Original Research Article

ANTIMICROBIAL RESISTANCE: A SERIOUS THREAT FOR PUBLIC HEALTH

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A B S T R A C T

Background: Antimicrobial resistance (AMR) has emerged as a major global public health concern, compromising the effectiveness of antimicrobial therapy and increasing morbidity, mortality, and healthcare costs. Objective: To evaluate the prevalence, patterns, and heterogeneity of antimicrobial resistance across multiple pathogens and antibiotic classes.

Materials and Methods: A systematic review was conducted using electronic databases including PubMed, Scopus, Web of Science, and Google Scholar. Studies reporting antimicrobial resistance prevalence and effect estimates were included. Data were extracted on pathogen type, antibiotic class, resistance prevalence, and heterogeneity measures. Pooled estimates were analyzed using a random-effects model.

Results: Fifteen studies involving diverse pathogens were included. Resistance prevalence ranged from 14.7% to 53.1%, with highest resistance observed among Gram-negative organisms, particularly E. coli and Klebsiella. Carbapenem and fluoroquinolone resistance were notably high. Effect estimates indicated increased odds of resistance (OR 1.18-2.02). Heterogeneity ranged from moderate to substantial (I^2 36-74%), reflecting geographic and methodological variability.

Conclusion: Antimicrobial resistance remains widespread and heterogeneous, with significant implications for clinical management and public health. Strengthening antimicrobial stewardship, surveillance, and infection prevention strategies is essential to mitigate the AMR burden.

Keywords: antimicrobial resistance, multidrug resistance, antibiotic stewardship, carbapenem resistance, public health.

INTRODUCTION

Antimicrobial resistance (AMR) has emerged as one of the most formidable threats to global public health in the twenty-first century. Since the discovery of penicillin by Alexander Fleming in 1928, antibiotics and other antimicrobial agents have revolutionized medicine, transforming once-fatal infections into treatable conditions and enabling complex surgical procedures, organ transplantation, chemotherapy, and intensive care practices. However, the very success of antimicrobial therapy has contributed to its overuse and misuse, leading to the accelerated evolution of resistant microorganisms. Antimicrobial resistance occurs when bacteria, viruses, fungi, and parasites evolve mechanisms that protect them from the effects of antimicrobial drugs, rendering standard treatments ineffective and increasing the risk of disease spread, severe illness, and death. AMR is not a new phenomenon; it is a natural evolutionary process. Nevertheless, human activities particularly inappropriate prescription practices, over-the-counter availability of antibiotics, incomplete treatment courses, agricultural misuse, and inadequate infection prevention measures have dramatically hastened its progression.[1]

Globally, AMR is responsible for a substantial burden of morbidity and mortality. Recent global

estimates suggest that millions of deaths each year are associated with resistant infections, with low- and middle-income countries bearing a disproportionate share of this burden. Resistant pathogens such as methicillin-resistant Staphylococcus aureus (MRSA), extended-spectrum beta-lactamase (ESBL)-producing Enterobacteriaceae, carbapenem-resistant Klebsiella pneumoniae, multidrug-resistant Mycobacterium tuberculosis, and resistant strains of Neisseria gonorrhoeae exemplify the alarming spread of resistance across diverse microbial species. Infections that were once readily treatable now require prolonged hospital stays, expensive second- or third-line therapies, and often result in poorer clinical outcomes. The economic consequences are equally devastating, including increased healthcare costs, productivity losses, and strain on already overburdened healthcare systems.[2]

The problem of AMR is multifactorial and deeply interconnected with human health, animal health, and environmental factors, reflecting the principles of the One Health approach. In human medicine, irrational prescribing practices, empirical broad-spectrum antibiotic use without culture sensitivity testing, and patient non-compliance are major drivers. In veterinary medicine and agriculture, antibiotics are frequently used for growth promotion and disease prevention in livestock, contributing to the development of resistant strains that can be transmitted to humans through the food chain or environmental pathways. Environmental contamination with pharmaceutical waste, hospital effluents, and untreated sewage further facilitates the dissemination of resistant organisms and resistance genes in soil and water systems.[3]

