MERAL Publications and Solutions Pvt. Ltd.

Review Article

Advances in understanding antimicrobial resistance and approaches for mitigation

Mohammed Ibrahim Mobarki[1], Abeer Abdulrahman Alkaabi[1], Mashael Hussien Alqahtani[1], Wed Abdulrahman Alasmri[1], Noura Fahad Alkhuwaiter[1], Saeed Ali Alasmary[2*], Dalia Saleh Alghamdi[3], Ibrahim Abdulrhman Alsharidah[4], Abdulkarim Mohsen Ali Alhakami[5], Rayan Mohammed Almohaimeed[6], Naif Abdulrahman Alarifi[7]

[1]Dental Assistant, Prince Sultan Military Medical City, Riyadh, Saudi Arabia. [2]Senior Pharmacist, Prince Sultan Military Medical city, Riyadh, Saudi Arabia. [3]Senior Pharmacist, Clinical Excellence Department, Riyadh, Saudi Arabia. [4]Dentist, Prince Sultan Military Medical City, Riyadh, Saudi Arabia. [5]Family Medicine Senior Registrar, Prince Sultan Military Medical City, Riyadh, Saudi Arabia. [6]Technician Nursing, Prince Sultan Military Medical City, Riyadh, Saudi Arabia. [7]Senior Specialist Laboratory, Armed Forces Medical Service, Riyadh, Saudi Arabia.

Correspondence: Saeed Ali Alasmary, Senior Pharmacist, Prince Sultan Military Medical city, Riyadh, Saudi Arabia. salasmary@psmmc.med.sa

Received: 18 May 2025; **Revised:** 07 August2025; **Accepted:** 08 August 2025

ABSTRACT

Antibiotics have transformed modern medicine, playing a pivotal role in healthcare and saving millions of lives globally. Nevertheless, the rapid rise of antimicrobial resistance (AMR) poses a significant and escalating threat, with the potential to trigger a major public health crisis. This review aims to summarize the microbial and human-driven factors contributing to AMR and highlight the implications of neglecting this challenge. Relevant literature was retrieved from international databases, including PubMed, Scopus, ScienceDirect, and Google Scholar, using combinations of keywords such as "antimicrobial resistance," "superbug," "antibiotic stewardship," "one health," and "surveillance." The article examines major drivers of AMR, including inappropriate antibiotic use and the proliferation of resistant bacterial strains, while also discussing strategies to counteract this threat. Proposed measures include implementation of the One Health framework, robust stewardship programs, and the integration of artificial intelligence in drug discovery. Moreover, the potential role of traditional and ethnic medicinal practices in therapeutic interventions has been explored. In summary, this review highlights the urgent need for coordinated, multifaceted action to combat AMR. Future research and innovative strategies are crucial to reducing the burden of resistance and protecting both human and animal health.

Keywords: Antimicrobial resistance, Antibiotics, Healthcare, Superbug, Surveillance

Introduction

Antibiotics are recognized as one of the most significant medical discoveries of the 20th century, credited with saving millions of lives from infectious diseases and hospital-acquired infections since their accidental discovery by Sir Alexander Fleming in the 1920s. However, their remarkable success is now threatened by the rising problem of antimicrobial resistance (AMR), which is progressively reducing the effectiveness of these drugs. As John Ray, the English taxonomist, noted, "Nothing is invented and perfected at the same time"—a reminder that even revolutionary drugs like antibiotics are vulnerable to limitations, particularly resistance.

Excessive prescribing, misdiagnosis, and the widespread misuse of antimicrobials have accelerated the emergence of resistant strains, making many infections increasingly challenging to treat. AMR occurs when microorganisms—including bacteria, viruses,

Access this article online	
Website: www.japer.in	**E-ISSN:** 2249-3379

How to cite this article: Mobarki MI, Alkaabi AA, Alqahtani MH, Alasmri WA, Alkhuwaiter NF, Alasmary SA, et al. Advances in understanding antimicrobial resistance and approaches for mitigation. J Adv Pharm Educ Res. 2025;15(3):167-77. https://doi.org/10.51847/5P5Jo37fEX

fungi, and some parasites—develop the ability to survive exposure to agents designed to eliminate them. This phenomenon has become a primary global health concern, as the failure of standard antibiotics threatens to render many infectious diseases untreatable [1].

The present review provides a comprehensive overview of the development and implications of AMR, alongside novel strategies for its control.

Materials and Methods

Literature was retrieved from international databases, including PubMed, Scopus, ScienceDirect, and Google Scholar, using search terms such as "antimicrobial resistance," "superbug," "antibiotic stewardship," "one health," and "surveillance," in various combinations. Out of the published studies, 71 relevant articles were selected for discussion. This review aims to provide researchers with updated insights into AMR, supporting the design of future investigations and interventions in this critical field.

Results and Discussion

Economic consequences of antimicrobial resistance

AMR represents not only a healthcare challenge but also an economic burden with potentially devastating global effects. The discovery and development of new antibiotics require significant financial investment and time, limiting accessibility for low- and middle-income populations [2]. In the United States, resistant infections associated with immigration have been identified as a key driver of healthcare costs, imposing substantial strain on national health budgets. This pattern is partly linked to migration from regions with underdeveloped health infrastructure, where resistant pathogens are more prevalent.

According to World Bank simulations, by 2050 AMR could reduce global annual GDP by approximately 1.1% [3]. Encouragingly, about half of these projected losses might be avoided through effective containment and stewardship measures. The direct costs of AMR are reflected in rising healthcare expenditures, which may compel governments to reallocate funds toward health at the expense of other sectors.

The economic burden extends beyond healthcare, encompassing reduced productivity, workforce losses, and higher morbidity and mortality rates. Some nations have also introduced travel and immigration restrictions to control the spread of resistant infections. Although the economic cost of AMR in India has not been fully quantified, it is expected to have significant implications for the country's economy in the future [4].

A global study estimated that 1.27 million deaths were attributable to bacterial AMR [5], and projections suggest mortality could reach 10 million annually by 2050 if the issue remains unaddressed [6]. Moreover, the livestock trade is likely to suffer considerable disruption, particularly in products such as meat and milk, due to the fear of zoonotic transmission from resistant strains of pathogens [7]. These consequences underscore the urgent need for coordinated global action to reduce both the health and economic toll of AMR.

Impact on the healthcare system

Antimicrobial resistance (AMR) exerts a profound burden on healthcare, disproportionately affecting vulnerable populations. Neonates experience elevated mortality rates due to resistant infections, while older adults with weakened immunity and immunocompromised patients are also at heightened risk. Individuals from economically disadvantaged backgrounds face additional challenges, as they often lack access to costly second-line antimicrobial therapies when first-line treatments fail. This disparity further amplifies the negative health consequences of AMR.

