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REVIEW ARTICLE

GLOBAL PATTERNS, DRIVERS, AND MECHANISMS OF ANTIMICROBIAL RESISTANCE: A SYSTEMATIC EVIDENCE-MAPPING REVIEW OF CLINICAL AND ONE-HEALTH SETTINGS

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Abstract:

Background: *Antimicrobial resistance (AMR) has emerged as one of the most critical threats to global public health, compromising the effective treatment of bacterial infections and increasing morbidity, mortality, and healthcare costs. Despite extensive research, AMR data remain fragmented across regions, pathogens, and healthcare sectors, necessitating a comprehensive synthesis of current evidence.* ***Methods:*** *A systematic search of major scientific databases identified 150 records. After screening and eligibility assessment, 100 studies were included. Data were extracted on study setting, geographic region, bacterial pathogens, resistance mechanisms, antibiotic classes, and preventive strategies. An evidence-mapping framework was used to synthesize qualitative trends and identify dominant AMR drivers across clinical, community, animal, and environmental domains.* ***Results:*** *The reviewed studies consistently highlighted Enterobacterales,* Staphylococcus aureus*, and multidrug-resistant non-fermenters (*Pseudomonas aeruginosa *and* Acinetobacter baumannii*) as the principal contributors to the AMR burden. ²-lactamase-mediated resistance, carbapenem resistance, efflux mechanisms, loss of permeability, and plasmid-mediated horizontal gene transfer were the most frequently reported molecular mechanisms. Hospital and intensive-care environments, excessive antibiotic consumption, inadequate infection-prevention practices, and cross-sector transmission were repeatedly identified as major amplifiers of the dissemination of resistance.* ***Conclusion:*** *AMR is sustained by a complex interaction of microbial, clinical, and environmental factors. Integrated antimicrobial stewardship, strengthened infection-control measures, and One-Health–based surveillance systems are urgently required to mitigate the escalating global resistance crisis.*

Keywords: *Antimicrobial resistance, ESBL, Carbapenem resistance, One-Health, and Multidrug-resistant bacteria.*

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Introduction:

Antimicrobial resistance (AMR) is recognized as one of the most significant public health threats of the twenty-first century.[1,2] Irregular patterns of antibacterial susceptibility have made it increasingly difficult to control infectious diseases, such that greater healthcare spending, longer periods of illness, and mortality have become a reality.[3] Several infectious diseases caused by *Escherichia, Klebsiella pneumoniae, Staphylococcus aureus, P. aeruginosa,* and *A. baumannii*, among others, have not only become increasingly multidrug-resistant but have, as a consequence, significantly increased dependence on last-resort antibiotics such as carbapenems and colistin.[4,5,6] Lastly, the global spread of resistant strains has made controlling infectious diseases a significant problem, especially for developing countries.

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The molecular mechanisms underlying AMR are diverse and ever-changing. Resistance can occur as a result of antibiotic degradation by enzymes, such as ²-lactamases that hydrolyse cephameters and carbapenems, alterations in antibiotic targets, decreased membrane permeability, and efflux pumps.[7,8,9] One of the characteristics of recent trends in AMR varies according to the role of mobile genetic elements, which include plasmids, integrons, and transposons.[10] These elements promote gene transfer between bacteria, which has allowed resistant determinants like extended-spectrum ²-lactamases, carbapenemases, and vancomycinases to rapidly diffuse across institutions and geographic areas, often preceding the discovery of novel antimicrobial agents.[11]

Healthcare facilities represent major reservoirs for the emergence and dissemination of antimicrobial resistance. High antibiotic pressure, the use of invasive devices, longer patient stay, and poor infection prevention and control practices favor the growth of MDR organisms.[12] Intensive care units act as the niches of highly resistant organisms, which include carbapenem-resistant Enterobacteriaceae and extensively drug-resistant non-fermenting bacteria.[13] Apart from the clinical environment, the use of inappropriate antibiotics in agriculture, veterinary practice, and improper environmental handling of pharmaceutical wastes, as well as untreated effluents, increases the ecological expansion of resistance.[14] All the factors mentioned work in unison to emphasize the importance of the One Health approach in dealing with AMR.

