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Prevalence and Antibiotic Resistance Patterns of Multidrug-Resistant Bacteria Isolated from Clinical Specimens

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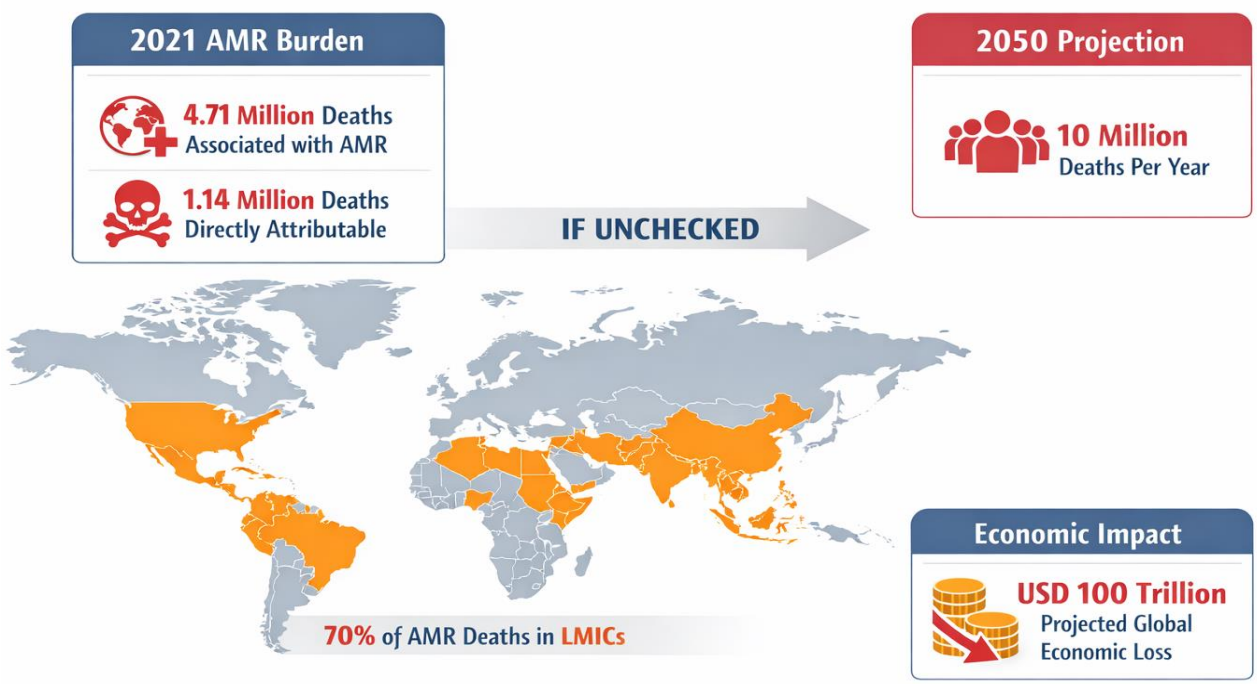
Abstract

The escalating global crisis of antimicrobial resistance (AMR) poses a severe threat to public health, with multidrug-resistant (MDR) bacteria responsible for an estimated 4.71 million deaths in 2021 and projected to cause 10 million annual deaths by 2050. This review synthesizes current epidemiological data on the prevalence and resistance patterns of MDR bacteria isolated from clinical specimens across diverse geographic regions, with particular emphasis on low- and middle-income countries (LMICs) in Africa and South Asia. High MDR rates were consistently observed across specimen types, with urine (up to 72%), blood (52.3%), and wound/pus samples showing the highest burden. ESKAPE pathogens (Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, and Enterobacter spp.) dominate, exhibiting resistance to multiple antibiotic classes through mechanisms including β-lactamase production (ESBLs, carbapenemases), target modification, efflux pumps, and biofilm formation. Regional hotspots include West Africa (59% overall MDR), Pakistan (high XDR Salmonella typhi and MRSA), and Nepal (52.3% MDR in tertiary care). The analysis underscores the critical role of inappropriate antibiotic use, environmental reservoirs, and healthcare-associated transmission in driving resistance. Strengthening antimicrobial stewardship, rapid diagnostics, enhanced surveillance (e.g., WHO GLASS), and a One Health approach are urgently required to curb the spread of MDR pathogens and preserve the efficacy of existing antimicrobials.

