The Review Of
DIABETIC
STUDIES OPEN ACCESS

Current Status And Future Direction Of Antibiotics: Therapeutic Potential And Resistance Mechanisms In Bacterial Infections

Talal Dhaifallah Musfir Al-Sayyali[1], Saleh Abdu Ali Alzaylaee[2], Ahmed Ibrahim Attia Al-Zahrani[2], Ali Ahmed Ali Alraeqi[2], Ohud Abdulqader Shatyan Aljohani[3], Osama Abdullah Alnazawi[3], Abdul Latif Hadyan Hussein Al-Dhuwaibi[4], Faisal Obaidallah Awadallah Al-Sayyali[5], Bader Ahmmad Algohne[6], Yousif Ali Alrshidi[7], Hala Awad Basaif[8*], Khulud Abdullah Husain Alali[9], Sajedah Saud Alnazga[9], Zakiah Marzouq B Albalawi[9], Mohammed Musallam Mohammed Alatawi[9]

[1]Ministry of Health Branch, Jeddah Governorate, Kingdom of Saudi Arabia
[2]Health Administration and Hospitals Director Specialist, Ministry of Health Office in Al-Qunfudhah Governorate, Saudi Arabia
[3]Yanbu General Hospital, Madinah Health Cluster, Yanbu 46421, Madinah Province, Saudi Arabia
[4]King Faisal Medical Complex, Taif Health Cluster, Shihar Road, Alhadaek, Taif 26514, Saudi Arabia
[5]Eradah Complex and Mental Health, Taif Health Cluster, Taif 21944, Saudi Arabia
[6]Ohud Hospital, Al Salam, Al-Madinah Al-Munawara 42354, Saudi Arabia
[7]Madinah Health Cluster, Ministry of Health, Pobox 4102, Madinah 42325, Saudi Arabia
[8]Makkah Healthcare Cluster, Ministry of Health, Makkah 24246, King Abdulaziz Hospital, Saudi Arabia
[9]Tabuk Health Cluster, KEAB-6774, POBox 47716, Tabuk 3734, Saudi Arabia
[*]Corresponding author: Hala Awad Basaif

Abstract
Antibiotics remain fundamental to the treatment of bacterial infections and the safe delivery of modern medical interventions, including surgery, transplantation, intensive care, and cancer chemotherapy. This review synthesizes their therapeutic value, key resistance mechanisms, and strategies required to sustain clinical effectiveness. A structured narrative approach was used to analyze peer-reviewed literature, clinical guidelines, and WHO reports, focusing on antibiotic classes, resistance burden, molecular pathways, One Health drivers, stewardship, and the antibacterial development pipeline. Despite substantial clinical benefits, resistance is increasingly concentrated among WHO priority pathogens, compromising empirical therapy and treatment outcomes. Major resistance mechanisms include enzymatic drug inactivation, target modification, reduced membrane permeability, active efflux, and biofilm-associated tolerance. Sustaining antibiotic efficacy will require coordinated global action, including strengthened stewardship programs, surveillance systems, infection prevention measures, equitable access to effective therapies, and continued innovation in antimicrobial development

Keywords Antibiotics; Antimicrobial Resistance; Bacterial Infections; Stewardship; WHO Priority Pathogens; One Health; Antibacterial Pipeline.

1. Introduction

Antibiotics remain one of the most important therapeutic advances in modern medicine because effective antibacterial therapy is central to the management of sepsis, pneumonia, urinary tract infection, skin and soft-tissue infection, and postoperative infection [1,2]. Their contribution also extends beyond direct infection treatment. Safe surgery, transplantation, neonatal care, and cancer chemotherapy all depend on reliable prophylactic and therapeutic antibiotic coverage [1]. The significance of antibiotics is therefore both therapeutic and enabling. In routine care, they reduce complications, shorten hospital stay, and improve survival in a wide range of bacterial diseases [2]. In specialized settings such as intensive care, oncology, and

organ transplantation, their effectiveness supports medical interventions that would otherwise carry substantially higher infectious risk [1].