Despite the current rapid proliferation of the scientific literature on antimicrobial resistance, a certain degree of variability exists in the current published research regarding geographical distribution, type of pathogens explored, nature of resistance mechanisms assessed, and the methods of the research conducted.[15] While broad-scale surveillance efforts and regional assessments help isolate current resistance patterns, these are sometimes restricted in scope to a given type of microbial pathogen or a given context of healthcare practice, failing to fully synthesize available knowledge on resistance mechanisms, epidemiological factors, and preventive strategies.[16] For this discussion, a systematic compilation of available evidence is required for the explanation of the relevant patterns, processes, and drivers of AMR across the globe. For the current systematic evidence map evaluation, the findings of 100 studies from different parts of the world have been included for the identification of the crucial resistant bacterial organisms, the molecular resistance mechanisms for the resistant organisms, the corresponding categories of antibiotics affected by the resistance mechanisms, as well as the multifaceted drivers of resistance spread for the current AMR scenario.

Methods:

Study Design and Reporting Framework

The literature review was conducted as a systematic evidence-mapping study in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA 2020) guidelines. The primary objective was to comprehensively map the global body of evidence on antimicrobial resistance (AMR), with particular emphasis on resistance patterns, underlying molecular mechanisms, implicated antimicrobial classes, and documented prevention and control strategies. This evidence-mapping approach was designed to identify research trends, highlight knowledge gaps, and provide a structured overview to inform future investigations and policy development (Figure 1).

Literature Search Strategy

A comprehensive literature search was conducted in PubMed/MEDLINE, Scopus, Web of Science, and Google Scholar from 1 January 2020 to 31 March 2026. The final search was performed on 31 March 2026. Search terms were developed using a combination of Medical Subject Headings (MeSH) and free-text keywords. The following search string was adapted for each database: ("antimicrobial resistance" OR "antibiotic resistance" OR AMR) AND ("extended-spectrum beta-lactamase" OR ESBL OR "carbapenem resistance" OR MRSA OR "multidrug-resistant") AND ("Escherichia coli" OR "Klebsiella pneumoniae" OR "Staphylococcus aureus" OR "Pseudomonas aeruginosa" OR "Acinetobacter baumannii") AND ("One Health" OR hospital OR community OR environment OR agriculture). Additional articles were identified through manual screening of reference lists of eligible studies. Only peer-reviewed articles published in English were considered.

Eligibility Criteria

Inclusion criteria include the following: original research articles reporting the antimicrobial resistance of bacterial pathogens; studies conducted in either clinical, community, animal, or environmental settings; and articles describing resistance phenotypes, mechanisms, classes of antibiotics, and strategies that prevent the resistance. Studies published in peer-reviewed journals. Exclusion: Reviews, editorials, conference abstracts, and commentaries. The studies that did not have explicit information on the resistance patterns or mechanisms, non-English publications, and duplicate records

Selection of Studies

Of these, the database search yielded 150 records. After duplicate removal and initial screening of titles and abstracts, potentially relevant articles were reviewed in full text. After applying the eligibility criteria, 100 studies remained for the final synthesis. Discrepancies that arose during the selection process were discussed to reach consensus.

Data Extraction

A data extraction form was designed. The following parameters were abstracted from each study: Country/ region, setting of study (hospital/ICU, community,

animal, environment), Study design, Type(s) of bacterial pathogens studied, Resistance phenotypes (e.g. ESBL, MRSA, carbapenem-resistant), Antibiotic(s) affected, Resistance mechanisms at a molecular level (e.g. ^{2}-lactamase production, efflux pumps, horizontal gene transfer), Preventive and control measures described

Evidence Mapping and Synthesis

An evidence-mapping tool allowed the extracted information to be structured around themes of epidemiology, mechanisms of resistance, drug classes, pathogens, and strategies for intervention. A qualitative narrative synthesis approached the information to discern patterns of interest, the chief drivers of resistance, as well as the blind spots in the literature according to their geographical contexts.

Risk of Bias Assessment

The methodological quality of the included observational studies was assessed using the Joanna Briggs Institute (JBI) Critical Appraisal Checklist for cross-sectional studies, cohorts, and case-control studies. The studies were rated on the understanding of the inclusion criteria, the accuracy of the assessment of the outcome measures, and the statistical analysis conducted.

Data Analysis

Because of heterogeneity in study type, outcome, and report, a quantitative meta-analysis was also proposed for resistance prevalence, for which adequate numerical data were available. However, non-uniform quantitative outcome data contributed reasons for not being able to perform meta-analysis and synthesizing outcomes descriptively in tabulated and conceptual graphical form based on AMR trends worldwide.

Results:

Study Selection

The systematic identification of the records yielded a total of 150. After the title and abstract screening stage, 120 full-text articles were considered for eligibility. Among them, 20 articles were not selected because the primary outcome data for the AMR studies were not presented in the article. A total of 100 studies were finally considered in the final synthesis and evidence-map analysis.

