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Original Research Article

ANTIMICROBIAL SUSCEPTIBILITY PATTERNS OF PSEUDOMONAS AEUROGINOSA ISOLATED FROM PATIENTS WITH RESPIRATORY DISEASES IN A TERTIARY CARE HOSPITAL

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Abstract: *Antimicrobial medicines have been extensively used since ancient times to treat various microbial infections, many of which can be life-threatening and contribute significantly to healthcare expenses worldwide. However, the increasing adaptability of these antibiotics has led to the emergence of resistance among microorganisms. This study aims to investigate the prevalence and susceptibility patterns of Pseudomonas aeruginosa among patients with respiratory disorders in a tertiary healthcare setting. A cross-sectional study was conducted at Civil Hospital Sialkot from September 2021 to June 2022, where 500 sputum samples were collected from both in and out-patients. Samples were collected following standard protocols and subjected to inoculation. Isolates were identified using standard biochemical protocols, and their antibiotic susceptibility patterns were determined using the Clinical and Laboratory Standards Institute (CLSI) guidelines and Kirby-Bauer's disc diffusion method. Out of the 500 sputum samples collected, 206 (41.2%) showed growth of microorganisms. Of these, 77 (37.38%) were identified as Pseudomonas aeruginosa. The isolates comprised 54.5% males and 45.5% females, with a mean age of 54.77 ± 11.16. The highest sensitivity was observed for Amikacin (93.5%), followed by Meropenem (92.21%), while the lowest sensitivity was observed for Cefoperazone (18.18%) and Tazocin (16.89%).*

Similarly, maximum resistance was seen in the case of Cefoperazone and Tazocin at (81.82%) and (83.11%) respectively. The results indicate that commonly used antibiotics against Pseudomonas aeruginosa are becoming increasingly resistant, with aminoglycosides and carbapenems remaining the two classes with the highest activity against this microorganism. These findings underscore the need for continued surveillance and appropriate use of antibiotics to minimize the development of resistance.

Keywords: Pseudomonas aeruginosa, Antibiotic susceptibility, Sputum Culture, Isolates

Introduction

In medicine, antimicrobial medicines are commonly used to treat microbial pathogens. However, the emergence of antimicrobial resistance has become a global concern mainly due to the numerous ways microbial populations have developed to combat these antimicrobial agents (Franco et al., 2009). This has increased healthcare expenses and the effects of Pseudomonas aeruginosa strains in hospitals and communities. Initially, antibiotics were considered miraculous; however, the abrupt use of such an inexpensive approach has caused significant resistance among the population, introducing more expensive and complicated antibiotics to cope with simpler infections (Rajat, 2012). Pseudomonas aeruginosa is a common and adaptable human opportunistic infection affecting morbidity, death, and healthcare expenses in hospitals and the community, and it is a Gram-negative bacterial species known for its specific properties and other characteristics (Gill et al., 2011). By using a variety of mechanisms, such as determining resistance and modifying enzymes, followed by changes in chromosomal genes, Pseudomonas aeruginosa is believed to develop resistance in the majority of cases (Franco et al., 2009).

Furthermore, the population's varied response and resistance patterns have been observed (Gill et al., 2011). The restricted and varied exposure to the vast range of antimicrobial agents has rapidly increased the isolation of resistant strains of microorganisms. Infections caused by Pseudomonas aeruginosa are more challenging to cure as the organism becomes more resistant to antibiotics (Poole, 2011). Despite several antipseudomonal medications, infections due to P. aeruginosa remain life-threatening and are

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considered a serious medical concern (S et al., 2014). The acquisition of specific genes, such as those encoding beta-lactamase and amino-glycoside modifying enzymes, has been shown to contribute to Pseudomonas aeruginosa's antimicrobial and multi-drug resistance (Zhao and Hu, 2010; Poole, 2005). Bacterial resistance patterns are location- and time-specific and fluctuate throughout time. Regular surveillance is required nationally and locally to treat the illness empirically and successfully (Alam et al., 2011). The current study aimed to determine the prevalence of Pseudomonas aeruginosa among patients with respiratory diseases visiting the hospital vicinity and to determine the antibiotic susceptibility pattern in the isolates.

Methodology

This investigation was carried out in the Department of Pulmonology, Civil Hospital Sialkot, from September 2021 to June 2022. The sputum samples of the selected patients were collected and stored in specialized vials before their biological characterization. A cross-sectional study was conducted, and Ethical approval was attained from the research and ethical committee. A total of 500 sputum samples were collected, of which 206 showed positive culture, of which 77 were identified as *P.aeruginosa* belonging *to* both genders, and all the age group patients were involved in the current study. Sputum samples were obtained using specialized sterile containers labeled with the serial numbers of each selected patient.