Causes of antimicrobial resistance

AMR represents one of the most significant challenges to modern medicine and spreads through both vertical gene transfer (from one generation to the next) and horizontal gene transfer mechanisms such as transformation, transduction, and conjugation [8]. Multiple factors contribute to the emergence of resistance, including active efflux pumps, reduced drug uptake, modification of drug targets, enzymatic inactivation of drugs, and other biochemical adaptations [8, 9].

Key drivers include plasmid-mediated resistance, biofilm formation, and various anthropogenic activities, all of which accelerate the dissemination of resistant traits across microbial populations.

Plasmid-mediated resistance

Among the diverse mechanisms, plasmid-mediated resistance plays a particularly significant role in the spread of AMR. Plasmids are extrachromosomal genetic elements capable of transferring resistance genes between bacterial cells, often through conjugation. These plasmids facilitate the acquisition and dissemination of antimicrobial resistance genes, making them central to the persistence of resistant strains.

For example, resistance to colistin has been widely documented in Enterobacteriaceae, attributed mainly to the plasmid-mediated *mcr-1* gene [10]. Importantly, implementation of One Health policies—such as restricting the use of colistin as a livestock growth promoter—has been shown to reduce the prevalence of colistin-resistant strains and the *mcr-1* gene across humans, animals, and the environment. Such sustainable interventions highlight the importance of the One Health approach in tackling antibiotic resistance.

Furthermore, plasmid-mediated horizontal gene transfer accelerates the spread of resistance genes more efficiently than other mechanisms [11]. Environmental contaminants, including heavy metals, nanoparticles, pharmaceuticals (both antibiotics

and non-antibiotics), and microplastics, have been shown to enhance plasmid transfer in both aquatic and terrestrial ecosystems, thereby compounding the problem of AMR.

Figure 1 shows the causes, mechanisms, and consequences of antimicrobial resistance (AMR).

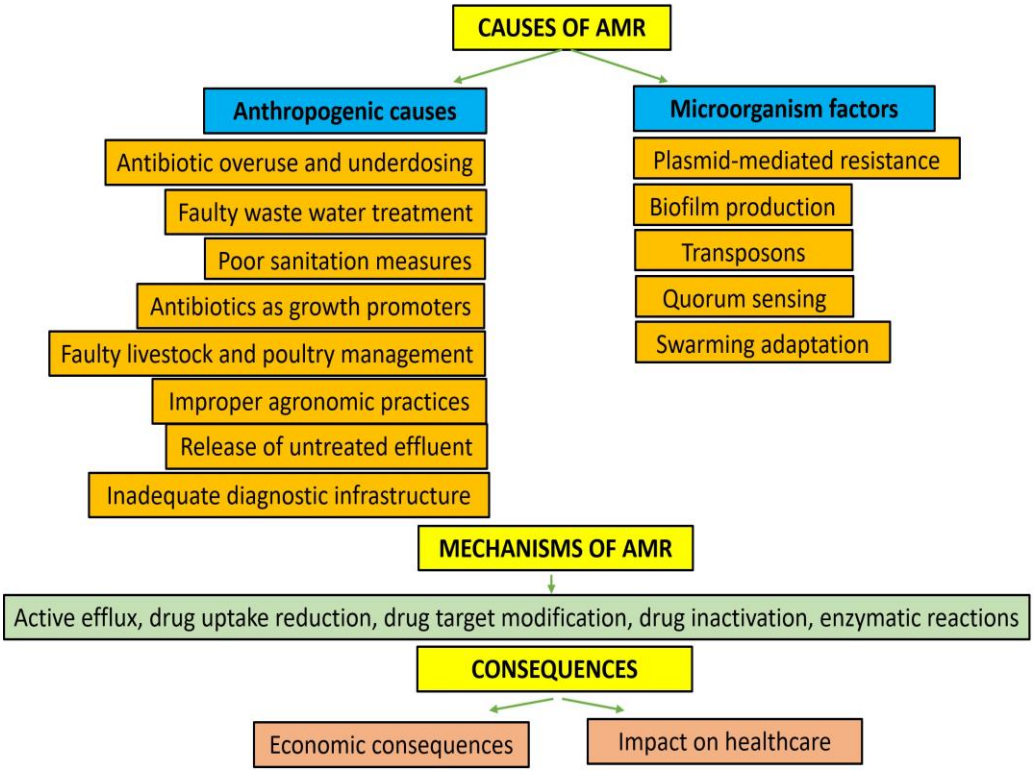

Figure 1. Causes, mechanisms, and consequences of antimicrobial resistance (AMR).

Future research should prioritize the rapid identification of environmental pollutants that enhance plasmid transfer and explore strategies to block such genetic exchanges, thereby limiting the spread of antibiotic resistance. Yassine *et al.* [12] reported a high prevalence of plasmid-mediated quinolone resistance (PMQR) in Arab countries, with Enterobacteriaceae showing increasing levels of quinolone resistance. Similarly, plasmid-encoded extended-spectrum β-lactamases (ESBLs) and carbapenemases have been identified as major contributors to resistance, as reviewed by Schultsz and Geerlings [13]. Certain drugs—such as colistin, fosfomycin, tigecycline, and temocillin—have demonstrated effectiveness against carbapenem-resistant Enterobacteria.

The plasmid-driven dissemination of resistance in Salmonella enterica has also been well documented. Carattoli [14] highlighted how enteric pathogens acquire resistance to expanded-spectrum cephalosporins, with integrons playing a crucial role in the incorporation and dissemination of resistance genes. An in vivo study revealed that the plasmid pOXA-48**,** conferring carbapenem resistance, was detected in enterobacterial colonies isolated from gut samples of hospitalized patients [15].

Guan *et al.* [16] reviewed mechanisms of quinolone resistance, noting that plasmid-mediated gene transfer, chromosomal mutations, altered efflux pump activity, and changes in cell membrane properties all contribute to the development of quinolone-resistant bacteria. A study on plasmid-mediated resistance among uropathogens in primigravid women with bacteriuria found that 65% of *Escherichia coli* isolates and 41% of *Klebsiella pneumoniae* isolates were ESBL-positive [17]. The predominant resistance genes were TEM-1 (66.7%) and CTX-M-15 (33.3%)**,** highlighting the increasing prevalence of plasmid-mediated ESBLs and quinolone-resistant organisms in community-acquired urinary tract infections among this population [17].

Additionally, Kivata *et al.* [18] reported plasmid-mediated penicillin and tetracycline resistance in *Neisseria gonorrhoeae* isolates from Kenya. The resistance was attributed to the TEM gene (penicillin resistance) and the TetM gene (tetracycline resistance), further demonstrating the role of plasmids in driving multidrug resistance.