Despite these benefits, the long-term effectiveness of antibiotics is increasingly threatened by antimicrobial resistance (AMR), which has become a major global health challenge. The burden of AMR is reflected not only in laboratory detection of resistant organisms, but also in mortality and health-system impact. A global analysis for 2019 estimated that bacterial AMR was directly responsible for approximately 1.27 million deaths, while updated projections based on 2021 data suggest that this burden may rise further by 2050 if current trends continue [3,4]. The urgency of this problem is reinforced by recent global prioritization efforts. The WHO 2024 Bacterial Priority Pathogens List identified 24 resistant bacterial pathogens across critical, high, and medium priority categories, with particular concern for carbapenem-resistant Gram-negative organisms because of their high mortality burden and limited treatment options [5,6]. These frameworks are important because they guide surveillance, research investment, and antimicrobial development toward the pathogens of greatest clinical and public-health concern.

Accordingly, the current AMR agenda requires more than a descriptive account of antibiotic classes or isolated resistance mechanisms. Recent analyses have framed AMR not only as a biomedical problem, but also as an issue of access, innovation, stewardship, and governance [7,8]. A contemporary review must therefore connect the therapeutic value of antibiotics with resistance biology and the health-system responses needed to preserve their long-term clinical utility.

2. Scope and search approach

This manuscript is a structured narrative review. Searches were conducted in PubMed, Scopus, and Web of Science, supplemented by WHO and society guidance documents. Priority was given to peer-reviewed research articles and review papers published from 2010 to 2026, with emphasis on recent surveillance, stewardship, and pipeline literature. The review focuses on antibiotics used against bacterial infections rather than the broader field of antiviral, antifungal, or antiparasitic therapy.

3. Therapeutic potential of antibiotics

Antibiotics can be grouped by chemical scaffold, antibacterial spectrum, or site of action, but a target-based classification is most useful for clinical interpretation. In practice, the major therapeutic targets are cell wall synthesis, protein synthesis, nucleic acid synthesis, membrane integrity, and folate metabolism [9,10]. Representative classes, clinical uses, and common resistance routes are summarized in Table 1.

Table 1. Major antibiotic classes, principal targets, representative uses, and common resistance routes.

Class	Principal target	Representative use	Typical resistance route
β-lactams	Peptidoglycan synthesis / PBPs	Sepsis, pneumonia, intra-abdominal infection	β-lactamases, altered PBPs, porin loss
Glycopeptides / lipopeptides	Cell wall precursor or membrane	MRSA and serious Gram-positive infection	Target remodeling, cell envelope adaptation
Aminoglycosides	30S ribosomal subunit	Severe Gram-negative infection, synergy	Drug-modifying enzymes, reduced uptake
Macrolides / tetracyclines / oxazolidinones	50S or 30S ribosomal targets	Respiratory infection, skin infection, step-down therapy	Methylation, protection proteins, efflux
Fluoroquinolones	DNA gyrase / topoisomerase IV	Urinary and selected systemic infections	Target mutation, efflux, permeability change
Sulfonamides / trimethoprim	Folate pathway	Urinary and community infections	Bypass enzymes, target alteration

Polymyxins	Outer membrane	Salvage therapy for MDR Gram-negative infection	Lipid A modification, heteroresistance

Note: Compiled from mechanism-based reviews of antibacterial action and resistance [11,12].

Cell wall-active agents remain central to therapy because peptidoglycan synthesis is essential to bacterial viability and absent from human cells. Beta-lactams, glycopeptides, and lipopeptides therefore continue to anchor treatment algorithms for common and severe infections, even in settings with substantial resistance [11,12]. Protein synthesis inhibitors, fluoroquinolones, and folate antagonists expand coverage and preserve oral options, step-down therapy, and site-specific utility when susceptibility is maintained. Their therapeutic value depends on exposure at the infection site, toxicity constraints, and local resistance prevalence rather than on class labels alone [1,13].

At the bedside, antibiotic efficacy is inseparable from timely administration, source control, and subsequent refinement of therapy. The practical message is that antibiotics remain highly potent drugs, but their benefit is conditional on matching the right agent to the pathogen, the patient, and the site of infection.