Obtained samples were subjected to routine microbiological processing for bacterial species identification. Inoculations were made on common culture media like Mac-Conkey agar, blood agar, and eosin-methylene blue agar using samples obtained from a variety of sources, including pus/wound, sputum, urine, tracheal aspirates, central venous (CV) catheter tip, broncho-alveolar lavage (BAL) fluid, catheters, and high vaginal swabs. Gram's staining, colony morphology, motility tests, sugar fermentation tests, and biochemical tests like the oxidase test, urease test, and IMViC (indole, methyl red, Voges-Proskauer, and citrate) tests were all conducted as part of the testing regimen to confirm that the isolates were *Pseudomonas aeruginosa* (Church et al., 2020). Antibiotic susceptibility of the attained samples was determined using *Kirby-Bauer's* disc diffusion method, where sensitive and resistant organisms were marked after measuring the zone of inhibition using CLSI guidelines. And later, the sensitivity and resistant pattern was determined. Demographic data of patients (age, gender, and nationality), data was attained, arranged, and subjected for their descriptive statistics.

Results

A total of 500 sputum samples were analyzed for the study. We found 206 patients with a positive culture. Among 206 patients, 77 showed positive cultures for P.aeruginosa, which were selected for further analysis. Out of the 77 selected samples, 42 (54.5%) were males, while 35 (45.5%) were females. The mean age was 54.78 ± 11.16, where most of the growth, 20 out of 77 were observed among patients aged 50-59. As shown in table 1 depicts the demographic characteristics of the patients.

Table 1: Demographic characteristics of the patients.

Characteristics	n (%)
Age (Mean ± S.D)	54.78 ± 11.16
Age groups	
0-19	6
20-29	4
30-39	8
40-49	10
50-59	20
60-69	19
70 or above	10
Gender	
Male	42 (54.5%)
Female	35 (45.5%)
Nationality	
Pakistani	77 (100%)

In-vitro antibiotic susceptibility pattern showed Amikacin (93.5%) had the highest sensitivity against *P.aeruginosa,* followed by Meropenem (92.21 %). Whereas the lowest sensitivity was observed in (16.89%). Other antibiotics showed sensitivity as follows Cefradine (66.24%), Imipenem (63.64%), Cefixime (62.34%), Ceftriaxone (46.76%), Septran (35.07%), Gentamicin (33.77%) as shown in Figure 1

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and 2 respectively. Similarly, the resistance patterns can be seen in the figure 1 and 2 as well. Shows (81.82%) and (83.11%) resistance were seen in Cefoperazone and Tazocin. (66.23%), (36.36%), (64.93%), and (53.24%) of resistance were reported in the case of Gentamicin, Imipenem, Septran, and Ceftriaxone, respectively. Amikacin (6.5%) and Meropenem (7.79%) recorded the least resistance in *Pseudomonas aeruginosa*.

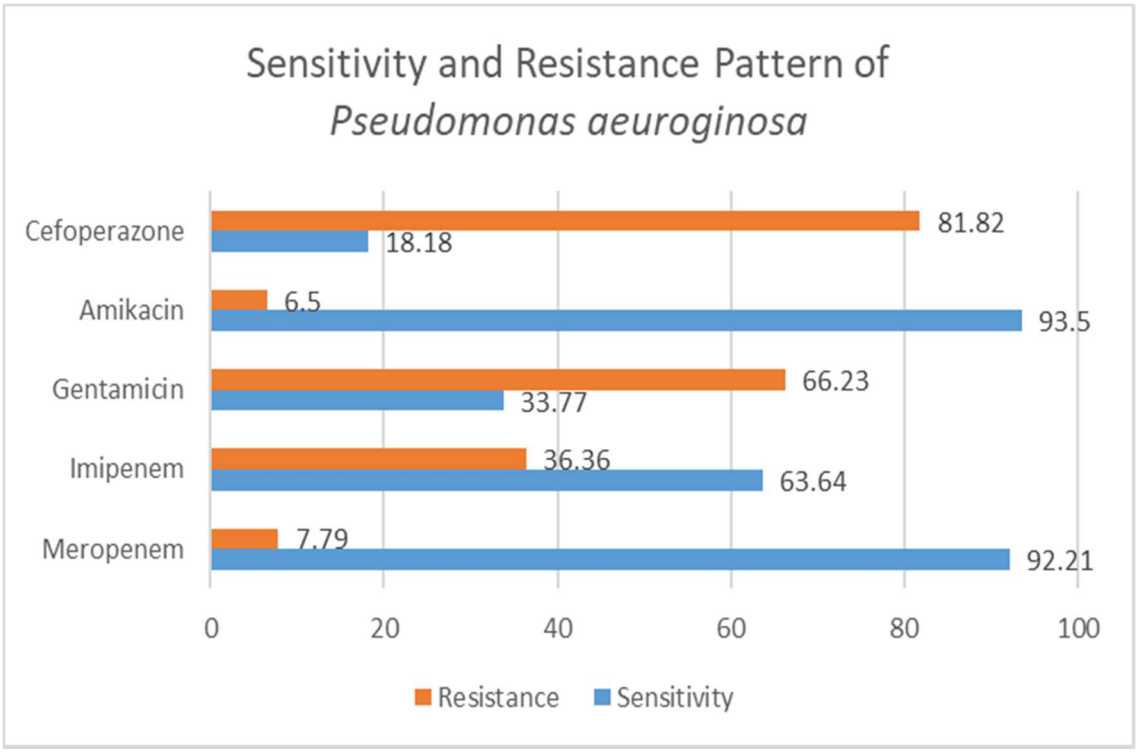

Figure 1: Part A of Sensitivity and Resistance Pattern of *Pseudomonas aeruginosa*