Resistance nodulation division (RND) and mobile genetic elements

Resistance nodulation division (RND) efflux systems, which are encoded by chromosomal genes, are essential contributors to multidrug resistance in Gram-negative organisms. Lv *et al.* described a novel plasmid-associated RND efflux pump gene cluster, tmexCD1-toprJ1, in *K. pneumoniae* of animal origin. Tigecycline is generally used as a therapeutic option against carbapenem-resistant *K. pneumoniae*; however, this plasmid-borne cluster has been shown to reduce susceptibility to tigecycline, creating serious clinical concerns [19]. Limiting the

spread of tmexCD1-toprJ1 through integrated one health strategies is therefore a priority.

Another example is *Bhargavaea beijingensis*, an environmental bacterium commonly isolated from soil and water. The PS04 strain was reported to harbor the plasmid repUS12, which carries the ermT and tet(L) genes, providing resistance to macrolides, lincosamides, and tetracyclines [20]. The emergence of this plasmid is likely linked to horizontal gene transfer, highlighting the importance of monitoring environmental bacteria in the surveillance of AMR.

Plasmid-mediated resistance has also been extensively reviewed in *Staphylococcus* and other Firmicutes, as noted by Schwarz *et al*. [21]. In addition to plasmids, mobile genetic elements such as transposons play a significant role. These "jumping genes" are capable of moving within the genome, often inserting resistance determinants that enhance the adaptability of bacteria and can transform them into multidrug-resistant strains [22].

Alongside these inheritable mechanisms, non-genetic adaptations, including biofilm development, quorum sensing, swarming, and the formation of persister cells, contribute substantially to antimicrobial resistance in clinical and environmental settings.

Role of biofilms in antimicrobial resistance

Biofilms represent a critical adaptation that enhances bacterial survival under stress conditions. Although the precise molecular relationship between biofilm development and the expression of resistance genes is not yet fully understood, evidence indicates that biofilms form a protective matrix that reduces the penetration and efficacy of antibiotics.

A review by Datta *et al*. [23], focusing on Indian clinical cases, found that biofilm-associated infections are particularly prevalent in organisms such as *Escherichia*, *Streptococcus*, *Staphylococcus*, and *Pseudomonas*. These bacteria are frequently implicated in respiratory tract infections, urinary tract infections, as well as dental and skin conditions [23].

There is growing concern over the increasing multidrug resistance observed in several microbial species, warranting further investigation. In *Salmonella typhi* (MTCC-733), biofilm formation was found to impair antibiotic efficacy significantly, with evidence suggesting that the cellulose fraction of the biofilm matrix plays a role in resistance development and could serve as a potential therapeutic target [24]. Research on *Mycobacteroides abscessus* indicated that smooth colony morphotypes, which readily form biofilms, display higher resistance to antimicrobials compared to rough morphotypes. Their biofilm-associated growth enhanced tolerance to amikacin and tigecycline, and also increased resilience against disinfectants such as peracetic acid [25].

Recent findings suggest that biofilm inhibition through small molecules and nanoparticles holds promise as an effective strategy to combat microbial resistance, as reviewed by Gattu *et al*. [26]. Pauze-Foixet *et al*. [27] further demonstrated that polymyxin B exerts more potent effects on biofilm suppression in *Vibrio cholerae* under anaerobic conditions. In addition, genetically engineered bacteriophages, along with phage-derived proteins and enzymes, have shown promise in targeting multidrug-resistant bacteria, either independently or in combination with conventional antibiotics [28].

During biofilm growth, bacterial communities rely on their extracellular matrix, which not only reduces antibiotic penetration but can also trap and inactivate antimicrobial compounds through its complex architecture [29]. Moreover, spatial heterogeneity within biofilms creates distinct physicochemical niches; for instance, oxygen-rich microenvironments in *Pseudomonas aeruginosa* are more susceptible to quinolones, whereas oxygen-depleted zones exhibit the opposite trend [22]. Overall, the structural and physiological complexity of biofilms diminishes the therapeutic efficiency of antibiotics and serves as a reservoir for antimicrobial resistance [30].

Quorum sensing, another pivotal mechanism, enables bacteria to modulate gene expression in response to cell density via chemical signals termed autoinducers [31]. This process regulates various behaviors, including motility, sporulation, swarming, and, in some instances, biofilm formation, thereby facilitating bacterial survival under antimicrobial stress. While quorum sensing often mediates host–pathogen interactions, it also contributes to the persistence of infections, underscoring the need for strategies that exploit its vulnerabilities to counteract resistant pathogens.

Anthropogenic drivers of antimicrobial resistance

Excessive and inappropriate antibiotic use in both human and veterinary contexts remains a significant contributor to the development of antibiotic resistance. In livestock production, antibiotics are frequently administered at sub-therapeutic doses to promote growth, inadvertently fostering the emergence of resistant strains. Similarly, in human medicine, practices such as incomplete treatment courses or incorrect dosing encourage bacterial adaptation and the rise of superbugs. Collectively, these anthropogenic pressures have accelerated the spread of antimicrobial resistance across healthcare facilities, animal husbandry, agriculture, and wastewater systems [32].

Key examples include the widespread use of antimicrobials in poultry and livestock farming, along with effluents from slaughterhouses, which introduce resistant bacteria into surrounding environments. Ciprofloxacin resistance has been reported at alarmingly high levels in slaughterhouses: 93% in Iran, 50% in Nigeria, and 20% in China. Comparable patterns have been observed in Europe, with poultry slaughterhouses in Germany showing resistance ranging from 21% to 81%, and in Spain, resistance levels reaching 56% [33]. Profiling of *Salmonella* spp. and *Escherichia coli* isolates from anthropogenic settings further revealed resistance to sulfisoxazole and streptomycin in *Salmonella*, and to sulfisoxazole, cefoxitin, and ampicillin in *E. coli* [34].

Navarro *et al*. [35] investigated antibiotic resistance in bacterial isolates from water samples collected in two rivers with minimal

anthropogenic influence—the Variola (pre-Alpine) and the Tiber (Apennine). Their results showed that the blaTEM gene, responsible for resistance to β-lactam antibiotics, was present in approximately 58% of isolates, whereas mefA/E, linked to macrolide resistance, appeared in only 9% [35]. These findings highlight the presence of co-resistant bacteria even in relatively pristine environments, raising concerns about their potential transmission to human and animal populations over time.

Further evidence comes from studies on nontuberculous *Mycobacteria* within hospital environments, where species such as *M. obuense* and *M. mucogenicum* demonstrated multidrug-resistant characteristics. Specifically, the erm (erythromycin resistance methylase) gene enabled *M. obuense* to resist clarithromycin, while *Corynebacterium* isolates exhibited resistance to penicillin, ciprofloxacin, and linezolid [36]. Similarly, Swift *et al*. [37] reported that the emergence of antimicrobial resistance in bacterial isolates from wildlife species is primarily driven by anthropogenic pressures, including exposure to antimicrobials and resistant strains originating from human activity.

