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| RESEARCH ARTICLE

Integrating Environmental Surveillance into One Health Responses to AMR: Challenges, Solutions and Global Perspectives

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| ABSTRACT

Antimicrobial resistance (AMR) poses a critical global health threat exacerbated by the complex interplay between humans, animals, and environmental reservoirs. Despite progress in clinical and agricultural surveillance, environmental AMR monitoring remains underdeveloped and fragmented, undermining comprehensive control efforts. This review synthesizes current knowledge on environmental compartments such as surface waters, wastewater systems, soils, and sediments as pivotal reservoirs and transmission pathways for resistance genes. It highlights the challenges in environmental AMR surveillance, including sampling heterogeneity, lack of standardized protocols, technical and financial constraints, and integration gaps within One Health frameworks. Global case studies from the Middle East, Africa, India and the European Union illustrate varied progress and persistent implementation barriers, especially regarding environmental data integration, laboratory capacity, and multisectoral coordination. The review underscores ethical considerations surrounding data sharing and privacy in the era of high-throughput technologies. Finally, it advocates for strategic investments in environmental surveillance infrastructure, harmonized methodologies, and inclusive governance models to strengthen One Health responses and curb the spread of antimicrobial resistance.

| KEYWORDS

Antimicrobial resistance (AMR); Antibiotics; Infection; Surveillance; One health

| ARTICLE INFORMATION

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Introduction & Background

Antibiotics refer to a diverse group of chemical agents that may be derived from natural sources, modified through semi-synthetic processes, or created entirely through synthetic means. Their primary role is to either suppress bacterial growth (*bacteriostatic*) or eliminate bacteria altogether (*bactericidal*) [1, 2]. These compounds are further classified based on their mode of action and range of activity some are effective only against specific types of bacteria (*narrow-spectrum*), while others target a broader array of pathogens (*broad-spectrum*) [1, 2]. These include β-lactams, tetracyclines, aminoglycosides, lincosamides, macrolides, pleuromutilins, and sulfonamides, all of which are increasingly scrutinized for their role in driving antimicrobial resistance (AMR) and the need for tighter regulatory oversight.

AMR arises when microorganisms including bacteria, viruses, fungi, and parasites adapt over time in ways that reduce or eliminate the effectiveness of drugs designed to eliminate them [3]. This growing threat is primarily driven by the widespread and often improper use of antimicrobials across multiple sectors. Contributing factors include excessive prescribing in human medicine, unregulated application in livestock and crop production, inadequate oversight in veterinary care, disruptions caused by war crisis, and misuse within the broader food industry [4]. These pressures accelerate the emergence and spread of resistant

strains, making common infections harder to treat. Resistance genes, often carried on mobile genetic elements, can spread across species and environments [5]. This not only undermines treatment effectiveness but also allows resistant bacteria to thrive across ecosystems [5]. Their movement driven by poor infection control, sanitation gaps, environmental contamination, and global travel poses a major threat to public health and health system resilience.

AMR is widely acknowledged as a complex challenge situated at the intersection of human, animal, and environmental health, underscoring its inherently One Health nature [6]. The One Health approach, a collaborative and interdisciplinary framework, recognizes the interdependence of these domains (Figure 1). Its origins trace back to the 19th century when Rudolf Virchow first articulated the link between human and animal health through the concept of zoonosis [7, 8], a notion further expanded by Calvin Schwabe's "One Medicine," which emphasized the shared aspects of human and veterinary medicine [9]. The modern One Health paradigm gained significant momentum with the 2004 Manhattan Principles, which called for coordinated global action to address health threats spanning humans, animals, and ecosystems [8, 10].

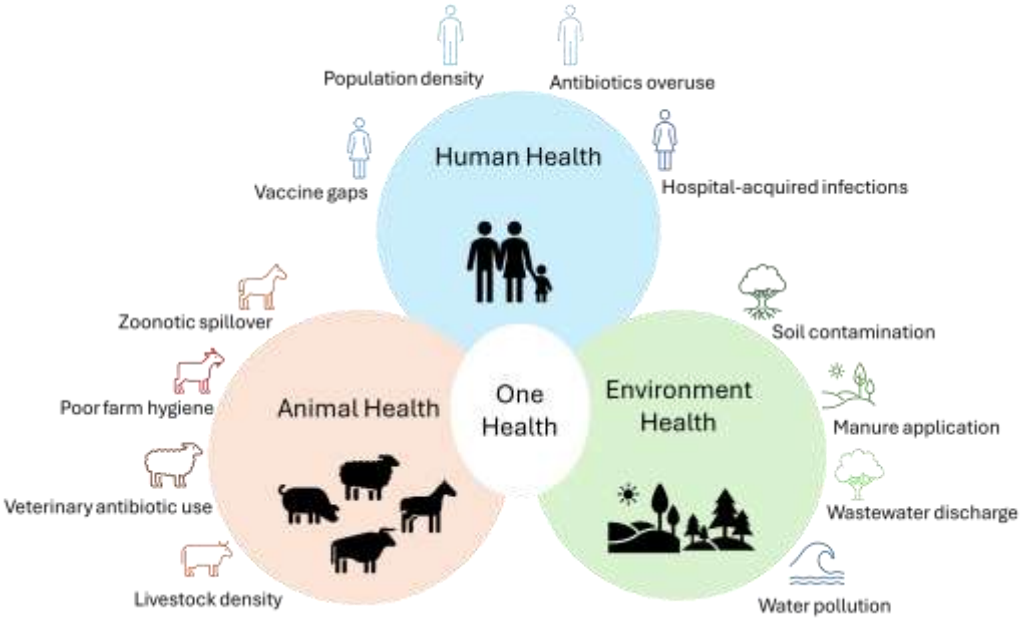

Figure 1: One Health Framework for Antimicrobial Resistance.

Interconnected drivers of AMR across humans, animals, and the environment. Created in https://BioRender.com.

