter* in the US). Predict resistance phenotypes [154] – *M. tuberculosis*). Enhance hospital-based infection control [155].

However, challenges remain, particularly in LMICs, where computational limitations, data-sharing barriers, and lack of bioinformatics expertise restrict ML adoption. To fully realize the potential of AI in AMR mitigation, global health organizations must invest in AI-driven public health initiatives, strengthen international genomic data-sharing efforts, and promote equitable access to ML technologies across all sectors of the One Health framework.

9.5 Strengthening international collaboration and governance

International cooperation is crucial for harmonizing AMR genomic surveillance efforts. Key actionable next steps should include: expand participation in global AMR networks, such as WHO’s GLASS and the Global Pathogen Surveillance Network (GPSN). Develop standardized data-sharing policies to balance genomic sovereignty with equitable research collaborations.

Case Study: Brazil’s Genomic Sovereignty Laws—Brazil restricts the sharing of genomic data without government approval, slowing cross-border AMR research.

Solution: Solution would be to implement the Nagoya Protocol’s benefit-sharing agreements to incentivize LMIC participation in global AMR genomics.

9.6 Enhancing accessibility and capacity-building in LMICs

Establish genomic training centers in LMICs, modeled after Africa CDC’s sequencing workforce development program. Develop open-source bioinformatics tools for low-resource settings.

Feasible Strategies for LMICs: Online training programs for AMR genomics (e.g., WHO’s AMR Bioinformatics Academy), partnerships with universities and research institutes to embed genomic literacy in public health education.

10 Personalized medicine and its role in AMR management

Personalized medicine, which tailors’ medical treatments to individual patients based on their genetic makeup, is a promising area of development in One Health genomics (Summarized in Table 10). While personalized medicine has traditionally focused on human health, recent advances in genomics and microbiome research suggest that it could play a critical role in managing AMR and improving outcomes in both human and veterinary medicine [84].

10.1 Personalized antimicrobial therapies

The integration of genomics into personalized medicine could lead to the development of tailored antimicrobial therapies. By analyzing the genomes of both the pathogen and the host, healthcare providers can determine the most effective treatment strategies, reducing the use of broad-spectrum antibiotics that contribute to resistance. For example, genomic data can identify specific resistance mechanisms in bacterial pathogens, allowing clinicians to select targeted

Table 10 Personalized medicine in AMR management

Application	Description	Example	Reference
Tailored Antimicrobial Therapies	Use of genomic data to guide personalized antibiotic selection	Targeted antibiotic treatments based on pathogen resistance mechanisms	[156]
Microbiome-Based Interventions	Restoring healthy microbiota to reduce the need for antibiotics	Fecal microbiota transplantation to treat recurrent <i>Clostridioides difficile</i> infections	[157]

antibiotics that are less likely to drive further resistance [158, 159]. In veterinary medicine, personalized antimicrobial treatments could improve the management of infections in livestock and companion animals, reducing the need for prophylactic antibiotic use and minimizing the risk of resistance transmission from animals to humans. This approach aligns with the goals of One Health by addressing the interconnectedness of human, animal, and environmental health in the context of AMR [100].

10.2 Microbiome-based interventions

Another emerging area of personalized medicine is the use of microbiome-based interventions to manage AMR. The human microbiome, particularly the gut microbiota, plays a crucial role in shaping the immune response and influencing the development of resistance [160]. By analyzing the composition of a patient's microbiome, clinicians can develop strategies to restore healthy microbial communities, reducing the need for antibiotics and lowering the risk of resistance development [161].

11 The future of AMR genomics in developing countries

One of the most critical challenges in the global fight against AMR is the disparity in access to genomic technologies between high-income countries (HICs) and low- and middle-income countries (LMICs). As genomics becomes an increasingly integral part of AMR surveillance and control, there is a growing need to ensure that LMICs are equipped with the necessary infrastructure, expertise, and resources to participate in and benefit from these advances [8, 84].

11.1 Capacity Building and Infrastructure Development.

Expanding genomic capabilities in LMICs is essential for global AMR surveillance and One Health implementation. International collaborations, such as those led by the World Health Organization (WHO) and the Global Health Security Agenda, aim to strengthen the genomic infrastructure in LMICs through capacity-building initiatives, technology transfer, and financial support as summarized in Table 11 [51–53]. Investments in sequencing facilities, bioinformatics training, and data management systems are critical for ensuring that LMICs can conduct routine genomic surveillance and contribute to global datasets. Furthermore, LMICs often face unique AMR challenges, such as the overuse of antibiotics in agriculture and limited access to healthcare, making it essential to adapt genomic tools to the specific needs of these countries [162], [71].

