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Drug Susceptibility Pattern of Multidrug Resistant Pseudomonas aeruginosa Causing Life threatening Infection among Intensive Care patients.

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I. INTRODUCTION

One of the most important issues facing worldwide public health in the 21st century is antimicrobial resistance. [1] The prevalence of drug resistance is growing, as is the number of resistant microbial strains, the geographic areas affected, and the degree of resistance in each organism. [2] In addition, the proportion of organisms displaying antimicrobial resistance, particularly resistance to several drugs, is steadily rising. [3] The danger of incorrect therapy is increased by resistant bacteria, which results in an increase in morbidity and mortality. [4, 5] This resistance could impede and postpone treatment, leading to problems or even fatalities. [6,7] Also, a patient can require additional care, the use of other, more expensive antibiotics that might have more severe side effects, or intrusive treatment like an intravenous injection that needs to be administered in a hospital. [6,8] Experiences from the antimicrobial use and resistance surveillance network demonstrate that data, whenever available, can be used for a variety of purposes, such as guiding treatment decisions, understanding antimicrobial trends, guiding public health policy, identifying priority areas for interventions, and tracking the effects of interventions on specific resistance. [1] As a result, the current study entails checking the antimicrobial resistance profile of medications called carbapenems that are used to treat infectious infections. In the 1970s, P. aeruginosa was shown to be the microbe that was specifically associated with neutropenic hosts, but about 50 years before, it was hardly ever thought to be a genuine pathogen. It is one of the most prevalent pathogens causing hospital acquired infections in the current situation. There are numerous sources for this infection, including respiratory devices, antiseptics, soaps, sinks, mops, and hydrotherapy pools. [9] Nosocomial infections are typically caused by P. aeruginosa, and 10–20% of patients with nosocomial infections were hospitalized to intensive care units [10].This pathogen is divided into various phenotypic variations, primarily depending on the pattern of treatment resistance. Pseudomonas species that are resistant to at least three different antimicrobial classes and multiple antimicrobial agents are referred to as MDR types. [11] Lower Respiratory Tract Infections (LRTI) are the most frequent and predominating gram negative, non-fermentative pathogen infections in ICU patients after urinary tract infections (UTI), surgical site infections, and bacteremia. Drug resistant phenotypes have evolved as a result of Pseudomonas species' capacity to create a wide range of drug resistance mechanisms. For the treatment of such a severe infection, this presents a difficulty to our clinician. This kind of circumstance calls attention to the need for the diagnosis of phenotypes that are developing various types of drug resistance mechanisms to prevent unsuccessful treatment and hospital acquired infections. [12] The current study's goal was to assess the prevalence of MDR P. aeruginosa and the antibiotic resistance patterns among ICU patients in a tertiary care hospital in Ghaziabad, Uttar Pradesh, India.

II. MATERIALS AND METHODS

The Department of Microbiology at Santosh Medical College and Hospital in Ghaziabad, Uttar Pradesh, conducted the current cross-sectional prospective study. The research was done between January 2019 and February 2021. Before beginning the investigation, IEC's approval was obtained (Reference No.SU/2021/092/3). Using the 2013 version of MS Excel, the results

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were statistically analyzed in terms of numbers and percentages.

Inclusion Criteria: All ICU samples, including those drawn from indwelling catheters and those drawn following invasive procedures, were included in the study.

Exclusion Criteria: Patients less than 10 years old were excluded from the current investigation because samples from the pediatric intensive care unit were not included. Also excluded from the trial were patients with signs of septicemia and a known diagnosis of P. aeruginosa infection.