In recent years, there has been a growing consensus among international organizations that combating AMR demands a coordinated, multisectoral response rooted in the One Health philosophy (Figure 2). This shift has catalyzed global initiatives focused on enhancing surveillance, promoting stewardship, and fostering collaboration across human, animal, and environmental sectors. Notably, the Global Action Plan on AMR jointly developed by the World Health Organization (WHO), the Food and Agriculture Organization (FAO), and the World Organisation for Animal Health (WOAH) calls for integrated surveillance systems and cross-sectoral data sharing to inform effective national strategies and curtail antimicrobial misuse across all domains [8].

To support these objectives, the WHO established the Global Antimicrobial Resistance Surveillance System (GLASS) in 2015 [11]. GLASS aims to standardize the collection, analysis, and reporting of AMR data at national and international levels. It focuses primarily on resistance in human pathogens but also encourages countries to expand their surveillance efforts into veterinary, agricultural, and environmental settings as capacity allows. Similarly, the FAO and WOAH have promoted antimicrobial use (AMU) and resistance monitoring in food-producing animals, contributing to a more comprehensive understanding of resistance patterns across the food chain. While these initiatives represent significant progress, they have largely centered on clinical and agricultural sectors, leaving a major blind spot in the global surveillance landscape: the environment. Despite growing evidence that rivers, wastewater, soil, and other environmental compartments are key reservoirs and transmission routes for resistant organisms and genes, environmental AMR surveillance remains severely underdeveloped [12, 13]. This underrepresentation limits the ability of countries to detect emerging resistance threats in non-clinical settings and undermines the effectiveness of national

AMR control strategies [13]. Without deliberate efforts to strengthen environmental monitoring and integrate it fully into One Health surveillance frameworks, the global response to AMR will remain incomplete.

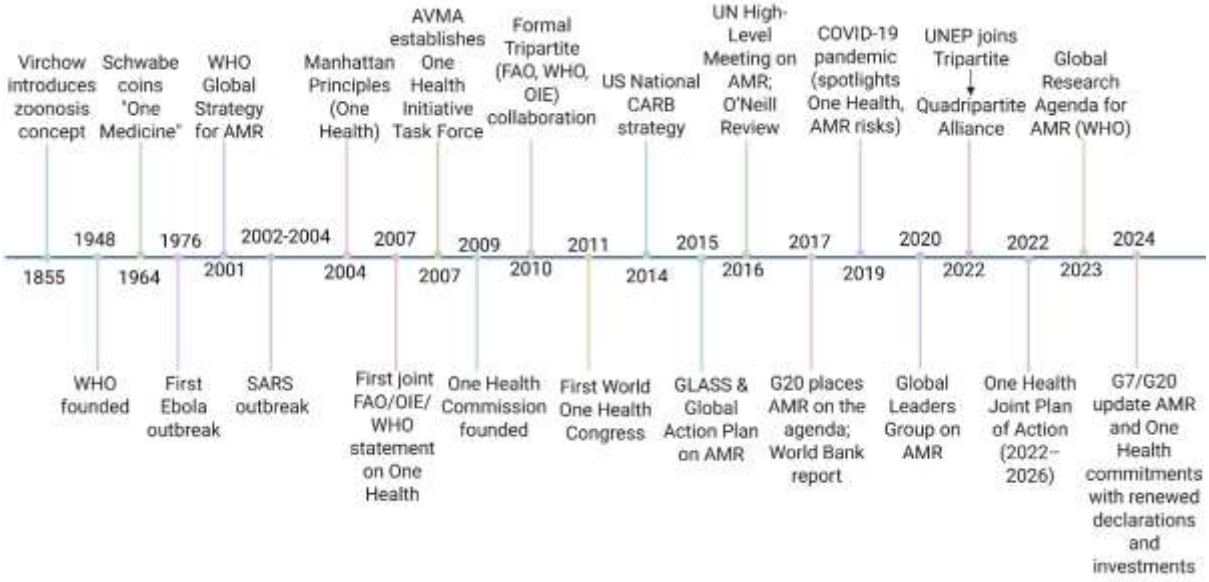

Figure 2: Key Milestones in the Evolution of One Health and Global Antimicrobial Resistance (AMR) Initiatives (1855–2024).

This timeline summarizes key milestones from 1855 to 2024 that shaped the One Health concept and the global response to AMR, highlighting major scientific discoveries, outbreaks, organizational foundations, and international collaborations that advanced multisectoral action across human, animal, and environmental health. Created in https://BioRender.com.

Environmental reservoirs such as rivers, wastewater systems, soils, and sediments act as major conduits and breeding grounds for AMR dissemination. Antibiotic residues, heavy metals, and resistant bacteria are often discharged into the environment through hospital effluents, agricultural runoff, and industrial waste, creating ecological niches where resistance can thrive and evolve [14]. From these reservoirs, AMR can be transmitted back to human and animal populations via contaminated water, food chains, and direct contact. Environmental surveillance refers to the systematic monitoring of antimicrobial residues, resistant microorganisms, and resistance genes in environmental matrices such as water (e.g., rivers, wastewater, groundwater), soil, sediments, and even air [14]. This form of surveillance serves multiple critical functions: it can detect emerging resistance threats before they appear in clinical or veterinary settings, reveal hotspots of contamination such as near pharmaceutical manufacturing sites or intensive farming operations, and provide insights into how AMR moves across ecological boundaries [15]. Despite increasing recognition that the environment plays a central role in the development and spread of AMR, environmental surveillance remains the most underdeveloped component of the global AMR response [16].

This review explores the untapped potential of environmental surveillance as a core component of the One Health response to AMR. It examines the role of environmental compartments in resistance transmission, reviews current surveillance challenges, highlights global case studies, and outlines key policy and implementation gaps.

