

**Review Article**

Tracking Antimicrobial Resistance beyond Healthcare: Role of Environmental Monitoring

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Abstract

Antimicrobial resistance (AMR) is an escalating global health threat, with environmental reservoirs playing a substantial yet often under recognized role in its emergence and dissemination. Antibiotic-resistant bacteria (ARB) enter the environment through various pathways, including anthropogenic activities, agricultural practices, and industrial processes. These contaminants infiltrate natural ecosystems such as soil, water, and air, where they may persist, proliferate, and transfer resistance genes to native microbial communities. Resistant microorganisms endanger both human and animal health and contribute to ecological and public health disturbances. This review focuses on how AMR spreads through the environment, emphasizing sources such as wastewater, soil, industry, and air. It also discusses current methods for detecting AMR in environmental matrices, encompassing traditional culture-based approaches, molecular techniques such as polymerase chain reaction (PCR) for rapid gene identification, metagenomics for comprehensive microbial community analysis, and biosensors for real-time, in situ detection. Furthermore, the review emphasizes the importance of environmental monitoring in identifying AMR hotspots, elucidating transmission pathways, assessing public health impacts, informing policy development, and guiding future research. The results indicate that environmental AMR noticeably drives the persistence and spread of resistance in both healthcare and community settings. Dealing with this issue requires strengthening monitoring systems through standardized protocols and advanced technologies. Governments and relevant stakeholders should prioritize the identification and control of AMR hotspots, such as wastewater treatment plants, agricultural runoff zones, and industrial discharge sites, to control the spread of resistance and safeguard public health.

Keywords: Antibiotic-resistant bacteria, Environmental contamination, Environmental reservoirs, Public health

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Introduction

Antibiotics are antimicrobial substances that can inhibit the growth of microorganisms or kill them. They are widely used to treat bacterial infections in humans and animals, as well as in various non-medical applications.¹ The annual global production of antibiotics is estimated to be between 100,000 to 200,000 tonnes, with over a one million tonnes produced since the 1940s.² Antibiotic resistance refers to the ability of certain bacteria to withstand the effects of antibiotic treatment. This resistance can be either innate or acquired, with the acquired form usually resulting from the use of antibiotics that eliminate susceptible bacteria in a population, thereby allowing resistant strains to thrive.³ The problem of drug resistance is exacerbated by the widespread use of antibiotics, not only for medical and veterinary purposes but also for growth promotion in livestock. Misuse and overuse accelerate

the emergence of antibiotic-resistant bacteria (ARB) and the spread of antibiotic resistance genes (ARGs) in the environment, increasing the risk of resistance transfer to humans.⁴ Antimicrobial resistance (AMR) is now recognized as one of the top ten global health threats, with rising trends in resistant infections suggesting an approaching post-antibiotic era. In such an era, common infections could become untreatable, surgeries riskier, and immunocompromised individuals more vulnerable to fatal infections. This underscores the urgent need for comprehensive, multi-pronged strategies to combat AMR. The growing global threat of AMR calls for immediate and innovative strategies.⁵ Both the World Health Organization (WHO) and the World Bank have recognized AMR as a critical crisis impacting human health, economic stability, and agricultural productivity, while simultaneously hindering progress toward achieving the Sustainable



Development Goals (SDGs).^{5,6} Current projections indicate that, by 2050, AMR could be responsible for more than 10 million deaths each year, exceeding the mortality rates of cancer and many other major diseases.⁷

Bacteria develop antibiotic resistance through gene mutation or horizontal gene transfer (Horizontal gene transfer (HGT) in bacteria is the process where bacteria exchange genetic material directly with other bacteria, rather than inheriting it from their parent cells).⁸ This allows bacteria to acquire resistance to a specific antibiotic and makes them susceptible to acquiring various mobile genetic elements. Consequently, bacteria can become resistant to multiple antibiotics, leading to multidrug-resistant strains, which pose significant challenges in the treatment of infections in clinical settings.⁹ Human exposure to environmental AMR can occur through waterborne or airborne pathways. This includes contamination of drinking water, food, and recreational water, potentially leading to the colonisation or infection of the skin, gastrointestinal tract, genitourinary tract, and respiratory tract by resistant microbes.¹⁰

Although the misuse and overuse of antibiotics in clinical and veterinary practices are well-recognized drivers of AMR, its environmental dimension remains comparatively underexplored and insufficiently regulated. Environmental compartments serve as both reservoirs and transmission pathways for antimicrobial residues, resistant bacteria, and resistance genes.¹¹ These environments not only sustain the persistence and selection of resistant strains but also promote horizontal gene transfer among microbial populations, thereby accelerating the propagation of resistance.¹²

The rationale for this review stems from a critical gap in both scientific research and policy attention. Most AMR studies have focused on clinical and veterinary aspects, often overlooking the role of environmental processes and pollution in resistance transmission across human and animal populations. This issue is particularly acute in low- and middle-income countries (LMICs), where inadequate waste management, poor sanitation infrastructure, and limited environmental surveillance amplify the risk of AMR proliferation. Although global efforts such as national action plans and international initiatives have begun to integrate environmental considerations, there is still a lack of cohesive data to guide effective interventions. The objective of this review is to synthesize existing scientific evidence on the role of environmental compartments in the emergence and dissemination of AMR. The primary objectives of this review are: (1) identifying key environmental sources, (2) evaluating current detection methodologies, and (3) highlighting the significance of environmental monitoring in controlling the spread of resistance. This review aims to explore the critical role of environmental monitoring in understanding and managing the spread of AMR. Additionally, it informs researchers, policymakers, and stakeholders of the urgent need to recognize and address environmental AMR as a

central component of the global resistance crisis.

Sources of AMR in the Environment

The environment can be contaminated with ARBs and ARGs from a variety of sources, including human activities, agricultural practices, and industrial processes. These contaminants find their way into natural ecosystems such as soil, water, and air, where they can persist, multiply, and potentially transfer resistance genes to native microbial communities. The major environmental sources of AMR include water and wastewater systems, soil, and airborne pathways.

Water and Wastewater

The presence of AMR in drinking water poses a significant public health concern, as it may lead to human exposure to resistant pathogens. Studies have detected various ARGs in drinking water systems, including those associated with resistance to β -lactams and fluoroquinolones.¹³ Additionally, private wells and household water supplies have been identified as reservoirs of ARBs, including opportunistic pathogens such as *Acinetobacter baumannii*.¹⁴ Environmental factors and human activities dramatically influence the dynamics of AMR in drinking water systems.¹⁵ Although water treatment processes can reduce the prevalence of ARBs and ARGs, they rarely achieve complete removal. For instance, chlorine dioxide disinfection exhibits variable efficiency against both free-living and particle-associated ARGs.¹³ Wastewater treatment plants (WWTPs) are critical nodes where ARB and ARGs can persist and multiply. Despite treatment processes designed to reduce microbial loads, many antibiotics and resistant bacteria remain in the treated effluent, which is subsequently discharged into surface waters.¹⁶ Also, the extensive use of antibiotics in livestock and crop production contributes to AMR through agricultural runoff, which carries resistant microbes and residues into rivers and lakes.¹⁷ Hospitals are hotspots for antibiotic-resistant pathogens, which can enter water systems through inadequately treated wastewater.¹⁸

Soil

Soil hosts diverse microbial communities whose interactions significantly influence the distribution and abundance of ARGs. Factors such as pH, moisture, and nutrient availability play key roles in shaping these microbial populations. Different agricultural systems, such as conventional and organic farming, can lead to variations in soil microbial communities and their resistomes. However, research suggests that such differences are generally minor, with similar resistance profiles observed across various farming systems.¹⁹ The use of antibiotics in livestock and the application of manure are major contributors to soil contamination. Soils treated with manure show a significant increase in ARG abundance over time, particularly tetracycline resistance genes, reflecting their widespread use in animal husbandry.²⁰ Irrigation

with treated municipal wastewater can also introduce antibiotics into soil, promoting increased resistance among soil bacteria.^{21,22} In addition to antibiotics, environmental contaminants such as heavy metals, polycyclic aromatic hydrocarbons (PAHs), and other pollutants can exert co-selective pressure on microbial communities, influencing ARG diversity and abundance. For instance, elevated heavy metal concentrations have been linked to greater ARG richness, as these metals can co-select for resistant bacteria.²³ Table 1 summarizes studies that have identified antimicrobial-resistant microorganisms isolated from various environmental sources.

