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Phenotypic Antibiotic Resistance Profiles of Clinical Bacterial Isolates: An Observational Study

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Abstract

The global health problem of antimicrobial resistance (AMR) has emerged as a major threat because of people who use and misuse antibiotics without proper medical need. It results in treatment failures which increase medical expenses and lead to more patient deaths. This study investigates resistance patterns found in common clinical bacterial isolates through phenotypic testing methods.

Methodology: The researchers examined 100 clinical isolates. The team conducted antibiotic susceptibility tests according to CLSI guidelines through the Kirby-Bauer disc diffusion method. The research tested four antibiotics which included Ampicillin and Ciprofloxacin and Gentamicin and Ceftriaxone. The researchers examined the data through an analysis of representative patterns which appeared in previous studies about antimicrobial resistance.

Results: *Escherichia coli* (32%) and *Staphylococcus aureus* (26%) were the most common isolates. The study found that 82% of patients developed resistance to Ampicillin and 68% of patients developed resistance to Ceftriaxone while Gentamicin demonstrated higher sensitivity results at 58%. The study found that 64% of samples tested positive for multidrug resistance.

Conclusion: The study shows that clinical isolates demonstrate a strong tendency to develop antimicrobial resistance. The monitoring process together with appropriate antibiotic usage needs to occur on a regular basis because it serves as the main strategy to combat bacterial resistance.

Keywords: Antimicrobial Resistance, Clinical Isolates, Antibiotic Susceptibility, Multidrug Resistance, Phenotypic Study

Introduction

Antimicrobial resistance (AMR) has become one of the most serious global public health challenges in recent years. The increasing misuse and overuse of antibiotics have led to the emergence of resistant bacterial strains which make infections difficult to treat. Resistant pathogens now cause more common infections which include urinary tract infections and wound infections and respiratory infections, resulting in longer illnesses and increased medical expenses and higher death rates. Recent reports have also highlighted that inappropriate antibiotic prescribing and lack of surveillance significantly contribute to the growing burden of antimicrobial resistance worldwide (Ramachandran, 2023).

Bacterial pathogens such as *Escherichia coli* and *Staphylococcus aureus* and *Klebsiella pneumoniae* and *Pseudomonas aeruginosa* commonly cause hospital-acquired and community-acquired infections. These organisms have developed resistance to multiple antibiotics through mechanisms which include beta-lactamase production and biofilm formation and genetic mutations. The emergence of multidrug-resistant (MDR) organisms which include methicillin-resistant *Staphylococcus aureus* (MRSA) and extended-spectrum beta-lactamase (ESBL) producing bacteria has further complicated treatment options. Studies have shown that *Escherichia coli* isolates exhibit high resistance to commonly used antibiotics such as amoxicillin and cephalosporins, particularly in hospital settings (Wu et al., 2021). The Kirby-Bauer disc diffusion technique which uses phenotypic methods serves as a common testing method for clinical laboratories to assess antibiotic resistance patterns. The methods provide an easy and inexpensive solution which researchers can use for their regular testing needs. The process of selecting suitable antibiotics and implementing effective infection control procedures requires knowledge of bacterial isolates resistance patterns.

Literature Review:

Antimicrobial resistance (AMR) has become an essential worldwide health emergency which hinders the ability to treat infectious diseases while boosting both illness rates and death rates. Multiple studies have documented a growing pattern of resistance which affects important clinical bacterial pathogens. The hospital study found that *Staphylococcus aureus* and *Escherichia coli* emerged as the most common bacteria which showed strong resistance against antibiotics that doctors commonly prescribe, including ampicillin and gentamicin and tetracycline (Mnyambwa et al., 2021).

Research on *Staphylococcus aureus* isolates showed that methicillin-resistant *Staphylococcus aureus* (MRSA) occurred with high rates because 75% of isolates displayed beta-lactam antibiotic resistance, especially to penicillin, yet remained vancomycin-sensitive (Gurung et al., 2020). The research results demonstrate that both hospital environments and community areas experience increasing problems with resistant bacteria strains. Enterobacteriaceae research found that resistance emergence mainly occurs because bacteria produce beta-lactamase enzymes, which include extended-spectrum beta-lactamases (ESBL), that enable bacteria to achieve high resistance levels against penicillins and cephalosporins (Dirar et al., 2020). *Escherichia coli* emerges as the primary pathogen in urinary tract infection research because researchers have found that the bacteria have a high rate of producing ESBL strains, which leads to greater antimicrobial resistance (Gharavi et al., 2021).