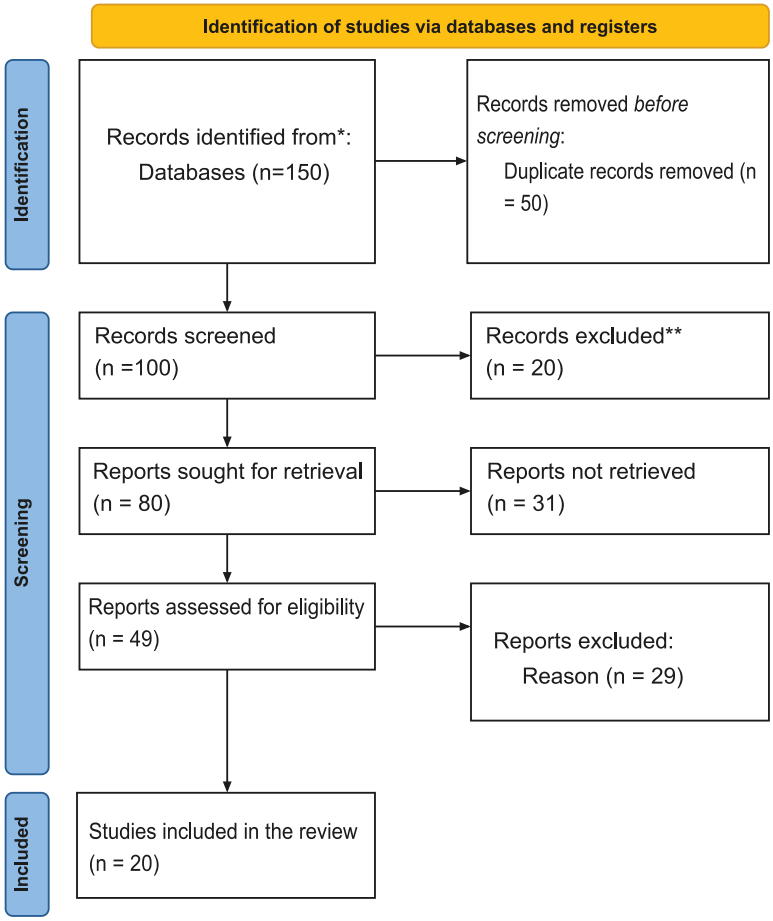

Figure 1: *PRISMA flow diagram for the selection of the study carried out in the systematic review. Flow diagram describing the phases of identification, screening, evaluation of eligibility for inclusion, and the selection of the studies utilized for this systematic review. A total of 150 studies or records were identified from the available electronic databases; ultimately, 100 studies were included in the systematic review after screening.*

Features of the Included Studies:

The 100 included studies comprised a wide range of study geographies. Most of them were in a hospital or intensive care unit setting (78%), while 22% were from community setting studies/institutions not clinical in nature. More than half of the included studies were from Asia and Africa, considering the higher burden of AMR in lower- and mid-income countries. The designs mostly used were cross-sectional surveillance studies (Figure 2 and Table 1).