Agricultural Practices

The emergence of AMR in agriculture is driven by several practices that promote the proliferation of ARBs and ARGs. These practices include the misuse of antibiotics in livestock farming, aquaculture, crop production, and the application of contaminated organic waste. In livestock farming, antibiotics are widely used for therapeutic purposes, disease prevention (prophylaxis), and as growth promoters. A significant proportion of the antibiotics administered to animals are excreted, often in metabolised form, in manure or urine. This waste introduces antibiotics into the environment, where they contribute to the development and spread of resistance.⁵³ Common antibiotics found in agricultural settings include sulphonamides, tetracyclines, and fluoroquinolones, which are commonly found in manure from cattle, chickens, and pigs.⁵⁴ While these practices play a significant role in the AMR crisis, some evidence suggests that organic farming, which restricts the use of antibiotics, can reduce the prevalence of AMR by approximately 31% across different types of livestock species.⁵⁵

In aquaculture, antibiotics are routinely added to water to prevent or treat diseases in farmed fish and other aquatic organisms. Unfortunately, this practice often leads to the direct release of antibiotics into the aquatic environments, promoting the growth of resistant bacteria in water bodies and sediments. These resistant bacteria can spread to other ecosystems through hydrological processes, exacerbating the AMR problem. Study show that up to 90% of aquatic bacteria may be resistant to at least one antibiotic, with significant proportion being multi-drug resistant.⁵⁶ In crop production, antibiotics such as streptomycin and tetracycline are occasionally used to control bacterial diseases. Although their use is less extensive than in livestock production, these applications contribute to the development of resistance in soil microbiota. Moreover, crops irrigated with contaminated water or fertilised with animal manure can accumulate resistant bacteria, that can eventually enter the human food chain.⁵⁷ The application of livestock manure and sewage sludge to agricultural soils is another significant contributor to the spread of resistance. These materials often contain significant levels of antibiotics and ARGs, introducing resistant bacteria into soil environments. Research suggests that manure

from antibiotic-treated animals can serve as a reservoir for ARB and resistance genes, thereby contributing to the spread of AMR in the environment.³⁸

Industrial Effluents

Industrial wastewater is a major contributor to the spread of AMR in the environment. These discharges often contain antibiotics, ARBs, and ARGs, which can contaminate water, soil, and sediments, creating reservoirs of resistance. Several industries including pharmaceutical manufacturing, healthcare, and food processing play significant roles in this process. In pharmaceutical manufacturing, the production of antibiotics frequently leads to the release of untreated or inadequately treated wastewater containing high concentrations of antibiotic residues. Countries such as China and India, which are among the world's largest antibiotic producers, face considerable challenges in managing these effluents, resulting in widespread environmental contamination.⁹ Studies indicate that wastewater from pharmaceutical plants can act as hotspots for resistant bacteria, as the high concentrations of antibiotics exert strong selective pressure, promoting the proliferation of ARBs and ARGs in nearby ecosystems.⁵⁸ Hospitals are critical sources of AMR due to improper disposal of medical waste and wastewater. Hospital wastewater typically contains multi-drug-resistant bacteria, including extended-spectrum beta-lactamase (ESBL) producers, which can persist despite wastewater treatment processes. Studies show that hospital effluents significantly contribute to the spread of resistant strains, particularly when reused for irrigation or discharged into natural water bodies.⁵⁹ This contamination poses a direct risk to public health, as resistant pathogens can spread through water supplies and into the broader community.^{60,61} Food processing facilities generate effluents that may contain antibiotic residues and ARBs from raw materials such as meat, milk, and other animal products. Runoff from these facilities often contains antibiotic residues and ARBs, contaminating soil and water systems.⁶² Moreover, improper handling and processing of food products can facilitate the transfer of resistant bacteria to consumers, further exacerbating the AMR crisis.⁶³

Airborne Transmission

Air is an important medium for the spread of antibiotic resistance, primarily through the transport of ARBs and ARGs via bioaerosols. Bioaerosols, which are airborne particles containing microorganisms, act as carriers of ARGs originating from sources such as agricultural operations, wastewater treatment plants, and industrial facilities. Research has showed that ARBs can travel considerable distances through the atmosphere. For example, atmospheric dispersion modelling has shown that ARGs from animal farms can be carried up to 10 kilometres downwind. This long-range transport poses a direct threat to human health, as inhalation of bioaerosols

Table 1. Antimicrobial-resistant bacteria isolated from various environmental reservoirs

AMR Microorganisms	Source	Study Location	Reference
Water and wastewater			
Cefotaxime-resistant <i>E. coli</i> and Multidrug-resistant (MDR) <i>V. cholerae</i>	Water supply system	Moamba, Mozambique	24
<i>Pseudomonas</i> spp., <i>Enterobacter</i> spp., <i>Escherichia coli</i> , <i>Citrobacter freundii</i> and <i>Citrobacter koseri</i> , <i>Acinetobacter</i> spp., and <i>Klebsiella oxytoca</i>	Drinking water samples and wastewater samples	Dhaka city	25
ESBL-producing, colistin-resistant, and multidrug-resistant <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i>	Wastewater of abattoirs	Greifswald, Germany.	26
<i>Klebsiella pneumoniae</i> and <i>Klebsiella oxytoca</i>	Hospital wastewater	Mexico	27
Methicillin-resistant <i>Staphylococcus aureus</i> (MRSA)	Municipal wastewater	Finland	28
<i>Bacillus</i> spp., <i>Enterococcus</i> spp., <i>Erythrobacter</i> spp., <i>Pseudomonas</i> spp., <i>Shigella</i> spp., <i>Serratia</i> spp., and <i>Staphylococcus</i> spp.	Drinking water sources.	Rivers State, Nigeria	15
<i>Staphylococcus aureus</i> , <i>Escherichia coli</i> , <i>Citrobacter</i> spp., <i>Acinetobacter</i> spp., <i>Enterobacter</i> spp., <i>Klebsiella pneumoniae</i> , and <i>Pseudomonas aeruginosa</i>	Hospital wastewater	Bahir Dar city, Ethiopia	29
Soil			
<i>Staphylococcus aureus</i>	Chickens, humans, rodents, and soil	Karatu district, Tanzania	30
<i>Pseudomonas</i> , <i>Stenotrophomonas</i> , <i>Sphingobacterium</i> , and <i>Chryseobacterium</i>	Soils from farming fields	Lithuania	20
<i>Proteus</i> sp., <i>Rahnella</i> sp., <i>Escherichia coli</i> , <i>Pseudomonas</i> spp., and <i>Bacillus</i> spp.	Heavy metal polluted soil	Lagelu, Nigeria	31
Multidrug-resistant <i>E. coli</i>	Household soil	Karatu district, Northern Tanzania	32
<i>Escherichia coli</i> ., <i>Klebsiella</i> spp., and <i>Staphylococcus</i> spp., <i>Bacillus</i> spp., <i>Pseudomonas</i> spp., and <i>Proteus</i> spp	Soil from dumpsites	Abraka, Delta State, Nigeria	33
Multidrug-resistant <i>Enterobacteriaceae</i>	Soil samples	Jos Metropolis, Plateau State, Nigeria	34
Agricultural setting			
Multidrug-resistant <i>Klebsiella pneumoniae</i>	Dairy farms	Blitar, Indonesia	35
<i>Bacillus</i> , <i>Acinetobacter</i> , <i>Stenotrophomonas</i> , <i>Enterobacteriaceae</i> genera, <i>Aeromonas</i> and <i>Cronobacter</i>	Irrigation ponds	São José do Vale do Rio Preto, Brazil	36
<i>Escherichia coli</i> and <i>Salmonella</i>	Food animal faeces	Rwanda	37
<i>Mycobacterium phlei</i> and <i>Bacillus anthracis</i>	Cow manure	Czech Republic	38
Multidrug-resistant <i>E. coli</i>	Poultry litter samples	Kano Metropolis, Nigeria	39
<i>Coliform</i> bacteria	Poultry cloaca	urban Arusha and Moshi districts, Tanzania	40
Multidrug-resistant <i>S. aureus</i>	Chickens	Karatu district, Tanzania	30
<i>Enterococcus</i> spp.	Poultry farms	North of Serbia.	41
<i>Escherichia coli</i>	Farm animals feces	Russia,	42
<i>Escherichia coli</i>	Layer farms	Mukono District, Uganda	43
Industries			
<i>Escherichia coli</i>	Commercial swine and poultry abattoirs	South Africa	44
<i>Enterobacter amnigenus</i> , <i>Pseudomonas aeruginosa</i> , <i>Enterobacter cloacae</i> and <i>Pseudomonas fluoresce</i> ,	Pharmaceutical Effluents	Accra, Ghana	45
<i>Pseudomonas aeruginosa</i> , <i>Bacillus</i> spp. and <i>Staphylococcus</i> spp.	Pharmaceutical Effluents	Dhaka and Gazipur.	46
Shiga-toxin-producing <i>E. coli</i> (STEC), <i>Listeria monocytogenes</i> , <i>Staphylococcus aureus</i> , and <i>Yersinia enterocolitica</i>	Meat Processing Plant	Gyeongki-do, South Korea.	47
Air			
<i>Staphylococcus aureus</i> , <i>Enterococci</i> species, <i>Enterococcus faecalis</i> , <i>Enterococcus faecium</i> , <i>Acinetobacter</i> spp, <i>Escherichia coli</i> and <i>Pseudomonas aeruginosa</i>	Hospital indoor air	South Ethiopia	48
<i>Staphylococcus</i> , <i>Aerococcus</i> , <i>Bacillus</i> , <i>Pseudomonas</i> , <i>Serratia</i> and <i>Acinetobacter</i>	Inside and outside of a dairy milking parlor	France	49
<i>Staphylococcus aureus</i> , and <i>Streptococcus pyogenes</i>	Hospital indoor air	General Hospital in Hawassa City, Sidama, Ethiopia	50
<i>Staphylococcus xylosum</i> , <i>Micrococcus luteus</i> and <i>Macroccoccus equiperficus</i> .	Office rooms	Southern Poland	51
<i>Staphylococcus aureus</i> , <i>Pseudomonas aeruginosa</i> , <i>P. stutzeri</i> , <i>Bacillus cereus</i> , <i>Acinetobacter schindleri</i> , <i>Proteus vulgaris</i> , <i>B. subtilis</i> , <i>Escherichia coli</i> , and <i>B. aerius</i> ,	Hospital indoor air	Dhaka region, Bangladesh.	52

