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Original Research

Prevalence and Patterns of Antibiotic Resistance in Clinical Isolates: A Cross-Sectional Study from India

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Abstract
An ever-increasing danger to world health, food stability, and progress is the rise of antibiotic resistance. Critical medical operations rely on reliable antibiotic prophylaxis, yet the efficiency of current therapies is undermined by the unregulated spread of resistant bacterial strains. Human actions and systemic problems, such as antibiotic abuse, a lack of regulation, and inadequate infection control practices, interact with biological processes, such as enzymatic drug degradation, target site alteration, and gene transfer, to drive antibiotic resistance, as this review has demonstrated. The consequences will have far-reaching effects, endangering millions of lives every year and causing economic losses estimated to be in the billions of dollars over the next several decades. There must be swift and concerted action in response to the rise of drug-resistant infections, which include multi drug resistant (MDR), extensively drug-resistant (XDR), and pan-drug-resistant (PDR) strains. Nevertheless, there remains hope for the international community. Antimicrobial stewardship, improved monitoring, public awareness initiatives, and legislative frameworks are starting to provide positive results. Artificial intelligence (AI) in medication development, bacteriophage treatment, and CRISPR-based technologies are just a few examples of how scientific and technological progress is opening up new avenues for creative interventions. In addition, the "One Health" perspective calls for a comprehensive solution to this complex problem by acknowledging the interdependence of human, animal, and environmental health. Antibiotic resistance may only be successfully combated if all relevant parties—including public and commercial entities—commit to a common goal. This involves bolstering healthcare infrastructure, especially in areas with low resources, investing in R&D, and strictly regulating antibiotic use.

Keywords: Antibiotic, CRISPR, Mechanisms, Operations, Resistance

Introduction

A significant number of people believe that antibiotics were the most significant medical discovery made in the 20th century. The usage of these products has resulted in a significant reduction in the amount of fatalities and diseases that are brought on by germs. In the years that have passed since Alexander Fleming's discovery of penicillin in 1928, antibiotics have been responsible for the preservation of a great number of lives and the facilitation of significant medical operations such as organ transplantation, chemotherapy-based treatments, and surgical procedures. The efficacy of antibiotics, however, has led to their misuse and excessive usage in a variety of situations, including human health and agricultural settings. The proliferation and spread of germs that are resistant to antibiotics has been made possible as a result of this. Microorganisms can become resistant to antibiotics by developing mechanisms that allow them to withstand the effects of medications that were formerly effective against them. This phenomenon is referred to as antibiotic resistance. Overprescribing antibiotics and patients not following prescribed treatments are two examples of human causes that contribute to the acceleration of the progression of this natural phenomenon. The extensive use of

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antimicrobials in livestock and agriculture is another factor that contributes to the acceleration of this natural phenomenon [1]. The establishment of an environment that is conducive to the selection and transmission of resistant strains brought about by these processes has resulted in diseases that were previously manageable becoming increasingly difficult to treat, and in some cases altogether incurable. This is owing to the fact that infections that were previously treatable are now becoming fully incurable. It is common knowledge that the threat posed by antibiotic resistance to public health all around the world is in the process of developing. As stated by the World Health Organization (WHO), antimicrobial resistance is currently ranked as one of the top ten global public health challenges that the human race is currently facing. It is estimated that over 1.2 million fatalities occur annually as a result of illnesses that are resistant to several drugs. According to the most recent forecasts, this number is expected to increase to 10 million by the year 2050 if the current trends continue. Furthermore, the high financial cost of resistance is a burden that is placed on healthcare systems as well as global economies. This is especially true in nations with middle-class and lower-class populations, where there are limited resources available for providing cutting-edge medical treatment. The purpose of this study is to investigate the molecular pathways that provide bacteria with the ability to develop resistance mechanisms. Some examples of such processes are the modification of genes and the transmission of genes that confer resistance from one generation to the next. In addition to this, it investigates the ways in which antibiotic resistance affects the quality of the environment, the safety of food, and the health of humans [2]. Last but not least, it investigates potential future treatments that might reduce the risk of resistance. These treatments include the creation of new antibiotics, complementary and alternative medicine, and worldwide policy campaigns that are centered on monitoring, education, and stewardship. When it comes to the development of medications that can endure the test of time, having a thorough understanding of the complexities of antibiotic resistance is absolutely necessary. Therefore, in order to tackle this obstacle, it is vital to use a collaborative and multidisciplinary strategy that combines education, public health policy, and scientific research [3]. With the expectation that our findings will contribute to the ever-increasing body of information that is required to solve one of the most critical health challenges of our day, we have decided to carry out study.