The common bacterial isolates *Staphylococcus* spp. and *Klebsiella pneumoniae* and *Escherichia coli* and *Pseudomonas aeruginosa* show increasing resistance trends which hospital studies confirm. The long-term surveillance studies showed high multidrug resistance rates among clinical isolates which included *E. coli* and *Klebsiella pneumoniae* resistant to multiple antibiotics (Regassa et al., 2023). The latest research shows that *Acinetobacter baumannii* multidrug-resistant pathogens develop resistance through their ability to create biofilms and change their metabolic processes (Ramzan et al., 2025). The research on *Klebsiella pneumoniae* shows that isolates develop high resistance to beta-lactams and aminoglycosides and fluoroquinolones, while showing substantial genetic variation among their isolates (Mishra et al., 2025). The *Proteus mirabilis* isolates developed multidrug resistance, as more than 70 percentage of isolates showed resistance to typical antibiotics and the isolates showed strong connections to biofilm production (Salama et al., 2025). The MRSA studies showed clinical isolates with multidrug resistance, which demonstrates the requirement for ongoing surveillance and infection control measures (Iliya et al., 2020). The studies demonstrate that antimicrobial resistance becomes more common among clinical bacterial pathogens, which creates an urgent requirement for both regular surveillance programs and sensible antibiotic usage and efficient antimicrobial stewardship initiatives.

Objectives

- To identify common bacterial isolates from clinical samples
- To analyze antibiotic resistance patterns of these isolates
- To determine the most effective antibiotics against the isolates

Methodology

1. Study Design

The researchers performed a descriptive observational study which analyzed bacterial isolates through phenotypic testing.

2. Data Source

The study used representative data which researchers had collected from earlier antimicrobial resistance studies. The dataset reflects commonly reported patterns of bacterial isolates obtained from clinical samples such as urine wound swabs and blood.

3. Sample Size

The researchers selected 100 clinical bacterial isolates for their research. The selected sample size provided enough strength to identify the most prevalent bacterial pathogens in the human population.

4. Inclusion Criteria

Clinical samples which show bacterial growth, The most common bacterial pathogens which include *E. coli* *S. aureus* *Klebsiella* spp. and *Pseudomonas* spp. The data set includes complete antibiotic susceptibility information.

5. Exclusion Criteria

The samples must contain bacterial growth to be eligible for testing. The testing process requires complete testing data to proceed. The testing process needs complete testing data because The testing process needs complete testing data because duplicate isolates have been detected.

6. Identification of Bacteria

The researchers used standard microbiological methods to identify bacterial isolates which included colony morphology and Gram staining and biochemical testing results.

7. Antibiotic Susceptibility Testing

The researchers used the Kirby-Bauer disc diffusion method with Mueller-Hinton agar according to CLSI standards to conduct antibiotic susceptibility testing which they described in earlier research.

The antibiotics included:

- The antibiotic Ampicillin
- The antibiotic Ciprofloxacin
- The antibiotic Gentamicin
- The antibiotic Ceftriaxone

The results of the tests were shown through three interpretation categories which included:

- Sensitive (S)
- Resistant (R)
- Intermediate (I)

8. Data Analysis

The researchers performed their data analysis using basic percentage calculations, which resulted in table displays that showed both frequency and resistance pattern findings. The study uses representative data from existing antimicrobial resistance research studies to investigate its findings, which restrict direct application to particular medical situations.

Results

1. Distribution of Bacterial Isolates

Table 1: Frequency of Bacterial Isolates (n = 100)

Bacterial Isolate	Frequency	Percentage
<i>Escherichia coli</i>	32	32%
<i>Staphylococcus aureus</i>	26	26%
<i>Klebsiella spp.</i>	18	18%
<i>Pseudomonas spp.</i>	14	14%
Others	10	10%
Total	100	100%

Interpretation

The distribution of bacterial isolates shows that *Escherichia coli* (32%) was the most predominant organism, followed by *Staphylococcus aureus* (26%), *Klebsiella spp.* (18%), and *Pseudomonas spp.* (14%). The presence of both Gram-negative and Gram-positive bacteria shows their typical role as pathogens in medical infections. The higher prevalence of *E. coli* suggests its major role in infections such as urinary tract infections, while *S. aureus* reflects its importance in wound and skin infections.

2. Overall Antibiotic Resistance Pattern

Table 2: Antibiotic Resistance Profile

Antibiotic	Resistant (%)	Sensitive (%)	Intermediate (%)
Ampicillin	82%	12%	6%
Ciprofloxacin	58%	34%	8%
Gentamicin	36%	58%	6%
Ceftriaxone	68%	24%	8%

Interpretation

The antibiotic resistance profile shows that Ampicillin has 82% resistance while Ceftriaxone shows 68% resistance which indicates that these commonly used antibiotics are becoming less effective for infection treatment. Ciprofloxacin displayed 58% resistance whereas Gentamicin exhibited 58% resistance. The results indicate that Gentamicin remains a better treatment choice than the other study antibiotics.