Introduction

The global landscape of clinical medicine is currently defined by a profound and escalating crisis in antimicrobial efficacy, driven by the emergence and dissemination of multidrug-resistant (MDR) bacterial pathogens (Gajic et al., 2025). This phenomenon, which represents a critical inflection point in infectious disease management, is characterized by the evolution of microorganisms that demonstrate non-susceptibility to at least one antimicrobial agent in three or more distinct antibiotic classes (GBD 2021 Antimicrobial Resistance Collaborators, 2024). Recent longitudinal assessments indicate a concerning 43% increase in multidrug-resistant infections on a global scale, with healthcare-associated infections (HAIs) rising by 67% and community-acquired infections increasing by 38% in geographic regions marked by significant antibiotic misuse (Pan et al., 2025). The human and economic tolls of this escalation are staggering; in 2021 alone, bacterial antimicrobial resistance (AMR) was associated with an estimated 4.71 million deaths, with 1.14 million of those deaths directly attributable to resistant pathogens (Karnwal et al., 2025). Projections based on current trajectories suggest that by 2050, the annual global mortality rate attributed to AMR could reach 10 million, with a cumulative economic burden nearing USD 100 trillion if containment strategies are not urgently optimized (Elmubark et al., 2025). The scale of the antimicrobial resistance crisis is illustrated in figure 1, which summarizes current global mortality and future projections associated with drug-resistant infections. The figure highlights the alarming increase in AMR-related deaths and underscores the urgent need for coordinated global interventions.

Figure 1: Global Burden and Projected Impact of Antimicrobial Resistance



Global and Regional Epidemiological Patterns of Resistance

The prevalence of MDR bacteria exhibits marked heterogeneity across different geographical regions, a variation largely dictated by local antibiotic stewardship practices, healthcare infrastructure, and environmental factors (Kashef Hamadani, 2023). While high-income countries face challenges related to the persistence of

resistant clones within specialized hospital units, low- and middle-income countries (LMICs) bear a disproportionate share of the global mortality burden, accounting for approximately 70% of all AMR-related deaths (Sah et al., 2023).

The African Continent: Surveillance Gaps and Escalating Prevalence

In the African region, the prevalence of MDR bacterial infections is an acute threat, with over one million deaths associated with bacterial AMR reported in 2021. In East Africa, research indicates that 50% to 60% of urinary tract infections are now caused by MDR bacteria, while in South Africa, over 80% of clinical isolates of Acinetobacter baumannii demonstrate an MDR phenotype (Sartorius et al., 2024). West African meta-analyses involving thirteen countries reveal an overall MDR prevalence of 59%, with significant contributions from Nigeria (34%) and Ghana (22%) (Khasapane et al., 2025). A critical observation in this region is the 7% increase in MDR prevalence recorded over the last decade, with nosocomial infections showing higher resistance rates (65%) compared to community-acquired infections (53%) (Diop et al., 2025).

In Rwanda, the healthcare system struggles with a high prevalence of extended-spectrum beta-lactamase (ESBL) producers. Studies at the University Teaching Hospital of Kigali identified that 75.9% of Gram-negative isolates were resistant to ceftriaxone, and 71.7% exhibited an ESBL-positive phenotype (Osena et al., 2025). This prevalence is directly linked to increased mortality, with deaths in patients infected by ESBL producers being more than double the general hospital mortality rate during the same period (Shamsrizi et al., 2020). Similarly, in Zambia, diagnostic stewardship data from 2020 to 2024 involving over 184,000 specimens show a statistically significant increasing trend in the isolation of priority pathogens like Escherichia coli, Staphylococcus aureus, and Klebsiella pneumoniae (Mudenda et al., 2024).

