Int. j. adv. multidisc. res. stud. 2025; 5(4):248-251

Received: 21-05-2025
Accepted: 01-07-2025

International Journal of Advanced Multidisciplinary Research and Studies

ISSN: 2583-049X

Rising Alarm of Bacterial resistance against Antibiotic threats: Global Health

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DOI: https://doi.org/10.62225/2583049X.2025.5.4.4571

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Abstract
The emergence and spread of antibiotic-resistant bacteria pose a significant threat to future healthcare and the effectiveness of treatments. Bacteria develop resistance through various mechanisms, with the presence of resistance genes being a primary factor. These genes enable the production of numerous enzymes that deactivate antibiotics by breaking down or altering their chemical structures. The resulting resistance hampers treatment efforts and contributes to the deaths of millions of patients globally. Poor hygiene and inadequate hospital management are major contributors to the spread of resistant bacteria. This mini-review explores the key causes of antibiotic resistance and the environmental factors that contribute to the dissemination of resistant bacterial strains. In Asia, due to lack of control of using antibiotics, selective pressure is high on bacteria to become resistance against antibiotics. Therefore, proper strategy of the countries in connection with world health organization is important against self-medication until we can protect the global health.

Keywords: Bacterial Resistant, Resistance Genes, Bacteria

1. Introduction

1.1 Antibiotic Resistance

Antibiotic resistance occurs when bacteria undergo changes that allow them to withstand the effects of antibiotics. These changes enable the bacteria to survive and continue multiplying, rendering the antibiotics ineffective. Infections caused by such bacteria are known as resistant infections, which are often difficult—and sometimes impossible—to treat. According to Magiorakos *et al*. (2012) [15], this phenomenon arises when bacteria evolve mechanisms that protect them from the action of antimicrobial agents. All bacterial species can potentially develop resistance to one or more antibacterial drugs, making standard treatments ineffective. In fungi, this phenomenon is termed antifungal resistance, while in bacteria, it is specifically referred to as antibiotic resistance. Collectively, these are classified under the broader category of antimicrobial resistance (AMR) (Magiorakos *et al*., 2012) [15].

Microorganisms that develop resistance to multiple antimicrobial agents are termed multidrug-resistant (MDR) and are commonly known as "superbugs" (Saha & Sarkar, 2021; Tanwar *et al*., 2014) [18, 20]. Although AMR is a natural evolutionary process, it is significantly accelerated by the misuse and overuse of antibiotics and improper infection management.

Bacterial resistance can emerge through spontaneous genetic mutations or by acquiring resistance genes from other bacterial species via horizontal gene transfer. The frequent and prolonged use of antibiotics promotes the selection of resistant strains, further complicating treatment strategies (Dabour *et al*., 2016; Fisher *et al*., 2022) [5, 7]. Similarly, antifungal resistance arises in fungi due to genetic mutations or chromosomal alterations like aneuploidy. Overuse of antifungal medications contributes to the development and spread of resistant fungal strains (Fisher *et al*., 2022) [7].

Antibiotic resistance poses a significant challenge in treating infections caused by certain bacteria, such as *Helicobacter pylori*, which has shown a particularly high resistance rate in the Middle East.Numerous studies have highlighted the alarming prevalence and severity of antibiotic resistance, particularly the spread of resistance genes in bacterial populations. This growing threat undermines the effectiveness of treatments in healthcare settings and signals an urgent public health concern. Research indicates that the rate of antibiotic resistance is especially high in regions such as the Middle East and Asia, across various bacterial species (Rahim *et al*., 2020) [17]. These findings emphasize the global nature of the issue and the urgent need for coordinated efforts to control its spread.

1.2 Factors Influencing Antibacterial Resistance

Antibiotic resistance occurs when bacteria develop mechanisms that allow them to survive exposure to drugs that were once effective against them. This adaptation leads to standard treatments becoming less effective, allowing infections to persist or worsen, sometimes with fatal consequences (Lee Ventola, 2015) [12]. Several factors contribute to this growing global issue.