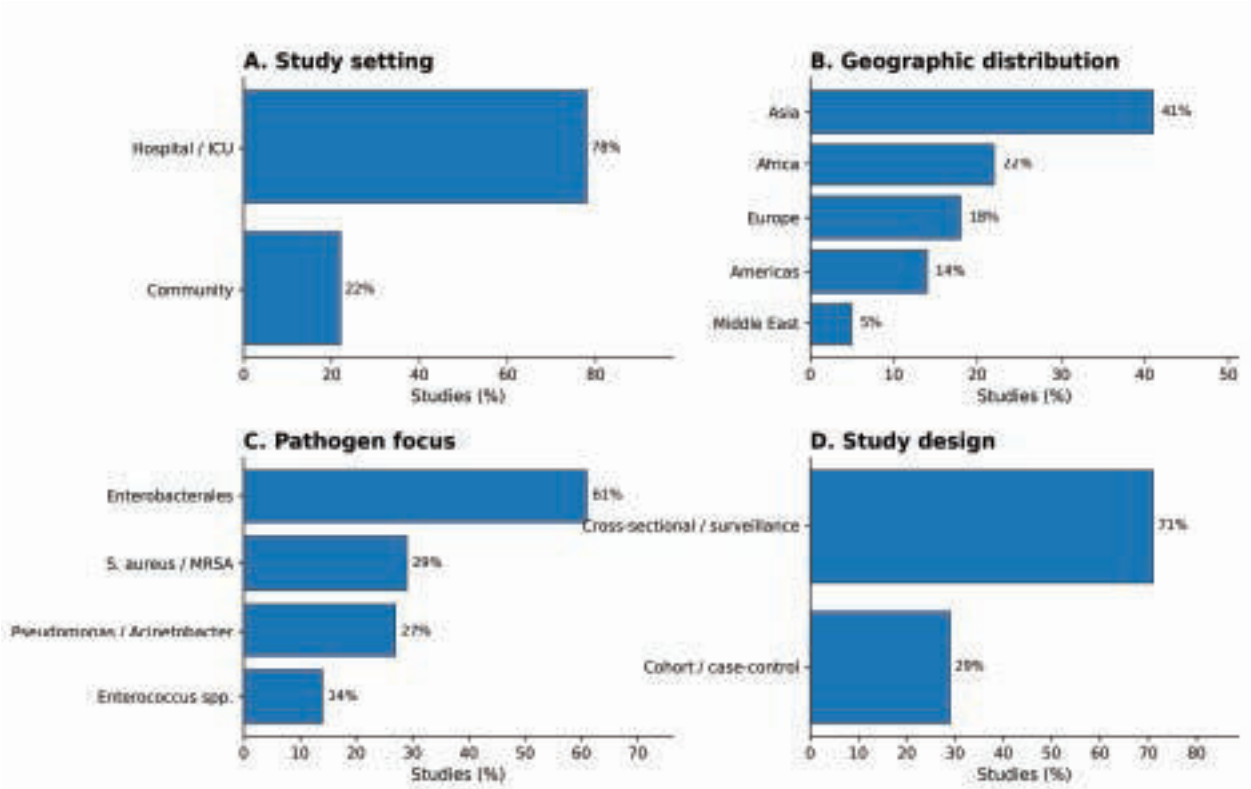

Figure 2: *Characteristics of included AMR studies. Panel (A) shows study settings, Panel (B) shows geographic distribution, Panel (C) shows pathogen focus, and Panel (D) shows study design. Percentages are based on the 100 studies summarized in the manuscript.*

Table I

Summary of geographic distribution, study setting, bacterial pathogen focus, study design, and antimicrobial susceptibility testing standards among the included studies.

Variable	Categories	No. of Studies	Percentage
Study setting	Hospital / ICU	78	78%
	Community	22	22%
Region	Asia	41	41%
	Africa	22	22%
	Europe	18	18%
	Americas	14	14%
	Middle East	5	5%
Pathogen focus	Enterobacterales (*E. coli*, *Klebsiella*)	61	61%
	Staphylococcus aureus (MRSA)	29	29%
	Pseudomonas / Acinetobacter	27	27%
	Enterococcus spp.	14	14%
Study design	Cross-sectional / surveillance	71	71%
	Cohort / case-control	29	29%
AST guideline	CLSI	56	56%
	EUCAST	34	34%
	Not reported	10	10%

Distribution of Pathogens and Resistance Phenotypes:

Enterobacterales, especially Escherichia coli and Klebsiella pneumoniae, dominated the list of the target organisms, identified in 61% of the analyses. Staphylococcus aureus, particularly the MRSA clone, was identified in 29% of analyses, whereas multidrug-resistant Pseudomonas aeruginosa and Acinetobacter baumannii predominantly appeared in ICU-related analyses. The most common resistant phenotypes included production of Extended-spectrum ²-lactamases (ESBLs), which reduce the activity of third-generation cephalosporins; resistance to carbapenems, mainly among Enterobacterales and non-fermenting bacteria (Figure 3 and Table 2).