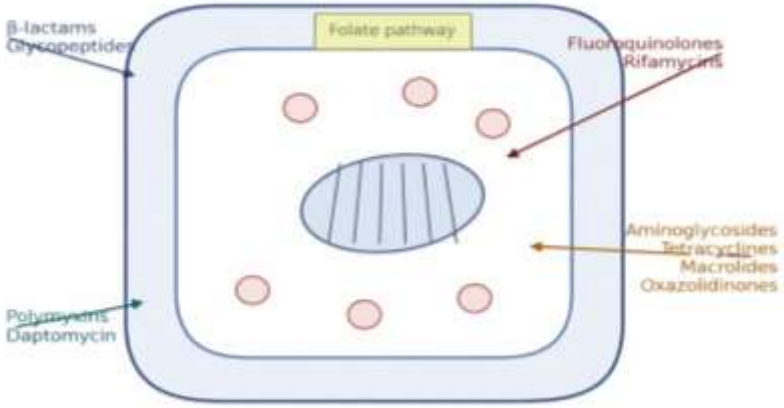

Figure 1. Representative antibacterial targets in a bacterial cell.

Note: Schematic placement of major antibiotic classes is based on target-focused descriptions in [9,10].

4. Current status of resistance in bacterial infections

Resistance is now concentrated in a relatively small number of organisms that generate disproportionate clinical harm. Figure 2 summarizes the global mortality burden reported by the major Lancet analyses [3,4].

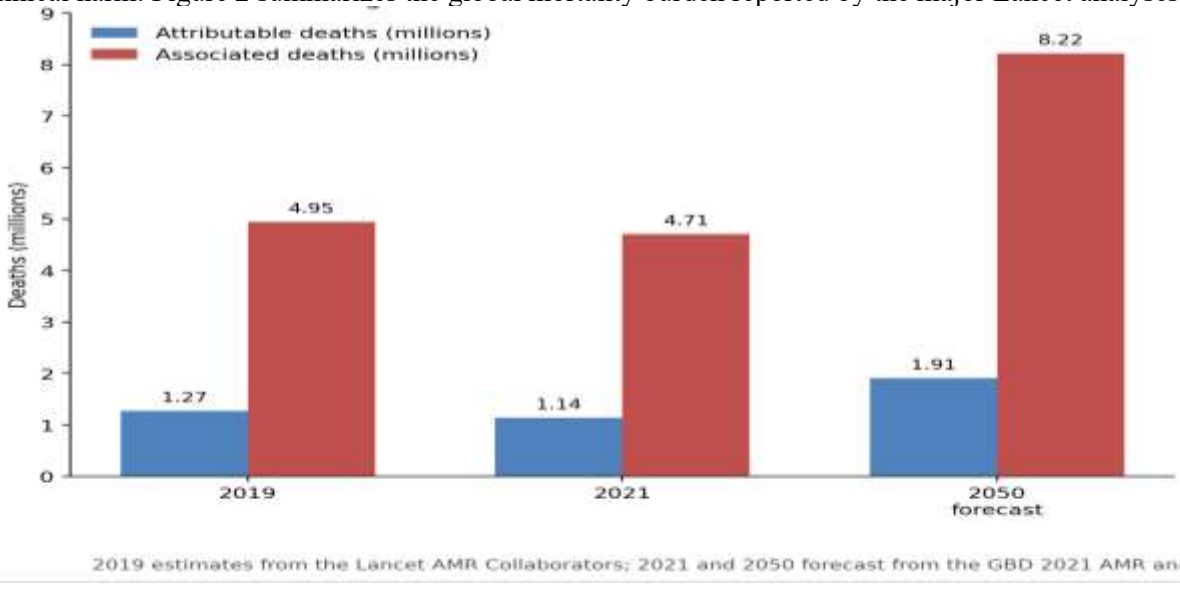

Figure 2. Global burden of bacterial antimicrobial resistance.

Note: Data shown in the figure are derived from the 2019 global burden analysis and the GBD 2021 AMR analysis [3,4].

The BPPL and the long-standing ESKAPE framework converge on the same warning: carbapenem-resistant Acinetobacter baumannii, Pseudomonas aeruginosa, and Enterobacterales, together with methicillin-resistant Staphylococcus aureus and vancomycin-resistant enterococci, are the organisms most likely to exhaust standard therapy [5,14]. Their major treatment implications are outlined in Table 2.

Table 2. Priority resistant pathogens and the main clinical problems they create.