Review

Environmental compartments as AMR reservoirs

Surface water and wastewater

Aquatic environments including surface waters, rivers, wastewater systems, and groundwater are now recognized as critical environmental reservoirs and transmission pathways for AMR. These ecosystems receive continuous inputs of antibiotics, antibiotic resistance genes (ARGs), and resistant bacteria through treated and untreated sewage, hospital effluent, industrial discharge, and agricultural runoff (Figure 3). A global metagenomic meta-analysis by Alhazmi et al. (2024) of untreated wastewater samples across five countries identified 2,483 ARGs, with

multidrug-resistant (MDR) genes being the most prevalent, comprising over 44% of detected ARGs in Europe [17]. The study revealed regional variations in ARG profiles, with distinct resistance patterns in Russia, China, the UK, Canada, and the USA. These findings underscore the growing global burden of ARGs. Complementing these findings, Zainab et al. (2020) highlighted that groundwater, which supplies drinking water to billions globally, is also increasingly contaminated with antibiotics and ARGs. Sources include leaky sewer systems, septic tanks, aquaculture runoff, and landfill leachate, all of which contribute to ARG dissemination [18].

A recent study in 18 drinking water source sites along the Wuhan section of the Yangtze River in China revealed the widespread presence of antibiotics and ARGs in drinking water source sites [19, 20]. Among 14 detected antibiotics, tetracycline showed the highest concentration, reaching up to 1,708 ng/L. The study also identified ten ARGs, with sul1 and sul2 being the most abundant, alongside macrolide (ermB) and fluoroquinolone (qnrS) resistance genes [19]. Importantly, the integron intI1, which facilitates horizontal gene transfer, showed strong correlations with multiple ARGs, suggesting its central role in ARG proliferation.
In a study of the Ter River in Spain, significant levels of antibiotics such as ciprofloxacin, clarithromycin, and sulfamethoxazole in both hospital effluents and downstream river sites were identified not only in raw wastewater but also in treated effluents and river water [21]. Despite partial removal during wastewater treatment, these compounds persisted and were even enriched downstream, illustrating the limited capacity of conventional wastewater treatment plants (WWTPs) to eliminate AMR determinants [21, 22].

La Rosa et al. (2025) emphasized that WWTPs not only serve as reservoirs of ARGs and antibiotic-resistant bacteria (ARB) but also as active hotspots for their amplification and evolution [23]. The close microbial contact, optimal nutrient levels, and favorable environmental conditions (e.g., temperature and pH) within WWTPs promote horizontal gene transfer (HGT), driven by mobile genetic elements (MGEs) such as plasmids, integrons, and transposons. This makes WWTPs ideal settings for the proliferation of multidrug resistance. Notably, ARGs were found to persist throughout various stages of treatment, and even advanced methods like membrane bioreactors (MBRs) did not consistently eliminate resistance genes. In some cases, ARGs remained transcriptionally active in effluents, posing risks to downstream environments [23].

Real-world cases have demonstrated striking genetic similarities between ARB found in treated hospital wastewater and those isolated from clinical patients, raising strong concerns about possible environmental-to-human transmission routes [23]. For instance, in one notable case [24], carbapenem-resistant *Acinetobacter baumannii* strains were isolated from treated hospital effluent and later detected in a patient admitted to the same facility three months afterward. Whole-genome sequencing revealed that the bacterial isolates from the environment and the patient were nearly clonal, differing by only four to nine single nucleotide polymorphisms (SNPs), and all carried the same resistance genes: *blaNDM-1* and *blaOXA-23* both of which encode enzymes that degrade last-resort carbapenem antibiotics. This genetic resemblance indicates a probable transmission link between the hospital wastewater system and the clinical setting. Another example involves the detection of extended-spectrum β-lactamase (ESBL)-producing *E. coli* and *Klebsiella pneumoniae* in municipal and hospital wastewater, which exhibited identical ARG profiles and plasmid types to those commonly found in local hospital patients.

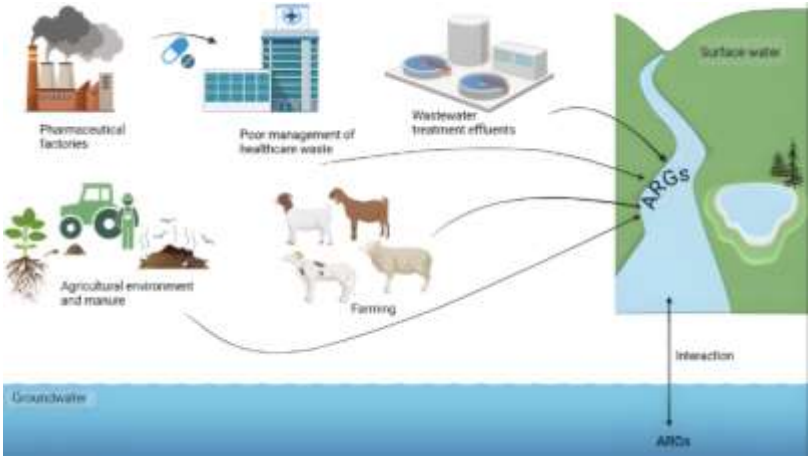

Figure 3: Environmental reservoirs and AMR gene transmission pathways.

This figure illustrates key environmental compartments contributing to the dissemination of antimicrobial resistance genes (ARGs). Sources include pharmaceutical factories, poor management of healthcare waste, wastewater treatment effluents, agricultural environments, and animal farming. These contribute to the release of ARGs into surface water, with potential interaction and seepage into groundwater. Created in https://BioRender.com.

Soil and agricultural runoff

Soil, particularly in agricultural settings, serves as a critical and complex reservoir for AMR. The intensification of agriculture and the widespread use of antibiotics in animal husbandry have significantly contributed to the accumulation of ARB and ARGs in soil environments. Slaughterhouse effluents are heavily contaminated with organic matter such as blood, animal waste, and residual veterinary antibiotics, making them critical zones for the emergence and spread of antimicrobial resistance [25]. One of the main pathways through which resistance spreads is the application of animal manure often rich in unmetabolized antibiotics and resistant microbes to fields as fertilizer. This practice introduces both ARB and ARGs directly into the soil ecosystem, creating a selective environment that promotes the persistence and propagation of resistance traits [26].
Moreover, animal farming practices often involve administering sub-therapeutic doses of antibiotics for growth promotion or prophylaxis, contributing to the development of multidrug-resistant organisms in manure. These resistant strains and their associated genes can then be horizontally transferred to indigenous soil microbes, further enriching the soil resistome [27].