Inadequate sanitation practices further accelerate the spread of infectious diseases, and non-compliance with hygiene measures remains a key driver of rising AMR worldwide [38]. In addition, weak diagnostic infrastructure often leads to misidentification of pathogens, encouraging inappropriate antibiotic prescriptions and facilitating cross-resistance. Other major anthropogenic contributors include the use of antimicrobials as growth promoters in animal husbandry, improper wastewater treatment, and the discharge of untreated effluents into natural ecosystems. These factors impose significant selection pressure, fostering the persistence of resistant strains and disseminating antibiotic resistance genes in aquatic environments. Consistently, studies have shown that effluent treatment plants harbor a higher prevalence of resistance genes compared to natural rivers, and insufficient treatment exacerbates their release into the environment [39].

Finally, the lack of awareness regarding antimicrobial stewardship, coupled with limited access to affordable alternatives to antibiotics, continues to exacerbate this global health crisis.

Novel approaches to address antimicrobial resistance and way forward

Addressing antimicrobial resistance (AMR) requires a combination of coordinated strategies and active engagement of all stakeholders, along with widespread awareness initiatives. The human gut serves as a reservoir for numerous antibiotic-resistant microorganisms, and conventional antibiotic therapy can disrupt the gut microbiome by altering both its taxonomic composition and functional profile. Such dysbiosis can facilitate colonization by pathogenic strains and increase the abundance of resistance genes, potentially leading to bloodstream infections and other diseases [40-42]. Advanced techniques such as functional metagenomics and long-read sequencing offer critical tools for detecting and characterizing resistance genes, aiding in the design of targeted strategies to combat resistant bacteria. **Tables 1 and 2** summarize emerging approaches and techniques, along with their potential advantages in mitigating AMR.

Development and discovery of new antibiotics

One promising strategy involves exploring antimicrobial compounds from microorganisms inhabiting extreme environments, which are largely unexposed to conventional antibiotics. Advances in nanobiotechnology and drug design allow for the creation of compounds that mimic physiological conditions and identify natural biomolecules capable of inhibiting microbial growth. The isolation chip (I-chip) technology exemplifies this approach by enabling the cultivation of previously unculturable bacteria within their native environments, facilitating the discovery of novel antimicrobial agents [43].

Targeting bacterial mechanisms of resistance

Another strategy focuses on inhibiting or neutralizing bacterial factors that confer drug resistance. This can involve coating drugs with protective compounds or inhibitors that bind to and deactivate bacterial enzymes responsible for resistance. In addition, routine hygiene measures—such as proper handwashing, the use of alcohol-based sanitizers, and effective disinfectants—can substantially reduce the transmission of infections, limiting reliance on antibiotics and curbing the spread of resistance. Anti-virulence strategies, including secretion system inhibitors, act by neutralizing bacterial virulence factors, preventing pathogen-mediated damage. In some cases, structural modification of antimicrobials or biofilm-based interventions can render bacterial resistance mechanisms ineffective.

Rapid diagnostics and continuous surveillance

Timely and accurate diagnosis of bacterial infections is critical to controlling AMR. Strengthening diagnostic infrastructure and supporting research for cost-effective tools are essential steps. Surveillance systems play a key role in monitoring local outbreaks and resistance patterns, while resource-rich nations can assist lower-income countries in expanding laboratory capacity and implementing vaccination programs. Establishing a global AMR surveillance database with standardized laboratory protocols is fundamental for coordinated response efforts.

Reducing antimicrobial use in agriculture and animal husbandry

Restricting the use of antimicrobials in agriculture and allied sectors is essential. Policies should be adapted to local and

national contexts, aiming to minimize unnecessary antimicrobial applications and limit access to drugs associated with high resistance potential. Effective implementation involves a combination of policy enforcement, improved animal nutrition, and biosecurity measures. Educating farmers about the long-term risks of excessive antibiotic use and incentivizing the production of organic animal products can also facilitate positive behavioral change. Regulatory oversight of antibiotic sales for food animals is critical for reducing the emergence of resistance [44].

Table 1. Novel approaches with their possible advantages to address AMR.

Strategy	Techniques	Advantages
Newer antibiotic development	Develop antibiotics that reduce reliance on existing ones	Explore unexplored bacteria for novel antibiotic molecules
Anti-virulence strategies	Protect antibiotics, find alternatives to minimize use	Use chelators, secretion system inhibitors, and sanitizers
Improved low-cost diagnostics	Accurate diagnosis, cost-effective healthcare	Portable devices, centralized sero-surveillance
Stricter control in agriculture	Reduce zoonotic antibiotic-resistant infections	Regulations promote organic farming
Antibiotic cycling	Preserve the effectiveness of susceptible antibiotics	Temporarily withhold and reintroduce susceptible antibiotics
Pulsed electromagnetic field	Increase antibiotic effectiveness	Use pulsed EMF with antimicrobial peptides
One health approach	Prevent emerging zoonotic superbugs	Integrate human, animal, and environmental health Evidence-based prescribing, incentives for development
Antibiotic	Proper antibiotic use reduces the impact on resources	Coat nanoparticles on antibiotics, use adjuvant molecules
Stewardship	Increase antibiotic efficacy, prevent resistance	Vaccination, probiotics for microbial flora alteration
Nano antibiotics	Reduce disease severity, an alternative to antibiotics	Use medicinal herbs, promote organic products
Host body immunomodulation, traditional medicinal practices, and artificial intelligence	Cost-effective alternative to antimicrobials, targeted drug design, and predicting emerging superbugs	Algorithm-based drug design, machine learning

Table 2. Strategies to address antimicrobial resistance (AMR).

Strategy and approach	Concept and methods	Benefits
1) Development of novel antibiotics	• Investigating new antibiotic compounds from untapped sources and cultivating hard-to-grow bacteria in lab conditions using isolation chip techniques that replicate their natural environment.	• Discovery of innovative antibiotic molecules reduces reliance on existing antibiotic classes.
2) Anti-virulence tactics and antibiotic modification	• Employing chelators and inhibitors of bacterial secretion systems to safeguard antibiotics. • Utilizing alcohol-based sanitizers and disinfectants as alternatives.	• Shields antibiotics from bacterial resistance mechanisms. • Reduces dependence on antibiotics by offering alternative bacterial elimination methods.
3) Enhanced diagnostics and cost-effective testing	• Creating affordable, precise, and portable diagnostic tools, combined with centralized serological surveillance and data analysis.	• Promotes accurate antimicrobial prescribing and cost-effective disease diagnosis for public health.
4) Stricter regulations on antibiotic misuse in agriculture	• Implementing stringent laws to curb antibiotic misuse as growth promoters in poultry and livestock. • Encouraging organic farming and antibiotic-free animal products.	• Decreases the rise of zoonotic and foodborne antibiotic-resistant infections.
5) Antibiotic rotation	• Temporarily halting the use of specific antibiotic classes and reintroducing them later.	• Prevents the development of resistance to vulnerable antibiotic classes, preserving their effectiveness.
6) Pulsed electromagnetic field (PEMF) application	• Using PEMF to enhance bacterial cell sensitivity alongside antimicrobial peptides, improving antibiotic penetration.	• Boosts the effectiveness of antimicrobial peptides against gram-negative bacteria via electroporation, enhancing antibiotic efficacy.
7) One health framework	• Integrating human, animal, and environmental health through research on emerging zoonotic infections and resistant microbes influenced by climate change.	• Fosters interdisciplinary research and data collection to prevent the emergence of zoonotic superbugs.