South Asian Dynamics: The Epicenter of Novel Resistance Mechanisms

South Asia, particularly Pakistan, India, and Nepal, has emerged as a global hotspot for the evolution and rapid dissemination of novel resistance determinants. Pakistan exhibits some of the highest age-standardized mortality rates associated with AMR, with substantial death tolls attributed to Klebsiella pneumoniae, E. coli, and S. aureus (da Silva et al., 2022). A major concern in this region is the emergence of extensively drug-resistant (XDR) Salmonella typhi, which has become resistant to almost all first- and second-line treatments (Mirha et al., 2024). Systematic reviews of S. typhi in Pakistan reveal alarming resistance to nalidixic acid (92%), ampicillin (80%), and ciprofloxacin (64%), with XDR strains significantly more common in pediatric populations (Ullah et al., 2025).

In Nepal, studies in tertiary care settings show that ESKAPE pathogens (Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, and Enterobacter spp.) are isolated in 32.1% of positive samples, with 52.3% of these being multidrug-resistant (Pandey et al., 2021). In burn units, the situation is even direr, with MDRO prevalence reaching 56.82% and significant predictors of infection including admission to the Intensive Care Unit (ICU) and the use of invasive devices like nasogastric tubes and ventilators (Maharjan et al., 2026).

European and North American Trends

While European data suggests a peak in the prevalence of certain isolates around 2021 followed by some declines, carbapenemase resistance remains high in specific species (Wise et al., 2024). In Palermo, Italy, carbapenemase resistance was observed in 55% of K. pneumoniae isolates, although Pseudomonas aeruginosa showed a significant decrease in meropenem resistance during the same study period (Pipitò et al., 2025). In the United States, Enterococcus species have become the third most frequent

nosocomial pathogen, accounting for 14% of hospital-acquired infections, a significant increase from 11% reported in 2007 (Thomsen et al., 2023).

Table 1: Regional Prevalence of Multidrug-Resistant (MDR) Bacteria and Primary Specimen Sources

Region/Country	MDR Prevalence (%)	Primary Specimen Source	Key Pathogen Trends
West Africa (Meta-analysis)	59%	Urine, Skin Swabs	Rising ESBL in E. coli (Diop et al., 2025)
Sudan (Wad Medani)	39.3%	Blood, Wound Swabs	Higher in males & age groups <5, >60 (Elmubark et al., 2025)
Nepal (Tertiary Care)	52.3%	Urine, Sputum	Predominance of K. pneumoniae (Sah et al., 2023)
India (Udaipur)	61.18% (GNB)	Urine, Pus	High resistance in Klebsiella and E. coli (Pan et al., 2025)
Pakistan (BSI)	29-55% (XDR)	Blood, Bone Marrow	XDR Salmonella and MRSA (Ullah et al., 2025)
Italy (University Hospital)	-	Urine, Respiratory	55% Carbapenem-R K. pneumoniae (Giordano et al., 2023)
China (National Data)	-	Blood, Urine	Fluctuating VREfm (2.2% in 2022) (Zhang et al., 2024)

Clinical Specimen Distribution and Resistance Phenotypes

The prevalence and antibiotic resistance patterns of bacterial isolates vary significantly according to the anatomical site of infection and the type of clinical specimen collected. This variation reflects the unique selective pressures present in different physiological microenvironments (Abebe et al., 2019).

Bloodstream and Systematic Infections

Blood cultures are critical for the identification of pathogens causing sepsis. In studies conducted in Sudan, blood samples demonstrated the highest MDRO detection rate at 52.3%. In Pakistan, Staphylococcus aureus (27.9%), Salmonella (25%), and Klebsiella (13.8%) were the most common isolates from blood cultures, with 88.6% of S. aureus being methicillin-resistant (MRSA) (Hoque et al., 2024). The high prevalence of XDR Salmonella typhi in blood cultures in South Asia underscores a critical failure of traditional oral and parenteral antibiotic regimens, requiring the use of last-resort carbapenems or azithromycin (Bale, 2021).

