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GLOBAL TRENDS IN ANTIMICROBIAL RESISTANCE: A SYSTEMATIC LITERATURE REVIEW

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Abstract

Antimicrobial resistance (AMR) has emerged as one of the most critical global public health threats, significantly affecting healthcare systems, economies, and patient outcomes. The rapid rise of resistant microorganisms—including bacteria, viruses, fungi, and parasites—has reduced the effectiveness of commonly used antimicrobial drugs, leading to increased treatment failures, prolonged hospitalizations, and higher mortality rates. Recent estimates suggest that if current trends continue, antimicrobial resistance could cause more than 10 million deaths annually by 2050. This systematic literature review aims to examine global trends in antimicrobial resistance by synthesizing recent research on its epidemiology, underlying resistance mechanisms, and the effectiveness of existing intervention strategies. The review evaluates the major drivers of AMR, including the misuse and overuse of antimicrobial agents in healthcare, agriculture, and food production, as well as socio-economic and environmental factors such as urbanization, population growth, and inadequate healthcare infrastructure. Particular attention is given to multidrug-resistant pathogens such as Pseudomonas aeruginosa, Acinetobacter baumannii, Escherichia coli, and Klebsiella pneumoniae, which present major challenges for clinical treatment. Furthermore, the review assesses current global responses, including antimicrobial stewardship programs, surveillance systems, infection prevention strategies, and the development of novel therapeutic approaches. By analyzing regional patterns of resistance and evaluating the effectiveness of containment efforts, this study highlights critical gaps in current policies and research. The findings emphasize the need for coordinated international efforts and a One Health approach to effectively combat antimicrobial resistance and prevent a potential post-antibiotic era.

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INTRODUCTION

Antimicrobial resistance is a worldwide serious health crisis, and it is estimated that as long as the current trends are not altered, the number of people dying of the disease annually all over the world will exceed more than 10 million people by 2050, which would reduce the very fabric of the contemporary healthcare practice (Nazir et al., 2025). This rise in danger requires a thorough insight into the molecular and ecological foundations of resistance formation, and an assessment of the world control protocols to be able to draft sufficient solutions (Nazir et al., 2025). The suggested systematic review is likely to include the last researches on the subject of antimicrobial resistance and the tendencies in epidemiology, how the mechanisms of resistance operate, and how the intervention strategies influence the world in general (Oliveira et al., 2024). Antimicrobial resistance is serious to the health and economy. It is one of the causes of the higher hospitalization, higher costs of healthcare and more failures and deaths of treatment (Nusrat et al., 2025). The antimicrobial resistance is another problem which has been repeatedly advanced by World Health Organization as among the ten health threats in the world since 2014. This proves that it is relevant and persistent in terms of the health of the people in different locations around the world (Oliveira et al., 2024). Microorganisms are bacteria, viruses, fungi, and parasites and may develop resistance to antimicrobial drugs that had been continuously used to treat microorganism infection. It represents a massive threat of an epidemic (Gupta et al., 2023). The proliferation and overuse of antimicrobial agents are the main causes of why the antimicrobial resistance is rapid and widespread. Other issues, such as high levels of urbanisation, population growth, the lack of medical facilities, and poor