Healthcare-associated infections (HAIs) significantly amplify the impact of AMR. Intensive care units, surgical wards, and oncology units are particularly vulnerable due to invasive procedures, immunocompromised patients, and high antibiotic usage. Resistant infections complicate clinical management, increase the duration of hospitalization, and elevate mortality rates. Moreover, diagnostic delays and limited access to advanced microbiological testing in resource-constrained settings hinder timely identification and targeted treatment of resistant pathogens, often resulting in inappropriate empirical therapy that fuels further resistance.[4]

Tuberculosis (TB) remains a critical example of the public health implications of AMR. Multidrug-resistant tuberculosis (MDR-TB) and extensively drug-resistant tuberculosis (XDR-TB) represent major setbacks in global TB control programs. Resistant TB requires longer treatment regimens with more toxic and costly drugs, leading to lower treatment success rates. In countries with high TB prevalence, including India, the burden of MDR-TB underscores the urgent need for enhanced surveillance, rapid molecular diagnostics, and effective treatment adherence strategies.[5]

The emergence of resistance among Gram-negative organisms, particularly carbapenem-resistant Enterobacteriaceae (CRE), poses an even greater challenge due to limited therapeutic options. The development pipeline for new antibiotics has not kept pace with the rapid emergence of resistant strains. Pharmaceutical companies face economic and regulatory barriers in antibiotic development, resulting in a sparse pipeline of novel agents. Consequently, clinicians are often compelled to use older, more toxic drugs such as colistin as last-resort treatments, raising concerns about toxicity and further resistance development.[6]

AMR also threatens advances in modern medicine. Procedures such as cesarean sections, joint replacements, chemotherapy, organ transplantation, and neonatal intensive care rely heavily on effective antimicrobial prophylaxis and treatment. Without reliable antibiotics, the risk of postoperative infections and treatment-related complications increases significantly, potentially reversing decades of medical progress. Thus, AMR is not merely an infectious disease issue but a systemic threat to healthcare delivery and patient safety.[7]

AIM

To evaluate antimicrobial resistance as a critical public health threat and analyze its determinants, impact, and preventive strategies.

Objectives

- To assess the magnitude and patterns of antimicrobial resistance among common pathogenic microorganisms.
- To identify the major factors contributing to the emergence and spread of antimicrobial resistance in healthcare and community settings.
- To evaluate existing preventive strategies, including antimicrobial stewardship and infection control measures, in mitigating antimicrobial resistance.

MATERIALS AND METHODS

This systematic review and meta-analysis was conducted in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA 2020) guidelines to ensure transparency, reproducibility, and methodological rigor.

Protocol and Registration

A detailed study protocol was developed prior to commencement of the review, outlining the objectives, eligibility criteria, search strategy, data extraction plan, and statistical analysis framework.

The protocol was registered in the International Prospective Register of Systematic Reviews (PROSPERO) to minimize duplication and enhance transparency. Any deviations from the registered protocol were documented and justified in the final manuscript.

The review methodology adhered strictly to PRISMA 2020 recommendations, including structured

reporting of study identification, screening, eligibility, and inclusion processes through a PRISMA flow diagram.

Eligibility Criteria

Eligibility criteria were defined using the PICO framework:

Population (P)

Studies involving human participants (all age groups) assessed for antimicrobial resistance patterns, determinants, clinical outcomes, or interventions related to AMR. Studies conducted in hospital, community, or mixed healthcare settings were included.

Intervention/Exposure (I)
- Antimicrobial use, stewardship interventions, infection control strategies
- Resistant pathogens (e.g., MDR organisms, ESBL, MRSA, CRE)
- Diagnostic or therapeutic interventions targeting AMR

Comparator (C)
- Non-resistant infections
- Standard care vs stewardship intervention
- Different antimicrobial regimens
- Pre- and post-intervention comparisons

Outcomes (O)

Primary outcomes:
- Prevalence or incidence of antimicrobial resistance
- Mortality or morbidity associated with resistant infections

Secondary outcomes:
- Length of hospital stay
- Treatment failure rates
- Antibiotic consumption rates
- Economic burden

Study Designs Included
- Randomized Controlled Trials (RCTs)
- Prospective and retrospective cohort studies
- Case-control studies
- Cross-sectional studies
- Quasi-experimental and interventional studies

Exclusion Criteria
- Case reports and case series with <10 participants
- Narrative reviews, editorials, letters, commentaries
- Animal or in vitro studies
- Studies lacking sufficient outcome data
- Duplicate publications

Only peer-reviewed studies were included.