One of the primary causes is the overuse and misuse of antibiotics. This includes taking antibiotics for viral infections, against which they have no effect, or failing to complete a full prescribed course. Additionally, the use of antibiotics in livestock and agriculture further accelerates the development of resistance. These practices expose bacteria to sub-lethal doses of antibiotics, encouraging them to adapt and survive. Another major factor is the natural evolutionary process of bacteria. Through genetic mutations or horizontal gene transfer, bacteria acquire resistance genes that help them withstand antibiotic action. These resistant strains are then naturally selected and proliferate, especially in environments where antibiotics are frequently used.

Poor hygiene and infection control measures in healthcare facilities and communities also play a significant role. When sanitation is lacking, resistant bacteria can spread rapidly, especially in hospitals, where patients are often vulnerable to infections. The consequences of antibiotic resistance are severe. Infections that were once easily treatable become difficult or even impossible to manage, leading to longer hospital stays, increased healthcare costs, and higher mortality rates. The reduced effectiveness of antibiotics also limits treatment options, forcing healthcare providers to rely on more expensive, less accessible, or more toxic alternatives. Moreover, the ease with which resistant bacteria can spread increases the likelihood of outbreaks that are hard to contain and control (Frieri *et al*., 2017; Lee Ventola, 2015) [8, 12].

To combat antibiotic resistance, a multifaceted approach is required. Responsible antibiotic use is essential—antibiotics should only be taken when prescribed by a healthcare professional, and patients must complete the entire course. Infection prevention and control through good hygiene, vaccination, and hospital protocols can also limit the spread of resistant bacteria. In addition, sustained investment in research and development is crucial to create new antibiotics and alternative therapies capable of countering emerging resistant strains. Global collaboration across sectors and countries is also necessary. Coordinated efforts involving public health initiatives, policy enforcement, education, and surveillance systems are needed to address this complex challenge (Frieri *et al*., 2017; Lee Ventola, 2015) [8, 12].

Furthermore, the rise of antibiotic resistance not only impacts treatment outcomes but also threatens the therapeutic use of beneficial bacteria. Some strains of bacteria are used in probiotic treatments, such as in managing infections, wound healing, and burn recovery. Resistance among these probiotic strains may reduce their effectiveness and limit their clinical utility. Therefore, the issue of antibiotic resistance goes beyond conventional infection treatment, affecting broader aspects of medical and therapeutic practices.

1.3 Drawbacks of Antibiotic Resistance

Antibiotic resistance presents a serious and growing threat to public health worldwide, with wide-ranging consequences that extend beyond individual patients to healthcare systems and global health infrastructure. One of the most immediate risks is treatment failure. When bacteria become resistant to standard antibiotics, infections become much harder to treat. This often results in prolonged illness, increased risk of complications, and the need to use alternative medications that may be more toxic, less effective, or significantly more expensive. The lack of effective treatment options jeopardizes patient recovery and increases the likelihood of recurrent infections.

A direct consequence of antibiotic resistance is increased morbidity and mortality. Resistant infections are associated with higher death rates, particularly among vulnerable populations such as infants, the elderly, and individuals with compromised immune systems. Infections that are not adequately treated can lead to severe health complications, systemic infections, and a higher probability of hospitalization. In turn, patients with resistant infections typically require extended hospital stays. Longer recovery times increase the risk of acquiring other healthcare-associated infections and place a significant financial and logistical burden on hospitals and medical systems.

The spread of resistant bacterial strains also poses a major concern. These strains can transmit from person to person, leading to community outbreaks and widespread transmission in healthcare settings. Additionally, resistant bacteria can enter the environment through hospital and agricultural waste, contributing to the global spread of resistance through water, soil, and food chains. This environmental contamination further complicates efforts to control resistance and increases the likelihood of cross-species transmission.

As resistance becomes more widespread, the availability of effective antibiotics continues to decline. This severely limits treatment options, especially for common infections, and increases reliance on last-resort antibiotics. The overuse or misuse of these critical drugs may lead to resistance against them as well, leaving healthcare providers with very few alternatives in life-threatening situations.

Economically, antibiotic resistance imposes a heavy burden on both healthcare systems and individual families. Treating resistant infections often requires costlier medications, longer hospitalizations, and more intensive care, all of which contribute to escalating healthcare expenses. For patients and their families, the financial impact of prolonged illness and lost income can be devastating, especially in low-resource settings.

The implications of antibiotic resistance extend to medical procedures that rely on effective prophylactic antibiotics, such as surgeries, chemotherapy, organ transplants, and intensive care treatments. Without reliable antibiotics, the risk of infection during or after these procedures increases, compromising their safety and success rates.