containing ARGs can lead to respiratory infections and contribute to the global burden of AMR.⁶⁴ Furthermore, Particulate Matter (PM), particularly fine particles such as PM_{2.5}, has been recognised as a vector for ARBs and ARGs. PM_{2.5} can facilitate horizontal gene transfer between bacteria, enhancing the exchange of resistance elements and increasing the likelihood of generating resistant strains emerging.⁶⁵ Environmental conditions, like temperature and humidity, further influence the survival, transport, and interaction of these resistant organisms with airborne pollutants, exacerbating the AMR problem.⁶⁶

The mechanism behind the spread of AMR through bioaerosols includes the aerosolization of resistant microbes from contaminated surfaces, liquids, or biological waste, followed by their transport and deposition. These airborne microbes may also engage in HGT, sharing resistance genes with other airborne or surface-dwelling bacteria.⁶⁷ Given the ability of bioaerosols to travel and persist in various environments, they pose a silent but significant threat to public health by facilitating the spread of AMR in both clinical and environmental contexts. **Figure 1** presents the mechanism of spread of bioaerosols.

The role of bioaerosols in the environmental dimension of AMR is particularly concerning in densely populated or enclosed spaces. For instance,⁶⁴ reported the presence of multidrug-resistant bacteria and diverse ARGs in indoor air samples collected from kindergartens in Hong Kong. Similarly, identified high levels of ARB in indoor environments of the hospitals in Dhaka Bangladesh, underscoring potential occupational exposure risks for healthcare personnel. These findings suggest that bioaerosols serve not only as passive carriers of resistant organisms but also as active environments where Horizontal Gene Transfer HGT can occur, further amplifying resistance dissemination.⁶⁸

Methods for Monitoring Environmental AMR

Cultural Methods

Culture-based methods represent conventional approaches for isolating and identifying microorganisms from environmental samples. These techniques depend on the morphological and biochemical traits of microbial colonies and enable quantification of cultivable bacteria within a specific growth medium. Owing to their high sensitivity, they are widely accepted as standard procedures for identifying particular microorganisms. Typically, the process starts with screening bacterial cultures on non-selective media, followed by the use of selective media formulated to suppress unwanted species while supporting the growth of target organisms. Phenotypic analyses such as microscopy, enzymatic assays, and antibiotic susceptibility testing (e.g., minimum inhibitory concentration (MIC) assays in broth or agar, disk diffusion, and E-test®) are subsequently performed to further characterize microbial lineages.^{69,70} Despite certain inherent limitations, culture-based methods remain among the most frequently applied techniques for AMR because of their simplicity (**Table 2**). Moreover, studies utilizing molecular techniques often commence with traditional methods, as they are straightforward to perform and provide a comprehensive overview of the microbial community and its resistance profiles⁷¹.

Molecular Methods

Molecular characterization of the genetic mechanisms underlying phenotypic results obtained from traditional antimicrobial susceptibility testing has become an essential aspect of environmental research. Molecular techniques have transformed the investigation of AMR by enabling the detection of resistance determinants in both culturable and non-culturable bacteria, thereby