Urinary Tract and Catheter-Related Infections

Urinary tract infections (UTIs) represent the most frequent source of clinical isolates globally. In Bangladesh, 47.5% of positive cultures were obtained from urine, with E. coli (37.2%) and Klebsiella sp. (11.5%) as the dominant pathogens (Bangladesh National Surveillance Team, 2024). In India, urine specimens were the most frequent source of Gram-negative bacilli, showing a 61.18% MDR rate (Pan et al., 2025). Research in West Africa indicates that urine samples exhibit the highest prevalence of MDR bacteria (72%), often associated with ESBL-producing Enterobacteriaceae (Diop et al., 2025). The high rate of resistance to third-generation cephalosporins and

fluoroquinolones in urinary isolates complicates the management of both uncomplicated and catheter-associated UTIs (Sah et al., 2023).

Respiratory and Wound Secretions

Respiratory specimens, including sputum and bronchial lavage, are frequently colonized by Acinetobacter baumannii and Pseudomonas aeruginosa, particularly in patients undergoing mechanical ventilation (Stamkou et al., 2025). In these samples, A. baumannii often demonstrates a difficult-to-treat resistance (DTR) phenotype, with resistance rates for commonly used antibiotics frequently exceeding 80% (Ullah et al., 2025). Wound swabs and pus samples also show high MDR rates, particularly in burn units and surgical wards. In Nepal, Pseudomonas aeruginosa (29.0%) and Klebsiella pneumoniae (18.1%) were the most common isolates from burn wounds (Ugochi Grace et al., 2025).

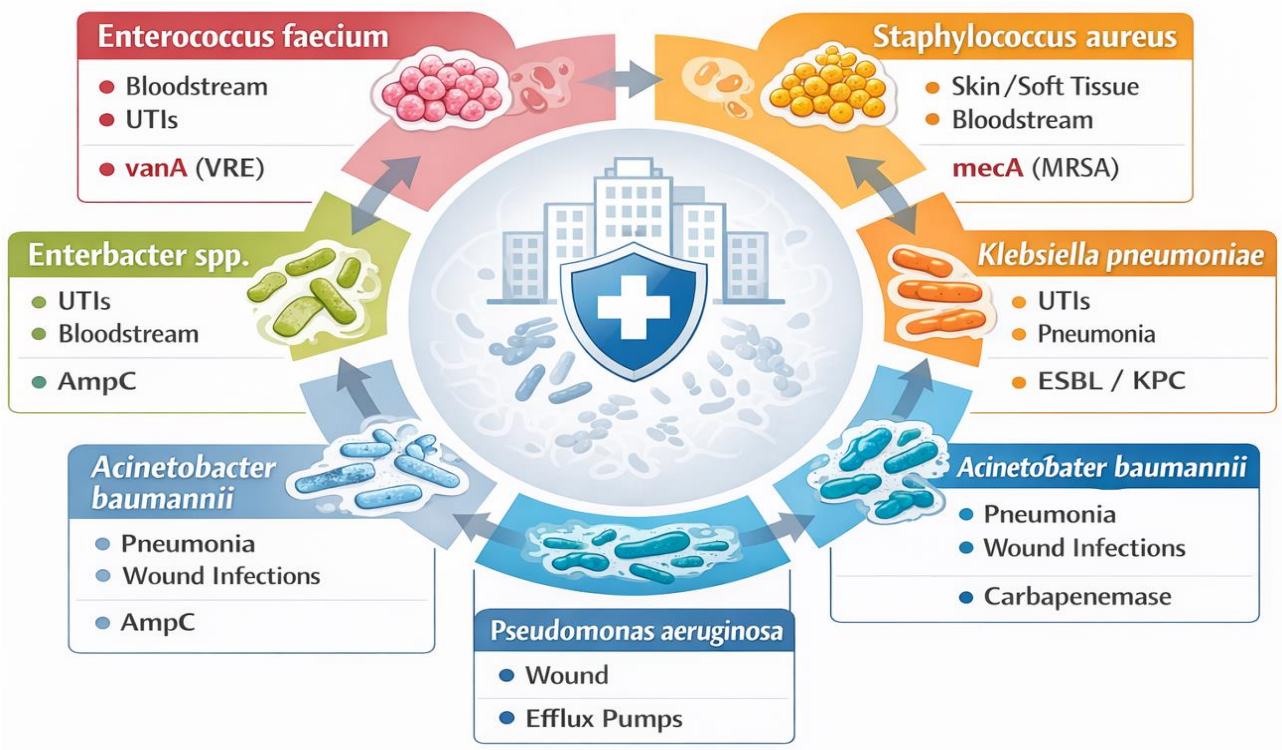
Table 2: Multidrug-Resistant (MDR) Detection Rates and Resistance Patterns by Clinical Specimen Type