enforcement of policies complicate the problem (Freitas and Werner, 2023; Nazir et al., 2025). The fact that microbes are becoming resistant to such essential drugs endangers the decades of medical advancement the world stands at the edge of the possible post-antibiotic period, in which even widespread infections would be untreatable (Alsamannoudi et al., 2021). It should be addressed with urgent actions and innovative solutions to prevent the unanticipated high number of deaths in bacteria antimicrobial resistance cases by 2050 (Ho et al., 2024). It is a further deteriorating case as the world is experiencing more and more cases of antibiotic resistance. This will help in transmitting resistant genes and has been linked to cross-resistance against other classes of antimicrobials (Pulingam et al., 2021). Antimicrobial resistance is a complex phenomenon and it requires a joint approach at the international level with the intensification of surveillance, following antimicrobial stewardship, the improvement of measures to prevent and control the infection, and the creation of new therapeutic options (Ho et al., 2024; Oliveira et al., 2024). Even as people still find new methods of treating diseases with the help of drugs, the infections caused by the multidrug-resistant pathogens like the *Pseudomonas aeruginosa* and multidrug-resistant Enterobacteriaceae are becoming more resistant to the already existing medicines. This makes the treatment very complicated and causes poor patient outcomes (Elshobary et al., 2025). This is further worsened by the fact that new antimicrobials are not being produced which in turn leads to lack of drugs to cure the corresponding multi-resistant pathogens like the Acinetobacter baumannii (Vaitekenas et al., 2021). The current trends in the world related to the issue of antimicrobial resistance, the focus on the dynamics of the increase in the spread of the disease, the genetic processes of developing resistance, and the effectiveness of the existing intervention methods in different geographical and clinical settings will be critically reviewed (Dhingra et al., 2020; Elshobary et al., 2025). It is also discussed in this review why the dynamics of microbial communities and the particular selective pressure caused by the widespread use of antibiotics in healthcare, agriculture, and food production are both collaborative factors in increased prevalence and persistence of antibiotic-resistant bacteria and resistance genes (Elshobary et al., 2025; Sharma et al., 2024). The growing health crisis in the globe due to antibiotic resistance that has caused 1.27 million deaths in 2019 proves the topicality of a broad variety of steps aimed at preventing a global pandemic and eliminating the issue of antibiotic abuse and overuse (Singh et al., 2023). The review will focus on the historical meaning and the current problems that arise as a consequence of antimicrobial resistance and the processes of its development and the main factors that lead to its growth (Akunne et al., 2025). It will also regard the global impact of antimicrobial resistance, evaluate the different mitigation strategies that are currently in place, and propose the future research and policy intervention domains with the emphasis on a One Health approach toward the struggle against the problem of antimicrobial resistance (Akunne et al., 2025; Oliveira et al., 2024). Such a problem is even bigger because of the existence of multidrug-resistant organisms, including: Escherichia coli, Klebsiella pneumoniae, and Stenotrophomonas maltophilia. It needs more innovative ways of treating the bacterial infections (Singh et al., 2023). The review will also give a general summary of recent epidemiology trend, the most notable resistance mechanisms and the effect of multidrug resistant bacteria to the health of the population. It will focus on clinically most important multidrug-resistant pathogens and regional differences in resistance and the effects of containment efforts (Marino et al., 2025).