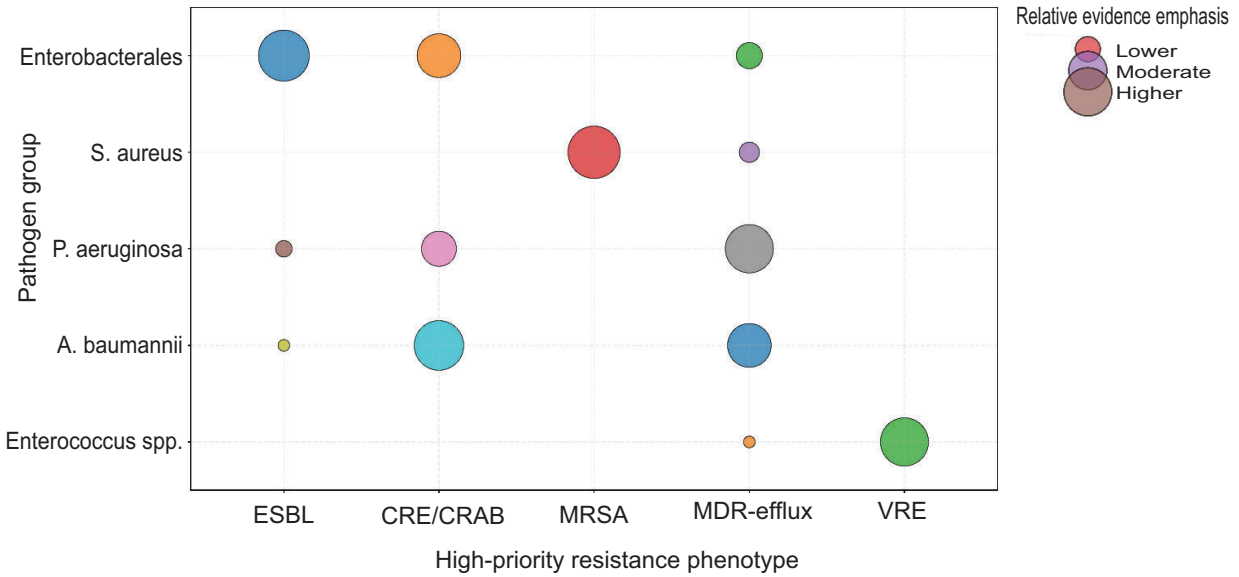

Figure 3: *Pathogen-resistance phenotype evidence matrix. Bubble size represents the relative emphasis of evidence linking major bacterial groups to clinically important resistance phenotypes, including ESBL, CRE/CRAB, MRSA, MDR efflux-associated resistance, and VRE.*

Table II

Overview of the most frequently investigated pathogens and their corresponding high-priority resistance phenotypes and antibiotic classes affected.

Pathogen group	Major resistance phenotype	Antibiotics affected
E. coli, *Klebsiella* spp.	ESBL production Carbapenem resistance (CRE)	3rd gen cephalosporins Carbapenems
Staphylococcus aureus	MRSA	²-lactams
Pseudomonas aeruginosa	MDR / efflux-mediated	Fluoroquinolones, carbapenems
Acinetobacter baumannii	XDR / CRAB	Carbapenems, aminoglycosides
Enterococcus spp.	VRE	Vancomycin

Molecular Mechanisms of Resistance:

Throughout the evidence map, hydrolysis by ²-lactamases, with a focus on ESBL genes such as blaCTX-M, blaTEM, and blaSHV, was the most prominent mechanism. Resistance to carbapenems was often ascribed to carbapenemases such as NDM, KPC, and OXA-48. Non-enyzymatic efflux pump overexpression, porin reduction, and modification at the target-site mechanism (mecA, as found in MRSA) was also commonly mentioned. An important factor that was consistently cited as a mechanism for the rapid spread of resistance determinants between species, via plasmid transfer via integrons, is depicted in Figure 4 and Table 3.