Specimen Type	MDR Detection Rate (%)	Most Common MDR Pathogens	Notable Resistance Pattern
Urine	72%	E. coli, K. pneumoniae	ESBL, Fluoroquinolone resistance (Pan et al., 2025; Diop et al., 2025)
Blood	52.3%	S. typhi, MRSA, Klebsiella	XDR, 3-Generation Cephalosporin resistance (Ullah et al., 2025; Elmubark et al., 2025)
Wound/Pus	41.2%	S. aureus, P. aeruginosa	MRSA, Biofilm-associated resistance (Shrestha et al., 2024; Elmubark et al., 2025)
Sputum	-	A. baumannii, P. aeruginosa	DTR, Carbapenem resistance (Ullah et al., 2025; Genovese et al., 2025)
CSF	-	Proteus sp., S. aureus	High mortality risk (Elmubark et al., 2025)

The ESKAPE Pathogens: Biology, Mechanisms, and Clinical Impact

The ESKAPE pathogens represent a group of microorganisms that have developed sophisticated strategies to evade antibiotic action, making them the primary contributors to nosocomial morbidity and mortality (Ma et al., 2020). The major multidrug-resistant organisms responsible for healthcare-associated infections are collectively known as the ESKAPE pathogens, as illustrated in figure 2. These organisms possess diverse resistance mechanisms that enable them to evade the effects of multiple antibiotic classes.

Figure 2: The ESKAPE Pathogens and Their Clinical Significance



Enterococcus faecium: The Resilient Commensal

Enterococcus faecium has transitioned from a commensal of the human gut to a major hospital-acquired pathogen, characterized by intrinsic resistance to many beta-lactams and its ability to acquire high-level vancomycin resistance (VRE) (Huang et al., 2025). Between 2011 and 2014, Enterococcus species accounted for 14% of hospital-acquired infections in the United States, with E. faecium showing higher resistance rates than E. faecalis (Fialho, 2025). In Africa, E. faecium resistance is particularly high against tetracycline (47%), while in China, the prevalence of VREfm reached 2.2% in 2022. The genetic basis for vancomycin resistance typically involves the vanA, vanB, or vanM genes (Luo et al., 2024).

Staphylococcus aureus: The Versatile Pathogen

Staphylococcus aureus is a versatile pathogen capable of causing infections ranging from minor skin abscesses to life-threatening endocarditis. Methicillin resistance, mediated by the mecA gene which encodes an alternative penicillin-binding protein (PBP2a), is the hallmark of MDR S. aureus (Khasapane et al., 2025).

Klebsiella pneumoniae: The Carbapenemase Producer

Klebsiella pneumoniae is a leading cause of healthcare-associated pneumonia and is a major reservoir for highly mobile resistance genes. It is a prominent producer of ESBLs and carbapenemases, including Klebsiella pneumoniae carbapenemases (KPC), New Delhi metallo-beta-lactamases (NDM), and OXA-48-like enzymes (Ghanbarinasab et al., 2023). In Pakistan, ESBL production was observed in 83.3% of Klebsiella isolates, while carbapenem-resistant Enterobacteriaceae (CRE) rates reached 62.8% (Zhang et al., 2018).