Repeated fertilization of agricultural soils with poultry or livestock manure, as well as irrigation with inadequately treated wastewater from livestock processing facilities, further intensifies this issue. These inputs deliver not only resistant bacteria and mobile genetic elements but also residual antibiotic compounds, particularly tetracyclines and sulfonamides, which apply selective pressure on soil microbial communities. The result is a marked increase in the abundance and diversity of resistance genes such as tetW, tetO, sul1, and sul2, often several times higher than in untreated soils [28]. Once present, these genes can persist independently of antibiotic selection and be horizontally transferred between environmental and potentially pathogenic bacteria. In addition, agricultural runoff carrying these contaminants contributes to the spread of ARGs into surrounding soil and water systems, sustaining environmental reservoirs of AMR and expanding their ecological footprint [25].

The depletion of soil fertility caused by continuous monoculture and intensive tillage places sustained stress on soil microbial communities. This pressure favors bacterial populations that are better adapted to survive under nutrient-poor conditions. As a result, mutations can occur in key regulatory genes such as *rpoS* and *rpoB*, which enhance bacterial survival in these harsh environments. These same mutations can also lead to resistance against antibiotics like rifampicin and nalidixic acid [29]. Pesticide use further exacerbates the issue. Many pesticides inadvertently affect non-target microbial populations, reducing microbial diversity and selecting for resistant strains. Some pesticide degradation enzymes, such as glutathione S-transferases and hydrolases, are linked to antibiotic degradation or resistance. Furthermore, co-resistance mechanisms allow resistance genes to pesticides and antibiotics to reside on the same plasmids, accelerating HGT and expanding the environmental AMR reservoir [29].

Surveillance challenges and solutions

Despite advancements in detection technologies, environmental AMR surveillance remains the least developed component of the global One Health response. It faces a constellation of challenges that span technical, economic, and policy domains, particularly in low- and middle-income countries (LMICs) (Figure 4).

Environmental and Sampling Heterogeneity

Environmental samples vary widely across locations and time, introducing significant variability in AMR detection. Water bodies, soil types, and sewage systems differ in microbial composition, pH, and pollutant levels, all of which influence the presence and detectability of resistance genes. Seasonal fluctuations, rainfall, and proximity to pollution sources like hospitals or farms further complicate surveillance efforts. In addition, methodological inconsistencies such as differences in sample collection, storage, filtration, and DNA extraction can substantially alter the outcome of surveillance studies. Studies from Havana's Almendares River clearly show that ARG levels vary significantly by both season and sampling site. In dry-season water samples, ARG abundance was significantly higher at stations near sewage outfalls, while wet-season patterns diverged completely, especially between water column and sediment matrices.

These findings demonstrate that relying on a single season or environmental compartment can severely bias AMR surveillance efforts [30].

In their 2018 study, Guo et al. performed a comprehensive four-season assessment of six key ARGs, sul1 and sul2 (conferring sulfonamide resistance), tetA and tetW (tetracycline resistance), aac(6')-Ib (aminoglycoside resistance), and qnrS (fluoroquinolone resistance) in surface sediments collected from eight strategically selected sites along the Yangtze Estuary [31]. For each sample, quantitative PCR (qPCR) was used to determine gene copy numbers per gram of dry sediment. Simultaneously, the researchers measured physicochemical parameters (temperature, pH, total organic carbon, total nitrogen, and clay content), quantified residual concentrations of relevant antibiotics, and analyzed bioavailable fractions of heavy metals (Ni, Zn, As, Cd) via acid-exchangeable extraction. The data revealed clear seasonal patterns: ARG abundances peaked in summer in July and declined in winter. This seasonal fluctuation suggests that warmer temperatures and increased hydrological inputs during summer months enhance microbial activity and facilitate ARG dissemination. Spatially, the highest ARG concentrations were detected at Shidongkou, immediately downstream of a major wastewater treatment plant, and at Wusongkou, located at a junction with an urban river; ARG levels in these hotspots were three- to five-times greater than at reference sites, implicating anthropogenic effluent discharges as primary sources of resistance genes [31].

To address these challenges, AMR surveillance programs should standardize protocols for sample collection and analysis, and adopt longitudinal, multi-site sampling designs that account for seasonal and spatial variability. Implementing harmonized methodologies and regularly sampling across diverse compartments (e.g., water, sediment, soil) and time points can greatly improve the reliability and comparability of environmental AMR data, enabling more accurate detection of trends and sources of resistance [32].

Absence of Standardized Protocols

A major barrier to global comparability of AMR data is the lack of standardized methodologies across countries and laboratories. While clinical surveillance benefits from well-established protocols, environmental AMR monitoring still suffers from inconsistent guidelines regarding sampling frequency, choice of environmental matrices, molecular targets, and data reporting formats. For instance, the WHO Tricycle Protocol, designed to foster integrated surveillance spanning human, animal, and environmental sectors, remains underutilized in many countries, often due to limited resources and fragmented institutional frameworks [33].

Building on this, recent literature underscores that these inconsistencies extend to the technical level, where variations in DNA extraction methods, primer design, and bioinformatics pipelines contribute to discrepancies in reported resistance gene prevalence. Such methodological heterogeneity complicates inter-study comparisons and hinders meta-analyses needed for global risk assessment. Moreover, lack of consensus on thresholds for clinically relevant resistance gene abundance limits actionable interpretation of environmental AMR data. To overcome these challenges, international collaborations have called for harmonized protocols and capacity-building initiatives that promote standardized laboratory and analytical procedures, thereby enhancing data quality and cross-border comparability [34]. A recent study [35] concluded that DNA extraction methods significantly impact the analysis of microbiomes and resistomes in activated sludge, which is an important component of WWTPs. The PowerSoil kit yielded higher DNA concentrations, while bead-beating disrupted DNA more effectively than vortexing. Although the extraction method had minimal effect on the total number of detected ARGs, bead-beating resulted in greater ARG diversity. These findings highlight the need for standardized DNA extraction protocols to improve the consistency and comparability of microbiome and resistome analyses in environmental studies, particularly in wastewater treatment monitoring.