Pathogen group	Priority problem	Why it matters clinically	Common therapeutic challenge
CRAB	Carbapenem resistance	High mortality in ventilator-associated and bloodstream infection	Limited active agents, toxicity of salvage therapy
DTR P. aeruginosa	Multiple resistance mechanisms	Frequent cause of hospital pneumonia and complicated infection	Rapid on-therapy emergence, need for phenotype-specific therapy
CRE / ESBL Enterobacterales	β-lactamase-mediated resistance	Common in urinary, bloodstream, and abdominal infection	Need for targeted β-lactam/β-lactamase inhibitor or carbapenem-sparing strategies
MRSA	Altered PBP target	Persistent burden in skin, lung, and invasive infection	Restricted oral options and need for anti-MRSA coverage
VRE	Glycopeptide resistance	Major problem in immunocompromised and hospitalized patients	Few reliable bactericidal choices

Note: Priority grouping is aligned with WHO 2024 pathogen prioritization and the ESKAPE concept [5,6].

At the clinical level, resistance narrows empiric options, increases the likelihood of discordant initial therapy, and complicates oral step-down planning. Current IDSA and ESCMID guidance illustrate this clearly for ESBL-producing Enterobacterales, carbapenem-resistant Enterobacterales, difficult-to-treat resistant P. aeruginosa, and carbapenem-resistant A. baumannii [15,16]. The bedside consequences are no longer theoretical. Resistant infections are associated with longer hospitalization, greater need for toxic reserve agents, and higher direct and indirect costs, while global surveillance reports show that susceptibility patterns remain dynamic and strongly region-specific [17,18].

5. Molecular basis of resistance

The molecular basis of resistance can still be organized into a practical framework: bacteria may inactivate the drug, alter the target, reduce intracellular accumulation, or survive within protected phenotypic states. Recent reviews emphasize that these pathways increasingly interact rather than operate in isolation [19,20]. Table 3 summarizes the dominant routes, and Figure 3 integrates them into a simple clinical model.

Table 3. Major resistance mechanisms and representative examples relevant to clinical practice.

Mechanism	Representative example	Effect on therapy	Typical organisms
Drug inactivation	ESBLs and carbapenemases	Loss of activity of β-lactams and older inhibitor combinations	Enterobacterales, A. baumannii

Target modification	Altered PBPs, ribosomal methylation, QRDR mutation	Reduced drug binding despite adequate exposure	MRSA, pneumococci, Enterobacterales
Reduced accumulation	Porin loss and active efflux	Lower intracellular concentration and multidrug resistance	P. aeruginosa, Enterobacterales
Phenotypic tolerance	Biofilm growth and persister cells	Microbiological failure without classical acquired resistance	Device-associated and chronic infections
Genetic dissemination	Plasmids, transposons, integrons	Rapid spread of resistance determinants across niches	Hospital, community, animal, and environmental reservoirs

Note: Compiled from major reviews of bacterial resistance mechanisms [12,21].

Enzymatic inactivation remains especially important for beta-lactams. Beta-lactamases now range from narrow-spectrum enzymes to ESBLs and carbapenemases, and the clinical usefulness of newer beta-lactam/beta-lactamase inhibitor combinations depends on which enzyme family is present [22,23]. Target modification is equally important. Altered penicillin-binding proteins, ribosomal methylation or protection, and fluoroquinolone target mutations can preserve bacterial survival despite otherwise adequate drug exposure [12,21]. Gram-negative bacteria also resist therapy by reducing intracellular drug concentration. Porin loss and tripartite efflux systems lower effective exposure and frequently combine with enzymatic resistance, producing high-level multidrug phenotypes [24,25].

Biofilms and persister states explain why microbiological failure can occur even when classical acquired resistance genes are absent. These phenotypes reduce penetration, slow metabolism, and increase tolerance during device-associated and chronic infection [26,27]. Resistance genes are then amplified and disseminated by mobile genetic elements. Plasmids, transposons, integrons, and horizontal gene transfer permit clinically important determinants to circulate across hospitals, communities, animals, and environmental reservoirs [28,29].