Sample Collection and processing: Each appropriate clinical sample that met the established inclusion criterion was acquired separately. As soon as possible, various clinical samples, including Endotracheal (ET) aspirate, Blood, Pus, and Urine, were collected with aseptic precaution in sterile universal containers and sent directly to the Microbiology laboratory. In case of an unavoidable circumstance, samples were kept in the refrigerator at 2-8°C temperature. The full clinical sample that was received by the microbiology lab was examined for AST, isolation, and identification. During the course of two years, 502 human clinical samples containing a total of 115 P. aeruginosa isolates were collected; each clinical sample was unique. These Pseudomonas isolates were recognized using traditional techniques in accordance with accepted microbiology laboratory protocol, and they were subsequently recognized by examining the cultural characteristics on common laboratory culture media, namely blood agar and MacConkey agar plates. Colonies of bacteria on MacConkey agar plates had a pale color and weren't lactose fermenting, and they tested positive for oxidase. In contrast, the bacterial colonies on nutrient agar had pigmented, non-pigmented, and oxidase positive colonies. The utilization of pure isolates of P. aeruginosa for future research came after species level identification was carried out using manual biochemical test procedures. In order to isolate and identify microorganisms, standard operating procedure was followed. [13]

ANTIBIOTIC SUSCEPTIBILITY TESTING:

All clinical isolates underwent AST using Hi-media Labs' standard Kirby-Bauer disc diffusion technique on Mueller Hinton agar (Mumbai, India). The study employed P. aeruginosa control strain ATCC (American Type Culture Collection) 27853. Clinical and Laboratory Standard Institute (CLSI) recommendations were used to interpret the zone of inhibition. [14] The data contained demographic details, such as age, sex, and length of ICU hospitalization.

STATISTICAL ANALYSIS

The data contained demographic details, such as age, sex, and length of ICU hospitalization. Moreover bacterial culture with respect to antibiotic resistance was looked at and data analysis was done using Microsoft Excel 2013, version.

III. RESULTS:

There were 115 P. aeruginosa isolates out of 502 clinical samples overall, representing a 23% prevalence. P. aeruginosa MDR phenotypes were frequently isolated from ET aspirates, then from urine, pus, and blood samples as shown in (Table.1). A total of 60 MDR phenotypes were identified; of these, 41 were separated from male patients and 19 from female patients.

Table1: Distribution of MDR Pseudomonas aeruginosa isolates by sample.

Types of Sample	MDR Pseudomonas aeruginosa (%)
ET aspirate	26(43.34)
Urine	18(30)
Pus	12(20)
Blood	2(3.33)
BAL fluid	2(3.33)

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Total	60

Drug resistance pattern of MDR P. aeruginosa: Cetazidime was shown to have the highest level of MDR resistance, and it was followed by gentamicin, cefepime, ciprofloxacin, amikacin, aztreonam, piperacillin, and ticarcillin/clavulanic acid piperacillin-tazobactam, with imipenem and meropenem having the lowest levels of resistance. The resistance profile of MDR P. aeruginosa to various anti-pseudomonal medications is displayed in (Table.3).A total of 115 Pseudomonas isolates were processed, out of which 60 (52%) were MDR phenotypes and 47 (41%) were Non Drug Resistant Pseudomonas aeruginosa (NDRPA). According to this study, mechanical ventilation and endotracheal intubation were the two main risk factors for P. aeruginosa infections in ICU patients. Long ICU stays were another key factor in ICU patients' infections and most recently, infections in ICU patients were strongly correlated with underlying illnesses like hypertension and Chronic Obstructive Pulmonary Disease (COPD). MDR was most prevalent in patients between the ages of 31 and 50, and a larger incidence of MDR in men was noted as shown in (Table.2)

Table2: Distribution of Pseudomonas aeruginosa MDR isolates by age and sex.

S.No.	Age Group(In Yeras)	MDR Isolates	
		Males(41)	Females(19)
1	11-20	2(4.9%)	2(10.5%)
2	21-30	4(9.8%)	2(10.5%)
3	31-40	16(39%)	4(21.1%)
4	41-50	14(34%)	6(31.6%)
5	51-60	2(4.9%)	2(10.5%)
6	>60	3(7.4%)	3(15.8%)

Table3: The MDR Pseudomonas aeruginosa resistance profile to several anti-pseudomonal medications.