Methodology

Study Design: A cross-sectional study was conducted from January 2024 to January 2025 in three tertiary hospitals located in Northern India (Sonipat, Muzaffarnagar, and Meerut).

Sample Collection: Clinical samples (urine, blood, sputum, pus) were collected from patients suspected of bacterial infections. Inclusion criteria involved patients who had not taken antibiotics in the past two weeks. A total of 500 non-duplicate isolates were randomly selected for this study.

Laboratory Procedures:

- **Bacterial Identification:** Standard biochemical tests and automated VITEK-2 Compact System.
- **Antibiotic Susceptibility Testing (AST):** Performed using the Kirby-Bauer disk diffusion method following CLSI 2023 guidelines.
- **Antibiotics Tested:** Amoxicillin-clavulanic acid, ceftriaxone, ciprofloxacin, gentamicin, imipenem, colistin.
- **Multidrug-resistant/ Extensively drug-resistant (MDR/XDR) Detection:** Defined as resistance to ≥1 agent in ≥3 antimicrobial categories.
- **ESBL Detection:** Confirmed by double-disk synergy test.

Data Analysis: Statistical analysis was performed using SPSS version 26. Descriptive statistics were used to report resistance percentages, and chi-square tests were used to evaluate the significance of resistance patterns between species.

Results

Out of 500 isolates:

- Escherichia coli (E. Coli) (35%) was the most frequently isolated organism, followed by Klebsiella pneumonia (K. pneumoniae) (25%), P. aeruginosa (15%), S. aureus (15%), and others (10%).
- **MDR:**

E. coli: 78% MDR, 45% ESBL-positive
K. pneumoniae: 72% MDR, 48% ESBL-positive
P. aeruginosa: 65% resistant to ciprofloxacin and gentamicin
S. aureus: 60% methicillin-resistant (MRSA)

- **Pan-drug resistance (PDR)** was observed in 2 isolates (one K. pneumoniae, one P. aeruginosa).
- **Carbapenem Resistance:** 32% of Gram-negative isolates showed resistance to imipenem.
- **Colistin Resistance:** 4% among Gram-negative organisms, all from ICU settings.

Statistical significance:

- MDR prevalence was significantly higher in ICU vs. OPD isolates ($p < 0.001$).
- Extended-spectrum beta-lactamase (ESBL) production was more common in urine isolates compared to blood ($p = 0.015$).

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Organism	Prevalence (%)	MDR (%)	ESBL Positive (%)	Carbapenem Resistance (%)	Colistin Resistance (%)	MRSA (%)
Escherichia coli	35	78	45	30	3	-
Klebsiella pneumoniae	25	72	48	34	4	-
Pseudomonas aeruginosa	15	65	-	32	5	-
Staphylococcus aureus	15	60	-	-	-	60
Others	10	-	-	-	-	-

Table 1: Prevalence and resistance patterns of major bacterial pathogens isolated from clinical samples in Northern India (2024–2025)

Table 1 presents data on the percentage prevalence of each bacterial species and their resistance rates to multiple antibiotics. MDR = Multidrug resistance; ESBL = Extended-spectrum beta-lactamase production; MRSA = Methicillin-resistant Staphylococcus aureus. A dash (–) indicates data not applicable or not tested.