Acinetobacter baumannii: The Hardest to Treat

Acinetobacter baumannii is often considered the most challenging ESKAPE pathogen to treat due to its rapid acquisition of resistance. It utilizes multiple mechanisms, including carbapenemase production, efflux pumps, and loss of porins (Mulani et al., 2019). In South Africa, over 80% of clinical isolates are MDR, and in Pakistan, 84%

are classified as difficult-to-treat resistance (DTR) strains (GBD 2021 Antimicrobial Resistance Collaborators, 2024).

Pseudomonas aeruginosa: The Efflux Specialist

Pseudomonas aeruginosa is notorious for its large genome and complex regulatory networks. It frequently employs RND-family efflux pumps and inducible AmpC beta-lactamases (Salleh et al., 2025). While it generally maintains higher susceptibility to colistin compared to Acinetobacter, resistance to carbapenems and fourth-generation cephalosporins is rising. In a five-year meta-analysis, the prevalence of MDR and XDR P. aeruginosa in Asia and Africa was 46.0% and 19.6%, respectively (Fong, 2023).

Enterobacter Species: The Inducible Resistor

Members of the Enterobacter genus are common causes of bacteremia in ICU settings. They are characterized by chromosomally encoded AmpC enzymes that can be induced by exposure to certain antibiotics, leading to clinical failure (Drozdinsky et al., 2021). In African studies, Enterobacter spp. showed the highest resistance to amoxicillin-clavulanate (95.3%) (Anju et al., 2020).

Table 3: Resistance Profiles and Last-Resort Therapeutic Options for ESKAPE Pathogens

Pathogen	Primary Resistance Genes	Typical Phenotype	Preferred Last-Resort Therapy
E. faecium	*vanA*, *vanB*, *vanM*	VRE, Linezolid-R (rare)	Linezolid, Daptomycin (Zhang et al., 2024; Pan et al., 2025)
S. aureus	*mecA*, *blaZ*	MRSA	Vancomycin, Linezolid (Sah et al., 2023; Khasapane et al., 2025)
K. pneumoniae	*blaCTX-M*, *blaKPC*, *blaNDM*, *blaOXA-48*	ESBL, CRE	Tigecycline, Colistin (Ghanbarinasab et al., 2023; Pan et al., 2025)
A. baumannii	*blaOXA-23-like*, *blaNDM*	MDR, XDR, DTR	Colistin, Cefiderocol (Giordano et al., 2023; Sah et al., 2023)
P. aeruginosa	*MexAB-OprM* (efflux), *blaVIM*	MDR, DTR	Colistin, Ceftolozane/tazobactam (Maleki et al., 2024)
Enterobacter spp.	*AmpC*, *qnrS*	3rd Gen Ceph-resistant	Carbapenems, Aminoglycosides (Sah et al., 2023; Khasapane et al., 2025)

Molecular Determinants and Mechanisms of Resistance

The adaptive evolution of MDR bacteria is driven by a sophisticated repertoire of molecular mechanisms (Fodor et al., 2020).

Enzymatic Inactivation and Modification

The production of beta-lactamases is the most prevalent mechanism of resistance against the beta-lactam class. ESBLs, predominantly of the CTX-M family, hydrolyze penicillins and third-generation cephalosporins but are inhibited by clavulanic acid (Akhtar et al., 2022). Carbapenemases represent a more severe threat. Molecular class B metallo-beta-lactamases (MBLs), such as NDM-1, require zinc ions and are not inhibited by common beta-lactamase inhibitors (Ahmed, 2021). Class D OXA-48 carbapenemases are notable for their ability to hydrolyze carbapenems while often

sparing extended-spectrum cephalosporins unless co-expressed with an ESBL (Hussain al., 2021).

Target Site Modification

Bacteria can also avoid antibiotic action by altering the molecular structure of the drug's target. This is seen in MRSA, where the mecA gene provides a penicillin-binding protein (PBP2a) with low affinity for beta-lactams (Otarigho et al., 2023). Similarly, vancomycin resistance in Enterococcus involves the modification of the cell wall precursor terminus to reduce vancomycin's binding affinity. Resistance to fluoroquinolones often arises from mutations in the gyrA and parC genes (Ambade et al., 2023).

