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Original Research Article

Antibiotic Susceptibility Patterns of Pseudomonas aeruginosa Isolated from ICU Patients

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Conflict of interest: Nil

Abstract:

Background: Pseudomonas aeruginosa is a prevalent opportunistic pathogen responsible for infections in patients with cancer. The objective of the study was to assess the antibiotic susceptibility of Pseudomonas aeruginosa and multidrug-resistant (MDR) isolates in ICU patients.

Methods: A retrospective study was performed from January 2024 to December 2024 at Netaji Subhas Medical College, Jamshedpur. A total of 111 unique clinical isolates of P. aeruginosa were collected from patients in several ICUs, encompassing medical, surgical, and neonatal units. The isolates were identified by established techniques utilizing biochemical assays. The antibiotic susceptibility profile of each isolate was assessed according to the Clinical and Laboratory Standards Institute (CLSI) guidelines 2022.

Results: Of the 111 clinical samples, the predominant P. aeruginosa isolates were obtained from respiratory specimens. The majority of isolates exhibited sensitivity to colistin (98.1%, n=109) and amikacin (66.6%, n=74); however, resistance to ciprofloxacin, ceftazidime, and levofloxacin was notably higher at 51.8%, 49.6%, and 49.6%, respectively.

Conclusions: This hospital-based retrospective study aims to enhance infection control tactics and augment doctors' understanding of antibiotic resistance patterns. Consequently, an antibiotic stewardship program is necessary to monitor resistance patterns at a tertiary care cancer hospital.

Keywords: Multidrug Resistance, Extensively Drug Resistance, Pseudomonas aeruginosa, Antibiotic Resistance, Clinical Samples, Surgical Wards, Hospital Environment.

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Introduction

Pseudomonas aeruginosa is a predominant etiological agent of healthcare-associated infections, especially in intensive care units (ICUs), where patients are severely ill, immunocompromised, and often subjected to invasive equipment and broad-spectrum antibiotics [1], [2]. This opportunistic bacterium causes ventilator-associated pneumonia, bloodstream infections, urinary tract infections, and surgical site infections, and is linked to elevated morbidity and mortality rates [3].

A significant difficulty in managing P. aeruginosa infections is its extraordinary capacity to build resistance to several antibiotic classes via intrinsic resistance mechanisms, acquisition of resistance genes, efflux pumps, and biofilm formation [4]. The rise of multidrug-resistant (MDR) and extensively drug-resistant (XDR) P. aeruginosa strains in intensive care units (ICUs) significantly restricts treatment alternatives [5], [6].

Understanding local antibiotic susceptibility patterns is crucial for directing empirical treatment, enhancing antimicrobial stewardship, and elevating patient outcomes [7]. This study sought to identify the antibiotic susceptibility profile of P. aeruginosa isolated from ICU patients.

Methods

Study Design and Setting: This retrospective cross-sectional study was conducted in the Netaji subhash medical college in India over a period of one year (January 2024–December 2024).

Study Isolates: A total of 111 non-duplicate clinical isolates of P. aeruginosa were obtained from patients admitted to various ICUs, including medical, surgical, and neonatal ICUs.

Inclusion Criteria

- Clinical samples from ICU patients yielding P. aeruginosa
- Only the first isolate per patient was included

Exclusion Criteria

- Duplicate isolates from the same patient
- Environmental isolates

Identification of P. aeruginosa: Isolates were identified based on colony morphology, Gram staining, oxidase test, pigment production, growth at 42°C, and standard biochemical tests.

Antibiotic Susceptibility Testing: Antibiotic susceptibility testing was performed using the Kirby–Bauer disc diffusion method on Mueller–Hinton agar. The antibiotics tested included:

- Piperacillin–tazobactam
- Ceftazidime
- Cefepime
- Amikacin
- Gentamicin
- Ciprofloxacin
- Levofloxacin
- Colistin

Results were interpreted according to Clinical and Laboratory Standards Institute (CLSI) guidelines.

Definition of Multidrug Resistance: MDR P. aeruginosa was defined as resistance to at least one agent in three or more antimicrobial classes.

Statistical Analysis: Data were entered into Microsoft Excel and analyzed descriptively. Results were expressed as frequencies and percentages.

Results

Distribution of Clinical Samples: The majority of P. aeruginosa isolates were recovered from respiratory samples.

Table 1: Distribution of Clinical Samples (n=111)

Sample Type	**Number**	**Percentage (%)**
Endotracheal aspirate	38	34.23
Sputum	23	20.7
Blood	18	15.0
Urine	20	16.7
Wound/pus	12	10.8

Antibiotic Susceptibility Pattern: Colistin showed the highest susceptibility, while fluoroquinolones and third-generation cephalosporins showed lower susceptibility rates.

Table 2: Antibiotic Susceptibility Pattern of P. aeruginosa

Antibiotic	Sensitive n (%)	Resistant n (%)
Piperacillin–tazobactam	72 (64.8)	39 (35.2)
Ceftazidime	56 (50.4)	55 (49.6)
Cefepime	60 (54.0)	51 (46)
Amikacin	74 (66.6)	37 (33.4)
Gentamicin	62 (55.8)	49 (44.2)
Ciprofloxacin	54 (48.6)	57 (51.8)
Levofloxacin	56 (50.4)	55 (49.6)
Colistin	109 (98.1)	2 (1.9)

Multidrug Resistance Pattern: Out of 111 isolates, 41 (38.3%) were identified as multidrug-resistant P. aeruginosa.

Table 3: Prevalence of Multidrug Resistance

Resistance Pattern	Number	Percentage (%)
MDR isolates	41	36.9
Non-MDR isolates	70	63.0

Discussion

This study emphasizes a troubling degree of antibiotic resistance in P. aeruginosa isolates collected from ICU patients. Respiratory specimens, especially endotracheal aspirates, were the predominant source, indicating the significant prevalence of ventilator-associated infections in intensive care units [8].

Moderate susceptibility to antipseudomonal beta-lactams was noted, however resistance to fluoroquinolones was significantly elevated. The identification of MDR P. aeruginosa in over one-third of isolates highlights the selection pressure imposed by extended ICU admissions and intensive antibiotic usage.

Colistin had exceptional efficacy against P. aeruginosa isolates, affirming its status as a last-resort antibiotic. The emergence of colistin resistance, however minimal, is concerning and necessitates rigorous antimicrobial stewardship and infection control measures [9].

Limitations

Testing for minimum inhibitory concentration (MIC) and molecular identification of resistance mechanisms were not conducted. This was a unicentric study.

Conclusion

Pseudomonas aeruginosa isolated from ICU patients showed elevated resistance to frequently utilized antibiotics, with a significant prevalence of multidrug-resistant isolates. Consistent monitoring of antibiotic susceptibility trends and prudent application of antimicrobials are crucial for informing empirical treatment and mitigating the dissemination of resistant P. aeruginosa in intensive care units.

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