8) Antibiotic stewardship programs	• Promoting evidence-based antibiotic prescribing and providing incentives for developing novel antibiotics while addressing development barriers.	• Reduces overuse and inappropriate use of antibiotics through careful prescribing. • Improves patient outcomes and minimizes the impact on available antibiotics.
9) Nanoantibiotics and antibiotic adjuvant	• Coating nanoparticles over antibiotics to increase their efficacy.	• Increases the efficacy of antibiotics manifold and is effective in preventing the emergence of resistance.
10) Host-body immunomodulation	• Use of adjuvant molecules.	• Monoclonal antibodies as an effective alternative to antibiotics.
11) Traditional and ethnic medicinal and veterinary practices	• Effective and regular vaccination to prevent the transmission of diseases and reduce the severity of diseases. • Use of probiotics as a medium to alter microbial flora.	• Vaccines prevent severe infections and minimize the need for antibiotics.
12) Application of artificial intelligence and computational	• Use of medicinal herbs to treat some infectious diseases. • Promotion of organic and antibiotic residue-free products. • Use of algorithms in drug designing. • Use of machine learning to predict newer emerging resistant superbugs.	• Faecal microbial transplants and probiotics to prevent drug-resistant infections. • An effective and relatively inexpensive way to reduce dependence on antimicrobials. • Whole genome sequencing to design the newer drugs to target pathogens. • AI-based prediction models to predict superbugs. • Use of AI to design drug combinations via 3D printing and antimicrobial peptide modelling.

The bacterial environment can be modified by introducing other microbes that exert inhibitory effects on pathogen growth, a phenomenon known as amensalism. A common application of this principle is the use of dietary probiotics, which suppress the proliferation of harmful bacteria within the gut.

Antimicrobial cycling

Antimicrobial cycling involves temporarily withdrawing a specific class of antibiotics from use and reintroducing it later to reduce the likelihood of bacterial resistance developing against that drug. Shortening the duration of antibiotic therapy can also help limit the development of resistance [45].

Overcoming antimicrobial resistance using electromagnetic forces

Emerging studies suggest that physical interventions, such as targeted electromagnetic fields, can enhance the susceptibility of resistant bacteria to antimicrobial agents. For example, nisin, an antimicrobial peptide, is typically ineffective against Gram-negative bacteria. However, applying pulsed electromagnetic fields (PEF) can increase bacterial cell membrane permeability, allowing nisin to exert bactericidal effects. Such approaches, which alter bacterial morphology and enhance drug uptake through electroporation, are gaining attention as innovative strategies to combat AMR [46].

A dedicated one health approach

The One Health framework emphasizes the interconnectedness of human, animal, and environmental health, fostering collaborative research and educational initiatives to prevent antimicrobial resistance and reduce zoonotic threats. Tools developed by the World Health Organization, such as WHONET, enable monitoring of veterinary antimicrobial use and evaluation of animal health services.

Implementing a robust One Health surveillance system is critical, although the benefits—such as reduced AMR risk—may take years to become evident [47]. Coordinated global efforts, including the joint commitment of FAO, WHO, WOAH, and UNEP, are essential for achieving AMR prevention objectives through awareness programs, research, and policy implementation [48, 49].

One health surveillance system

Implementing a robust One Health surveillance system is essential, although the benefits may take years to materialize in the form of reduced antimicrobial resistance risk [47]. The One Health approach emphasizes the integration of human, animal, and environmental health, with global coordination through quadripartite organizations such as FAO, WHO, WOAH, and UNEP. Their collective commitment facilitates AMR prevention by promoting awareness programs, research, and coordinated policy actions [48, 49].

Antibiotic stewardship

Antibiotic stewardship comprises systematic interventions designed to optimize clinical outcomes while minimizing unintended consequences, including the emergence of resistance. This involves selecting the most appropriate agent at an optimal dose and duration, and educating prescribers to follow evidence-based guidelines [50]. Tools such as telemedicine can support rational antibiotic use, particularly in regions where patients cannot readily access healthcare facilities. Additionally, reserving newly developed antibiotics until clinically necessary, alongside incentives for pharmaceutical companies (e.g., tax deductions, streamlined clinical trials, and support for research infrastructure), can balance public health needs with commercial interests [51]. Effective stewardship also requires addressing cognitive biases

among prescribers, promoting rational decision-making, and establishing feedback systems, quality indicators, and surveillance networks to ensure optimal antibiotic utilization [52, 53].

Nano-antibiotics and antibiotic adjuvants

Nanoparticle-coated antibiotics, utilizing metals such as silver, gold, or copper, have demonstrated enhanced efficacy against infections, including those complicated by biofilm formation, and have promoted wound healing in previously non-responsive cases [54]. Antibiotic adjuvants act by potentiating antimicrobial activity—either by improving targeting of pathogens, protecting antibiotics from degradative enzymes, disrupting biofilms, increasing bacterial oxidative stress, or inhibiting efflux pumps [52]. Permeabilizers, for example, destabilize the outer lipopolysaccharide layer of Gram-negative bacteria, facilitating antibiotic penetration and restoring susceptibility [55, 56]. The dual benefits of adjuvants include extending the lifespan of existing antimicrobials and reducing pressure to develop new drugs. Examples of adjuvants include polymyxins, aminoglycosides, and polyamines [57].

Host immunomodulation

Modulating the host immune system through probiotics or microbiome transplantation is emerging as an effective strategy to reduce pathogenic bacterial loads in the gut. Monoclonal antibodies have also shown promise in treating specific infections, offering potential alternatives to conventional antibiotics to address the shortage of new antimicrobial agents.

Traditional medicines and ethnobotanical practices

Traditional medicine has long contributed to infection management, with systems such as Ayurveda offering cost-effective and sustainable approaches. These practices reduce dependence on antibiotics, promote One Health principles, and support the production of antibiotic residue-free animal products, enhancing market value [58, 59]. Ethno-veterinary practices, such as using neem (*Azadirachta indica*) and turmeric (*Curcuma longa*) pastes for lumpy skin disease or herbal formulations to prevent mastitis, have demonstrated clinical efficacy and underline the potential of traditional knowledge in combating AMR [60, 61].