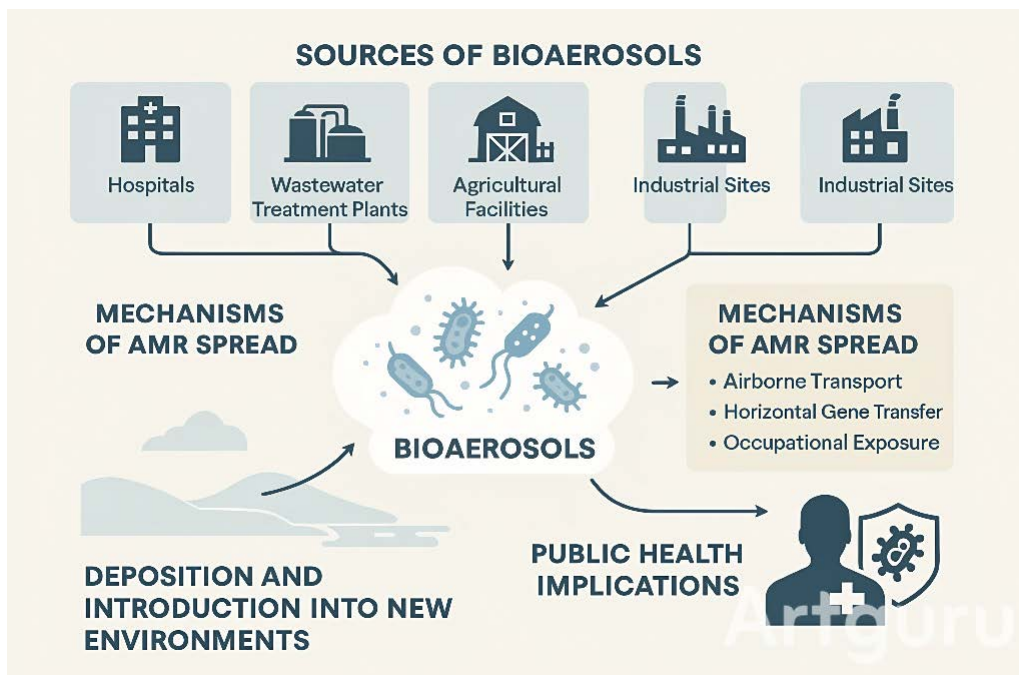


Figure 1. Pathways and mechanisms linking bioaerosols to the spread of AMR

Table 2. Advantages and limitations of environmental AMR monitoring methods

Detection Method	Advantages	Limitations	References
Culture-Based Methods	<ul style="list-style-type: none"> - Provide key data on multiple antibiotic resistance. - Established protocols - Cost-effective for routine use 	<ul style="list-style-type: none"> - Time-consuming (days to weeks) - Labour-intensive - Not suitable for all pathogens 	70,72
Molecular Techniques	<ul style="list-style-type: none"> - Rapid results (hours) - High specificity and sensitivity - Can detect unculturable organisms 	<ul style="list-style-type: none"> - Requirement for specialized equipment and expertise - Potential for false positives/negatives 	73
Metagenomics	<ul style="list-style-type: none"> - Broad identification of microorganisms - No need for culturing - High-throughput capabilities 	<ul style="list-style-type: none"> - Complex data analysis - Database-dependent identification - Requires specialized knowledge - high cost and technical expertise 	74–76
Biosensors	<ul style="list-style-type: none"> - Rapid and real-time detection - High sensitivity and specificity - Potential for point-of-care use 	<ul style="list-style-type: none"> - May require calibration - Susceptible to sample matrix effects - Initial development costs can be high 	77,78

providing a more comprehensive insight into microbial communities. These approaches are designed to identify specific DNA or RNA sequences of pathogens through hybridization between target nucleic acids and synthetic oligonucleotides, facilitating the detection of species-specific genes and virulence factors. Molecular methods are generally rapid, efficient, and independent of pathogen cultivation. Commonly used approaches include polymerase chain reaction (PCR)-based assays such as conventional PCR, real-time or quantitative PCR (qPCR), droplet digital PCR (ddPCR), and multiplex PCR (mPCR). Other advanced tools include microarrays, loop-mediated isothermal amplification (LAMP), sequencing technologies, and fluorescence in situ hybridization (FISH).^{73,79} Collectively, these molecular techniques have markedly enhanced the speed and precision of AMR detection in diverse environmental settings.

Metagenomics Method

Metagenomics involves the study of genetic material (genomes) derived from mixed communities of organisms, commonly present in environmental samples such as soil or water.⁸⁰ It represents a cutting-edge approach that enables the direct investigation of microbial communities within their natural habitats by analysing DNA extracted from environmental or clinical samples. Unlike conventional microbiological methods that depend on culturing organisms, metagenomics allows researchers to explore the immense diversity of microorganisms, including those that cannot be cultured. The process generally includes several key stages: sample collection, DNA extraction, and high-throughput sequencing to produce large-scale genetic data. Metagenomic sequencing can be categorized into two main types: targeted metagenomics, which focuses on specific genetic markers such as the 16S rRNA gene for identifying and classifying microbial taxa, and shotgun metagenomics, which randomly sequences all DNA within a sample, providing comprehensive insights into both the taxonomic composition and functional potential of microbial communities.⁷⁵ As a non-targeted approach, metagenomics is highly effective for exploring taxonomic and functional genetic diversity in complex

environments. It enables the quantification of gene or sequence categories, offering valuable information on the occurrence and relative abundance of different microbial groups. Owing to this capability, metagenomics has emerged as one of the most powerful tools for investigating natural ecosystems. In particular, metagenomic analysis of the environmental resistome the complete collection of ARGs present within a microbial community, including those in pathogenic and non-pathogenic bacteria as well as their precursors has been greatly enhanced by the availability of public databases of ARGs and mobile genetic elements (MGEs). These resources have facilitated in-depth exploration of microbial resistance dynamics across diverse ecosystems.⁷⁶

Biosensor-based Methods

Biosensor-based methods are advanced analytical techniques that combine biological recognition elements with transducers to detect specific analytes such as pathogens or biomarkers in real time. These systems are designed to deliver rapid, sensitive, and accurate measurements, making them valuable tools in healthcare, environmental monitoring, and food safety applications.⁸¹ A typical biosensor consists of two main components: a bioreceptor (e.g. enzymes, antibodies, or nucleic acids) that specifically interacts with the target analyte, and a transducer that converts this biological interaction into a quantifiable signal, which may be electrical, optical, or mass-based.⁷⁷ Biosensors provide several key advantages: they produce quick results, require only small sample volumes, and can be used for on-site detection, reducing reliance on complex laboratory infrastructure. Moreover, they can be designed to detect multiple analytes simultaneously, increasing their effectiveness when analyzing complex environmental or biological samples.⁷⁸

Significance of Environmental Monitoring of AMR

Hotspots Identification

AMR hotspots are specific locations characterized by a high occurrence, emergence, or dissemination of AMR. These areas serve as reservoirs or amplifiers that promote the spread of ARB and ARGs. Implementing effective

containment strategies in high-risk environments, such as wastewater treatment plants, healthcare facilities, and agricultural sites, can significantly reduce the likelihood of community, level transmission.⁸² Identifying these hotspots enables health authorities, regulatory agencies, and environmental organizations to focus their monitoring and intervention efforts where they are most needed. This targeted approach not only enhances the efficiency of AMR control programs but also optimizes resource allocation by preventing unnecessary expenditure on non-priority areas.⁸³

Understanding Reservoirs and Routes of Transmission

Reservoirs of AMR are environments, organisms, or materials in which ARBs and ARGs persist, proliferate, or transfer. The transmission routes represent the pathways through which AMR disseminates among humans, animals, and the surrounding environment. Key reservoirs comprise healthcare facilities, the microbiota of humans and animals, and soil, water, and air contaminated by the utilization or disposal of antibiotics.⁸⁴ The pathways of transmission include human-to-human interactions, zoonotic transfers from animals, environmental exposures via contaminated water or air, food chain contamination, and horizontal gene transfer among bacterial populations.⁸⁵ Understanding the concepts of reservoirs and transmission pathways is of paramount importance for the formulation of targeted interventions, the mitigation of AMR proliferation, and the development of policies that deal with the AMR crisis at its source. It will also facilitate the implementation of effective containment strategies, minimise risks to public health, and enhances global initiatives aimed at reduce AMR.⁸⁶

Impact Assessment

Impact assessment critically examines the consequences of AMR for public health, economic stability, ecological systems, and societal frameworks. It elucidates the severity of the issue and guides the formulation of policy and intervention methodologies. The presence of antibiotic residues and resistant microorganisms in aquatic, terrestrial, and atmospheric environments disrupts natural microbial consortia, thereby influencing essential ecosystem services such as nutrient cycling.⁸⁷ The escalation of resistance observed in both wildlife and aquatic species serves as an indicator of human-induced environmental pollution. Environments such as wastewater treatment facilities and agricultural runoff zones function as critical reservoirs for the propagation of resistance genes into natural ecological systems. Evaluating these impacts is imperative for the development of effective interventions, the prioritization of research agendas, and the promotion of international cooperation.⁸⁸

Policy Development

Effective policies and regulations aimed at addressing AMR are predicated on the acquisition of precise data, rigorous scientific inquiry, and collaborative engagement

among stakeholders to curtail its proliferation. The processes of environmental monitoring and assessment are instrumental in the development of evidence-based guidelines and the establishment of enforcement mechanisms.⁸⁸ These activities furnish policymakers with comprehensive data regarding AMR trends, geographical hotspots, and transmission pathways, thereby facilitating the formulation of targeted interventions.