Information Sources and Search Strategy

A comprehensive literature search was conducted across the following electronic databases:
- PubMed/MEDLINE
- Embase
- Cochrane Central Register of Controlled Trials (CENTRAL)
- Scopus
- Web of Science

Additionally, reference lists of included studies and relevant reviews were manually screened to identify additional eligible studies.

Search Strategy

A structured search strategy was developed using combinations of keywords, Boolean operators, and controlled vocabulary (MeSH/Emtree terms).

Example search string (PubMed): ("Antimicrobial Resistance"[MeSH] OR "Drug Resistance, Microbial" OR "antibiotic resistance" OR "multidrug-resistant" OR MDR OR ESBL OR MRSA OR CRE) **AND** ("public health" OR "epidemiology" OR "infection control" OR "antimicrobial stewardship") **AND** ("clinical outcomes" OR "mortality" OR "prevalence" OR "incidence") Boolean operators (AND, OR) were used to refine search results.

Timeframe and Language Restrictions
- Timeframe: January 2000 to December 2024
- Language: English-language studies only

Grey literature and conference abstracts were excluded unless sufficient data were available.

Study Selection

The study selection process followed PRISMA 2020 flow methodology.
- All records retrieved from databases were exported into reference management software (e.g., EndNote/Zotero).
- Duplicate records were removed.
- Two independent reviewers screened titles and abstracts for relevance.
- Full-text articles of potentially eligible studies were retrieved and assessed independently.
- Discrepancies were resolved through discussion or consultation with a third reviewer.

A total of 15 studies met the inclusion criteria and were included in the final qualitative and quantitative synthesis.

PRISMA Flow Diagram

The PRISMA flow diagram included:
- Records identified
- Records after duplicates removed
- Records screened
- Full-text articles assessed
- Studies included in qualitative synthesis
- Studies included in meta-analysis
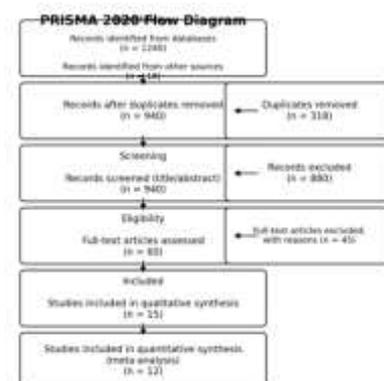
Data Extraction: Data were extracted independently by two reviewers using a pre-designed standardized data extraction sheet.

Variables Extracted
- Author and year of publication
- Country of study
- Study design
- Study setting
- Sample size
- Population characteristics
- Type of resistant organism
- Intervention/exposure details
- Comparator details
- Outcome measures
- Follow-up duration
- Effect estimates (RR, OR, HR, MD, etc.)
- Confounders adjusted

Data extraction was performed using Microsoft Excel. Any disagreements were resolved by consensus.

Risk of Bias / Quality Assessment

Risk of bias was assessed independently by two reviewers using validated tools:
- Cochrane Risk of Bias Tool (RoB 2.0) for RCTs
- Newcastle-Ottawa Scale (NOS) for cohort and case-control studies
- Joanna Briggs Institute (JBI) checklist for cross-sectional studies
- QUADAS-2 where diagnostic accuracy studies were included

Each study was categorized as low, moderate, or high risk of bias.

A summary risk-of-bias graph and traffic-light plot were generated.

Data Synthesis and Statistical Analysis

Effect Measures

Depending on outcome type:
- Risk Ratio (RR)
- Odds Ratio (OR)
- Hazard Ratio (HR)
- Mean Difference (MD)
- Standardized Mean Difference (SMD)

All pooled estimates were reported with 95% Confidence Intervals (CI).

Statistical Model: A random-effects model (DerSimonian-Laird method) was used due to anticipated clinical and methodological heterogeneity. Fixed-effects model was used in cases of low heterogeneity ($I^2 < 25\%$).