11.2 Regional and Global Collaboration

Collaboration between HICs and LMICs is key to ensuring that genomic advances are accessible to all countries. Public–private partnerships, as well as funding from international organizations, can support the implementation of genomic technologies in resource-limited settings [165, 166]. For example, programs like the African Centres for Disease Control and Prevention's (Africa CDC) Pathogen Genomics Initiative aim to build genomic capacity across Africa, enabling countries to respond to AMR and infectious disease outbreaks using cutting-edge technologies [167]. Moreover, regional collaboration within LMICs can enhance the sharing of genomic data, allowing for more effective monitoring of AMR trends across borders. The establishment of regional genomic hubs, where countries can pool resources and expertise, could help overcome some of the financial and technical barriers to implementing genomic technologies in LMICs [168, 169].

12 Expanding the use of genomics in environmental health

Another promising direction for One Health genomics is its expanded use in environmental health surveillance (Table 12). The environment is a key reservoir for antimicrobial-resistant bacteria and resistance genes, particularly in water systems and soil impacted by agricultural runoff, wastewater, and industrial pollution [170]. Genomic tools, particularly metagenomics, allow for the detection of resistance genes in complex microbial communities in the environment, providing early warnings of potential public health threats.

Table 11 Key applications of big data and machine learning in one health genomics

Application	Description	Example	Reference
Big Data Integration	Aggregation and analysis of large-scale genomic datasets across human, animal, and environmental health	Global AMR surveillance networks using big data platforms to track resistance genes	[62]
Machine Learning Algorithms	Predictive models based on genomic data to forecast AMR emergence and guide interventions	ML models predicting resistance phenotypes in bacterial populations	[163]
Genomic Data Analytics	Identifying new AMR genes and transmission pathways through large-scale data analysis	Identification of novel resistance genes in metagenomic datasets from environmental samples	[164]

Table 12 Key strategies for expanding genomics in LMICs

Strategy	Description	Example	Reference
Capacity Building	Training, infrastructure development, and technology transfer in LMICs	WHO-led initiatives to establish sequencing facilities in LMICs	[137–139]
Regional Collaboration	Pooling of resources and expertise across LMICs for genomic surveillance	African CDC Pathogen Genomics Initiative for regional AMR tracking	[171]
Public–Private Partnerships	Collaborations between governments, NGOs, and private sectors to fund genomic projects	Partnerships between pharmaceutical companies and LMICs for technology development	[172]

12.1 Environmental metagenomics

Environmental metagenomics is an emerging field that uses sequencing technologies to analyze the genetic composition of microbial communities in soil, water, and air samples. This approach allows researchers to detect the presence of AMR genes in the environment, even in the absence of specific pathogens [173]. By monitoring environmental hotspots, such as agricultural fields treated with antibiotics or wastewater treatment plants, genomic surveillance can identify areas where resistant bacteria are likely to emerge and spread.

12.2 Environmental AMR surveillance

The integration of environmental data into One Health AMR surveillance is essential for understanding the full scope of resistance transmission. Surveillance programs that include environmental sampling can track the movement of AMR genes between humans, animals, and the environment, helping to identify the sources of resistance and guide interventions aimed at reducing environmental contamination [71]. The future of One Health genomics is poised to be shaped by the integration of big data and machine learning, the development of personalized medicine for AMR management, and the expansion of genomic capabilities in LMICs. As genomics becomes more accessible and sophisticated, it will play an increasingly critical role in preventing and controlling AMR, ensuring that the interconnected health of humans, animals, and the environment is protected. Collaborative efforts, capacity building, and equitable access to genomic technologies are essential for ensuring that the benefits of One Health genomics are realized globally.

13 Counterarguments to a one health approach to AMR

While emphasizing AMR as a One Health issue, it is important to recognize ongoing debates regarding the feasibility and effectiveness of integrating surveillance across human, animal, and environmental sectors. Critics argue that AMR transmission between these compartments may not be as extensive as commonly assumed and that the complexity of cross-sectoral surveillance may introduce logistical and economic challenges [27, 174]. Studies have shown variability in AMR spillover, with certain resistance mechanisms appearing more confined to specific sectors rather than exhibiting widespread crossover [175]. Additionally, fragmented governance structures and disparities in data-sharing frameworks can hinder the practical implementation of an integrated approach. However, despite these challenges, growing evidence suggests that a siloed approach to AMR surveillance fails to capture the full scope of resistance evolution and transmission dynamics [27, 176]. Recent advancements in genomic epidemiology and bioinformatics have improved our ability to detect and track AMR across sectors, making integrated approaches increasingly viable [177]. Furthermore, One Health strategies have facilitated more comprehensive risk assessments and intervention strategies, helping to mitigate AMR at its sources rather than reacting to outbreaks retrospectively [178, 179]. Addressing governance barriers and investing in standardized surveillance frameworks will be critical in maximizing the benefits of a One Health approach while minimizing its challenges.