To improve global comparability and interpretability of environmental AMR data, policymakers and research networks should prioritize the adoption of harmonized sampling, DNA extraction, and reporting protocols ideally guided by international frameworks like the WHO Tricycle Protocol alongside targeted capacity-building initiatives that ensure these standards are practically implementable across diverse country settings [36, 37].

Financial, Technical and Knowledge Gaps

Advanced surveillance techniques such as metagenomics, qPCR, and high-throughput sequencing demand well-equipped laboratories, consistent electricity and internet access, cold-chain management, and skilled personnel. In many low- and middle-income countries (LMICs), these requirements are often only met in select academic or urban institutions. As a result, national surveillance programs frequently rely on basic phenotypic assays, which lack the sensitivity to detect the full diversity of resistance genes [38]. Moreover, ongoing costs such as equipment maintenance, data storage, and analytical software make long-term implementation of comprehensive environmental AMR

monitoring programs financially unsustainable [38]. Major obstacles identified in these countries include inadequate laboratory infrastructure, inconsistent standard operating procedures, lack of qualified personnel, and challenges with equipment maintenance and reagent supply [39]. Chronic understaffing, limited training of clinical microbiologists, and weak leadership further erode data management and quality oversight [15]. Additionally, issues related to external quality assurance, sample shipping delays, and poor data management systems are critical areas for improvement [39]. The absence of harmonized specimen-handling protocols, under-participation in external quality assessments, and inconsistent adoption of international AST guidelines (e.g., CLSI, EUCAST) produce variable susceptibility data [15]. Meanwhile, harsh environmental conditions and fragmented supply chains impede the timely delivery and cold-chain integrity of diagnostics and reagents, while low-quality substitutes jeopardize result reliability [15]. Although initiatives such as the Fleming Fund and GLASS have provided essential seed funding to enhance surveillance capacity, these gains are inherently transient and cannot be maintained without ongoing domestic funding allocations and strong governmental policy support.

Environmental AMR research often struggles to secure financial resources, as it must compete with other urgent environmental issues such as climate change [40]. Historically, the majority of AMR research funding has been allocated to clinical settings, particularly hospitals, due to the direct impact on human health. As a result, the environmental dimensions of AMR have been comparatively neglected, and basic information on prevalence, transmission pathways, and risk factors remains limited. In recent years, however, there has been a noticeable increase in research attention directed toward environmental AMR [40]. This shift appears to be driven by a growing awareness of the serious health and economic burdens associated with drug-resistant infections worldwide. In countries with publicly funded healthcare systems, the escalating costs of treating resistant infections have highlighted the need for broader surveillance and prevention strategies that include environmental sources. Despite these encouraging developments, large research and knowledge gaps persist [40]. The limited availability of environmental data not only constrains scientific understanding but also hinders the creation and implementation of evidence-based policies. Without a robust body of research, policy development in the environmental sector lags behind efforts in human and animal health, where evidence is more abundant. Ultimately, these research shortcomings perpetuate a cycle where the lack of evidence leads to weak policy, and weak policy further limits investment in research and surveillance for environmental AMR [40].

To address these persistent barriers, governments and funding agencies should prioritize sustained investment in environmental AMR research and surveillance infrastructure, including dedicated funding streams for laboratory upgrades, equipment maintenance, workforce development, and the adoption of harmonized protocols [40].

Ethical and Data-Sharing Constraints

Integrating technological solutions in AMR management introduces significant ethical and security considerations, especially relating to patient privacy, informed consent, and data ownership. Utilizing patient data in research contexts has sparked considerable debate, notably in LMICs, where established consent procedures might be insufficient or inconsistently applied [41, 42]. As a result, developing clear and comprehensive ethical frameworks to guide technology usage in AMR prevention and control is becoming increasingly important and necessitates further focused research [41]. In response to these issues, experts advocate for increased funding and strengthened policies to enhance cybersecurity infrastructure and better protect healthcare data against potential threats [41]. Furthermore, applying a One Health perspective fostering cooperation among diverse sectors and stakeholders has been recommended to improve the overall security and management of antimicrobial resistance (AMR) [41].

A critical ethical concern also involves the potential overreliance on technology-driven solutions, possibly leading to neglect of essential traditional epidemiological practices. For instance, while advanced techniques like whole-genome sequencing effectively detect resistant pathogens, these methods must supplement rather than substitute traditional practices such as contact tracing and outbreak investigations [41]. Hence, it is vital that technological tools are responsibly integrated alongside behavioral interventions and antimicrobial stewardship efforts to provide a balanced and holistic approach to managing AMR. Moreover, the collection and handling of extensive datasets such as patient medical histories, laboratory results, and antibiotic prescribing information present significant ethical challenges regarding patient privacy and informed consent [43]. Concerns persist about potential privacy breaches and misuse of sensitive information, particularly when individuals are unaware or inadequately informed about how their data will be utilized in AMR surveillance initiatives [41]. These risks underscore the critical importance of implementing rigorous safeguards to protect patient confidentiality and prevent detrimental impacts on patient welfare.

Addressing the balance between technological advancement and ethical and cybersecurity challenges represents another notable research gap. Robust governance structures and clearly defined policy frameworks are essential for ensuring that technology is employed responsibly, equitably, and securely. Policies need to clearly outline procedures for safeguarding sensitive data while simultaneously enabling necessary data sharing for research and public health interventions. Governance frameworks must also ensure protection against potential exploitation of vulnerable populations during the development and testing of new antimicrobial agents. Additionally, there is a notable research gap in the governance and policy dimensions concerning data handling in AMR contexts. Defining and implementing best practices for secure data sharing and integration, protecting patient privacy, and effectively utilizing emerging technologies such as blockchain and distributed ledger systems for secure data management are crucial areas requiring further exploration [44].