Vaccination strategies

Vaccination remains a critical tool for AMR mitigation, as it decreases the need for antibiotics by preventing widespread infections. Expanding coverage among humans and livestock, coupled with efforts to reduce vaccine hesitancy, is essential [62]. Advances in vaccine development, including broader serotype coverage and combined vaccine–antibiotic approaches, can further reduce the selection pressure driving resistance [63, 64].

Emerging therapeutic approaches

Additional innovative strategies include immunotherapeutics, quorum-sensing inhibitors, biofilm-disrupting compounds, RNA-based therapies, and phage therapy. Genetically modified bacteriophages have shown particular promise against multidrug-resistant bacteria [65-67]. Antimicrobial peptides (AMPs) also offer a potential solution, though cross-resistance to host AMPs may arise, which could compromise innate immunity in humans and animals [68].

Use of artificial intelligence and advanced computational biology

Artificial intelligence (AI) provides powerful computational tools capable of learning from existing datasets to enhance predictive accuracy and reduce errors [69]. Machine learning algorithms can forecast the likelihood of bacterial strains evolving into superbugs, as well as identify the specific pathways through which resistance develops [70]. Applying AI to analyze and classify AMR surveillance data can facilitate early detection of emerging resistance trends and help anticipate future AMR crises [71]. Furthermore, AI-driven models can efficiently explore a vast array of potential drug combinations, optimizing therapeutic efficacy while minimizing adverse effects. Coupled with advances in whole genome sequencing, these computational approaches enable the identification of novel antimicrobial targets and the rational design of new antimicrobial peptides, representing a transformative avenue in the fight against AMR.

Conclusion

The use of antimicrobials in animals is a well-established contributor to the emergence of antibiotic resistance in humans. To prevent the spread of zoonotic infections, antibiotics must be used judiciously, supported by regulatory frameworks that promote the rational application of these medications. Failure to implement such measures could lead to the proliferation of mutant superbugs, posing a threat to both global food security and healthcare systems.

Awareness campaigns targeting school children, frontline health workers, and relevant stakeholders are essential to disseminate knowledge about the risks posed by antimicrobial resistance. Effective mitigation requires collaborative efforts among veterinarians, livestock producers, medical professionals, public health authorities, and the general public. The declining pipeline of novel antibiotics, combined with diminishing efficacy of existing drugs, underscores the urgent need to rethink antibiotic usage policies and take coordinated global action.

Increased investment in research and development (along with enhanced international collaboration for sharing AMR surveillance data) is critical. Addressing AMR as an urgent, worldwide threat demands compelling evidence to inform decision-makers and stakeholders at national and global levels,

ensuring it is prioritized on par with other significant public health challenges.

Acknowledgments: None

Conflict of interest: None

Financial support: None

Ethics statement: None

References

1. Bernier SP, Surette MG. Concentration-dependent activity of antibiotics in natural environments. Front Microbiol. 2013;4:20. doi:10.3389/fmicb.2013.00020
2. Chandy SJ, Naik GS, Balaji V, Jeyaseelan V, Thomas K, Lundborg CS. High-cost burden and health consequences of antibiotic resistance: the price to pay. J Infect Dev Ctries. 2014;8(9):1096-102. doi:10.3855/ jidc.4745
3. World Bank. Drug-Resistant Infections: a threat to our economic future. Washington, DC: World Bank. License: Creative Commons Attribution CC BY 3.0 IGO. 2017. doi:10.1596/26707
4. Dixit A, Kumar N, Kumar S, Trigun V. Antimicrobial resistance: progress in the decade since emergence of New Delhi Metallo-β-Lactamase in India. Indian J Community Med. 2019;44(1):4-8.
5. Antimicrobial Resistance Collaborators. Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis. Lancet. 2022;399(10325):629-55. doi:10.1016/S0140-6736(21)02724-0
6. O'Neill J. Review on antimicrobial resistance. Antimicrobial resistance: tackling a crisis for the health and wealth of nations, 2014(4).
7. Palma E, Tilocca B, Roncada P. Antimicrobial resistance in veterinary medicine: an overview. Int J Mol Sci. 2020;21(6):1914. doi 10.3390/ijms21061914
8. Nadeem SF, Gohar UF, Tahir SF, Mukhtar H, Pornpukdeewattana S, Nukthamna P, et al. Antimicrobial resistance: more than 70 years of war between humans and bacteria. Crit Rev Microbiol. 2020;46(5):578-99. doi:10.1080/1040841X.2020.1813687
9. Alaali Z, Thani BAS. Patterns of antimicrobial resistance observed in the Middle East: environmental and health care retrospectives. Sci Total Environ. 2020;740:140089. doi:10.1016/j.scitotenv.2020.140089
10. Rhouma M, Madec JY, Laxminarayan R. Colistin: from the shadows to a One Health approach for addressing antimicrobial resistance. Int J Antimicrob Agents. 2023;61(2):106713. doi:10.1016/j.ijantimicag.2023.106713
11. Li LG, Zhang T. Plasmid-mediated antibiotic resistance gene transfer under environmental stresses: insights from laboratory-based studies. Sci Total Environ. 2023;887:163870. doi:10.1016/j.scitotenv.2023.163870
12. Yassine I, Rafei R, Osman M, Mallat H, Dabboussi F, Hamze M. Plasmid-mediated quinolone resistance: mechanisms, detection, and epidemiology in the Arab countries. Infect Genet Evol. 2019;76:104020. doi:10.1016/j.meegid.2019.104020
13. Schultsz C, Geerlings S. Plasmid-mediated resistance in Enterobacteriaceae: changing landscape and implications for therapy. Drugs. 2012;72(1):1-16. doi:10.2165/11597960-000000000-00000
14. Carattoli A. Plasmid-mediated antimicrobial resistance in Salmonella enterica. Curr Issues Mol Biol. 2003;5(4):113-22.
15. DelaFuente J, Toribio-Celestino L, Santos-Lopez A, León-Sampedro R, Alonso-del Valle A, Costas C, et al. Within-patient evolution of plasmid-mediated antimicrobial resistance. Nat Ecol Evol. 2022;6(12):1980-91. doi:10.1038/s41559-022-01908-7
16. Guan X, Xue X, Liu Y, Wang J, Wang Y, Wang J, et al. Plasmid-mediated quinolone resistance--current knowledge and future perspectives. J Int Med Res. 2013;41(1):20-30. doi:10.1177/0300060513475965
17. Kammili N, Rani M, Styczynski A, Latha M, Pavuluri PR, Reddy V, et al. Plasmid-mediated antibiotic resistance among uropathogens in primigravid women-Hyderabad, India. PLoS One. 2020;15(5):e0232710. doi:10.1371/journal.pone.0232710
18. Kivata MW, Mbuchi M, Eyase F, Bulimo WD, Kyanya CK, Oundo V, et al. Plasmid mediated penicillin and tetracycline resistance among Neisseria gonorrhoeae isolates from Kenya. BMC Infect Dis. 2020;20(1):703. doi:10.1186/s12879-020-05398-5
19. Lv L, Wan M, Wang C, Gao X, Yang Q, Partridge SR, et al. Emergence of a plasmid-encoded resistance-nodulation-division efflux pump conferring resistance to multiple drugs, including tigecycline, in klebsiella pneumoniae. mBio. 2020;11(2):e02930-19. doi:10.1128/mBio.02930-19
20. Seethalakshmi PS, Prabhakaran A, Kiran GS, Selvin J. Genomic insights into plasmid-mediated antimicrobial resistance in the bacterium Bhargavaea beijingensis strain PS04. Arch Microbiol. 2023;206(1):33. doi:10.1007/s00203-023-03746-y
21. Schwarz S, Shen J, Wendlandt S, Feßler AT, Wang Y, Kadlec K, et al. Plasmid-mediated antimicrobial resistance in staphylococci and other firmicutes. Microbiol Spectr. 2014;2(6). doi:10.1128/microbiolspec.PLAS-0020-2014
22. Lahiri D, Nag M, Ghosh A, Das D, Dey A, Mukherjee D, et al. Biofilm and antimicrobial resistance. Biofilm-Mediated Diseases: Causes and Controls. 2021:183-208. doi:10.1007/978-981-16-0745-5_8
23. Datta S, Nag S, Roy DN. Biofilm-producing antibiotic-resistant bacteria in Indian patients: a comprehensive