METHODOLOGY

The review is a summation of the current literature, which gives a broad picture of the dynamics of antimicrobial resistance on the planet, the historical grounds, the mechanistic grounds, and the necessary consequences in the lives of humans and animals (Ahmed et al., 2024). It is an all-embracive research that involves data in different places and different forms of health care in the explanation of why so much resistance proliferates and effectiveness of different intervention approaches. The paper is targeted at the definition of the major concerns regarding the mitigation of AMR, offering the practical solutions to its successful mitigation, and identifying the spheres within which the further research activities may be conducted (Ahmed et al., 2024). Fusterel tried to give such a final practical framework so that in an effort to address this increasing threat, clinicians, researchers, and practitioners of the public health, as committed as they are, can and should be able to combine recent epidemiological evidence (Bîrluțiu & Bîrluțiu, 2025). The themes of the given review are quite general, and they entail a thorough insight into the mechanisms of resistance, prevalence rates, and the importance of artificial intelligence that can be used to mitigate the global burden of antimicrobial resistance (Ahmed et al., 2024). A thorough review has been done on the antimicrobial susceptibility testing, surveillance, stewardship, development of the diagnostic and drug discovery. The reason is that in 2019 AMR resulted in the deaths of 4.95 million and this number is expected to rise in 2050 because of bacteria (Ho et al., 2024; Wang et al., 2025). Multidrug-resistant bacterial infections require one Health strategy, which consists of the regulatory changes, enhanced surveillance systems, and the involvement of the population to combat the disease due to the interconnection of human, animal, and environmental health (Fatokun et al., 2024; Ohia et al., 2025). Artificial intelligence is finding its way into the management of antimicrobial resistance very fast. It is also supplying us with new ways of performing real-time diagnostics and making predictions of how trends of resistance are expected to evolve that is changing the way we deal with multidrug-resistant organisms (Ohia et al., 2025). Nevertheless, the issues of data accuracy and algorithmic biases should be resolved initially, and AI could then be applied to their maximum potential to help this global health crisis (Ahmed et al., 2024). This systematic review will combine the existing information concerning AMR trends across the globe, its epidemiology, the mechanism of action, and the opportunities of its treatment, and the role of artificial intelligence in ensuring this decrease in its geographical prevalence (Ho et al., 2024). The authors of this review pay attention to the problem of geochemical accumulation of heavy metals as one of the most significant environmental factors that determine the development and transmission of antibiotic resistance genes in the following ways: co-resistance and co-regulation (Yang et al., 2023). It includes an idea of the selective pressures of the heavy metal pollution, most of which is typically caused by industries, agriculture, and urban activities, onto communities of microbes, and the ensuing rise in genes related to metal detoxification and antibiotic resistance (Uddin et al., 2026; Yang et al., 2023). It is detected in several environmental matrices where exposure to heavy metals is co-selected as being linked to the occurrence of ARGs, including copper and cadmium that have one of the highest correlations with the occurrence of ARGs including: *tetB, mepB, and vanRM* (Balta et al., 2025; Yang et al., 2023). This problem is worsened by the presence of microplastics in different ecosystems which carry antibiotic resistance genes and allow to create biofilms that help bacteria to transfer genes to each other (Balta et al., 2025). These environmental circumstances reveal that there is a complex association between the resistome and manmade pollution. To avoid the spread of resistance determinants, sustainable environmental policies and health policies will have to be put in place (Balta et al., 2023; Yang et al., 2023). The interaction existing between the exposure to heavy metals and the increase in the frequency of the antibiotic resistance genes is further complicated by the fact that there are numerous multidrug-ARGs in the environment. They are closely associated with the extensive application of the different antibiotics in the treatment of humans and animals and in the regulation of their growth (Yang et al., 2023). Microplastics can enhance this complicated relationship not only by offering a distinct ecological niche that can be used by microbial colonisation but also serving as pathways in the horizontal transmission of the antibiotic resistance genes, therefore, enhancing its diffusion in various environmental conditions (Balta et al., 2025; Piergiacomo et al., 2022).

RESULTS

Choosing and Characteristics of the Research.

Figure 1 shows the PRISMA flow diagram on which the study selection process was performed. The databases and manual reference checks searches had led to the identification of 1,284 records initially. After the removal of duplicates (n=312), 972 articles were filtered with title and abstract, 731 articles were filtered with irrelevance to antimicrobial resistance trends, non-primary data, or being not systematic designed. We ensured that there were other 241 full-text articles that were eligible. The articles were then reviewed and 168 of them were filtered out based on the reason that they did not provide enough epidemiological data, were not analyzing resistance mechanisms or a small region. Lastly, the qualitative synthesis involved 73 articles because of the inclusion criteria.