To address these challenges, national authorities and research networks should prioritize the development and enforcement of robust ethical frameworks and data governance policies tailored to AMR surveillance. This includes standardizing consent procedures, enhancing transparency in data use, investing in secure digital infrastructure, and ensuring regular training in data protection for all personnel involved [41, 42].

Poor Integration into One Health Systems

Environmental AMR surveillance is often siloed from clinical and veterinary data, resulting in fragmented monitoring systems [45]. Environmental data such as from rivers, wastewater, and agricultural runoff rarely feed into the same databases or reporting streams used for human or animal AMR monitoring. This disconnect impairs early warning capabilities and weakens national response strategies. A recent scoping review of integrated surveillance systems further highlights that true implementation of One Health remains limited in practice. It found that most surveillance systems operate in isolation within individual sectors, with few achieving genuine data sharing or operational coordination across human, animal, and environmental components. Barriers include conceptual misalignment between sectors, lack of interoperable data infrastructure, limited stakeholder engagement, and weak governance mechanisms. Without addressing these structural limitations particularly in LMIC settings surveillance lacks representativeness and sustainability, undermining its utility in informing national AMR strategies [46].

To improve integration, countries should establish national One Health coordination platforms that bring together stakeholders from human, animal, and environmental sectors, develop interoperable data systems that enable real-time sharing and joint analysis, and invest in joint training, governance, and regular cross-sectoral meetings to ensure effective, sustained collaboration in AMR surveillance [47, 48].

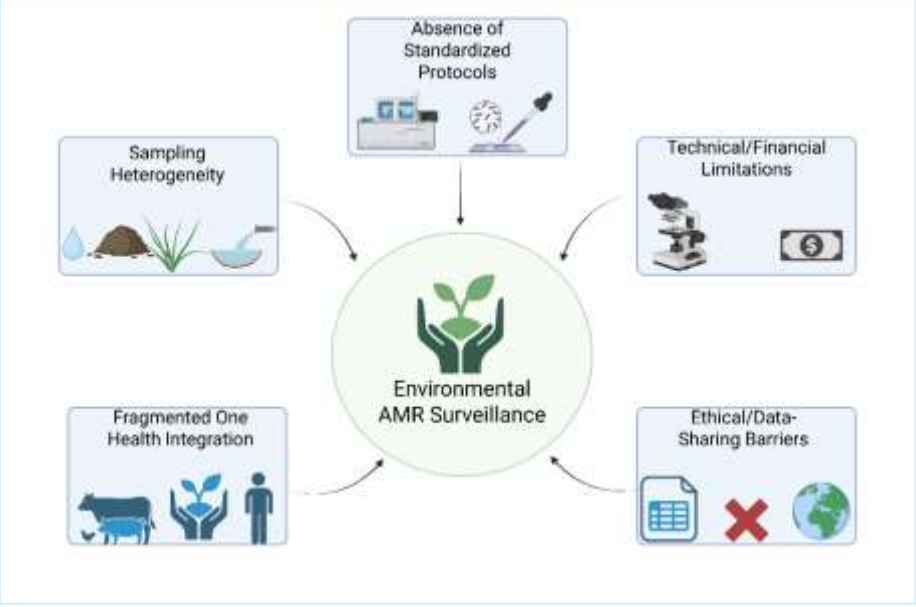

Figure 4: Major Challenges in Environmental AMR Surveillance: A One Health Perspective.

This schematic shows the main barriers to environmental AMR surveillance, including sampling variability, lack of standard protocols, technical and financial constraints, limited One Health coordination, and ethical/data-sharing issues all of which hinder effective global monitoring. Created in https://BioRender.com.

Global responses to environmental AMR: progress and implementation gaps

Middle East response

The Middle East region has made some important strides in establishing surveillance systems and antimicrobial stewardship (AMS) frameworks, yet these efforts remain uneven across countries. For instance, the United Arab Emirates (UAE) stands out as one of the first countries in the Gulf region to adopt a structured national AMR surveillance program. This program was developed in alignment with the WHO GLASS and has been operational since 2015, building on earlier efforts initiated in Abu Dhabi. A comprehensive national protocol was introduced, which standardized surveillance across all seven Emirates, integrating 317 reporting sites and 45 microbiology laboratories. Between 2010 and 2021 alone, the UAE reported over 1.2 million isolates, allowing for the first time the development of national treatment guidelines based on local resistance trends. Moreover, annual national AMR reports are now produced, informing both public health strategies and clinical practice, a milestone in evidence-based policy within the Gulf region [49].

Beyond the UAE, other Gulf states like Saudi Arabia and Qatar have also taken steps to improve surveillance through hospital-based monitoring and infection control measures. Qatar launched its first NAP in 2018 and recently introduced its second phase for 2024–2030, which reinforces its commitment to the One Health approach. Key achievements include establishing a National AMR Committee, conducting its first Point Prevalence Survey (PPS) on antimicrobial use in hospitals, and setting up a multisectoral governance structure. The country has prioritized integrated AMR surveillance systems across human, animal, food, and environmental sectors while promoting antimicrobial stewardship and infection prevention programs. Additionally, research initiatives involving institutions such as Hamad Medical Corporation and Qatar University have grown significantly [50].

Saudi Arabia's 2022–2025 AMR Action Plan reflects a strengthened governance framework led by the Public Health Authority (Weqaya) and a National AMR Committee. The plan includes antimicrobial stewardship programs, improved infection prevention and control, and measures to monitor antimicrobial consumption across sectors. Saudi Arabia has also emphasized collaboration between health, agriculture, and environmental sectors to ensure a coordinated response [51]. However, the systems in Gulf countries primarily hospital-centric and lack strong environmental integration. The GCC developed a strategic plan in 2014, endorsed by all member states, to address AMR through harmonized policies, multisectoral coordination, and alignment with WHO recommendations. This plan underpins national strategies in Saudi Arabia, Qatar, the UAE, and other Gulf states, ensuring that AMR remains a top regional health priority [52].