review. Curr Med Res Opin. 2024;40(3):403-22. doi:10.1080/03007995.2024.2305241

24. Upadhyay A, Pal D, Kumar A. Interrogating salmonella typhi biofilm formation and dynamics to understand antimicrobial resistance. Life Sci. 2024;339:122418. doi:10.1016/j.lfs.2024.122418
25. Oschmann-Kadenbach AM, Schaudinn C, Borst L, Schwarz C, Konrat K, Arvand M, et al. Impact of Mycobacteroides abscessus colony morphology on biofilm formation and antimicrobial resistance. Int J Med Microbiol. 2024;314:151603. doi:10.1016/j.ijmm.2024.151603
26. Gattu R, Ramesh SS, Ramesh S. Role of small molecules and nanoparticles in effective inhibition of microbial biofilms: a ray of hope in combating microbial resistance. Microb Pathog. 2024;188:106543. doi:10.1016/j.micpath.2024.106543
27. Pauze-Foixet J, Mathieu-Denoncourt A, Duperthuy M. Elevated concentrations of polymyxin B elicit a biofilm-specific resistance mechanism in Vibrio cholerae. Res Microbiol. 2024:104179. doi:10.1016/j.resmic.2023.104179
28. Boroujeni MB, Mohebi S, Malekian A, Shahraeini SS, Gharagheizi Z, Shahkolahi S, et al. The therapeutic effect of engineered phage, derived protein and enzymes against superbug bacteria. Biotechnol Bioeng. 2024;121(1):82-99. doi:10.1002/bit.28581
29. Abebe GM. The role of bacterial biofilm in antibiotic resistance and food contamination. Int J Microbiol. 2020;1705814. doi:10.1155/2020/1705814
30. Zhao X, Yu Z, Ding T. Quorum-Sensing regulation of antimicrobial resistance in bacteria. Microorganisms. 2020;8(3):425. doi:10.3390/microorganisms8030425
31. Erasmus V, Daha TJ, Brug H, Richardus JH, Behrendt MD, Vos MC, et al. Systematic review of studies on compliance with hand hygiene guidelines in hospital care. Infect Control Hosp Epidemiol. 2010;31(3):283-94. doi:10.1086/650451
32. Tripathi V, Cytryn E. Impact of anthropogenic activities on the dissemination of antibiotic resistance across ecological boundaries. Essays Biochem. 2017;61(1):11-21. doi:10.1042/EBC20160054
33. Foyle L, Burnett M, Creaser A, Hens R, Keough J, Madin L, et al. Prevalence and distribution of antimicrobial resistance in efluent wastewater from animal slaughter facilities: a systematic review. Environ Pollut. 2023;318:120848. doi:10.1016/j.envpol.2022.120848
34. Balbin MM, Hull D, Guest C, Nichols L, Dunn R, Thakur S. Antimicrobial resistance and virulence factors profile of Salmonella spp. and Escherichia coli isolated from different environments exposed to anthropogenic activity. J Glob Antimicrob Resist. 2020;22:578-83. doi:10.1016/j.jgar.2020.05.016
35. Navarro A, Sanseverino I, Cappelli F, Lahm A, Niegowska M, Fabbri M, et al. Study of antibiotic resistance in freshwater ecosystems with low anthropogenic impact. Sci Total Environ. 2023;857(Pt 3):159378. doi:10.1016/j.scitotenv.2022.159378
36. Pereira SG, Alarico S, Tiago I, Reis D, Nunes-Costa D, Cardoso O, et al. Studies of antimicrobial resistance in rare mycobacteria from a nosocomial environment. BMC Microbiol. 2019;19(1):62. doi:10.1186/s12866-019-1428-4
37. Swift BM, Bennett M, Waller K, Dodd C, Murray A, Gomes RL, et al. Anthropogenic environmental drivers of antimicrobial resistance in wildlife. Sci Total Environ. 2019;649:12-20. doi:10.1016/j.scitotenv.2018.08.180
38. Marston HD, Dixon DM, Knisely JM, Palmore TN, Fauci AS. Antimicrobial resistance. JAMA. 2016;316(11):1193-204. doi:10.1001/jama.2016.11764
39. Ryan M. Assessing national action plans on antimicrobial resistance in animal production: What lessons can be drawn? OECD Food, Agriculture and Fisheries Papers. 2021;134:1-28. doi:10.1787/18156797
40. Anthony WE, Burnham CD, Dantas G, Kwon JH. The gut microbiome as a reservoir for antimicrobial resistance. J Infect Dis. 2021;223(12 Suppl 2):S209-13. doi:10.1093/infdis/jiaa497
41. Sorbara MT, Pamer EG. Interbacterial mechanisms of colonization resistance and the strategies pathogens use to overcome them. Mucosal Immunol. 2019;12(1):1-9. doi:10.1038/s41385-018-0053-0
42. Iacob S, Iacob DG. Infectious threats, the intestinal barrier, and its Trojan Horse: dysbiosis. Front Microbiol. 2019;10:1676. doi:10.3389/fmicb.2019.01676
43. Kollef MH. Is antibiotic cycling the answer to preventing the emergence of bacterial resistance in the intensive care unit? Clin Infect Dis. 2006;43(Suppl 2):S82-8. doi:10.1086/504484
44. Novickij V, Stanevičienė R, Vepštaitė-Monstavičė I, Gruškienė R, Krivorotova T, Sereikaitė J, et al. Overcoming antimicrobial resistance in bacteria using bioactive magnetic nanoparticles and pulsed electromagnetic fields. Front Microbiol. 2018;8:2678. doi:10.3389/fmicb.2017.02678
45. Queenan K, Hasler B, Rushton J. A one health approach to antimicrobial resistance surveillance: is there a business case for it? Int J Antimicrob Agents. 2016;48(4):422-7. doi:10.1016/j.ijantimicag.2016.06.014
46. Collignon PJ, McEwen SA. One health-its importance in helping to better control antimicrobial resistance. Trop Med Infect Dis. 2019;4(1):22. doi:10.3390/tropicalmed4010022
47. Schooneveld VT. Antimicrobial stewardship: attempting to preserve a strategic resource. J Community Hosp Intern Med Perspect. 2011;1(2):7209. doi:10.3402/jchimp.v1i2.7209
48. Laxminarayan R, Duse A, Wattal C, Zaidi AK, Wertheim HF, Sumpradit N, et al. Antibiotic resistance-the need for global solutions. Lancet Infect Dis. 2013;13(12):1057-98. doi:10.1016/S1473- 3099(13)70318-9