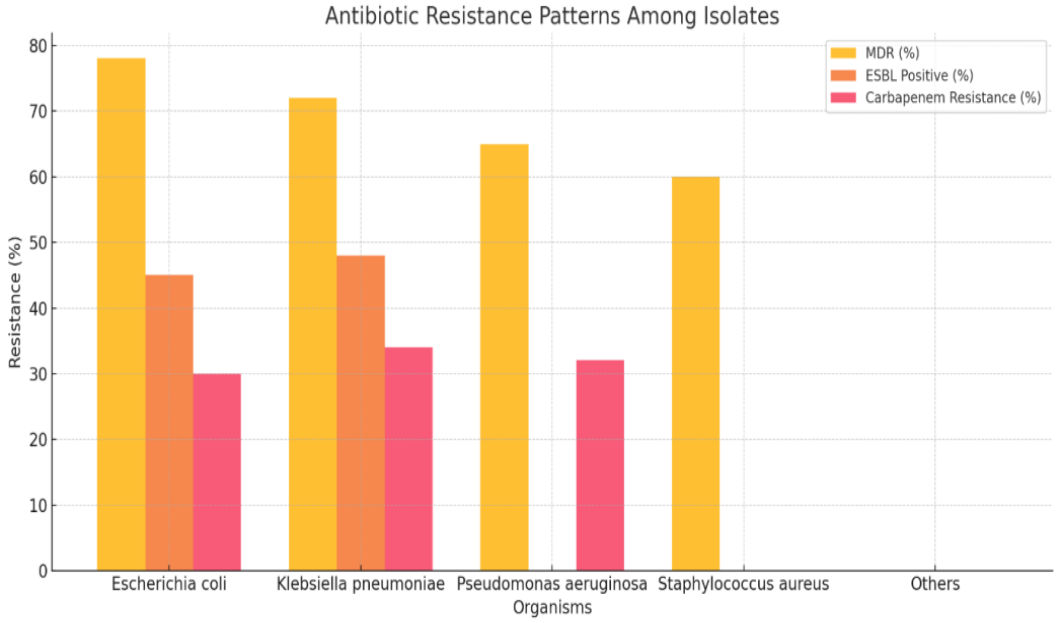

Figure 1. Comparative antibiotic resistance profiles among common clinical bacterial isolates.

This bar chart illustrates the percentage of isolates exhibiting multidrug resistance (MDR), ESBL production, and carbapenem resistance across four predominant organisms. Data highlights the significant burden of resistance, especially among E. coli and K. pneumoniae.

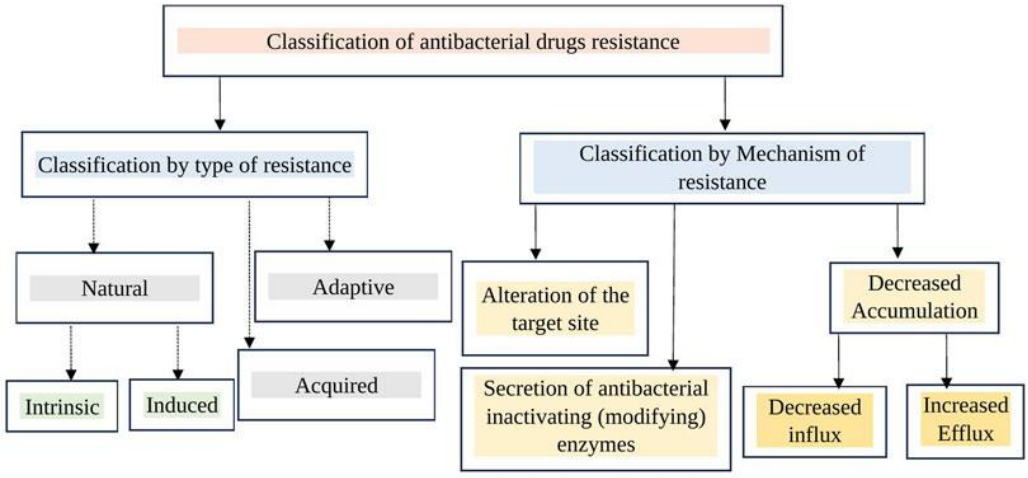

Figure 2. Antibacterial drug resistance can be categorized based on its mechanism and type. The three main types of antibiotic resistance are intrinsic (natural), acquired, and adaptive.

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Discussion

The findings of this study reveal a concerning trend in the growing prevalence of MDR and extended-spectrum beta-lactamase (ESBL)-producing organisms among clinical isolates in Northern India. The dominance of E.Coli and K. pneumoniae among the isolates is consistent with global and national trends, especially in urinary and respiratory tract infections. High rates of resistance to third-generation cephalosporins and fluoroquinolones, as shown in our results, align with previous studies and reflect the widespread misuse and overprescription of these antibiotics in both outpatient and hospital settings.