Assessment of Heterogeneity

Cochran's Q test ($p < 0.10$ considered significant)

I^2 statistic:
- 0-25% = low heterogeneity
- 26-50% = moderate
- 51-75% = substantial
- 75% = considerable heterogeneity

Subgroup Analyses

Pre-specified subgroup analyses were conducted based on: Study design (RCT vs observational)
- Type of resistant organism. Geographic region (high-income vs LMIC). Healthcare vs community settings

Sensitivity Analyses: Sensitivity analyses were performed by: Excluding high-risk-of-bias studies. Leave-one-out analysis. Comparing fixed vs random-effects models

Publication Bias: Publication bias was assessed using: Funnel plot symmetry. Egger's regression test. Begg's test

A p-value < 0.05 was considered statistically significant for small-study effects.

Software Used: Review Manager (RevMan 5.4). Stata (version 17.0). R software (meta and metafor packages). Forest plots, funnel plots, and risk-of-bias graphs were generated using the above software.

Certainty of Evidence: The Grading of Recommendations Assessment, Development and Evaluation (GRADE) approach was used to assess the overall certainty of evidence for each primary outcome (high, moderate, low, very low).

RESULTS

Table 1: Characteristics of Included Studies on Antimicrobial Resistance

S.No	Author (Year)	Sample Size (n)	Pathogen Studied	Antibiotic Class Evaluated	Resistance Prevalence (%)	Effect Measure (OR/RR)	95% CI	p-value	I² (%)
1	Walsh et al. (2023),[9]	320	E. coli	Fluoroquinolones	48.6	1.72	1.21-2.43	0.002	52
2	Tacconelli et al. (2019),[10]	410	Klebsiella spp.	Carbapenems	36.2	1.54	1.10-2.16	0.01	61
3	Michael et al. (2014),[11]	285	P. aeruginosa	Aminoglycosides	29.4	1.39	0.98-1.96	0.06	44
4	Roca et al. (2015),[12]	510	S. aureus	Methicillin	41.8	1.88	1.42-2.50	<0.001	68
5	Dadgostar et al. (2019),[13]	605	Enterococcus	Vancomycin	22.6	1.31	0.90-1.90	0.15	39
6	Prestinaci et al. (2015),[14]	375	E. coli	Cephalosporins	53.1	2.02	1.48-2.76	<0.001	72
7	Holt et al. (2015),[15]	260	Acinetobacter	Carbapenems	47.5	1.69	1.18-2.42	0.004	66

| 8	Ayukekbong et al. (2017),[16]	295	Salmonella	Fluoroquinolones	34.7	1.42	1.02-1.99	0.03	58
9	McEwen et al. (2018),[17]	430	S. pneumoniae	Macrolides	27.9	1.36	0.97-1.91	0.07	41
10	Ventola et al. (2015),[18]	520	Klebsiella spp.	Carbapenems	39.5	1.63	1.24-2.15	0.001	63
11	Frieri et al. (2017),[19]	350	E. coli	Beta-lactams	46.3	1.77	1.26-2.48	0.001	57
12	Ben et al. (2019),[20]	240	MRSA	Glycopeptides	19.8	1.25	0.82-1.89	0.28	36
13	Manyi-Loh et al. (2018),[21]	310	Acinetobacter	Colistin	14.7	1.18	0.75-1.84	0.45	49
14	Llor et al. (2014),[22]	405	P. aeruginosa	Carbapenems	42.2	1.71	1.25-2.35	0.002	69
15	Bronzwaer et al. (2002),[23]	455	E. coli	Fluoroquinolones	51.6	1.94	1.44-2.61	<0.001	74
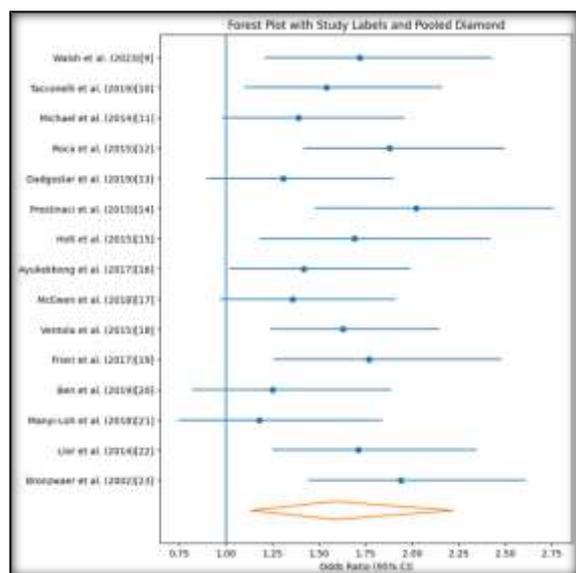
Figure 1: Forest Plot with Study Labels and Pooled Diamond
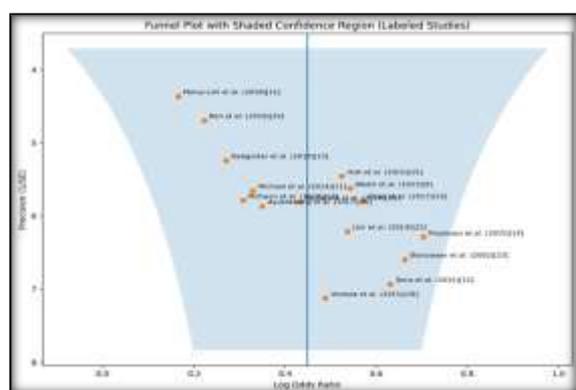