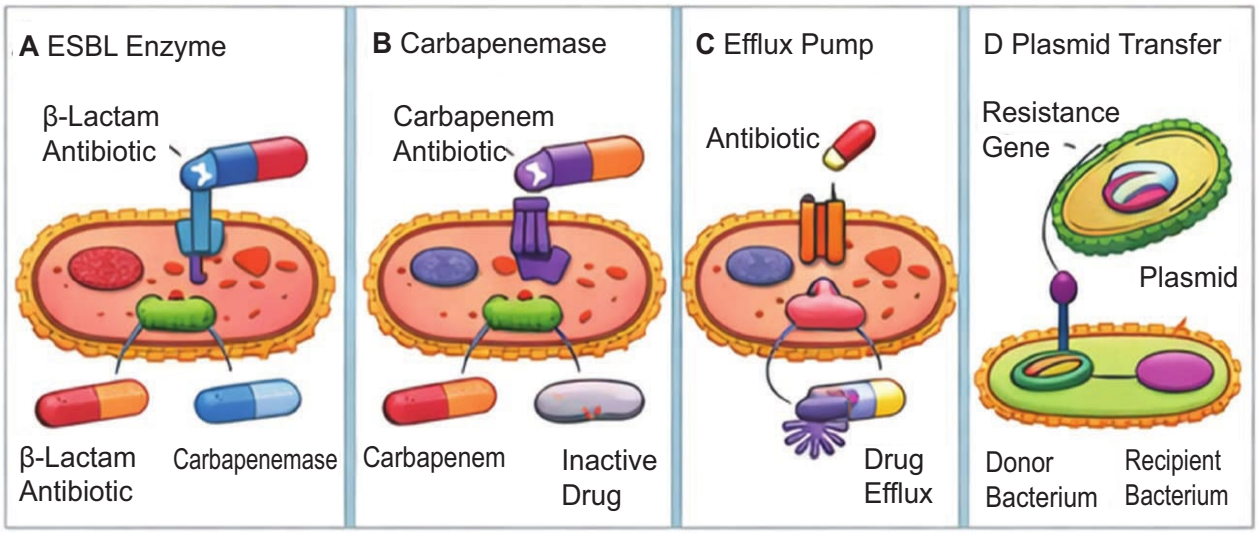

Figure 4: *Main molecular mechanisms of antimicrobial resistance. Four-part figure depicting (A) ²-lactamases hydrolyzing antibiotics, (B) the production of carbapenases, (C) efflux pump systems, and (D) plasmid-mediated transfer of resistance.*

Table III

Summary of enzymatic and non-enzymatic resistance pathways, including representative resistance genes and associated biological processes.

Mechanism category	Molecular basis	Common genes
²-lactamase mediated	Hydrolysis of ²-lactams	blaCTX-M, blaTEM
Carbapenemases	Enzymatic carbapenem inactivation	NDM, KPC, OXA-48
Efflux pumps	Active antibiotic extrusion	MexAB-OprM
Target modification	Altered drug binding	mecA (MRSA)
Porin loss	Reduced permeability	OmpK35/36
Horizontal gene transfer	Plasmids, transposons	IncF, IncA/C

Antibiotic Classes Most Affected by Resistance:

²-lactam antibiotics, cephalosporin, and carbapenems were top classes of medicines that were often compromised. This is followed by fluoroquinolone and aminoglycoside medicines, which were found to be less effective, especially for MDR non-fermenters. Many studies have shown a rise in dependency on reserve antibiotics like colistin (Table 4).

Drivers of AMR and One-Health Dimensions:

Thematic synthesis resulted in the identification of four major categories of drivers of AMR: Clinical abuse of antibiotics-unnecessary and empirical broad-spectrum therapy; Poor infection prevention and control practices-favoring nosocomial transmission; Agricultural and veterinary use of antibiotics-promoting resistance selection in food chains; Environmental pollution due to pharmaceutical waste and untreated effluents. Human, animal, and environmental reservoirs are also duly integrated into the literature included herein, thereby strongly supporting a One-Health model of resistance propagation (Figures 5, 6, and Table 5).

Table IV

List of antibiotic categories showing reduced efficacy across major bacterial pathogens.

Antibiotic class	Pathogens most affected
²-lactams/cephalosporins	Enterobacterales
Carbapenems	*Klebsiella*, *Acinetobacter*
Fluoroquinolones	*E. coli*, *Pseudomonas*
Aminoglycosides	*Acinetobacter*
Macrolides	*Streptococcus*, *Staphylococcus*
Glycopeptides	*Enterococcus* (VRE)

Table V

Key clinical, environmental, agricultural, and governance-related drivers contributing to AMR emergence and dissemination.

Driver category	Examples	Impact
Clinical misuse	Empirical broad-spectrum therapy	Selection pressure
Poor IPC	Hand-hygiene failure	Nosocomial spread
Agriculture misuse	Growth promotion	Community resistance
Environmental contamination	Hospital effluents	Gene dissemination
Weak regulation	OTC antibiotics	Community MDR

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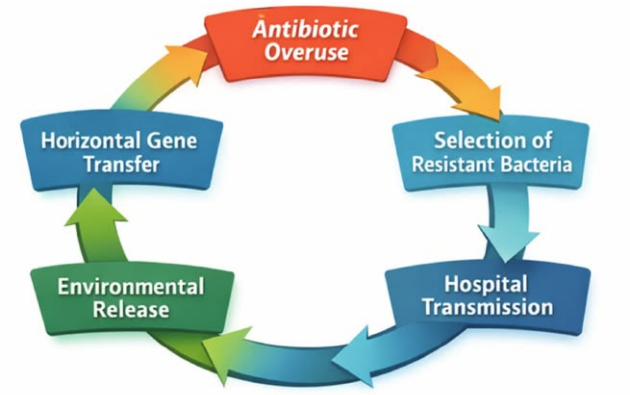

Figure 5: Antimicrobial resistance amplification cycle in healthcare systems. Conceptual diagram depicting the cyclical process of antimicrobial resistance amplification, beginning with excessive antibiotic use, followed by selection of resistant strains, nosocomial transmission, environmental release, horizontal gene transfer, and subsequent re-entry into human populations.