Efflux Pumps and Reduced Permeability

The active expulsion of antibiotics is mediated by efflux pumps, particularly those of the RND family. These pumps can transport a wide range of structurally unrelated compounds, conferring an MDR phenotype (Colclough et al., 2020). Reduced membrane permeability, often through the loss of outer membrane porins, restricts antibiotic entry (Henderson et al., 2021).

Horizontal Gene Transfer and Plasmid Dissemination

The rapid spread of resistance is largely facilitated by horizontal gene transfer. Plasmids serve as major vectors for resistance genes, often carrying multiple genes that allow a single antibiotic to select for a strain resistant to many drug classes (Singh et al., 2025).

Table 4: Molecular Mechanisms of Resistance and Associated Antibiotic Classes

Mechanism Category	Molecular Examples	Targeted Antibiotic Classes	Primary Host Pathogens
Enzymatic Degradation	*blaNDM-1*, *blaKPC-2*, *blaCTX-M-15*	Beta-lactams, Carbapenems	*K. pneumoniae*, *E. coli* (Ghanbarinasab et al., 2023; Sah et al., 2023)
Target Modification	*mecA*, *vanA*, *gyrA* mutations	Methicillin, Vancomycin, Quinolones	*S. aureus*, *E. faecium* (Zhang et al., 2024; Sah et al., 2023)
Efflux Overexpression	*MexAB-OprM*, *AcrAB-TolC*	Macrolides, Tetracyclines, Quinolones	*P. aeruginosa*, *A. baumannii* (GBD 2021 Antimicrobial Resistance Collaborators, 2024; Maleki et al., 2024)
Target Protection	*qnrA*, *qnrB*, *qnrS*	Fluoroquinolones	*Enterobacter* spp., *E. coli* (Sah et al., 2023)
Altered Permeability	*OmpK35/36* loss	Carbapenems	*K. pneumoniae* (Ghanbarinasab et al., 2023)

The Role of Biofilms in Persistent and Recalcitrant Infections

A biofilm is a group of microorganisms encased in a self-produced extracellular matrix of polysaccharides, proteins, and extracellular DNA. It is estimated that up to 80% of human bacterial infections involve biofilms, particularly those associated with indwelling medical devices (Zafer et al., 2024).

Physical and Chemical Barriers to Antibiotic Action

The extracellular polymeric substance (EPS) matrix acts as a significant physical and chemical barrier. Infrared spectroscopy has demonstrated that the rate of transport for antibiotics like ciprofloxacin is significantly lower on colonized surfaces compared to sterile ones (Pipitò et al., 2025). The matrix also contains adsorption sites that can trap and accumulate antibiotic-degrading enzymes, such as beta-lactamases (Thomsen et al., 2023).

Metabolic Heterogeneity and "Persister" Cells

Within a biofilm, nutrient and oxygen gradients create diverse microenvironments, leading to stratified metabolic rates. Cells in the inner layers enter a state of dormancy, making them less sensitive to antibiotics that target actively dividing cells (Shamsrizi et al., 2020). Furthermore, biofilms harbor small subpopulations of "persister" cells that can survive extreme conditions only to repopulate the environment once the stress is removed (Sartorius et al., 2024).

Quorum Sensing and Genetic Exchange

Biofilm formation and maturation are regulated by quorum sensing, a cell-to-cell communication system that coordinates gene expression based on population density. Quorum sensing facilitates the upregulation of genes associated with drug resistance and efflux pumps (Mulani et al., 2019). Moreover, the close proximity of bacteria within a biofilm provides an ideal environment for the transfer of mobile genetic elements carrying resistance genes (Bale, 2021).