Jordan, on the other hand, faces an added layer of complexity due to severe environmental stressors, particularly acute water scarcity and pollution from untreated wastewater, which heighten the risk of AMR gene dissemination. While environmental regulations exist, implementation remains inconsistent, and agricultural practices such as overuse of pesticides and untreated irrigation water exacerbate bacterial resistance pressures [53].

At the broader regional level, Egypt, Iraq, Jordan, and Lebanon have adopted the WHO Global Action Plan framework and joined GLASS. AMS initiatives have been implemented to varying degrees, but these efforts are fragmented. Hospitals in these countries report widespread use of carbapenems and β-lactam/β-lactamase inhibitor combinations as empirical therapy for multidrug-resistant (MDR) infections, especially those caused by Klebsiella pneumoniae, Acinetobacter baumannii, and Pseudomonas aeruginosa. In addition, the region has seen an alarming rise in resistance to critical antibiotic classes such as carbapenems and fluoroquinolones, particularly during the COVID-19 pandemic. The pandemic triggered a surge in unsubstantiated antibiotic prescriptions, supply shortages, and reduced focus on AMR surveillance, leading to a noticeable increase in MDR infections in ICUs [54].

Despite progress, substantial gaps hinder the Middle East from achieving robust AMR control (Table 1). Surveillance remains fragmented, with limited integration of environmental monitoring; a critical omission in water-stressed countries such as Jordan, where untreated wastewater and agricultural runoff are widely reused for irrigation, creating hotspots for resistance dissemination [53]. Laboratory infrastructure and diagnostic capacity are another bottleneck, as most hospitals lack access to molecular testing and advanced susceptibility methods, forcing reliance on empirical therapy without genotypic confirmation [54]. AMS programs, while present in some hospitals, are inconsistently

implemented and lack standardized national enforcement, resulting in wide variations in prescribing practices across facilities [54]. The COVID-19 pandemic further amplified these challenges, triggering an unprecedented surge in unsubstantiated antibiotic use and disrupting surveillance priorities, which fueled multidrug resistance, particularly among gram-negative pathogens in intensive care units [54]. These gaps, compounded by socioeconomic and environmental stressors (including severe water scarcity and outdated wastewater infrastructure in Jordan) underscore the urgent need for integrated One Health strategies that encompass environmental, clinical, and agricultural sectors [53].

Table 1: AMR Surveillance Systems in the Middle East Region

Country	Surveillance Status	Key Achievements	Implementation Gaps	Key Challenges	References
UAE	Operational since 2015	317 sites, national guidelines, annual reports	Limited environmental monitoring	Lack of environmental AMR data	[49]
Qatar	NAP since 2018, updated 2024	Multisectoral governance, PPS, research growth	Hospital-centric, limited environmental data	Data sharing across sectors	[50]
Saudi Arabia	NAP 2022–2025	Weqaya-led governance, AMS, IPC improvements	Hospital-focused, environmental gaps	Inconsistent lab infrastructure	[51]
Jordan	WHO GLASS participant	Environmental awareness, water scarcity focus	Poor enforcement, inconsistent implementation	Wastewater reuse & pollution	[53]
Egypt, Iraq, Lebanon	WHO GLASS participants	AMS and hospital surveillance efforts	Fragmented, hospital-centric	Limited diagnostic capacity	[54]

Urban wastewater monitoring in Africa

Urban wastewater in Africa has emerged as both a critical surveillance opportunity and a hotspot for the evolution and dissemination of AMR. Major cities such as Nairobi and Lagos, characterized by rapid population growth, limited sanitation coverage, and inadequate infrastructure, underscore the urgency of environmental monitoring within a One Health framework [55, 56].

Recent initiatives have begun to explore wastewater as a practical tool for AMR surveillance. The Global Sewage Surveillance Project demonstrated the power of metagenomic approaches to capture the breadth of resistance genes in untreated sewage across 60 countries, including multiple African cities. Results from this effort revealed that samples from Africa harbored some of the highest AMR gene abundances globally, with notable enrichment of genes conferring resistance to β-lactams, tetracyclines, sulfonamides, and aminoglycosides. Importantly, clinically significant resistance determinants such as blaNDM, blaCTX-M, and mcr were detected, confirming the feasibility of sewage-based monitoring as an ethically acceptable, cost-effective approach to population-level AMR surveillance [57].

In East Africa, targeted studies have corroborated these findings, highlighting the environmental dimensions of AMR. For instance, investigations in Nairobi documented substantial antimicrobial pollution in municipal and hospital effluents. These streams frequently contain high concentrations of β-lactams, fluoroquinolones, and sulfonamides, which apply strong selective pressure for the persistence and propagation of ARGs. Overburdened facilities like

Nairobi's Ruai wastewater treatment plant often release untreated or partially treated sewage into rivers, exacerbating contamination and expanding AMR hotspots [56]. Such evidence demonstrates the growing recognition of wastewater as an early-warning system for emerging resistance trends.

Similarly, in West Africa, recent data from Lagos has provided a stark picture of the scale of the problem. A cross-sectional survey of wastewater canals across 20 Local Government Areas (LGAs) isolated 123 bacterial pathogens, with Escherichia coli (28.5%), Salmonella spp. (16.3%), Vibrio cholerae (10.6%), and Shigella spp. (5.7%) being the most prominent. Alarmingly, extended-spectrum β-lactamase (ESBL) genes were detected in 87.5% of sampled sites, with 42.5% harboring both SHV and CTX-M genes. These findings highlight untreated wastewater canals as major reservoirs and amplifiers of multidrug-resistant organisms in Lagos and, by extension, other urban centers in sub-Saharan Africa [55].