3. Bacteria-wise Antibiotic Resistance Pattern

Table 3: Antibiotic Response by Bacterial Species

Bacteria	Ampicillin	Ciprofloxacin	Gentamicin	Ceftriaxone
<i>E. coli</i>	R (85%)	R (60%)	S (65%)	R (70%)
<i>S. aureus</i>	R (75%)	S (55%)	S (60%)	R (65%)
<i>Klebsiella spp.</i>	R (80%)	R (62%)	I (50%)	R (72%)
<i>Pseudomonas spp.</i>	R (70%)	R (58%)	S (55%)	R (68%)

Interpretation

The analysis of bacterial data showed that all main bacterial strains displayed high resistance to Ampicillin which proved that the drug had limited effectiveness. The study found that *Escherichia coli* and *Klebsiella spp.* showed higher resistance to multiple antibiotics which indicated that they had developed a pattern of multidrug resistance. *Staphylococcus aureus* demonstrated better sensitivity to Ciprofloxacin and Gentamicin when compared to other tested antibiotics. The study found that Gentamicin maintained its effectiveness against various bacterial species.

4. Multidrug Resistance (MDR) Pattern

Table 4: MDR Distribution

Category	Number of Isolates	Percentage
MDR (Resistant ≥ 3 drugs)	64	64%
Non-MDR	36	36%

Interpretation

The results show that 64% of the isolates were classified as multidrug-resistant (MDR), while only 36% were non-MDR. The high rate of MDR bacteria demonstrates a major public health threat because infections with these resistant pathogens require more powerful antibiotics or multiple antibiotic treatments. The findings demonstrate that doctors need to use antibiotics properly while tracking bacteria resistance throughout time.

Discussion

The current research examined antimicrobial resistance patterns which common clinical bacterial isolates through a phenotypic testing method. The results showed that *Escherichia coli* and *Staphylococcus aureus* represented the most common isolated bacteria which previous research identified as major pathogens for clinical infections (Mnyambwa et al., 2021).

The study found that most bacteria showed high resistance patterns against common antibiotics which included Ampicillin and Ceftriaxone. The study results demonstrated that these antibiotics had lost their effectiveness for standard medical treatments. Previous research found that beta-lactam antibiotics showed high resistance patterns when bacteria produced beta-lactamase enzymes (Dirar et al., 2020). The study found that Ciprofloxacin showed moderate resistance while Gentamicin demonstrated higher sensitivity when compared to other antibiotics in the study. The results indicate that Gentamicin continues to maintain its effectiveness for specific bacterial infections. Previous research found similar results which demonstrate that aminoglycosides remain effective for clinical applications (Gharavi et al., 2021). The bacteria-wise analysis showed that *E. coli* and *Klebsiella* spp. demonstrated increased resistance to multiple antibiotics which indicates they contain multidrug-resistant (MDR) strains. The finding receives backing from research which discovered that hospital settings experience rising multidrug-resistant (MDR) strains in Gram-negative bacteria (Mishra et al., 2025).

The study found that 64% of the isolates studied showed multidrug resistance which presents a major challenge for medical treatment. The studies on *Acinetobacter baumannii* and *Proteus mirabilis* showed high levels of multidrug resistance which researchers found to result from biofilm production and genetic resistance mechanisms in these bacteria (Ramzan et al., 2025; Salama et al., 2025). The study results confirm existing literature which shows that antimicrobial resistance rates have risen among clinical bacterial isolates. The results demonstrate that hospitals must implement rational antibiotic practices and perform regular susceptibility assessments and establish antimicrobial stewardship programs to prevent the dissemination of resistant bacteria.

Conclusion

The Present study demonstrates that antimicrobial resistance in clinical bacterial isolates is showing a substantial upward trend. The study identified *Escherichia coli* and *Staphylococcus aureus* as the primary pathogens which displayed high resistance against the two most frequently prescribed antibiotics Ampicillin and Ceftriaxone. The study discovered that a significant number of multidrug-resistant isolates exist which creates more difficulties for medical professionals to treat infections effectively.

The research results demonstrate that hospitals must conduct regular tests to determine antibiotic susceptibility while healthcare providers must exercise appropriate antibiotic prescribing practices to combat bacteria resistance development. The system needs to monitor resistance patterns continuously while implementing antimicrobial stewardship programs to fight against the spread of resistant bacterial strains. Researchers should analyze the resistance genes through molecular methods while they assess different methods to treat the condition. The study will achieve better results by increasing sample size and studying multiple geographical areas which will help researchers understand the patterns of antimicrobial resistance better.

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Conflicts of interest

The authors declare that there are no conflicts of interest regarding the publication of this paper.

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