Advancing Scientific Research

Advancing the scientific understanding of AMR necessitates an in-depth examination of its underlying mechanisms, contributing factors, and potential solutions to effectively guide intervention strategies.⁸⁹ Systematic surveillance elucidates the influence of environmental factors, including pollutants, climatic variations, and microbial interactions, on the emergence and dissemination of AMR. Environmental surveillance serves as a crucial methodology for identifying previously unrecognized resistance genes in natural reservoirs, thereby enhancing our comprehension of AMR.⁹⁰

Conclusion

The environmental dimension of AMR represents a critical, yet often underappreciated, component of the global AMR crisis. Human activities including wastewater discharge, agricultural runoff, industrial effluents, and air pollution play a major role in introducing and disseminating ARB and ARGs into natural ecosystems. These resistant organisms not only threaten biodiversity and compromise essential ecosystem services but also pose significant public health risks. Consequently, governments and stakeholders must prioritize the identification and management of AMR hotspots, such as wastewater treatment plants, agricultural runoff areas, and industrial effluent sources. Developing integrated global surveillance systems that link environmental, clinical, and agricultural data is essential, particularly in resource-limited settings, to achieve a comprehensive understanding of AMR dynamics and to guide targeted interventions.

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References

- Kariuki S. Antimicrobial resistance in enteric pathogens in developing countries. In: Sosa A, Byarugaba DK, Amábile-Cuevas CF, Hsueh P-R, Kariuki S, Okeke IN, eds. *Antimicrobial Resistance in Developing Countries*. New York: Springer; 2010. p. 177-97. doi: [10.1007/978-0-387-89370-9_11](https://doi.org/10.1007/978-0-387-89370-9_11).
- Aslam B, Khurshid M, Arshad MI, Muzammil S, Rasool M, Yasmeen N, et al. Antibiotic Resistance: One Health One World Outlook. *Front Cell Infect Microbiol*. 2021;11:771510. doi: [10.3389/fcimb.2021.771510](https://doi.org/10.3389/fcimb.2021.771510).
- Iskandar K, Murugaiyan J, Hammoudi Halat D, Hage SE, Chibabhai V, Adukkadukkam S, et al. Antibiotic discovery and resistance: the chase and the race. *Antibiotics (Basel)*. 2022;11(2):182. doi: [10.3390/antibiotics11020182](https://doi.org/10.3390/antibiotics11020182).
- Carlet J, Collignon P, Goldmann D, Goossens H, Gyssens IC, Harbarth S, et al. Society's failure to protect a precious resource: antibiotics. *Lancet*. 2011;378(9788):369-71. doi: [10.1016/s0140-6736\(11\)60401-7](https://doi.org/10.1016/s0140-6736(11)60401-7).
- Cartledge K, Short FL, Hall A, Lambert K, McDonald MJ, Lithgow T. Ethical bioprospecting and microbial assessments for sustainable solutions to the AMR crisis. *IUBMB Life*. 2025;77(1):e2931. doi: [10.1002/iub.2931](https://doi.org/10.1002/iub.2931).
- Aslam B, Asghar R, Muzammil S, Shafique M, Siddique AB, Khurshid M, et al. AMR and sustainable development goals: at a crossroads. *Global Health*. 2024;20(1):73. doi: [10.1186/s12992-024-01046-8](https://doi.org/10.1186/s12992-024-01046-8).
- Chinemerem Nwobodo D, Ugwu MC, Oliseloke Anie C, Al-Ouqaili MT, Chinedu Ikem J, Victor Chigozie U, et al. Antibiotic resistance: the challenges and some emerging strategies for tackling a global menace. *J Clin Lab Anal*. 2022;36(9):e24655. doi: [10.1002/jcla.24655](https://doi.org/10.1002/jcla.24655).
- Moura de Sousa J, Lourenço M, Gordo I. Horizontal gene transfer among host-associated microbes. *Cell Host Microbe*. 2023;31(4):513-27. doi: [10.1016/j.chom.2023.03.017](https://doi.org/10.1016/j.chom.2023.03.017).
- Larsson DG, Flach CF. Antibiotic resistance in the environment. *Nat Rev Microbiol*. 2022;20(5):257-69. doi: [10.1038/s41579-021-00649-x](https://doi.org/10.1038/s41579-021-00649-x).
- Xie J, Jin L, He T, Chen B, Luo X, Feng B, et al. Bacteria and antibiotic resistance genes (ARGs) in PM2.5 from China: implications for human exposure. *Environ Sci Technol*. 2019;53(2):963-72. doi: [10.1021/acs.est.8b04630](https://doi.org/10.1021/acs.est.8b04630).
- Liguori K, Keenum I, Davis BC, Calarco J, Milligan E, Harwood VJ, et al. Antimicrobial resistance monitoring of water environments: a framework for standardized methods and quality control. *Environ Sci Technol*. 2022;56(13):9149-60. doi: [10.1021/acs.est.1c08918](https://doi.org/10.1021/acs.est.1c08918).
- Baquero F. Threats of antibiotic resistance: an obliged reappraisal. *Int Microbiol*. 2021;24(4):499-506. doi: [10.1007/s10123-021-00184-y](https://doi.org/10.1007/s10123-021-00184-y).
- Kimbell LK, LaMartina EL, Kohls S, Wang Y, Newton RJ, McNamara PJ. Impact of corrosion inhibitors on antibiotic resistance, metal resistance, and microbial communities in drinking water. *mSphere*. 2023;8(5):e0030723. doi: [10.1128/mSphere.00307-23](https://doi.org/10.1128/mSphere.00307-23).