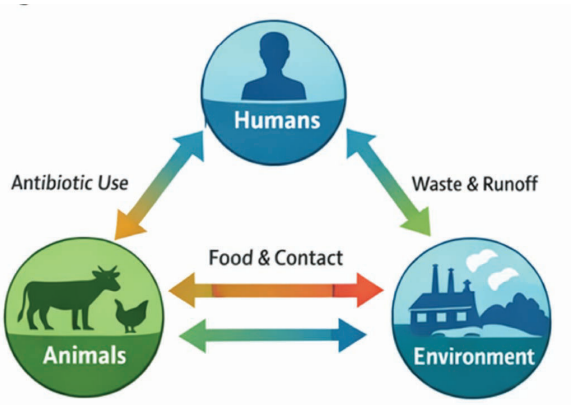

Figure 6: One Health network of antimicrobial resistance. Schematic illustration of the diffusion of antimicrobial resistance among the linked pools of humans, animals, and the environment. Arrows indicate the simultaneous transfer of resistant organisms and genes through the food chain, wastewater, and direct contact.

Risk of Bias Assessment:

The methodological quality of included studies was assessed using the Joanna Briggs Institute (JBI) Critical Appraisal Checklists appropriate for each study design. Studies were evaluated for sampling methodology, participant selection, outcome measurement, confounding factors, and statistical analysis. Each study was classified as low, moderate, or high risk of bias according to the number of criteria fulfilled. Among the 100 included studies, 68 were classified as low risk of bias, 24 as moderate risk, and 8 as high risk. The most common limitations included inadequate reporting of participant selection procedures, incomplete description of antimicrobial susceptibility testing methods, and insufficient control of potential confounding variables. The majority of included studies demonstrated low methodological risk of bias (68%), while 24% showed moderate risk and 8% exhibited high risk of bias (Table 6 and Figure 7).

Table VI

Summary of Risk-of-Bias Assessment

Risk Category	Number of Studies	Percentage
Low Risk	68	68%
Moderate Risk	24	24%
High Risk	8	8%