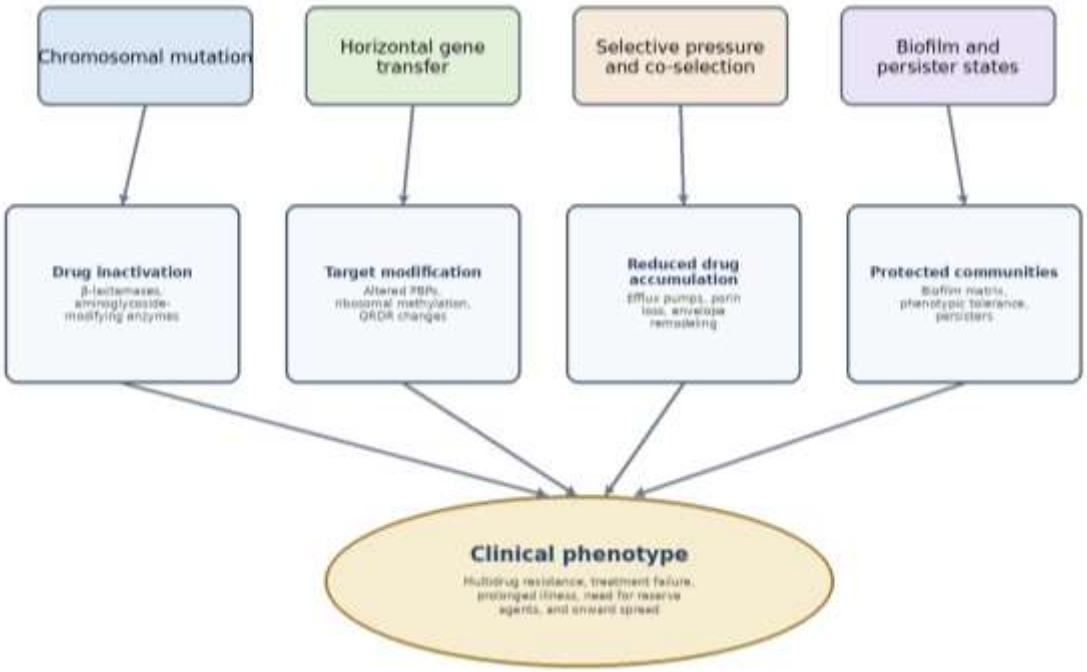

Figure 3. Integrated view of the main pathways that generate clinical resistance phenotypes.

Note: Conceptual summary adapted from contemporary mechanism reviews and gene dissemination literature [19,28].

6. Drivers of resistance across the One Health continuum

Resistance is accelerated by antibiotic exposure itself. In human medicine, unnecessary prescriptions, overly broad empiric regimens, prolonged courses, and repeat community prescribing all increase selection pressure at individual and population levels [30,31]. The problem is also ecological. One Health analyses show that antibiotic use in animals, environmental contamination, and inadequate sanitation create linked reservoirs that maintain and redistribute resistance determinants beyond hospitals [32,33].

Environmental selection does not act only through antibiotics. Co-selective pressures from biocides, heavy metals, and wastewater exposures can maintain resistance even when antibiotic use falls, which helps explain why reversal is slower than emergence [27,34]. At the same time, stewardship must address the global paradox of excess and lack of access. Some health systems overuse broad-spectrum agents, whereas others still face preventable mortality because active antibiotics, diagnostics, and basic infection control remain unavailable [7,35].

Table 4. Major drivers that accelerate antibiotic resistance beyond single-patient prescribing decisions.

Driver	How it acts	Illustrative setting	Practical implication
Inappropriate human use	Selects for resistant flora and amplifies transmission	Unnecessary outpatient prescriptions, prolonged hospital courses	Need for diagnostic support and review at 48–72 h
Animal and food-chain use	Maintains reservoirs under chronic selection	Livestock and aquaculture	Need for One Health regulation and surveillance
Environmental contamination	Sustains genes and co-selection outside healthcare	Wastewater, pharmaceutical discharge, poor sanitation	Need for environmental controls
Weak laboratory capacity	Prevents timely narrowing of therapy	Settings without culture or AST support	Empiric broad-spectrum use persists
Inequitable access	Delays active treatment and distorts antibiotic use patterns	Low-resource health systems	Access and stewardship must be developed together

Note: Compiled from reviews of AMR drivers, One Health ecology, and environmental selection [30,34].

7. Preserving antibiotic efficacy

Antibiotic stewardship is the most immediate tool for preserving efficacy. In operational terms, stewardship means starting the right agent quickly when infection is likely, then narrowing, stopping, or switching to oral therapy once microbiology and clinical trajectory are known [36,37]. Figure 4 outlines this workflow.