The observed MDR prevalence among E. coli (78%) and K. pneumoniae (72%) significantly limits therapeutic options and necessitates the use of higher-generation antibiotics, such as carbapenems. However, the resistance to carbapenems—found in 30–34% of E. coli and K. pneumoniae isolates—further narrows the treatment window. These carbapenem-resistant strains are alarming, as they have been linked to higher morbidity and mortality rates, especially in critically ill patients.

Our study also detected colistin resistance (3–5%) in a small subset of Gram-negative isolates. Though low in prevalence, colistin resistance is particularly worrisome due to its role as a last-resort antibiotic. Its emergence suggests potential overuse in ICUs and highlights the need for more stringent stewardship protocols in critical care environments.

Interestingly, S. aureus isolates demonstrated a 60% methicillin resistance rate (MRSA), consistent with earlier Indian surveillance data. This further emphasizes the importance of routine screening and decolonization protocols to prevent hospital-acquired infections.

One strength of this study is its multicenter approach, capturing data across three tertiary hospitals and increasing its regional applicability. However, limitations include its cross-sectional nature, which may not reflect long-term resistance trends, and the exclusion of molecular typing methods to confirm resistance genes.

Overall, these results underscore the urgent need for localized antimicrobial resistance surveillance and data-driven policies to combat the growing threat of antibiotic resistance. Infection control practices, judicious prescribing, and public health education must be intensified to mitigate this crisis.

Mechanisms of Antibiotic Resistance

There has been a significant amount of research conducted on the methods that bacteria use to gain resistance to antibiotics. According to Munita and Arias (2016), bacteria have the potential to resist antibiotics through a variety of innate and acquired techniques. These methods include a number of different approaches. Techniques such as enzymatic degradation, changed target locations, enhanced efflux pump activity, decreased membrane permeability, and penicillin-binding proteins are examples of some of the methods that are included in this category [4]. Another essential approach that enables the fast transmission of resistance genes from one species to another is known as horizontal gene transfer (HGT). The authors Davies and Davies (2010) state that this can take place through the processes of transformation, transduction, or conjugation [5]. It has been claimed by Patterson and Bonomo (2005) that the advent of carbapenemases and extended-spectrum β-lactamases (ESBLs) is a cause for concern [6].The presence of enzymes such as these has the potential to render several β-lactam antibiotics ineffective, even those that are considered to be therapies of last resort, such as carbapenems. According to the findings of the research (Magiorakos et al., 2012), with the rising incidence of organisms that are MDR, XDR, and PDR, there has been a significant reduction in the number of treatment choices available [7].

Contributing Factors

The primary factors that contribute to antibiotic resistance and the extent to which they have been studied extensively. In human healthcare, overprescribing is still a major issue. According to studies conducted by Llor and Bjerrum (2014), a large number of antibiotic prescriptions, particularly for respiratory infections, are unnecessary or have no use [8]. A lack of patient compliance exposes germs to antibiotic dosages below the threshold of mortality, which exacerbates the condition and encourages antibiotic resistance. A study by Van Boeckel et al. (2015) found that antibiotic resistance has been steadily increasing in the agricultural sector due to the widespread usage of these drugs as growth boosters in cattle [9]. Contaminations of the environment, human interaction, or the food chain are three ways that these bacteria resistant to antibiotics might make it to people. O'Neill (2016) cites a lack of access to diagnostic tools, global inequalities in regulatory compliance, and poor sanitation as causes of resistance in low- and middle-income nations [10].

Public Health and Economic Implications

There is a significant impact that antibiotic resistance has on the global economy as well as healthcare systems. According to the Centres for Disease Control and Prevention (CDC, 2019), each year in the United States alone, there are over 2.8 million reported cases of illnesses that are resistant to antibiotics, which results in over 35,000 fatalities. This is a problem that exists in other countries as well. The number is far greater on a worldwide basis, and it is increasing at a speed that is quite quick. Antimicrobial resistance places a significant financial load on healthcare systems, which are already struggling to meet that cost. Research conducted by the World Bank in 2017 indicates that both increases in healthcare spending and decreases in productivity might be detrimental to the achievement of global development goals.

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According to the paper, it was anticipated that antimicrobial resistance might be responsible for a possible loss of 3.8% of the global GDP by the year 2050 [11].