- Alawi M, Smyth C, Drissner D, Zimmerer A, Leupold D, Müller D, et al. Private and well drinking water are reservoirs for antimicrobial resistant bacteria. *NPJ Antimicrob Resist*. 2024;2(1):7. doi: [10.1038/s44259-024-00024-9](https://doi.org/10.1038/s44259-024-00024-9).
- Wilcox IM, Sokari TG, Akani NP, Amadi N. Antimicrobial profiling of resistant genes in bacteria isolated from drinking water sources in Bonny island, Rivers state, Nigeria. *J Adv Microbiol*. 2023;23(10):146-57. doi: [10.9734/JAMB/2023/v23i10766](https://doi.org/10.9734/JAMB/2023/v23i10766).
- Singh AK, Kaur R, Verma S, Singh S. Antimicrobials and antibiotic resistance genes in water bodies: pollution, risk, and control. *Front Environ Sci*. 2022;10:830861. doi: [10.3389/fenvs.2022.830861](https://doi.org/10.3389/fenvs.2022.830861).
- World Economic Forum (WEF). *Antimicrobial Resistance and Water: The Risks and Costs for Economies and Societies*. WEF; 2021.
- Kusi J, Ojewole CO, Ojewole AE, Nwi-Mozu I. Antimicrobial resistance development pathways in surface waters and public health implications. *Antibiotics (Basel)*. 2022;11(6):821. doi: [10.3390/antibiotics11060821](https://doi.org/10.3390/antibiotics11060821).
- Han B, Ma L, Yu Q, Yang J, Su W, Hilal MG, et al. The source, fate and prospect of antibiotic resistance genes in soil: A review. *Front Microbiol*. 2022;13:976657. doi: [10.3389/fmicb.2022.976657](https://doi.org/10.3389/fmicb.2022.976657).
- Armalytė J, Skerniškytė J, Bakienė E, Krasauskas R, Šiugždinienė R, Kareivienė V, et al. Microbial diversity and antimicrobial resistance profile in microbiota from soils of conventional and organic farming systems. *Front Microbiol*. 2019;10:892. doi: [10.3389/fmicb.2019.00892](https://doi.org/10.3389/fmicb.2019.00892).
- Franklin AM, Kariyawasam S, Andrews DM, McLain JE, Watson JE. Presence of antimicrobial-resistant bacteria and resistance genes in soil exposed to wastewater treatment plant effluent. *Sustainability*. 2024;16(16):7022. doi: [10.3390/su16167022](https://doi.org/10.3390/su16167022).
- Phan D, Bhattacharjee AS, Hanan D, Park S, Herrera D, Ashworth D, et al. Dissemination of antimicrobial resistance in agricultural ecosystems following irrigation with treated municipal wastewater. *Sci Total Environ*. 2024;934:173288. doi: [10.1016/j.scitotenv.2024.173288](https://doi.org/10.1016/j.scitotenv.2024.173288).
- Pagalung E, Hough R, Avery L, Robinson L, Freitag T, Coull M, et al. Antibiotic resistance patterns in soils across the Scottish landscape. *Commun Earth Environ*. 2023;4(1):403. doi: [10.1038/s43247-023-01057-0](https://doi.org/10.1038/s43247-023-01057-0).
- Taviani E, van den Berg H, Nhassengo F, Nguluve E, Paulo J, Pedro O, et al. Occurrence of waterborne pathogens and antibiotic resistance in water supply systems in a small town in Mozambique. *BMC Microbiol*. 2022;22(1):243. doi: [10.1186/s12866-022-02654-3](https://doi.org/10.1186/s12866-022-02654-3).
- Akhtar K, Farhana N, Hossain A, Khanam F. Molecular characterization of antimicrobial resistance organisms from drinking water and wastewater in a metropolitan city. *medRxiv [Preprint]*. April 15, 2024. Available from: <https://www.medrxiv.org/content/10.1101/2024.04.12.24305711v1>.
- Homeier-Bachmann T, Heiden SE, Lübcke PK, Bachmann L, Bohnert JA, Zimmermann D, et al. Antibiotic-resistant *Enterobacteriaceae* in wastewater of abattoirs. *Antibiotics (Basel)*. 2021;10(5):568. doi: [10.3390/antibiotics10050568](https://doi.org/10.3390/antibiotics10050568).
- Galarde-López M, Velazquez-Meza ME, Bobadilla-Del-Valle M, Carrillo-Quiroz BA, Cornejo-Juárez P, Ponce-de-León A, et al. Surveillance of antimicrobial resistance in hospital wastewater: identification of carbapenemase-producing *Klebsiella* spp. *Antibiotics (Basel)*. 2022;11(3):288. doi: [10.3390/antibiotics11030288](https://doi.org/10.3390/antibiotics11030288).
- Al-Mustapha AI, Tiwari A, Johansson V, Heljanko V, Kirsimaarit L, Lipponen A, et al. Characterization of methicillin resistant *Staphylococcus aureus* in municipal wastewater in Finland. *One Health*. 2024;19:100881. doi: [10.1016/j.onehlt.2024.100881](https://doi.org/10.1016/j.onehlt.2024.100881).
- Endalamaw K, Tadesse S, Asmare Z, Kebede D, Erkihun M, Abera B. Antimicrobial resistance profile of bacteria from hospital wastewater at two specialized hospitals in Bahir Dar city, Ethiopia. *BMC Microbiol*. 2024;24(1):525. doi: [10.1186/s12866-024-03693-8](https://doi.org/10.1186/s12866-024-03693-8).
- Sonola VS, Misinzo G, Matee MI. Occurrence of multidrug-resistant *Staphylococcus aureus* among humans, rodents, chickens, and household soils in Karatu, Northern Tanzania. *Int J Environ Res Public Health*. 2021;18(16):8496. doi: [10.3390/ijerph18168496](https://doi.org/10.3390/ijerph18168496).