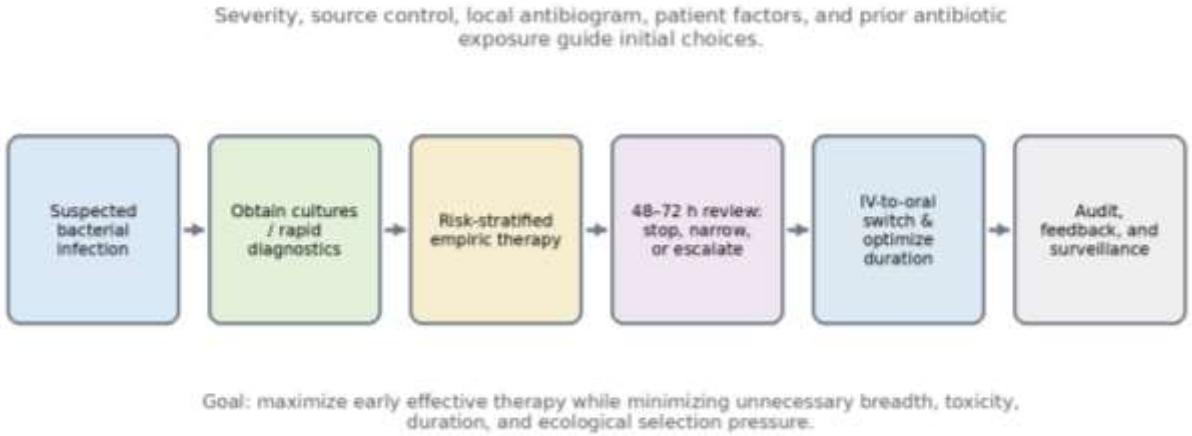

Figure 4. Core stewardship workflow from initial suspicion of infection to review and optimization.

Note: The sequence reflects major antimicrobial stewardship guidance and evidence syntheses [36,38].

Evidence syntheses show that stewardship programs reduce inappropriate prescribing, Clostridioides difficile infection, and colonization or infection with resistant organisms, especially when audit-and-feedback, guideline implementation, and diagnostic support are combined [38,39]. Stewardship, however, works best when paired with resistance-aware therapeutics. Current IDSA recommendations, ESCMID guidance, and up-to-date breakpoint interpretation help clinicians match specific agents to specific resistance phenotypes instead of relying on outdated class generalizations [15,40].

WHO's AWaRe framework adds a population lens by encouraging access to essential first-line agents while protecting higher-risk Watch and Reserve antibiotics from indiscriminate use. Surveillance systems such as GLASS make that framework more actionable by linking policy to observed resistance trends [18,41]. Stewardship alone cannot solve established resistance, so the antibacterial pipeline remains important. WHO pipeline reviews show that discovery activity continues but is still thin relative to clinical need, especially for critical Gram-negative pathogens [42,43].

Future discovery will likely combine classical microbiology with newer search platforms. Natural-product rediscovery, mechanism-guided chemistry, and AI-enabled screening have already produced notable proof-of-concept examples, including teixobactin and machine-learning-derived candidate scaffolds [44,45]. Teixobactin remains an especially useful proof of principle because it demonstrated the value of targeting highly conserved cell-wall precursors outside conventional protein targets [46]. Broader management frameworks also continue to emphasize infection prevention, vaccination, and new-agent access alongside therapeutic innovation [8,13].

Table 5. Complementary strategies for preserving and extending antibiotic effectiveness.

Strategy	Primary goal	Representative actions	Current status
Stewardship	Reduce unnecessary exposure	Prospective audit, de-escalation, IV-to-oral switch	Standard of care in many hospitals
Diagnostics and AST	Improve precision of early therapy	Rapid diagnostics, culture, susceptibility testing, antibiograms	Expanding but uneven globally
Infection prevention	Reduce need for antibiotics	Hand hygiene, source control, vaccination, IPC bundles	Highly effective when sustained
Access and equity	Ensure patients receive active first-line therapy	Reliable supply chains, laboratory capacity, guideline adoption	Persistent gap in many settings

Innovation and incentives	Expand options against priority pathogens	Pipeline support, pull incentives, AI discovery, novel agents	Active but still insufficient

Note: Strategy framework synthesized from stewardship guidance, AWaRe policy, and pipeline analyses [41,42].

8. Future directions

The future of antibiotics will be determined less by a single new drug than by how well health systems align access, diagnostics, surveillance, and innovation. The recent Lancet AMR series argues that durable control requires coordinated investment in antibiotics, vaccines, diagnostics, and delivery systems rather than pipeline expansion alone [7,8]. This also means correcting inequity. Affordable supply, laboratory capacity, and context-specific guidelines are as important to antibiotic effectiveness as new molecules because untreated or undertreated bacterial infection also drives resistance and mortality [35,41]. A realistic near-term goal is therefore durable antibiotic efficacy rather than eradication of resistance. That goal depends on integrating stewardship, infection prevention, environmental control, and innovation within a One Health governance model [32,42].