Table 5: Biofilm-Mediated Resistance Mechanisms Compared to Planktonic States

Biofilm Mechanism	Impact on Resistance	Comparison to Planktonic State	Clinical Significance
EPS Matrix Barrier	Reduced drug penetration	10 to 1,000-fold MIC increase (Yasir et al., 2024)	Failure of standard therapy (Yasir et al., 2024)
Metabolic Stratification	Tolerance in dormant cells	Inactive cells survive beta-lactams (Yasir et al., 2024)	Persistent/Chronic infections (Yasir et al., 2024)
Persister Cells	Spore-like survival state	100% susceptibility in planktonic (Yasir et al., 2024)	Recurrent infections after treatment (Yasir et al., 2024)
Quorum Sensing	Coordinated gene expression	Enhanced efflux and virulence (Maleki et al., 2024)	Targeted for "Quorum Quenching" (Yasir et al., 2024)
HGT Stability	Facilitated plasmid transfer	Higher rate of gene dissemination (Yasir et al., 2024)	Evolution of "Superbugs" (Yasir et al., 2024)

Socio-Economic and Environmental Drivers of Resistance

The emergence of MDR bacteria is rooted in human activities and environmental conditions (Ma et al., 2020).

Inappropriate Antibiotic Use and Stewardship Challenges

The misuse and overuse of antibiotics exert strong selective pressure that favors the survival of resistant strains. In LMICs, the situation is compounded by unregulated sales of antibiotics and lack of access to proper diagnostics (Stamkou et al., 2025). Healthcare professionals often face a dilemma in the emergency department, where the

need for rapid empirical treatment to prevent sepsis must be balanced against the risk of driving resistance (Ugochi Grace et al., 2025).

Environmental Reservoirs and "One Health" Perspective

AMR is increasingly detected in environmental reservoirs, including wastewater from hospitals and agricultural runoff. A "One Health" approach, which recognizes the interconnected health of people, animals, and the environment, is essential for understanding transmission cycles (Abebe et al., 2019).

Socio-Demographic Factors and Infrastructure

Overcrowded healthcare facilities, limited access to clean water, and inadequate sanitation infrastructure propagate the rapid transmission of resistant pathogens. Furthermore, global travel and trade act as conduits for the rapid transborder dissemination of resistant clones (Noreen et al., 2025).

Strategies for Containment and Antimicrobial Stewardship

Addressing the global health crisis of MDR bacteria requires effective antimicrobial stewardship (ASP), diagnostic innovation, and international collaboration (Pandey et al., 2021).

Diagnostic Innovations and Stewardship

The integration of rapid diagnostic tests (RDTs) is essential. Techniques such as polymerase chain reaction (PCR) and MALDI-TOF mass spectrometry can identify resistant strains much faster than traditional culture-based methods. "Diagnostic-driven de-escalation" leveraging biomarkers and rapid microbial identification allows for personalized therapy (World Health Organization, 2021).

Surveillance and Global Collaboration

Strengthening surveillance systems, particularly the WHO Global Antimicrobial Resistance and Use Surveillance System (GLASS), is critical. Standardized approaches for reporting resistance data enable reliable comparisons across different settings and countries (Pan et al., 2025).

Conclusion

Multidrug-resistant bacterial infections have evolved from a localized concern into a global public health emergency, with profound clinical, economic, and societal consequences. This review highlights alarmingly high MDR prevalence across clinical specimens particularly urine, blood, and wound samples and the dominance of ESKAPE pathogens that exhibit complex, multi-mechanism resistance profiles, including enzymatic inactivation, target alteration, efflux overexpression, reduced permeability, and robust biofilm formation. The situation is especially dire in LMICs of Africa and South Asia, where limited diagnostic capacity, unregulated antibiotic access, and inadequate infection control amplify transmission and mortality. The data clearly demonstrate that current empirical treatment regimens are increasingly ineffective, leading to prolonged hospital stays, higher treatment costs, and excess deaths. Without immediate intervention, the projected 10 million annual AMR-related deaths by 2050 will become reality. Effective containment demands a multifaceted strategy: rigorous antimicrobial stewardship programs, widespread adoption of rapid diagnostics and culture-guided therapy, strengthened national and global surveillance systems, and implementation of the One Health framework to address resistance at the human–animal–environment interface. Investment in new antibiotics, alternative therapies (e.g., phage therapy, anti-biofilm agents), and infection prevention infrastructure is equally critical. Only through coordinated, sustained global action can we slow the spread of MDR bacteria and safeguard the future of modern medicine.

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