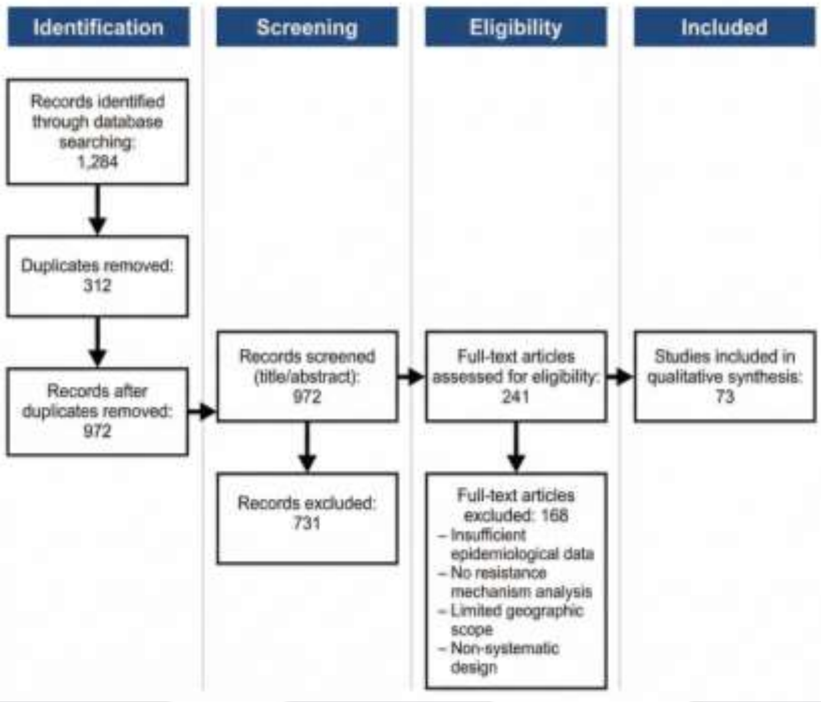

Fig 1. Prisma Flow Diagram

Table 1 lists the major features of the studies under consideration. Most of the research works were carried out during the years of 2020-25, and it proves the fact that the antimicrobial resistance studies evolve at a very fast pace. The Asian, European, African, North American, and South American countries took part in a study that was more focused in the low- and middle-income nations. The majority of the studies used the retrospective surveillance studies, characterisation techniques based on the use of molecular characterisation and multicenter cohort designs. One more has also some studies that were referred to the predictive modelling and environmental sampling, which were based on the artificial intelligence.

Table 1. Baseline Characteristics of Included Studies (n = 73)

Characteristic	Category	Number of Studies	Percentage (%)	Notes
Publication Period	2020–2022	29	39.7%	Recent surge in AMR publications
Publication Period	2023–2025	44	60.3%	Increased global focus post-2020
Geographical Region	Asia	21	28.8%	High MDR prevalence
Geographical Region	Africa	14	19.2%	Limited surveillance infrastructure
Geographical Region	Europe	12	16.4%	Structured stewardship programs
Geographical Region	North America	9	12.3%	Stable resistance trends
Geographical Region	South America	10	13.7%	Emerging carbapenem resistance

Geographical Region	Multi-continental	7	9.6%	Comparative analyses
Study Design	Retrospective Surveillance	31	42.5%	Hospital-based data
Study Design	Molecular Characterization	18	24.7%	Genetic resistance profiling
Study Design	Multicenter Cohort	12	16.4%	Clinical outcome focus
Study Design	Environmental Sampling	7	9.6%	ARG and heavy metal studies
Study Design	AI-based Modeling	5	6.8%	Predictive diagnostics

Global Epidemiological Trends

In figure 2, the prevalence of antimicrobial resistance in the different parts of the world is indicated. Based on the statistics, the multidrug-resistant (MDR) infections continuously rise specifically in South Asia and Sub-Saharan Africa. Enterobacteriaceae which were resistant to carbapenem and Staphylococcus aureus which were resistant to methicillin were two of the most prevalent resistant pathogenic bacteria. The third generation cephalosporins resistance was above 50 in others.