- 10.3390/ijerph18168496.
31. Joseph OJ, Ogunleye GE, Oyinlola KA, Balogun AI, Olumeko DT. Co-occurrence of heavy metals and antibiotics resistance in bacteria isolated from metal-polluted soil. *Environ Anal Health Toxicol.* 2023;38(4):e2023024-0. doi: [10.5620/eaht.2023024](https://doi.org/10.5620/eaht.2023024).
 32. Sonola VS, Katakweba AS, Misinzo G, Matee MIN. Occurrence of multidrug-resistant *Escherichia coli* in chickens, humans, rodents and household soil in Karatu, Northern Tanzania. *Antibiotics (Basel).* 2021;10(9):1137. doi: [10.3390/antibiotics10091137](https://doi.org/10.3390/antibiotics10091137).
 33. Odum EI, Idise OE, Ogogo DI. Multidrug resistant bacteria in dumpsite soils within Abraka, Delta state, Nigeria. *FUDMA J Sci.* 2020;4(2):639-44. doi: [10.33003/fjs-2020-0402-196](https://doi.org/10.33003/fjs-2020-0402-196).
 34. Ngene AC, Ohaegbu CG, Awom IE, Egbere JO, Onyimba IA, Coulthard OD, et al. High prevalence of multidrug-resistant *Enterobacteriaceae* isolated from wastewater and soil in Jos metropolis, Plateau state, Nigeria. *Afr J Bacteriol Res.* 2021;13(2):22-9. doi: [10.5897/jbr2021.0336](https://doi.org/10.5897/jbr2021.0336).
 35. Permatasari DA, Witaningrum AM, Wibisono FJ, Effendi MH. Detection and prevalence of multidrug-resistant *Klebsiella pneumoniae* strains isolated from poultry farms in Blitar, Indonesia. *Biodiversitas.* 2020;21(10):4642-7. doi: [10.13057/biodiv/d211024](https://doi.org/10.13057/biodiv/d211024).
 36. Lopes ES, Parente CE, Picão RC, Seldin L. Irrigation ponds as sources of antimicrobial-resistant bacteria in agricultural areas with intensive use of poultry litter. *Antibiotics (Basel).* 2022;11(11):1650. doi: [10.3390/antibiotics11111650](https://doi.org/10.3390/antibiotics11111650).
 37. Manishimwe R, Moncada PM, Musanayire V, Shyaka A, Scott HM, Loneragan GH. Antibiotic-resistant *Escherichia coli* and *Salmonella* from the feces of food animals in the east province of Rwanda. *Animals (Basel).* 2021;11(4):1013. doi: [10.3390/ani11041013](https://doi.org/10.3390/ani11041013).
 38. Stiborova H, Kracmarova M, Vesela T, Biesiekierska M, Cerny J, Balik J, et al. Impact of long-term manure and sewage sludge application to soil as organic fertilizer on the incidence of pathogenic microorganisms and antibiotic resistance genes. *Agronomy.* 2021;11(7):1423. doi: [10.3390/agronomy11071423](https://doi.org/10.3390/agronomy11071423).
 39. Ibrahim A, Habibu UA. Isolation and characterization of multidrug-resistant *Escherichia coli* from poultry litter samples from selected farms in Kano metropolis, Nigeria. *Niger J Microbiol.* 2021;35(1):5623-9.
 40. Maganga R, Sindiyo E, Musyoki VM, Shirima G, Maina B, Mmbaga BT. Antimicrobial resistant coliforms across four poultry production systems in Arusha and Moshi, Tanzania. *PAMJ One Health.* 2022;7(4):1-15. doi: [10.11604/pamj-oh.2022.7.4.29800](https://doi.org/10.11604/pamj-oh.2022.7.4.29800).
 41. Velhner M, Prunić B, Aleksić N, Todorović D, Knežević S, Ljubojević Pečić D. Antimicrobial resistance of *Enterococcus* isolates from poultry farms in the Republic of Serbia (autonomous province of Vojvodina). *Microorganisms.* 2024;12(7):1483. doi: [10.3390/microorganisms12071483](https://doi.org/10.3390/microorganisms12071483).
 42. Timofeeva AM, Galyamova MR, Krivosheev DM, Karabanov SY, Sedykh SE. Investigation of antibiotic resistance of *E. coli* associated with farm animal feces with participation of citizen scientists. *Microorganisms.* 2024;12(11):2308. doi: [10.3390/microorganisms12112308](https://doi.org/10.3390/microorganisms12112308).
 43. Kakooza S, Tayebwa DS, Njalira KR, Kayaga EB, Asiimwe I, Komugisha M, et al. Reflections on drivers for the emergence and spread of antimicrobial resistant bacteria detected from chickens reared on commercial layer farms in Mukono district, Uganda. *Vet Med (Auckl).* 2023;14:209-19. doi: [10.2147/vmrr.S418624](https://doi.org/10.2147/vmrr.S418624).
 44. Ogundare ST, Fasina FO, Makumbi JP, van der Zel GA, Geertsma PF, Kock MM, et al. Epidemiology and antimicrobial resistance profiles of pathogenic *Escherichia coli* from commercial swine and poultry abattoirs and farms in South Africa: a One Health approach. *Sci Total Environ.* 2024;951:175705. doi: [10.1016/j.scitotenv.2024.175705](https://doi.org/10.1016/j.scitotenv.2024.175705).
 45. Logtong EG, Zakpaa HD. The assessment of antibiotic resistant bacteria in pharmaceutical effluents from major pharmaceutical companies in Accra, Ghana. *Ghana J Sci Technol Dev.* 2024;10(1):50-68.
 46. Mahmud MS, Hosen MA, Hossion MI, Sadik Sabuj MS, Rumi NA, Hossain MK, et al. Isolation, identification, and characterization of resistant bacteria to antibiotics from pharmaceutical effluent and study of their antibiotic resistance. *Front Microbiol.* 2023;14:1307291. doi: [10.3389/fmicb.2023.1307291](https://doi.org/10.3389/fmicb.2023.1307291).
 47. Bae D, Macoy DM, Ahmad W, Peseth S, Kim B, Chon JW, et al. Distribution and characterization of antimicrobial resistant pathogens in a pig farm, slaughterhouse, meat processing plant, and in retail stores. *Microorganisms.* 2022;10(11):2252. doi: [10.3390/microorganisms10112252](https://doi.org/10.3390/microorganisms10112252).
 48. Solomon FB, Wadilo FW, Arota AA, Abraham YL. Antibiotic resistant airborne bacteria and their multidrug resistance pattern at university teaching referral hospital in South Ethiopia. *Ann Clin Microbiol Antimicrob.* 2017;16(1):29. doi: [10.1186/s12941-017-0204-2](https://doi.org/10.1186/s12941-017-0204-2).
 49. Bayle S, Drapeau A, Rocher J, Laurent F, Métayer V, Haenni M, et al. Characterization of cultivable airborne bacteria and their antimicrobial resistance pattern in French milking parlour. *Environ Sci Pollut Res Int.* 2021;28(9):11689-96. doi: [10.1007/s11356-020-11974-8](https://doi.org/10.1007/s11356-020-11974-8).
 50. Atalay YA, Mengistie E, Tolcha A, Birhan B, Asmare G, Gebeyehu NA, et al. Indoor air bacterial load and antibiotic susceptibility pattern of isolates at Adare General Hospital in Hawassa, Ethiopia. *Front Public Health.* 2023;11:1194850. doi: [10.3389/fpubh.2023.1194850](https://doi.org/10.3389/fpubh.2023.1194850).
 51. Bągoszewska E, Biedroń I. Indoor air quality and potential health risk impacts of exposure to antibiotic resistant bacteria in an office rooms in Southern Poland. *Int J Environ Res Public Health.* 2018;15(11):2604. doi: [10.3390/ijerph15112604](https://doi.org/10.3390/ijerph15112604).
 52. Khan BA, Roy S, Tahsin N, Baidya K, Das KC, Islam MS, et al. Antibiotic resistance of bioaerosols in particulate matter from indoor environments of the hospitals in Dhaka Bangladesh. *Sci Rep.* 2024;14(1):29884. doi: [10.1038/s41598-024-81376-0](https://doi.org/10.1038/s41598-024-81376-0).
 53. Cheng G, Ning J, Ahmed S, Huang J, Ullah R, An B, et al. Selection and dissemination of antimicrobial resistance in agri-food production. *Antimicrob Resist Infect Control.* 2019;8:158. doi: [10.1186/s13756-019-0623-2](https://doi.org/10.1186/s13756-019-0623-2).
 54. Wu J, Wang J, Li Z, Guo S, Li K, Xu P, et al. Antibiotics and antibiotic resistance genes in agricultural soils: a systematic analysis. *Crit Rev Environ Sci Technol.* 2023;53(7):847-64. doi: [10.1080/10643389.2022.2094693](https://doi.org/10.1080/10643389.2022.2094693).
 55. Kelbrick M, Hesse E, O'Brien S. Cultivating antimicrobial resistance: how intensive agriculture ploughs the way for antibiotic resistance. *Microbiology (Reading).* 2023;169(8):001384. doi: [10.1099/mic.0.001384](https://doi.org/10.1099/mic.0.001384).
 56. Pepi M, Focardi S. Antibiotic-resistant bacteria in aquaculture and climate change: a challenge for health in the Mediterranean area. *Int J Environ Res Public Health.* 2021;18(11):5723. doi: [10.3390/ijerph18115723](https://doi.org/10.3390/ijerph18115723).
 57. Taylor P, Reeder R. Antibiotic use on crops in low and middle-income countries based on recommendations made by agricultural advisors. *CABI Agric Biosci.* 2020;1(1):1. doi: [10.1186/s43170-020-00001-y](https://doi.org/10.1186/s43170-020-00001-y).
 58. Hubeny J, Harnisz M, Korzeniewska E, Buta M, Zieliński W, Rolbiecki D, et al. Industrialization as a source of heavy metals and antibiotics which can enhance the antibiotic resistance in wastewater, sewage sludge and river water. *PLoS One.* 2021;16(6):e0252691. doi: [10.1371/journal.pone.0252691](https://doi.org/10.1371/journal.pone.0252691).
 59. Gashaw M, Gudina EK, Tadesse W, Froeschl G, Ali S, Seeholzer T, et al. Hospital wastes as potential sources for multidrug-resistant ESBL-producing bacteria at a tertiary hospital in