Despite notable progress, several critical gaps impede the effective integration of wastewater surveillance into AMR monitoring frameworks in Africa. Infrastructure remains a fundamental challenge, as centralized treatment facilities such as those in Nairobi operate far beyond their design capacity, while cities like Lagos treat only a fraction of their enormous daily wastewater output (over 2.2 billion liters) resulting in widespread discharge of untreated effluents into open waterways [55]. Surveillance systems are fragmented and largely research-driven, lacking harmonized sampling protocols, sequencing standards, or structured data reporting mechanisms. Consequently, environmental AMR data rarely inform national action plans, leaving a major blind spot in One Health strategies [57]. Technological and capacity limitations compound these problems, as advanced tools such as metagenomic sequencing, which offer the most comprehensive resistome insights, remain inaccessible to most African laboratories due to cost, infrastructure gaps, and shortages of trained personnel [57]. Finally, weak governance and regulatory enforcement exacerbate the situation, allowing untreated hospital and industrial effluents to bypass control measures and enter aquatic systems unchecked. Without addressing these interlinked weaknesses, wastewater surveillance will remain an underutilized yet critical component of AMR mitigation in Africa.

European Union's approach: EFSA and ECDC guidance

The European Union has established one of the most advanced frameworks for AMR monitoring, underpinned by the One Health concept and coordinated by the European Food Safety Authority (EFSA), the European Centre for Disease Prevention and Control (ECDC), and the European Medicines Agency (EMA). This collaborative system integrates surveillance across humans, food-producing animals, and food products, while also monitoring antimicrobial consumption in both human and veterinary medicine [58]. A significant milestone in this effort was the development of harmonized outcome indicators, enabling Member States to assess trends and progress using standardized metrics. Indicators include the proportion of Escherichia coli isolates fully susceptible to a defined antimicrobial panel and the prevalence of ESBL-/AmpC-producing E. coli in food-producing animals and derived meat [58].

Recent EU reports reveal notable progress in controlling AMR in the agri-food sector. Commission Implementing Decision (EU) 2020/1729 mandated harmonized surveillance protocols for 2021–2027, ensuring consistent sampling across poultry, pigs, cattle, and derived meat products, while aligning human health monitoring with Decision 1082/2013/EU on cross-border threats [59]. Data from 2021–2022 show significant declines in ESBL-producing E. coli in broilers, broiler meat, and pig meat at the EU level, reflecting successful antimicrobial stewardship at farm level [59]. Furthermore, key outcome indicators (KOICS and KOIESC) which measure complete susceptibility and absence of ESBL-/AmpC-producers have shown encouraging upward trends over the last seven years, particularly in poultry [59].

The adoption of whole-genome sequencing (WGS) in 2021 as an alternative to phenotypic confirmatory testing for extended-spectrum cephalosporin and carbapenem resistance marks another major advancement, enhancing traceability of resistance determinants [59, 60]. Member States like the Netherlands and Sweden have consistently maintained some of the lowest resistance rates and antimicrobial consumption levels across the EU. Their success is attributed to early adoption of restrictive veterinary prescribing, proactive infection prevention strategies, and strong regulatory frameworks limiting antimicrobial use in livestock [59, 60].

Despite these achievements, several gaps persist. Environmental surveillance remains outside the formal harmonized monitoring framework, leaving a critical link in the AMR transmission chain largely unaddressed [58]. Variability in reporting completeness and timeliness among Member States also undermines data comparability and weakens the capacity for real-time response [59, 60]. Furthermore, while WGS has been authorized, its uptake remains uneven, restricting the EU's ability to track mobile genetic elements such as blaNDM and other emerging resistance genes. Finally, current indicators lack the granularity to assess sector-specific interventions or capture environmental contamination, which limits their effectiveness in guiding targeted One Health policies [58].

India's Ganges River

The Ganges River, particularly in its upper region, serves not only as a crucial cultural and religious site but has also become a hotspot for antimicrobial resistance (AMR), especially due to the emergence of the New Delhi Metallo-beta-lactamase-1 (NDM-1) gene. NDM-1 is an enzyme that makes bacteria resistant to a broad range of beta-lactam antibiotics, leaving few treatment options available [61].

Progress in detecting NDM-1 in the Ganges River includes identifying its extensive presence in urban areas such as Delhi, where high concentrations of the gene were first detected in clinical settings but later also identified in environmental water bodies [62]. Studies conducted in the pristine areas of Rishikesh and Haridwar, particularly during seasonal pilgrimages, have demonstrated a concerning increase in NDM-1 gene abundances, correlating significantly with fecal coliform levels. This spike in resistance genes is largely attributed to the influx of pilgrims from urban regions, whose waste, often inadequately managed, contributes significantly to contamination [62].

Additionally, clinical isolates from the Kashmir valley have shown alarming trends where various bacteria, including Escherichia coli, Klebsiella pneumoniae, Citrobacter freundii, and Acinetobacter spp., harboring the blaNDM-1 gene, were resistant to almost all antibiotics except polymyxin B and tigecycline. This demonstrates the critical issue of multi-drug resistance associated with NDM-1 positive bacteria, posing a substantial threat to public health [61].

Despite these advancements in understanding, substantial gaps remain. A primary concern is the inadequate wastewater treatment infrastructure in pilgrimage cities, unable to manage the surge in population during peak pilgrimage seasons. This deficiency directly leads to higher blaNDM-1 gene dissemination in the environment. Moreover, standardized, longitudinal surveillance efforts remain insufficient, limiting effective public health interventions. Without coordinated environmental monitoring and improved waste management systems, efforts to control the spread of resistant genes will likely remain reactive rather than preventive [62].

Conclusions

AMR is a complex issue that extends beyond clinical and agricultural settings into the environment, which remains under-monitored and poorly integrated into global surveillance efforts. Challenges such as inconsistent methodologies, limited infrastructure, and fragmented data hinder effective detection and response. While some regions show progress through One Health frameworks, widespread gaps persist. Strengthening environmental AMR surveillance with standardized methods, improved capacity, and coordinated multisectoral collaboration is essential to effectively manage and reduce the spread of resistance worldwide.

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