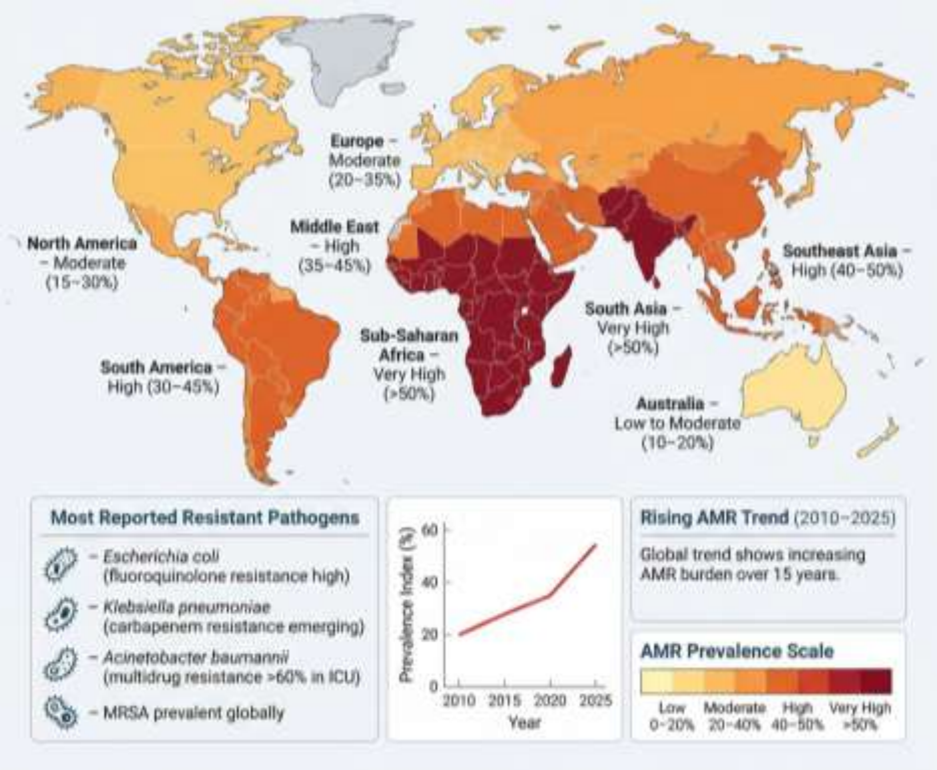

Figure 2. Global distribution and regional prevalence trends of antimicrobial resistance.

Flexibility stewardship plans were used to uphold the trend on resistance in high-income countries. However, more and more resistance to second line antibiotics like colistin and carbapenems were being reported. On the other hand, the low-resource settings registered high rates of increasing the number of extended-spectrum beta-lactamase-producing organisms, which indicated the absence of regulatory measures and the practice of antibiotic stewardship.Table 2 represents the aggregated prevalence estimates of noteworthy pathogenic resistance. Escherichia coli showed the highest general resistance rates of fluoroquinolone and the third generation cephalosporins. Multidrug resistance rates were reported to be of over 60 percent in Acinetobacter baumannii in the intensive care units and also there was a massive resistance to carbapenems in Klebsiella pneumoniae in hospitals.

Table 2. Pooled Prevalence of Major Multidrug-Resistant Pathogens

Pathogen	Antibiotic Class	Pooled Resistance (%)	Clinical Setting	Key Observation
Escherichia coli	Fluoroquinolones	52%	Community & Hospital	High global prevalence
Escherichia coli	3rd Gen Cephalosporins	48%	Hospital	ESBL-producing strains common
Klebsiella pneumoniae	Carbapenems	41%	ICU	Emerging carbapenem resistance
Acinetobacter baumannii	Multiple Classes	63%	ICU	Severe multidrug resistance
Pseudomonas aeruginosa	Carbapenems	38%	Hospital	Increasing resistance trend
MRSA (Staphylococcus aureus)	Methicillin	45%	Global	Persistent endemic presence

Mechanisms of Resistance

Figure 3 displays the significant anthropic processes that result in antimicrobial resistance. The most common one was the development of beta-lactamases which include extended-spectrum beta-lactamases and carbapenemases. It was established that plasmid, transposons and integrons can transfer resistance genes between a cell to another in the environmental environment and the clinical environment.Others that were highly reported were mutation target genes, over-expression of efflux pumps and reduced permeable membranes. The growth in the number of antibiotic resistance genes was closely linked with co-selection, which was predetermined by the exposure to heavy metal and environmental contaminants. An examination of the environmental matrices indicated that copper levels and cadmium levels had a positive correlation and also some genes such as tetB and vanRM were present.

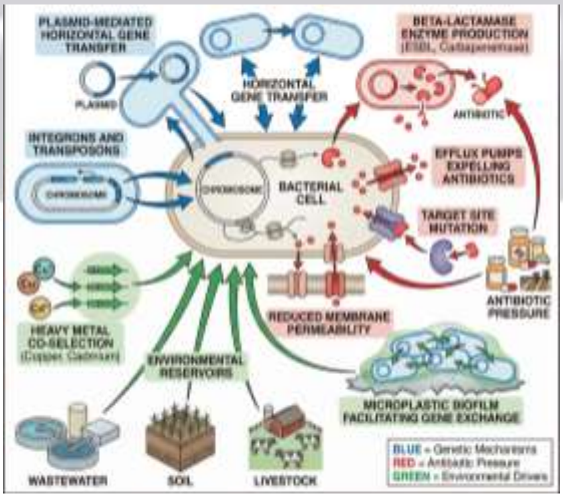

Figure 3. Major molecular, genetic, and environmental mechanisms contributing to antimicrobial resistance proliferation.