On a global scale, antibiotic resistance is a pressing international health threat. Resistant strains can easily cross borders through travel, trade, and migration, undermining disease control efforts worldwide. Addressing these risks requires coordinated global action, including responsible antibiotic usage, stricter infection control, investment in the development of new antimicrobial agents, and strong public health collaboration across nations (Cassini *et al*., 2019; Piri *et al*., 2018) [4, 16].

2. Global Distribution of Antibiotic Resistance Genes bacteria

Numerous studies across Asia and the Middle East have documented a concerning prevalence of antibiotic resistance genes in bacterial populations. Countries such as China, Pakistan, India, Bangladesh, Iran, Iraq, Egypt, and Turkey have all reported high levels of resistance genes, indicating a widespread regional issue involving various bacterial strains and resistance mechanisms.

In **Pakistan**, significant resistance has been observed in *Pseudomonas aeruginosa*, with 23.94% of clinical isolates producing ESBL, 40.84% producing MBL, and 35.21% producing AmpC β-lactamases. A considerable number of strains also co-produced multiple enzymes. Notably, 19.71% of isolates carried the CTX-M-15 gene, commonly linked with ESBL, MBL, and AmpC phenotypes (Ullah *et al*., 2017) [21]. Another study highlighted the presence of β-lactamase genes among Enterobacteriaceae, identifying 15% of strains positive for the blaSHV gene and 43% for the blaOXA gene (Waheed *et al*., 2019) [22].

In **China**, 2.2% of *Klebsiella pneumoniae* isolates were found to possess inactivated blaSHV genes, some of which still exhibited mRNA transcription (Xu *et al*., 2014) [23]. Additional research revealed that clinical *Enterobacter cloacae* isolates predominantly carried blaCTX-M (70.8%) and blaSHV (63.9%) genes. A high frequency of plasmid-mediated quinolone resistance (PMQR) genes was also detected, along with carbapenemase genes IMP-4 and IMP-8, and class I integrons in 40.3% of the isolates (Cao *et al*., 2017) [3].

In **Bangladesh**, several resistance genes have been identified, including blaTEM-type in 82.5% and blaOXA-1-type in 47.5% of isolates. Half of the isolates also carried class-1 integrons (Lina *et al*., 2014) [14]. Resistance to tetracyclines, fluoroquinolones, and streptomycin was also common, with genes such as tetA, qnrA, qnrB, and aadA1 found at high frequencies (Islam *et al*., 2022) [11].

Iraq has also shown high prevalence of β-lactamase-producing bacteria. In *E. coli* isolates from both humans and animals, 20.6% were positive for blaCTX-M and blaTEM genes, particularly among heavy antibiotic users (Alaa *et al*., 2020) [1]. In *Proteus* species, 17.2% of isolates carried resistance genes, with blaTEM-1 and blaSHV detected (Hama-Soor *et al*., 2021 [10]; Salih *et al*., n.d.). Diarrheal *E. coli* isolates predominantly carried blaOXA genes (57.5%) and blaSHV (22.3%), with some studies reporting even lower rates for OXA (11.7%) (Alaa *et al*., 2021). Furthermore, *Pseudomonas* isolates were found to carry blaOXA (7.4%) and blaCMY (3.7%) resistance genes (Ghafour *et al*., 2021a, 2021b).

In **Iran**, antibiotic resistance gene prevalence is also significantly high. One investigation revealed that among 1,275 isolates resistant to third-generation cephalosporins, 475 (12%) were ESBL producers. TEM was identified as the most prevalent ESBL gene (Armin *et al*., 2020) [2]. In another study on *Acinetobacter baumannii*, 59% of 100 isolates were ESBL-positive, with blaTEM detected in 42% of strains. However, blaSHV and blaVEB genes were not detected by PCR (Ghasemian *et al*., 2018; Leylabadlo *et al*., 2017; Detektiert Werden, n.d.) [9, 13, 6].

These findings collectively indicate that antibiotic resistance genes are not only widespread across Asia and the Middle East but are also found across various bacterial species and clinical settings. The data underscore the urgent need for coordinated surveillance, effective antibiotic stewardship, and enhanced infection control measures in these regions.

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