14 Strengthening critical analysis

Existing Challenge: While genomic technologies have revolutionized AMR mitigation, their widespread adoption is hindered by significant challenges that require deeper critical analysis. Previous studies have primarily focused on the benefits of whole-genome sequencing (WGS) and metagenomics, but gaps in implementation remain unaddressed.

New Insights Added:

- *Bioinformatics limitations* Many LMICs lack the computational resources necessary to analyze large genomic datasets effectively. This gap has led to a reliance on high-income country databases, which may not reflect local AMR trends.
- *Regulatory and governance barriers* Genomic surveillance requires harmonized policies, yet inconsistencies in data-sharing regulations among public health, veterinary, and environmental sectors hinder collaborative mitigation strategies.

- *Interpretation challenges* Unlike phenotypic testing, genomic sequencing detects resistance genes that may not always translate into clinical resistance, leading to discrepancies in reporting and intervention strategies.

To advance the field, future research must integrate AI-driven analytics to streamline interpretation, prioritize context-specific genomic surveillance, and develop regulatory frameworks to support cross-sectoral collaboration.

14.1 Providing novel insights into genomic applications

Existing Understanding: Current reviews highlight genomic tools such as CRISPR-based diagnostics and metagenomics but often overlook their integration with other cutting-edge technologies.

New Synthesis:

- *Machine learning in AMR prediction models:* The convergence of AI and genomics has the potential to improve AMR prediction accuracy. For example, AI models trained on genomic datasets can predict resistance trends, allowing proactive interventions before outbreaks occur.
- *Personalized antimicrobial therapy:* Genomic sequencing enables targeted antimicrobial prescribing, reducing the reliance on broad-spectrum antibiotics and slowing resistance development. However, challenges such as high costs and ethical concerns surrounding patient genomic data must be addressed.
- *Microbiome-based interventions:* Instead of focusing solely on resistant pathogens, research should expand to microbiome restoration techniques, such as fecal microbiota transplantation, to mitigate AMR spread.

14.2 Expanding future directions and policy implications

Existing Approach: Discussions around future genomic applications often focus on technological advancements without addressing policy and governance challenges.

New Directions

- *Global Policy Standardization:* The absence of uniform genomic surveillance policies creates fragmented data that limits global AMR tracking. A One Health approach should advocate for an international regulatory framework governing genomic data-sharing.
- *Equitable Access to Genomic Technologies:* While high-income countries lead genomic research, LMICs struggle with accessibility. Expanding public–private partnerships and increasing investment in local sequencing infrastructure can bridge this gap.
- *Ethical Considerations in Genomic Data Use:* As genomic technologies become integral to AMR mitigation, ethical challenges related to data ownership, privacy, and equitable benefit-sharing must be addressed. Policymakers should establish clear guidelines on data governance to ensure responsible use.

15 Conclusion

The intersection of genomics, antimicrobial resistance (AMR), and public health within the One Health framework offers a transformative approach to addressing some of the most pressing global health challenges. The integration of genomics into One Health enhances our understanding of the genetic mechanisms driving AMR and strengthens our ability to conduct real-time surveillance, outbreak response, and predictive modeling to prevent the spread of resistant pathogens across human, animal, and environmental health sectors. This review set out to achieve three primary objectives:

To analyze the application of genomic tools in understanding AMR mechanisms and improving pathogen surveillance – Throughout this review, we have demonstrated how technologies such as whole-genome sequencing (WGS), metagenomics, and CRISPR-based diagnostics have revolutionized the detection and tracking of resistant pathogens. These advancements enable researchers and public health authorities to pinpoint the origins of resistance genes, monitor their transmission across One Health compartments, and design more targeted interventions.

To identify the challenges hindering the integration of genomics into AMR management, particularly in low- and middle-income countries (LMICs) – The discussion has highlighted several key barriers, including the technical complexities of data sharing, the lack of bioinformatics expertise, economic constraints limiting access to genomic

technologies, and fragmented governance structures that hinder cross-sectoral collaboration. These factors present significant obstacles to the seamless adoption of genomics in AMR mitigation, particularly in resource-limited settings.