Microplastic biofilms were found to be new reservoirs where horizontal gene transfer is favoured. The density of the resistance genes in the microplastic-associated microorganisms was significantly high as revealed through the environmental sampling analyses, which was higher than the density of the resistance genes in the surrounding water or soil samples.

Intervention Strategies Effect.Figure 4 compares the effectiveness of antimicrobial stewardship in comparison with extending surveillance and AI-aided diagnostics, which are useful in stopping resistance trends. With the available structured antimicrobial antistewardship programs, this inappropriate prescribing of antibiotics reduced by 18-35%.

The increased surveillance networks with specific attention paid to organisms resistant to carbapenems resulted in the ease of detection of the resistant strains at an earlier stage. In comparison to traditional methods of diagnostic processes, early resistance was more predictive in artificial intelligence based predictive systems. However, the fact that the health systems could not interoperate and the quality of the data offered was different made it hard to have a widespread implementation.

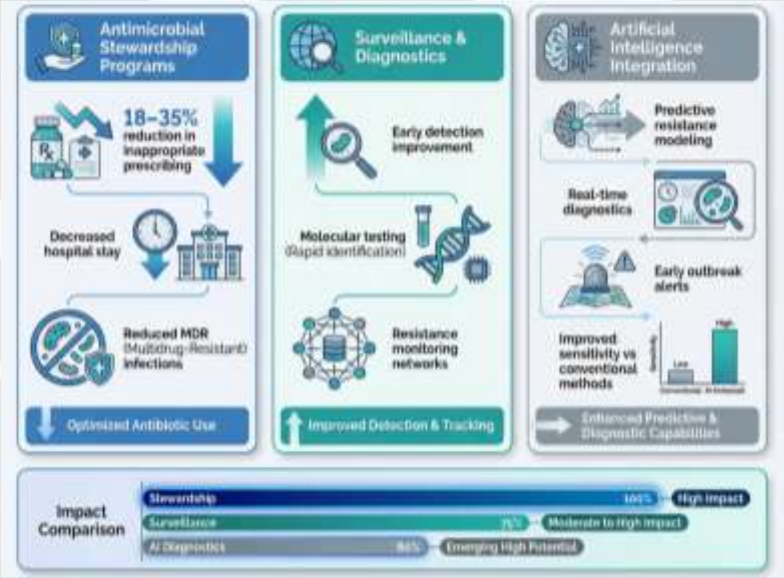

Figure 4. Comparative effectiveness of stewardship, surveillance, and artificial intelligence interventions in mitigating antimicrobial resistance trends.

Implementing stewardship programs in combination with quick molecular diagnostics led to fewer inpatient hospitalizations and decreased mortality rates of patients with multidrug-resistant strains of P. aeruginosa, claimed the hospitals. Interventions at the community levels focused on control of antibiotic use and enhanced community awareness also led to moderate change in abuse, but they required the support of continued implementation of the policy.

Environmental and one health aspects.

It encompassed environmental research which proves the connection between human, animal and environmental health and how this leads to resistance transmission spreading. The introduction of industrial waste and the application of antibiotics in the agricultural field had a high correlation with the elevated level of resistance genes in the local ecosystems. The genetically-related isolates of livestock were comparable to human clinical isolates and this signifies the potential of transfer of animals to human disease.The co-selective force was contamination of heavy metal which increased the duration of multidrug resistance determinants. The wastewater treatment plants and surface waters were among the places where commensal and pathogenic bacteria might exchange the genes.

Combined, the generated evidence demonstrates that the issue of antimicrobial resistance is increasingly becoming widespread throughout the globe, with a lot of regional diversity depending on the healthcare system, regulatory policies, as well as environmental factors. The misuse of the clinical setting, as well as the methods of agriculture, environmental pollution, and genetic adaptation of microorganisms, is a pointer of how complicated is this global crisis.