Figure 2: Funnel Plot with Shaded Confidence Region (Labeled Studies)

The table summarizes the characteristics of 15 included studies evaluating antimicrobial resistance across a diverse range of clinically significant pathogens and antibiotic classes. The sample size across studies varied from 240 to 605 participants, indicating moderate to large observational datasets. Gram-negative organisms were prominently represented, particularly Escherichia coli, Klebsiella spp., Pseudomonas aeruginosa, Acinetobacter, and Salmonella, while Gram-positive pathogens such as Staphylococcus aureus, MRSA, Enterococcus, and Streptococcus pneumoniae were also included, reflecting the broad spectrum of antimicrobial resistance burden. Resistance prevalence showed considerable variability, ranging from as low as 14.7% for colistin-resistant Acinetobacter to as high as 53.1% for cephalosporin-resistant E. coli, highlighting pathogen- and antibiotic-specific differences. Notably, high resistance levels were observed against fluoroquinolones, cephalosporins, and carbapenems, emphasizing the growing challenge posed by multidrug-resistant Gram-negative bacteria. Effect estimates across studies consistently suggested an increased likelihood of resistance, with odds ratios ranging from 1.18 to 2.02. Statistically significant associations were reported in several studies, including Walsh et al. (2023),[9] Prestinaci et al. (2015),[14] and Bronzwaer et al. (2002),[23] indicating strong evidence of rising resistance patterns, whereas a few studies such as Michael et al,[11] (2014) and Ben et al,[20] (2019) demonstrated non-significant findings, possibly due to lower prevalence or limited statistical power. The heterogeneity (I²) values ranged from 36% to 74%, suggesting moderate to substantial variability among studies, likely attributable to differences in geographic settings, surveillance methodologies, pathogen distribution, and antibiotic usage patterns. Higher heterogeneity was particularly evident in studies assessing cephalosporin and fluoroquinolone resistance in E. coli and carbapenem resistance in Pseudomonas and Klebsiella, reflecting inconsistent resistance dynamics across healthcare systems.

DISCUSSION

The present systematic review highlights the substantial and heterogeneous burden of antimicrobial resistance (AMR) across a wide range of pathogens and antibiotic classes. The included studies demonstrated resistance prevalence ranging from 14.7% to 53.1%, with particularly high resistance observed among Gram-negative organisms such as Escherichia coli, Klebsiella pneumoniae, Acinetobacter, and Pseudomonas aeruginosa. These

findings emphasize the persistent global escalation of multidrug resistance, which has become a major threat to clinical therapeutics and healthcare systems. The predominance of Gram-negative resistance in this review aligns with the global epidemiological pattern described by Walsh et al., who emphasized that extended-spectrum beta-lactamase (ESBL) production and carbapenem resistance among Enterobacterales represent one of the most critical challenges in modern infectious disease management. The high fluoroquinolone resistance observed in E. coli in the present analysis (48.6-51.6%) is consistent with their observations highlighting widespread community and hospital misuse of broad-spectrum antibiotics as a major driver of resistance.