49. World Health Organization. One health joint plan of action (2022-2026): working together for the health of humans, animals, plants and the environment. 2022. https://www.who.int/ publications/i/item/9789240059139.
50. Charani E, Cooke J, Holmes A. Antibiotic stewardship programmes--what's missing. J Antimicrob Chemother. 2010;65(11):2275-7. doi:10.1093/jac/dkq357
51. Dyar OJ, Huttner B, Schouten J, Pulcini C. What is antimicrobial stewardship. Clin Microbiol Infect. 2017;23(11):793-8. doi:10.1016/j.cmi.2017.08.026
52. Kumar SB, Arnipalli SR, Ziouzenkova O. Antibiotics in food chain: the consequences for antibiotic resistance. Antibiotics. 2020;9(10):688. doi:10.3390/ antibiotics9100688
53. Li C, Budge LP, Driscoll CD, Willardson BM, Allman GW, Savage PB. Incremental Conversion of Outer-Membrane Permeabilizers into Potent Antibiotics for Gram-Negative Bacteria. J Am Chem Soc.1999;121:931-40. doi:10.1021/ja982938m
54. Kwon DH, Lu CD. Polyamines increase antibiotic susceptibility in Pseudomonas aeruginosa. Antimicrob Agents Chemother. 2006;50(5):1623-7. doi:10.1128/AAC.50.5.1623-1627.2006
55. Gonzalez-Bello C. Antibiotic adjuvants - a strategy to unlock bacterial resistance to antibiotics. Bioorg Med Chem Lett. 2017;27(18):4221-8. doi:10.1016/j. bmcl.2017.08.027
56. Nair MNB, Punniamurthy N. Ethno-Veterinary Practices (EVP) as a new approach for management of cattle health without antimicrobial and other chemical veterinary drugs. EC Vet Sci. 2021;6(5):22-5.
57. Pradhan S, Mishra S. Ethnoveterinary practice: an alternative treatment approach in contemporary India. Pharm Innov. 2018;7(9):362-5.
58. Nair BMN, Punniamurthy N, Mekala P, Ramakrishnan N, Kumar SK. Ethnoveterinary formulation for treatment of bovine mastitis. Res Rev: J Vet Sci. 2017;18(S1):377-82.
59. Kumar SK, Deepa PM, Punnimurthy N. Study on the prevention of mastitis in cattle during dry period using herbal formulation. Res Asp Agric Vet Sci. 2021;4:1-5. doi:10.9734/bpi/ raavs/v4/13490D
60. Michael CA, Dominey-Howes D, Labbate M. The antimicrobial resistance crisis: causes, consequences, and management. Front Public Health. 2014;2:145. doi:10.3389/fpubh.2014.00145
61. Mitchell PK, Lipsitch M, Hanage WP. Carriage burden, multiple colonization and antibiotic pressure promote emergence of resistant vaccine escape pneumococci. Philos Trans R Soc Lond B Biol Sci. 2015;370(1670):20140342. doi:10.1098/ rstb.2014.0342
62. Buchy P, Ascioglu S, Buisson Y, Datta S, Nissen M, Tambyah PA, et al. Impact of vaccines on antimicrobial resistance. Int J Infect Dis. 2020;90:188-96. doi:10.1016/j.ijid.2019.10.005
63. Westwater C, Kasman LM, Schofield DA, Werner PA, Dolan JW, Schmidt MG, et al. Use of genetically engineered phage to deliver antimicrobial agents to bacteria: an alternative therapy for treatment of bacterial infections. Antimicrob Agents Chemother. 2003;47(4):1301-7. doi:10.1128/ AAC.47.4.1301-1307.2003
64. Thiel K. Old dogma, new tricks-21st century phage therapy. Nat Biotechnol. 2004;22(1):31-6. doi:10.1038/nbt0104-31
65. Lu TK, Collins JJ. Engineered bacteriophage targeting gene networks as adjuvants for antibiotic therapy. Proc Natl Acad Sci. 2009;106(12):4629-34. doi:10.1073/ pnas.0800442106
66. Roscher R, Bohn B, Duarte MF, Garcke J. Explainable machine learning for scientific insights and discoveries. IEEE Access. 2020;8:42200-416. doi:10.1109/ ACCESS.2020.2976199
67. Rabaan AA, Alhumaid S, Mutair AA, Garout M, Abulhamayel Y, Halwani MA, et al. Application of Artificial Intelligence in Combating High Antimicrobial Resistance Rates. Antibiotics. 2022;11(6):784. doi:10.3390/antibiotics11060784
68. Jangir PK, Ogunlana L, Szili P, Czikkely M, Shaw LP, Stevens EJ, et al. The evolution of colistin resistance increases bacterial resistance to host antimicrobial peptides and virulence. Elife. 2023;12:e84395. doi:10.7554/eLife.84395
69. Lv J, Deng S, Zhang L. A review of artificial intelligence applications for antimicrobial resistance. Biosaf Health. 2021;3(1):22-31. doi:10.1016/j. bsheal.2020.08.003
70. Das P, Delost MD, Qureshi MH, Smith DT, Njardarson JT. A survey of the structures of US FDA approved combination drugs. J Med Chem. 2018;62(9):4265-311. doi:10.1021/acs.jmedchem.8b01610
71. Sharma P, Dahiya S, Kaur P, Kapil A. Computational biology: role and scope in taming antimicrobial resistance. Indian J Med Microbiol. 2023;41:33-8. doi:10.1016/j.ijmmb.2022.12.005