DICUSSION

This systematic review presents on a synthesis of the current tendencies in antimicrobial resistance in the globe, listing the major drivers and evaluating the effects of various intervention measures, thereby offering a comprehensive review of the dynamic threat. It details how the microbial evolution, human activities, and the environment are interconnected in complex, which combined guarantee the appearance and the spread of resistant pathogens (Elbehiry and Abalkhail, 2025). AMR is a serious and acute threat to the global health. It is caused by different complicated processes, such as genetic mutations, horizontal gene transfer, and adaptive responses of the bacteria, such as biofilm formation and efflux pumps overexpression (Elbehiry and Abalkhail, 2025; Nusrat et al., 2025). It is further aggravated by the fact that it is a highly expensive project that requires about 730 billion annually to treat AMR related diseases (Ye et al., 2025). This economic liability will only become a reality as it hits US$100 trillion in different parts of the world by 2050 unless we take action to tame it (Fatokun et al., 2024). Huge quantities of antimicrobials used in human health, in agriculture, and in animal treatment of course have an enormous impact on the problem, leading to the selection and dispersion of resistant strains into other ecological environments (Puvača et al., 2022). This systematic review will critically examine the available data concerning the topic of acquisition, diversity, and interspecies transmission of antimicrobial resistance (AMR) and bring together microbial, clinical, and environmental viewpoints in a One Health framework (Elbehiry et al., 2025; Meier et al., 2022). It is necessary to agree that the careless use of antibiotics in humans and animal breeding is one of the primary causes of resistant antimicrobial strains (Sudhakari and Ramisetty, 2022). The 21 st century is a century of antimicrobial resistance as one of the important health dangers. It makes the contemporary medical treatment ineffective and turns back decades of the advancements that had been achieved, in the field of infection control (Elbehiry et al., 2025). Resistance mechanisms such as extended-spectrum beta-lactamases have been widely spread and are an issue of serious concern with resistance to the common infections, which results in higher morbidity and mortality (Khan et al., 2025). The effects of AMR on the economy and health are dire, and both the international and domestic levels should be made to initiate an urgent and collective action to decrease its occurrence and assure the sustainability of the efficacy of the antimicrobial agents (Altevogt et al., 2025; Momani et al., 2025). Therefore, a deeper insight into the environmental factors and genetic mechanisms that cause AMR is proposed to the formulation of new measures aimed at its reversal of the unstoppable course (Meier et al., 2022). The most important reason of this global health disaster is the overuse and abuse of antibiotics whereby the micro organisms have become simpler to resist at present (Sinha & Upadhyay, 2025). The causes of this issue include bad infection control, poor hygiene, and the fact that, as much as the world has become interconnected, resistant strains can be transmitted at a very fast rate across continents (Joshua et al., 2022; Mohammad et al., 2022). Financial consequences in particular refer to the urgency of the problem of AMR because it is estimated that the world economy would lose USD 100 trillion, and every year 10 million people would die unless the current trends are minimized (AB, 2024; Mohammad et al., 2022). In recognition of this threat in the near future, there has been an increased focus on the notion of the One Health approach, which underscores the high interconnectedness between human, animal, and environmental health in the context of interpreting and combating AMR (Li et al., 2023; Meier et al., 2022). This integrated model underscores the fact that the indiscriminate use of antibiotics in such industries increases the evolution speed and spread of resistant bacteria, which are a complex problem to the community health (Das et al., 2024).

CONCLUSION

As discussed in this review, antimicrobial resistance is a complex global problem that arises because of various factors in human, animal, and environmental settings and requires a combined One Health solution to be solved effectively. The fact that the global AMR came up as a result of improper use and overuse of the antimicrobial agents not only in farming but also in health care and the evolution of microorganisms do not mean the conclusion. The governments, medical practitioners, researchers and ordinary people should also work in unison to avoid further deterioration of drug efficacy and rise in healthcare costs. The antimicrobial resistance is a complicated process that demands the creation of new diagnostic and treatment opportunities since the discussed phenomenon is linked to various microbial mechanisms and human factors. Also, there should be extensive monitoring mechanisms that could be used to track the trends of resistance and provide feedback on certain response measures. The management of the infections is getting harder due to the growing prevalence of antibiotic resistant bacteria especially in hospitals. This proves that it is crucial to find new ways of containing infections and novel antibiotics. AMR would spread uncontrollably and with 10 million deaths per year, and 100 trillion to the global economy, it would grow. AMR also possesses inadequate environmental effects. In this example, researchers identified 212 different resistive genes of antibiotics in the river sediments some of which were not visible using the standard method.

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