Conclusion

Antibiotics remain among the most consequential therapeutic tools in medicine, but their value can no longer be assumed to persist without deliberate protection. The current evidence supports a dual conclusion: antibiotics still deliver major clinical benefit, yet resistance is concentrating in priority pathogens, narrowing empiric therapy, and increasing reliance on reserve agents. Durable efficacy will depend on stewardship, surveillance, infection prevention, equitable access, and sustained innovation.

Declarations

Funding: No specific funding was received for this review article.
Conflicts of interest: The authors declare they don’t have any conflict of interest.
Ethics approval: Not applicable for this review article.

Author contributions

Each author contributed to the manuscript's writing, gathered information, edited it, made tables, and received approval to submit it to a journal for publication. The first author wrote the first draft of the paper, which was supervised by a cross-responding author.

Acknowledgement

The authors thank numerous resources for their open access publications, including DOAJ, Google Scholar, PubMed, Cochrane Library, BMJ Clinical Evidence, Embase, and Medline.

References

1. Hutchings MI, Truman AW, Wilkinson B. Antibiotics: past, present and future. Current Opinion in Microbiology. 2019.
2. Davies J, Davies D. Origins and evolution of antibiotic resistance. Microbiology and Molecular Biology Reviews. 2010.
3. Antimicrobial Resistance Collaborators. Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis. The Lancet. 2022.
4. GBD 2021 Antimicrobial Resistance Collaborators. Global burden of bacterial antimicrobial resistance 1990–2021: a systematic analysis with forecasts to 2050. The Lancet. 2024.
5. World Health Organization. WHO bacterial priority pathogens list, 2024. Geneva: WHO. 2024.
6. Sati H, Carrara E, Savoldi A, et al. The WHO bacterial priority pathogens list 2024: a prioritisation study to guide research, development, and public health strategies against antimicrobial resistance. The Lancet Infectious Diseases. 2025.