Emerging Strategies and Future Directions

Several novel approaches are now being investigated as part of an attempt to counteract the development of antibiotic resistance. It has been demonstrated via research that antimicrobial stewardship programs contribute to the promotion of responsible antibiotic use, particularly in healthcare settings (Barlam et al., 2016) [12]. Within the framework of the WHO, there are surveillance initiatives such as the worldwide Antimicrobial Resistance Surveillance System (GLASS) that are designed to facilitate the better sharing of data and the monitoring of resistance on a worldwide scale. Moreover, novel approaches to therapy are now being researched and developed. The invention of novel antibiotics, the utilization of bacteriophages, antimicrobial peptides, and gene editing based on CRISPR are all examples of things that Aslam et al. (2018) consider to be victories in the fight against antibiotic resistance [13]. In addition, artificial intelligence (AI) is being utilized to develop models for the prediction of resistance and to assist in the identification of new drugs (Stokes et al., forthcoming) [14]. If we want to attain a One Health (Robinson et al., 2016) that incorporates human, animal, and environmental health, then the management of antibiotic resistance has to have a holistic and long-term perspective. Within the framework of this approach, the welfare of all living things is taken into consideration [15].

Types of antibacterial drug resistance

There is a possibility that the presence of antimicrobial medications that are either bacteriostatic or bactericidal might make it easier for resistant germs to proliferate at doses that would normally prevent their formation. On the majority of occasions, the creation of such resistance may be attributed to either mutations or acquired resistance, which refers to the transmission of genes that are resistant to antibiotics. The idea of intrinsic resistance, which involves cellular characteristics and wild-type genes (Cox and Wright, 2013; Blair et al., 2015), is the opposite side of this coin [16, 17]. They are the two sides of the same coin. Intrinsic resistance, acquired resistance, and adaptive resistance are the three primary categories of drug resistance that may be distinguished from one another. The growing pattern of resistance is what sets these groupings apart from one another. It is possible that various literature sources do not consistently classify some kinds of drug resistance in the same manner over and over again. In any case, it seems that a decent place to begin is by classifying drug resistance into three distinct categories: innate, acquired, and adaptive [18].

Natural resistance

When antibacterial treatments stimulate the expression of genes that are typically present in bacteria to become more resistant, this is an example of induced natural resistance. Intrinsic natural resistance is a type of natural resistance that is inherent to the species and cannot be altered. One type of natural resistance is induced natural resistance.On the other hand, horizontal gene transfer (HGT) has nothing to do with the phenomenon of intrinsic resistance, which is a characteristic that all bacteria have and which is unaffected by previous treatments with antibiotics. The term "intrinsic antimicrobial resistance" refers to a natural characteristic of bacteria that confers resistance to specific antibacterial agents. According to Melander et al. (2023), this type of resistance can render antimicrobial therapy ineffective [19].Two of the most prevalent bacterial mechanisms that contribute to intrinsic resistance are the presence of lipopolysaccharides (LPS) in Gram-negative bacteria and the intrinsic functioning of efflux pumps. Both of these processes give rise to the phenomenon of intrinsic resistance. A decrease in the permeability of the outer membrane is another effect that is brought about by LPS. Multidrug-efflux pumps are another common factor that contributes to the development of induced resistance. Natural resistance is distinguished from acquired resistance by the existence of genes in bacteria that exhibit both forms of resistance. This is the case despite the fact that there are two subtypes of natural resistance: intrinsic resistance and induced resistance. Further, the majority of natural resistance is comprised of factors that are internal to the system [20].

It is not the administration of antibacterial medications that is responsible for the development of intrinsic resistance in bacteria; rather, it is the structural characteristics of the bacteria themselves. Beta-lactam antibiotics, for example, are designed to inhibit the creation of cell walls. However, bacteria such as Ureaplasma and Mycoplasma do not possess cell walls, and as a result, they are inherently resistant to these antibiotics. Research conducted in the year 2020 by Christaki and colleagues reveals that Gram-negative bacteria have the ability to change the glycopeptides in their cell membranes in order to demonstrate innate resistance. This modification resulted in an increase in the impermeability of the outer membrane, which was the end result [21]. Porin proteins are responsible for preventing antibacterial agents from entering the body, which is another factor that contributes to the development of antibiotic resistance. There are a few examples that highlight how antibiotics can be naturally resistant to infections: An oxidative metabolism is not present in anaerobic bacteria, which is the reason why aminoglycosides are ineffective against these germs. As a result of their inability to convert metronidazole into its active form, aerobic bacteria are resistant to the antibiotic [22]. On the other hand, Gram-negative bacteria are resistant to