- Ethiopia. *Antibiotics* (Basel). 2024;13(4):374. doi: [10.3390/antibiotics13040374](https://doi.org/10.3390/antibiotics13040374).
60. Mehanni MM, Gadow SI, Alshammari FA, Modafar Y, Ghanem KZ, El-Tahtawi NF, et al. Antibiotic-resistant bacteria in hospital wastewater treatment plant effluent and the possible consequences of its reuse in agricultural irrigation. *Front Microbiol.* 2023;14:1141383. doi: [10.3389/fmicb.2023.1141383](https://doi.org/10.3389/fmicb.2023.1141383).
 61. Perry MR, Lepper HC, McNally L, Wee BA, Munk P, Warr A, et al. Secrets of the hospital underbelly: patterns of abundance of antimicrobial resistance genes in hospital wastewater vary by specific antimicrobial and bacterial family. *Front Microbiol.* 2021;12:703560. doi: [10.3389/fmicb.2021.703560](https://doi.org/10.3389/fmicb.2021.703560).
 62. Samtiya M, Matthews KR, Dhewa T, Puniya AK. Antimicrobial resistance in the food chain: trends, mechanisms, pathways, and possible regulation strategies. *Foods.* 2022;11(19):2966. doi: [10.3390/foods11192966](https://doi.org/10.3390/foods11192966).
 63. Oniciuc EA, Likotrafiti E, Alvarez-Molina A, Prieto M, López M, Alvarez-Ordóñez A. Food processing as a risk factor for antimicrobial resistance spread along the food chain. *Curr Opin Food Sci.* 2019;30:21-6. doi: [10.1016/j.cofs.2018.09.002](https://doi.org/10.1016/j.cofs.2018.09.002).
 64. Lee G, Yoo K. A review of the emergence of antibiotic resistance in bioaerosols and its monitoring methods. *Rev Environ Sci Biotechnol.* 2022;21(3):799-827. doi: [10.1007/s1157-022-09622-3](https://doi.org/10.1007/s1157-022-09622-3).
 65. Zhou Z, Shuai X, Lin Z, Yu X, Ba X, Holmes MA, et al. Association between particulate matter PM_{2.5} air pollution and clinical antibiotic resistance: a global analysis. *Lancet Planet Health.* 2023;7(8):e649-59. doi: [10.1016/s2542-5196\(23\)00135-3](https://doi.org/10.1016/s2542-5196(23)00135-3).
 66. Wang W, Weng Y, Luo T, Wang Q, Yang G, Jin Y. Antimicrobial and the resistances in the environment: ecological and health risks, influencing factors, and mitigation strategies. *Toxics.* 2023;11(2):185. doi: [10.3390/toxics11020185](https://doi.org/10.3390/toxics11020185).
 67. Jin L, Xie J, He T, Wu D, Li X. Airborne transmission as an integral environmental dimension of antimicrobial resistance through the “One Health” lens. *Crit Rev Environ Sci Technol.* 2022;52(23):4172-93. doi: [10.1080/10643389.2021.2006537](https://doi.org/10.1080/10643389.2021.2006537).
 68. Oliveira M, Antunes W, Mota S, Madureira-Carvalho Á, Dinis-Oliveira RJ, Dias da Silva D. An overview of the recent advances in antimicrobial resistance. *Microorganisms.* 2024;12(9):1920. doi: [10.3390/microorganisms12091920](https://doi.org/10.3390/microorganisms12091920).
 69. Warren J, Schmidt W. *Environmental Antimicrobial Resistance: Review of Biological Methods.* Bristol: Environment Agency; 2023.
 70. Yamin D, Uskoković V, Wakil AM, Goni MD, Shamsuddin SH, Mustafa FH, et al. Current and future technologies for the detection of antibiotic-resistant bacteria. *Diagnostics* (Basel). 2023;13(20):3246. doi: [10.3390/diagnostics13203246](https://doi.org/10.3390/diagnostics13203246).
 71. Hassall J, Coxon C, Patel VC, Goldenberg SD, Sergaki C. Limitations of current techniques in clinical antimicrobial resistance diagnosis: examples and future prospects. *NPJ Antimicrob Resist.* 2024;2(1):16. doi: [10.1038/s44259-024-00033-8](https://doi.org/10.1038/s44259-024-00033-8).
 72. Awang MS, Bustami Y, Hamzah HH, Zambry NS, Najib MA, Khalid MF, et al. Advancement in *Salmonella* detection methods: from conventional to electrochemical-based sensing detection. *Biosensors* (Basel). 2021;11(9):346. doi: [10.3390/bios11090346](https://doi.org/10.3390/bios11090346).
 73. Zhang S, Li X, Wu J, Coin L, O'Brien J, Hai F. Molecular methods for pathogenic bacteria detection and recent advances in wastewater analysis. *Water.* 2021;13(24):3551. doi: [10.3390/w13243551](https://doi.org/10.3390/w13243551).
 74. Xing X, Liu JS, Zhong W. MetaGen: reference-free learning with multiple metagenomic samples. *Genome Biol.* 2017;18(1):187. doi: [10.1186/s13059-017-1323-y](https://doi.org/10.1186/s13059-017-1323-y).
 75. Lema NK, Gameda MT, Woldeesemayat AA. Recent advances in metagenomic approaches, applications, and challenge. *Curr Microbiol.* 2023;80(11):347. doi: [10.1007/s00284-023-03451-5](https://doi.org/10.1007/s00284-023-03451-5).
 76. Deutschbauer AM, Chivian D, Arkin AP. Genomics for environmental microbiology. *Curr Opin Biotechnol.* 2006;17(3):229-35. doi: [10.1016/j.copbio.2006.04.003](https://doi.org/10.1016/j.copbio.2006.04.003).
 77. Huang CW, Lin C, Nguyen MK, Hussain A, Bui XT, Ngo HH. A review of biosensor for environmental monitoring: principle, application, and corresponding achievement of sustainable development goals. *Bioengineered.* 2023;14(1):58-80. doi: [10.1080/21655979.2022.2095089](https://doi.org/10.1080/21655979.2022.2095089).
 78. Gavrilaş S, Ursachi C, Perța-Crișan S, Munteanu FD. Recent trends in biosensors for environmental quality monitoring. *Sensors* (Basel). 2022;22(4):1513. doi: [10.3390/s22041513](https://doi.org/10.3390/s22041513).
 79. Galhano BS, Ferrari RG, Panzenhagen P, de Jesus AC, Conte-Junior CA. Antimicrobial resistance gene detection methods for bacteria in animal-based foods: a brief review of highlights and advantages. *Microorganisms.* 2021;9(5):923. doi: [10.3390/microorganisms9050923](https://doi.org/10.3390/microorganisms9050923).
 80. Méndez-García C, Bargiela R, Martínez-Martínez M, Ferrer M. Metagenomic protocols and strategies. In: Nagarajan M, ed. *Metagenomics.* Academic Press; 2018. p. 15-54. doi: [10.1016/b978-0-08-102268-9.00002-1](https://doi.org/10.1016/b978-0-08-102268-9.00002-1).
 81. Mach KE, Mohan R, Baron EJ, Shih MC, Gau V, Wong PK, et al. A biosensor platform for rapid antimicrobial susceptibility testing directly from clinical samples. *J Urol.* 2011;185(1):148-53. doi: [10.1016/j.juro.2010.09.022](https://doi.org/10.1016/j.juro.2010.09.022).
 82. Karp BE, Tate H, Plumblee JR, Dessai U, Whichard JM, Thacker EL, et al. National antimicrobial resistance monitoring system: two decades of advancing public health through integrated surveillance of antimicrobial resistance. *Foodborne Pathog Dis.* 2017;14(10):545-57. doi: [10.1089/fpd.2017.2283](https://doi.org/10.1089/fpd.2017.2283).
 83. Ng C, Gin KY. Monitoring antimicrobial resistance dissemination in aquatic systems. *Water.* 2019;11(1):71. doi: [10.3390/w11010071](https://doi.org/10.3390/w11010071).
 84. Hendriksen RS, Munk P, Njage P, van Bunnik B, McNally L, Lukjancenko O, et al. Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage. *Nat Comm.* 2019;10(1):1124. doi: [10.1038/s41467-019-08853-3](https://doi.org/10.1038/s41467-019-08853-3).
 85. Fuhrmeister ER, Larson JR, Kleinschmit AJ, Kirby JE, Pickering AJ, Bascom-Slack CA. Combating antimicrobial resistance through student-driven research and environmental surveillance. *Front Microbiol.* 2021;12:577821. doi: [10.3389/fmicb.2021.577821](https://doi.org/10.3389/fmicb.2021.577821).
 86. World Health Organization (WHO), Food and Agriculture Organization of the United Nations (FAO), World Organisation for Animal Health (OIE). *Monitoring and Evaluation of the Global Action Plan on Antimicrobial Resistance: Framework and Recommended Indicators.* WHO, FAO, OIE; 2019.
 87. Honda R, Kumar M, Mardalisa, Wang R, Sabar MA, Chaminda T, et al. Recommendations of key elements within an integrated monitoring framework of antimicrobial resistance for Asian countries. *Environ Sci Technol Lett.* 2023;11(1):5-8. doi: [10.1021/acs.estlett.3c00820](https://doi.org/10.1021/acs.estlett.3c00820).
 88. Frost I, Kapoor G, Craig J, Liu D, Laxminarayan R. Status, challenges and gaps in antimicrobial resistance surveillance around the world. *J Glob Antimicrob Resist.* 2021;25:222-6. doi: [10.1016/j.jgar.2021.03.016](https://doi.org/10.1016/j.jgar.2021.03.016).
 89. Burch TR, Newton RJ, Kimbell LK, LaMartina EL, O'Malley K, Thomson SM, et al. Targeting current and future threats: recent methodological trends in environmental antimicrobial resistance research and their relationships to risk assessment. *Environ Sci Water Res Technol.* 2022;8(9):1787-802. doi: [10.1039/d2ew00087c](https://doi.org/10.1039/d2ew00087c).
 90. Kaiser RA, Taing L, Bhatia H. Antimicrobial resistance and environmental health: a water stewardship framework for global and national action. *Antibiotics* (Basel). 2022;11(1):63.