7. Okeke IN, Laxminarayan R, Bhutta ZA, et al. The scope of the antimicrobial resistance challenge. The Lancet. 2024.
8. Laxminarayan R, Outterson K, Pécoul B, et al. Expanding antibiotic, vaccine, and diagnostics development and access to tackle antimicrobial resistance. The Lancet. 2024.
9. Kohanski MA, Dwyer DJ, Collins JJ. How antibiotics kill bacteria: from targets to networks. Nature Reviews Microbiology. 2010.
10. Kapoor G, Saigal S, Elongavan A. Action and resistance mechanisms of antibiotics: a guide for clinicians. Journal of Anaesthesiology Clinical Pharmacology. 2017.
11. Fair RJ, Tor Y. Antibiotics and bacterial resistance in the 21st century. Perspectives in Medicinal Chemistry. 2014.
12. Munita JM, Arias CA. Mechanisms of antibiotic resistance. Microbiology Spectrum. 2016.
13. Ventola CL. The antibiotic resistance crisis: part 2: management strategies and new agents. P&T. 2015.
14. Boucher HW, Talbot GH, Bradley JS, et al. Bad bugs, no drugs: no ESKAPE! An update from the Infectious Diseases Society of America. Clinical Infectious Diseases. 2009.
15. Tamma PD, Heil EL, Justo JA, Mathers AJ, Satlin MJ, Bonomo RA. Infectious Diseases Society of America 2024 guidance on the treatment of antimicrobial-resistant Gram-negative infections. Clinical Infectious Diseases. 2024.
16. Paul M, Carrara E, Retamar P, et al. ESCMID guidelines for the treatment of infections caused by multidrug-resistant Gram-negative bacilli. Clinical Microbiology and Infection. 2022.
17. Ventola CL. The antibiotic resistance crisis: part 1: causes and threats. P&T. 2015.
18. World Health Organization. Global antibiotic resistance surveillance report 2025. Geneva: WHO. 2025.
19. Blair JMA, Webber MA, Baylay AJ, Ogbolu DO, Piddock LJV. Molecular mechanisms of antibiotic resistance. Nature Reviews Microbiology. 2015.
20. Darby EM, Trampari E, Siasat P, et al. Molecular mechanisms of antibiotic resistance revisited. Nature Reviews Microbiology. 2023.
21. Reygaert WC. An overview of the antimicrobial resistance mechanisms of bacteria. AIMS Microbiology. 2018.
22. Bush K. Past and present perspectives on beta-lactamases. Antimicrobial Agents and Chemotherapy. 2018.
23. Bush K, Bradford PA. Interplay between beta-lactamases and new beta-lactamase inhibitors. Nature Reviews Microbiology. 2019.
24. Du D, Wang-Kan X, Neuberger A, et al. Multidrug efflux pumps: structure, function and regulation. Nature Reviews Microbiology. 2018.
25. Alav I, Kobylka J, Kuth MS, et al. Structure, assembly, and function of tripartite efflux and type 1 secretion systems in Gram-negative bacteria. Chemical Reviews. 2021.
26. Hall CW, Mah TF. Molecular mechanisms of biofilm-based antibiotic resistance and tolerance in pathogenic bacteria. FEMS Microbiology Reviews. 2017.
27. Andersson DI, Hughes D. Antibiotic resistance and its cost: is it possible to reverse resistance? Nature Reviews Microbiology. 2010.
28. Partridge SR, Kwong SM, Firth N, Jensen SO. Mobile genetic elements associated with antimicrobial resistance. Clinical Microbiology Reviews. 2018.
29. von Wintersdorff CJH, Penders J, van Niekerk JM, et al. Dissemination of antimicrobial resistance in microbial ecosystems through horizontal gene transfer. Frontiers in Microbiology. 2016.
30. Holmes AH, Moore LSP, Sundsfjord A, et al. Understanding the mechanisms and drivers of antimicrobial resistance. The Lancet. 2016.
31. Costelloe C, Metcalfe C, Lovering A, Mant D, Hay AD. Effect of antibiotic prescribing in primary care on antimicrobial resistance in individual patients: systematic review and meta-analysis. BMJ. 2010.
32. McEwen SA, Collignon PJ. Antimicrobial resistance: a One Health perspective. Microbiology Spectrum. 2018.
33. Berendonk TU, Manaia CM, Merlin C, et al. Tackling antibiotic resistance: the environmental framework. Nature Reviews Microbiology. 2015.
34. Larsson DGJ, Flach CF. Antibiotic resistance in the environment. Nature Reviews Microbiology. 2022.

35. Laxminarayan R, Duse A, Wattal C, et al. Antibiotic resistance—the need for global solutions. The Lancet Infectious Diseases. 2013.
36. Barlam TF, Cosgrove SE, Abbo LM, et al. Implementing an antibiotic stewardship program: guidelines by the Infectious Diseases Society of America and the Society for Healthcare Epidemiology of America. Clinical Infectious Diseases. 2016.
37. Dyar OJ, Huttner B, Schouten J, Pulcini C. What is antimicrobial stewardship? Clinical Microbiology and Infection. 2017.
38. Schuts EC, Hulscher MEJL, Mouton JW, et al. Current evidence on hospital antimicrobial stewardship objectives: a systematic review and meta-analysis. The Lancet Infectious Diseases. 2016.
39. Baur D, Gladstone BP, Burkert F, et al. Effect of antibiotic stewardship on the incidence of infection and colonisation with antibiotic-resistant bacteria and Clostridioides difficile infection: a systematic review and meta-analysis. The Lancet Infectious Diseases. 2017.
40. European Committee on Antimicrobial Susceptibility Testing. Breakpoint tables for interpretation of MICs and zone diameters, version 16.0. EUCAST. 2026.
41. World Health Organization. The WHO AWaRe (Access, Watch, Reserve) antibiotic book. Geneva: WHO. 2022.
42. World Health Organization. 2023 antibacterial agents in clinical and preclinical development: an overview and analysis. Geneva: WHO. 2024.
43. Silver LL. Challenges of antibacterial discovery. Clinical Microbiology Reviews. 2011.
44. Lewis K. The science of antibiotic discovery. Cell. 2020.
45. Stokes JM, Yang K, Swanson K, et al. A deep learning approach to antibiotic discovery. Cell. 2020.
46. Ling LL, Schneider T, Peoples AJ, et al. A new antibiotic kills pathogens without detectable resistance. Nature. 2015.