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vancomycin due to the fact that their outer membranes are impermeable to large glycopeptides (Miller et al., 2014) [23]. When it comes to treating illnesses that are caused by certain bacteria, antibacterial therapies have mostly been rendered ineffectual due to the advent of innate resistance. It does not present a substantial obstacle since the bacteria possesses intrinsic resistance, which is a property of the bacterium rather than an exogenous component [24].

Acquired resistance

An acquired resistance arises when a bacterium that was previously responsive to an antibacterial drug acquires a tolerance to the medicine. This process is known as acquired resistance. There are two ways that additional genetic material may be introduced into a cell: mutations and HGT. Both of these methods can increase a cell's resistance to certain illnesses. Mutations or alterations to the structure of chromosomes or other genetic components (such as plasmids or transposons), according to the authors Salih Cesur Ali and Demiroz (2013), are the perpetrators in this case [25, 26]. It is the naturally occurring changes that take place inside the chromosomes of bacteria that are responsible for the chromosomal resistance that bacteria exhibit. Several different types of chemical and physical stresses, such as ultra violet (UV) light, have the potential to influence the cellular structure of bacteria, which can result in mutations. Depending on the circumstances, this may either change the drug targets that are already present within the cell or decrease the permeability of the cell to medications [27].As a result of the extremely uncommon occurrence of spontaneous chromosomal changes, this route is responsible for the production of clinical resistance that is extremely uncommon and frequently negligible. There are several different vectors that may be used to transmit the extrachromosomal genetic elements that are necessary for resistance. Some of these vectors include plasmids, transposons, and integrons. In many cases, plasmid genes are responsible for encoding enzymes that hinder the effectiveness of antibacterial medications. The formation of integrons occurs when genes that confer resistance to bacteria are located in close proximity to one another and to certain combinations of integration sites. There is a possibility that these genes are situated on chromosomes or plasmids. The fact that extrachromosomal resistance may be easily and quickly passed on from one bacterial population to another within the same population makes it a more serious type of resistance. Illnesses that are resistant to more than one treatment represent a higher hazard, and the management of these illnesses is not a walk in the park. In a nutshell, the two primary factors that lead to acquired resistance are genes that have been altered or the introduction of new genes through the process of HGT [28].

Multi-drug resistance and pan-resistance

MDR organisms are bacteria that have developed the ability to resist the effects of multiple antibacterial medications.In light of this, it may be deduced that antibacterial agents are becoming less efficient in eliminating or managing different types of pathogens. Both of these biological processes have the potential to give birth to MDR in bacteria. The fact that bacteria are capable of acquiring a wide variety of resistance genes is something that should be kept in mind. The genes in question are typically carried by resistance plasmids. Enzymatic inactivation, changes in target structure, and increased expression of genes responsible for multidrug efflux pumps are some of the additional mechanisms that have the potential to result in MDR. Other processes that may also contribute to MDR include mutations in target structures. For the purpose of this discussion, the term "multidrug-resistant bacteria" refers to bacterial strains that demonstrate resistance to three or more types of antimicrobial products [29]. We claim that a strain of bacteria is extensively drug-resistant when it demonstrates resistance to practically all types of antimicrobials, while they only exhibit resistance to a handful of them. When referring to bacterial strains, PDR is used to characterize those that are able to resist every antimicrobial agent that is currently available. Bacteria that are resistant to several drugs pose a rising risk to public health because they are able to avoid the effects of a wide variety of antibacterial medications. Because of this, MDR is turning into a more significant problem. Since this is the case, it is becoming increasingly difficult to treat diseases that are brought on by bacteria that are resistant to several treatments. It is clear from this that there is an urgent requirement for both the creation of novel antimicrobials and the cautious application of antibacterials that are already in existence [30]. The classification of the many categories of antibacterial medicine resistance is illustrated in Figure 2. This classification is based on the reported mechanism of resistance.