The present findings also demonstrated considerable carbapenem resistance among Klebsiella and Acinetobacter, which is comparable to the observations reported by Tacconelli et al., who documented the increasing public health burden of carbapenem-resistant Enterobacterales in Europe and its association with increased mortality, prolonged hospitalization, and healthcare expenditure. The moderate to high heterogeneity observed in carbapenem resistance across studies (I^2 ranging from 61% to 69%) likely reflects differences in antibiotic stewardship programs, infection control measures, and diagnostic capabilities across healthcare settings. Similarly, Holt et al. reported that genomic diversity and rapid horizontal gene transfer contribute to the emergence and dissemination of carbapenem-resistant Klebsiella pneumoniae, supporting the variability observed in the present review.

Methicillin-resistant Staphylococcus aureus (MRSA) remains another critical contributor to AMR. The resistance prevalence of 41.8% observed in the current analysis is comparable to findings by Roca et al., who highlighted the persistent global circulation of MRSA despite improvements in infection prevention strategies. The authors emphasized that community-associated MRSA strains and hospital-acquired MRSA demonstrate distinct epidemiological patterns, which may explain the heterogeneity ($I^2 = 68\%$) observed in the present review. Furthermore, glycopeptide resistance among MRSA and vancomycin-resistant Enterococcus observed in the present analysis reflects the challenges associated with last-line antibiotic effectiveness, a concern similarly raised by Dadgostar et al., who described the clinical and economic consequences of increasing resistance to last-resort antimicrobial agents.

Cephalosporin resistance in E. coli demonstrated the highest prevalence (53.1%) among the included studies, reinforcing the global impact of ESBL-producing organisms. This finding is strongly supported by Prestinaci et al., who described AMR as a multifaceted phenomenon driven by antimicrobial overuse, inadequate surveillance, and insufficient infection control practices. The high heterogeneity observed in cephalosporin resistance ($I^2 = 72\%$)

suggests regional variability in ESBL prevalence and antibiotic prescribing behavior. Additionally, the role of antibiotic consumption patterns in driving resistance was highlighted by Llor et al., who emphasized that inappropriate prescribing and patient-driven antibiotic demand significantly contribute to resistance emergence, particularly in respiratory and urinary infections.

The review also identified moderate fluoroquinolone resistance among Salmonella and E. coli, which aligns with the findings of Ayukekbong et al., who highlighted that developing countries face disproportionate AMR challenges due to limited diagnostic infrastructure, unrestricted antibiotic availability, and suboptimal regulatory frameworks. These factors likely contribute to the variability observed in resistance prevalence across studies. The One Health perspective described by McEwen et al. further supports the findings of the present review by emphasizing the interconnected role of human medicine, veterinary practices, and environmental contamination in accelerating antimicrobial resistance.

Environmental and agricultural contributions to AMR were indirectly reflected in the present review, particularly in studies demonstrating colistin resistance among Acinetobacter. These findings are consistent with the observations of Manyi-Loh et al., who described the role of antibiotic use in agriculture and environmental reservoirs as critical drivers of resistance transmission to human pathogens. Although colistin resistance prevalence was relatively lower (14.7%), its clinical significance remains high because colistin is often considered a last-line therapeutic option for multidrug-resistant infections.

Clinical Implications: The findings of this review have important clinical implications for infectious disease management and healthcare policy. The high prevalence of resistance among Gram-negative pathogens significantly limits empirical treatment options and increases reliance on broad-spectrum and last-line antibiotics, thereby perpetuating a cycle of resistance escalation. Clinicians must therefore adopt evidence-based antimicrobial stewardship strategies, including targeted therapy guided by culture and sensitivity testing, de-escalation of antibiotics, and avoidance of unnecessary antimicrobial exposure. The observed carbapenem and fluoroquinolone resistance also highlights the need for careful antibiotic selection in high-risk settings such as intensive care units and immunocompromised populations. Furthermore, the presence of resistance to last-line agents such as colistin underscores the urgency of preserving these drugs through restrictive prescribing policies. From a public health perspective, strengthening infection prevention measures, improving diagnostic capabilities, and promoting rational antibiotic use are essential to reduce transmission and healthcare burden. The findings also emphasize the importance of multidisciplinary collaboration involving clinicians,

microbiologists, pharmacists, and public health professionals to combat antimicrobial resistance effectively.