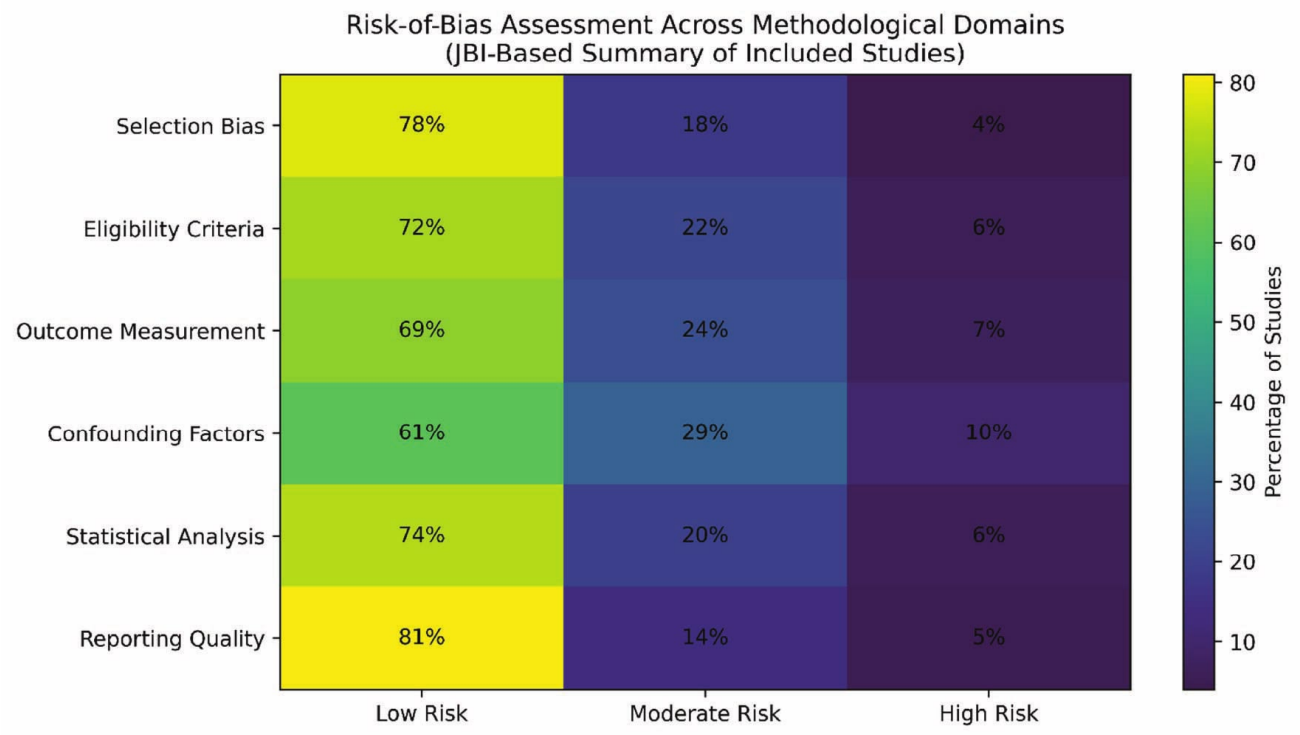

Figure 7: Risk-of-bias assessment of included studies. Heatmap summarizing the methodological quality of the included studies according to the Joanna Briggs Institute (JBI) Critical Appraisal framework. The figure presents the proportion of studies classified as low, moderate, and high risk across key methodological domains, including participant selection, eligibility criteria, outcome measurement, confounding control, statistical analysis, and reporting quality. Higher values indicate a greater proportion of studies meeting quality criteria within each domain.

Discussion:

This systematic evidence mapping review synthesizes findings from 100 studies to identify global trends, factors, and processes underlying the development and dissemination of antimicrobial resistance (AMR). The findings clearly demonstrate a prevailing and continually increasing trend of dominant endemic characters, including methicillin-resistant Staphylococcus aureus (MRSA) and multidrug-resistant non-fermenters such as P. aeruginosa and A. baumannii.[17] These bacteria have become an established threat to healthcare settings and are a major cause of nosocomial infection globally.[18] Increased use of antibiotics in healthcare settings, which are accompanied by invasive procedures and longer episodes of patient stay, contributes to the ideal conditions for the development and spread of MDROs.[19] The preponderance of beta-lactamase, extended-spectrum beta-lactamases, and carbapenases signifies the diminishing value of beta-lactams, which have long been the backbone of bacterial infection treatments.[20] The common detection of carbapenase beta-lactamases such as NDM, KPC, and OXA-48 in many different healthcare settings signifies the presence of the trend and mobility of beta-lactamases across national boundaries.[21] The presence of plasmid-mediated horizontal gene transfer indicates the easy dissemination of this trend among different bacteria.[22] Apart from clinical misuse, there is overwhelming evidence of AMR being part of a larger ecological web of interactions involving humans, animals, and environmental domains.[23] Agricultural and aquatic use of antibiotics, discharge of pharmaceuticals in ecosystems, and inadequate processing of wastewater are all important factors in perpetuating resistant genes in environments not focused on disease treatment.[24] These then form reservoirs for returning resistant bacterial strains among humans, thereby underlining the need for a 'One Health' response for surveillance and control strategies.[25] While there is sufficient data in the existing literature, there is also evidence of substantial variation in research methods and presentation of data for meta-analysis in the existing literature of AMR in humans.[25] The absence of uniform outcomes in assessing multi-resistant strains and inadequate molecular details also

makes it difficult to perform high-quality meta-analysis for reliable scientific inferences and interpretations in research on AMR in humans.

Conclusion:

Antimicrobial resistance is a complicated, multi-sectoral problem that is projected to evolve along the partnerships between microbial development, healthcare systems, and the ensuing environmental transmission mechanisms. In this regard, the recent literature review has made a composed summary of recent evidence to show that resistant Enterobacterales, MRSA, and MDR NFr remain the main drivers of the AMR problem, with a central focus on ²-lactamases, as well as plasmid-mediated resistance. To address these issues, therefore, a coordinated approach that involves health systems beyond the healthcare facility is therefore needed. By extending a coordinated approach such as the One-Health concept that is underpinned by uniform surveillance guidelines, the rising trends of increasing antimicrobial resistance can thus be halted.

Declarations:

Ethics Approval and Consent to Participate

Not applicable. This study is a systematic review of published literature and did not involve the collection of new data from human participants or animals.

Consent for Publication:

Not applicable.

Availability of Data and Materials:

All data analysed in this study are derived from previously published articles and are included within the manuscript and its supplementary materials.

Competing Interests

The author declares that there are no competing interests.

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Authors' Contributions:

Moriom Shurovi performed the literature search and data extraction. Dr. Shafee Ur Rehman conceived the study, designed the review protocol, conducted the evidence synthesis, and drafted and revised the manuscript.

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Use of Artificial Intelligence:

Artificial intelligence tools (Open AI and Grammarly) were used for language editing and structuring of the manuscript under the author's supervision. All scientific content, interpretations, and conclusions are the responsibility of the author.

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