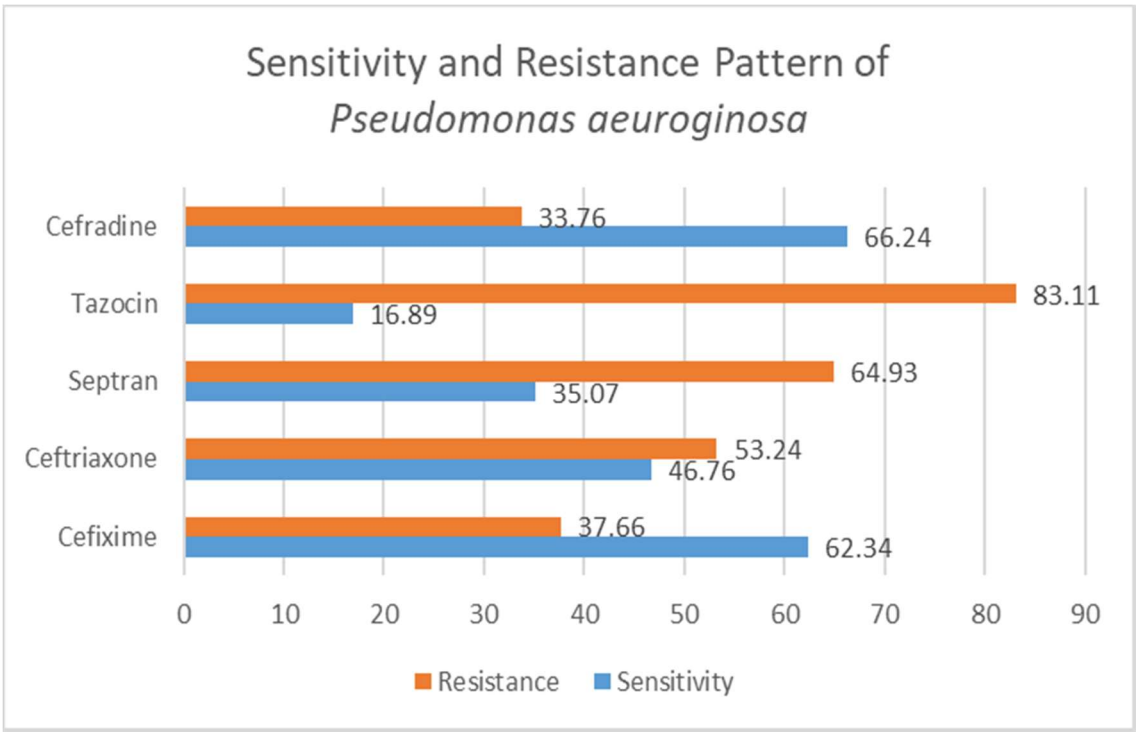

Figure 2: Part B of Sensitivity and Resistance Pattern of *Pseudomonas aeruginosa*

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Discussion

Numerous studies have been conducted worldwide in different populations and regions to investigate antibiotic resistance incidences and avoid future interventions. The more rational use of antibiotics has contributed to increased antibiotic resistance among populations (Lambert et al., 2022). Furthermore, statistics indicate that older individuals are more susceptible to developing antibiotic resistance due to the rational and irrational use of antibiotics in the population (Steinberg and Monahan, 2007). A study in Peshawar reported the highest sensitivity among the carbapenem and aminoglycoside classes of antibiotics (Samad et al., 2017). Gram-negative bacteria, particularly anaerobic and non-fermenting bacteria, are frequently associated with various infections. Pseudomonas aeruginosa is known to develop resistance against nearly all antibiotics, making infections caused by this pathogen increasingly life-threatening (Pachori et al., 2019). The development of antibiotic resistance is primarily due to the more rational use of antibiotics, resulting from various factors (Hueston and Dickerson, 2001). Our study has some limitations. The study was conducted on a limited number of patients visiting a particular center; therefore, conducting the study on a larger scale is recommended for more precise results.

Conclusion

The present analysis reveals that Pseudomonas aeruginosa is becoming increasingly resistant to commonly used antibiotics, including carbapenems and aminoglycosides. Drug distributors' misuse and irrational dispensing of these medications may contribute to this emerging problem. Therefore, it is crucial to implement strict policies for the sale and distribution of antibiotics to prevent the development and spread of antibiotic resistance.

Conflict of interest

The authors declared absence of conflict of interest.

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