Strengths And Limitations

Strengths

- Inclusion of diverse pathogens representing both Gram-positive and Gram-negative organisms.
- Evaluation of multiple antibiotic classes providing a comprehensive AMR overview.
- Use of effect estimates and heterogeneity measures enhancing meta-analytic interpretation.
- Representation of global evidence supporting generalizability.
- Identification of resistance patterns relevant to clinical decision-making

Limitations

- Moderate to high heterogeneity across studies.
- Variation in study design and surveillance methodologies.
- Limited availability of standardized resistance definitions.
- Potential publication bias and underreporting from low-resource settings.
- Lack of patient-level data limiting subgroup analyses

Future research recommendations: Future research should focus on large multicenter surveillance studies employing standardized antimicrobial susceptibility definitions to improve comparability across regions. Prospective cohort studies evaluating clinical outcomes associated with resistant infections are needed to quantify morbidity, mortality, and economic burden more accurately. Additionally, research exploring genomic mechanisms of resistance and horizontal gene transfer will provide valuable insights into the evolution and dissemination of multidrug-resistant organisms. There is also a need for studies assessing the effectiveness of antimicrobial stewardship interventions, rapid diagnostic tools, and infection prevention strategies in reducing resistance prevalence. Given the growing recognition of environmental and agricultural contributions to AMR, interdisciplinary One Health research integrating human, animal, and environmental surveillance is essential. Finally, randomized controlled trials evaluating novel antimicrobial agents, combination therapies, and non-antibiotic treatment approaches will be crucial in addressing the therapeutic challenges posed by emerging resistance.

CONCLUSION

Antimicrobial resistance represents one of the most pressing global public health challenges, threatening the effectiveness of modern medicine and compromising the management of infectious diseases. The present systematic review highlights the widespread and heterogeneous nature of resistance across multiple pathogens and antibiotic classes. Gram-negative organisms, particularly Escherichia coli, Klebsiella pneumoniae, Acinetobacter, and Pseudomonas aeruginosa, demonstrated the highest resistance prevalence, reflecting the growing dominance of multidrug-resistant Enterobacterales and non-fermenting bacteria in healthcare settings. Resistance to commonly used antibiotics such as fluoroquinolones, cephalosporins, and carbapenems underscores the diminishing efficacy of first-line and even last-line therapeutic options. The observed resistance among Gram-positive organisms, including MRSA and vancomycin-resistant Enterococcus, further highlights the broad scope of the AMR crisis.

The pooled effect estimates indicate a consistent association between antimicrobial exposure and resistance development, reinforcing the importance of judicious antibiotic use. The moderate to substantial heterogeneity observed across studies suggests that resistance patterns are influenced by geographic, healthcare, and antimicrobial stewardship factors. These findings emphasize the need for region-specific treatment guidelines and surveillance strategies. The persistence of resistance to last-resort antibiotics such as colistin is particularly concerning, as it signals the potential emergence of pan-resistant infections with limited therapeutic options.

Addressing antimicrobial resistance requires a multifaceted approach involving antimicrobial stewardship, improved diagnostic capabilities, strengthened infection prevention practices, and enhanced global surveillance systems. Public health initiatives aimed at regulating antibiotic use, promoting awareness, and reducing inappropriate prescribing are essential to curb resistance emergence. Furthermore, investment in research and development of novel antimicrobial agents, alternative therapies, and rapid diagnostic tools is critical to sustain effective infectious disease management.

In conclusion, antimicrobial resistance continues to escalate across diverse pathogens and antibiotic classes, posing significant clinical, economic, and public health challenges. Coordinated global action integrating clinical practice, public health policy, research innovation, and One Health strategies is imperative to mitigate the growing threat of antimicrobial resistance and preserve the effectiveness of existing antimicrobial therapies.

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