To examine emerging innovations, such as machine learning, big data analytics, and microbiome-based interventions, in advancing AMR control – We have explored how integrating artificial intelligence and big data with genomic surveillance is enhancing the prediction of resistance trends and optimizing antimicrobial stewardship. Additionally, the rise of personalized medicine and microbiome-based therapies presents new opportunities to reduce dependence on broad-spectrum antibiotics and mitigate resistance evolution.

One of the most promising developments in AMR mitigation is the *integration of big data and machine learning (ML) with genomic tools*, which has the potential to transform how we predict, monitor, and respond to AMR threats in both high-income countries (HICs) and LMICs.

In HICs, where large-scale genomic sequencing programs and electronic health record (EHR) systems are well established, integrating ML with genomic data can significantly enhance AMR surveillance and intervention strategies. The key benefits include: *Early Detection of Emerging Resistance Trends* – ML algorithms can rapidly analyze vast amounts of sequencing data from hospitals, wastewater, and livestock to detect subtle patterns indicative of new resistance mechanisms before they become widespread. *Optimized Antibiotic Stewardship Programs* – By leveraging real-time genomic and epidemiological data, ML-driven decision-support systems can recommend the most effective antimicrobial treatments, reducing unnecessary antibiotic use. *Personalized AMR Risk Prediction* – Advanced predictive models can assess a patient's risk of developing a resistant infection based on genomic, microbiome, and medical history data, allowing clinicians to tailor treatment strategies accordingly. *Automated Pathogen Surveillance* – AI-powered genomic epidemiology tools can map and track AMR hotspots at a national or regional level, guiding policymakers in deploying targeted public health interventions.

For LMICs, where genomic surveillance infrastructure is still developing, the integration of big data and ML can bridge critical gaps in AMR monitoring and response. The advantages include: *Cost-Effective Resistance Surveillance* – ML algorithms can analyze genomic data even in settings with limited computational resources, enabling LMICs to maximize insights from smaller sequencing datasets without requiring high-end computing infrastructure. *Portable AI-Driven Diagnostic Tools* – Mobile sequencing devices (e.g., Oxford Nanopore MinION) coupled with AI-powered resistance detection algorithms allow real-time AMR diagnostics in remote or resource-limited healthcare settings. *Strengthening Regional AMR Monitoring* – Cloud-based data-sharing platforms can connect LMIC public health agencies with global AMR surveillance networks, ensuring that data from LMICs contributes to and benefits from international research efforts. *Reducing the Burden on Overstretched Healthcare Systems* – Automated data analysis reduces reliance on specialized bioinformatics personnel, addressing a critical workforce gap in many LMICs.

While big data and ML provide unprecedented opportunities for AMR surveillance, addressing disparities in access to these technologies is essential for ensuring that both HICs and LMICs can effectively leverage genomic advancements. Key strategies to achieve this include: *Strengthening International Collaboration* – Partnerships between HICs and LMICs (e.g., WHO's Global Health Security Agenda, Africa CDC's Pathogen Genomics Initiative) should focus on technology transfer and capacity-building. *Developing Affordable AI-Driven AMR Tools* – Public-private collaborations can facilitate the creation of cost-effective, open-source AI-powered surveillance platforms accessible to LMICs. *Improving Data Accessibility and Standardization* – Standardizing genomic and epidemiological data collection across HICs and LMICs will enhance global AMR monitoring efforts and reduce disparities in data quality.

Despite these advancements, significant challenges remain in fully integrating genomics, big data, and ML into the One Health framework. Addressing these challenges requires sustained investment in research, infrastructure, and international collaboration. Looking ahead, efforts must focus on: *Scaling up genomic sequencing and bioinformatics training in LMICs* to build local expertise. *Ensuring sustainable funding mechanisms* to support long-term genomic AMR surveillance programs. *Harmonizing AMR data governance policies* to promote ethical and equitable global data sharing. Developing AI-driven, real-time AMR surveillance systems that can be deployed across human, animal, and environmental health sectors.

By continuing to expand genomic capabilities and fostering interdisciplinary partnerships, genomics—when combined with big data and machine learning—can fulfill its potential as a cornerstone of the global strategy to mitigate AMR. A coordinated One Health approach—supported by scientific innovation, policy alignment, and capacity-building initiatives—will be essential to safeguarding public health and ensuring a sustainable future for humans, animals, and the environment.

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Declarations

Ethics approval and consent to participate The study employed a narrative review methodology that utilized publicly available data and peer-reviewed literature. Since no human participants, animals, or private data were directly involved in this research, ethical approval was not required. However, the study adhered to ethical principles for conducting and reporting research, including transparency, accuracy, and integrity in data analysis and interpretation.

Consent for publication Not applicable.

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