The Rise of Multidrug-Resistant Organisms and Antibiotic Resistance

Within the context of his acceptance address for the Nobel Prize in Medicine in 1945, Sir Alexander Fleming predicted the potential risks associated with the abuse of penicillin and its eventual resistance [31]. There are several bacteria and other microbes that have acquired resistance mechanisms that were already present prior to the development of antimicrobial drugs. Consequences of the widespread use of antibiotics in animals and people include the development of selection pressure and the spread of antibiotic-resistant isolates. Both of these outcomes are considered to be undesirable outcomes. A selection pressure is exerted on microbial populations as a result of the usage of antibiotics, and the intensity of this impact rises as the amount of antibiotics used

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increases. Over the course of nearly seven decades, antibiotics have been utilized effectively in the treatment of bacterial illnesses [32]. On the other hand, throughout the course of time, a great number of hazardous organisms have developed resistance to the treatments that were formerly supposed to exterminate them, which has rendered such remedies worthless. There has been an increase in the percentage of infectious illnesses that have developed resistance to at least one antimicrobial drug. This progression has occurred very recently. Over the course of the past few years, antibiotic-resistant bacteria have been rapidly expanding in both human and animal populations. This alarming trend has been seen in both countries. In both of these environments, this trend has been seen [33].

Because antibiotics are the usual therapy for many bacterial disorders, such as urinary tract infections (UTIs), sexually transmitted infections (STIs), diarrhoea, sepsis, and hospital-acquired infections (HAIs), a significant number of bacteria have evolved resistance to antibiotics. Consequently, there is a shortage of the appropriate drugs that are necessary to treat these disorders [34]. According to a fact sheet on antimicrobial resistance published by the WHO, the resistance to the antibiotic ciprofloxacin, which is routinely used to treat UTIs, varied from 8.4% to 92.9% for E.coli and from 4.1% to 79.4% for K.pneumoniae. In the event that all other options have been exhausted, carbapenem medications are no longer effective against K. pneumoniae, a bacterium that has the potential to produce infections that are fatal on a mass scale [35].A number of nations and places have discovered instances of bacteria that are resistant to colistin, which is the last medicine that has the potential to be used in the treatment of illnesses that are brought on by carbapenem-resistant Enterobacteriaceae, which might be lethal. As a direct result of this, new illnesses have shown themselves for which there is now no available antibiotic treatment that is viable. There is a common bacterium known as Staphylococcus aureus that is responsible for infections in both individuals and healthcare institutions. This bacterium may also be found among the beneficial microorganisms that populate the skin. The death rate for individuals infected with MRSA was significantly higher than that of infections caused by drug-sensitive germs, which accounted for over 64 percent of the cases. On the other hand, drug-resistant P. aeruginosa infections are the cause of a rising number of fatalities; these infections account for approximately 11% of all bacterial infections that are acquired in hospitals [36].

Conclusion

This study highlights the high burden of antibiotic resistance among bacterial pathogens in Northern India, particularly among E. coli, K. pneumoniae, and S. aureus. The significant presence of MDR, ESBL, and carbapenem-resistant isolates emphasizes the critical need for robust antimicrobial stewardship, surveillance systems, and policy interventions. Immediate, coordinated action involving clinicians, microbiologists, and policymakers is vital to curb the spread of resistant infections and preserve the efficacy of existing antibiotics for future generations.An ever-increasing danger to world health, food stability, and progress is the rise of antibiotic resistance. Critical medical operations rely on reliable antibiotic prophylaxis, yet the efficiency of current therapies is undermined by the unregulated spread of resistant bacterial strains. Human actions and systemic problems, such as antibiotic abuse, a lack of regulation, and inadequate infection control practices, interact with biological processes, such as enzymatic drug degradation, target site alteration, and gene transfer, to drive antibiotic resistance, as this review has demonstrated. The consequences will have far-reaching effects, endangering millions of lives every year and causing economic losses estimated to be in the billions of dollars over the next several decades. There must be swift and concerted action in response to the rise of drug-resistant infections, which include MDR, XDR, and PDR strains. Nevertheless, there remains hope for the international community. Antimicrobial stewardship, improved monitoring, public awareness initiatives, and legislative frameworks are starting to provide positive results. AI in medication development, bacteriophage treatment, and CRISPR-based technologies are just a few examples of how scientific and technological progress is opening up new avenues for creative interventions.

Conflicts of interest: Nil

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