Antibiotcs	MDR P.aeruginosa N (%)
Colistin(10 µg)	Nil
Amikacin(30 µg)	46(76%)
Piperacillin-Tazobactam (100 µg/10 µg)	23(38%)
Piperacillin (100 µg)	36(60%)
Gentamicin (10 µg)	51(85%)
Meropenem (10 µg)	10(16%)
Imipenem (10 µg)	11(18%)

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Ciprofloxacin (5 µg)	48(80%)
Ticarcillin/clavulanic acid (75 µg/10 µg)	29(48%)
Aztreonam (30 µg)	46(76%)
Cefepime (30 µg)	48(80%)
Ceftazidime (30 µg)	52(86%)
Polymyxin B (300 Units)	Nil

IV. DISCUSSION

Recent years have seen an increase in the threat posed by the emergence of MDR, XDR, and PDR phenotypes in P. aeruginosa, and treating these phenotypes is a very difficult challenge for physicians. The synthesis of various b-lactamases, integron-mediated integration of bla genes, inability of porin genes to increase their expression level, and target site modification are just a few examples of the several molecular mechanisms that lead to resistance to these antibiotics. [2] In this investigation, Pseudomonas aeruginosa was more prevalent than previously reported by Gill JS et al. [2], where it was reported at a rate of 23% versus 14.7%. Senthamarai S et al. reported a prevalence rate of 2.76% in Tamilnadu, but Gupta R et al. reported a prevalence rate of 28%. [15, 16] In the current study, MDR P. aeruginosa prevalence was 52%. Yet in Iran, Gill JS et al. discovered a prevalence rate of 50%, Saderi H and Owlia P observed a frequency of 54.5% for MDR P. aeruginosa, and Mirzaei B et al. in Tehran discovered a prevalence rate of 16.5% for MDRPA. [10, 17, 18] The lower respiratory tract, urine, pus, and blood samples were where MDR P. aeruginosa phenotypes were most commonly identified in the current investigation. Gupta R et al. have observed similar findings. [16] The bulk of the positive isolates, however, were found in urine and wound samples, according to Gill JS et al. [10] Moreover, Prakash V et al. [19] concurred with our findings. In the current investigation, it was discovered that male patients (68%) outnumbered female patients (32%), when it came to MDR P. aeruginosa. These outcomes were consistent with those of Mirzaei B et al. [18] According to the findings of the current study, ceftazidime had the highest level of MDR P. aeruginosa resistance, whereas imipenem and meropenem had the lowest levels, Studies by Biswal I et al. in burn victims also produced comparable outcomes.[20] The current study's findings concurred with those reported by Gupta R et al. and Nasser M et al. [16, 21], who also observed comparable results regarding the resistance pattern of MDRPA.

Carbapenems are the preferred medication for MDR P. aeruginosa isolates, however there is now a severe threat from rising carbapenem resistance. Imipenem and Meropenem had the lowest resistance patterns in this investigation, at 18% and 16%, respectively. The resistance pattern for MDR P. aeruginosa isolates, however, was reported by Bhatt P et al. to be 61% and 54%, respectively. [22]

More than 50% of the isolates were found to be resistant to fluroquinolones, gentamicin, cephalosporins, and aminoglycosides in the current investigation, which examined drug resistance trends. Such bacterial strains have few therapy and management options, which could lead to treatment failures and cause severe morbidity and mortality. The excellent effectiveness of carbapenems as an antibiotic in the treatment of nosocomial infections and as a priceless tool against MDR P. aeruginosa infections. In the current study, MDR P. aeruginosa isolates had the lowest resistance to carbapenems, whereas piperacillin alone had a 60% resistance rate and beta-lactam/b-lactamase inhibitor piperacillin/Tazobactam had a 38% resistance rate. This suggests that beta-lactamase inhibitor

significantly broadens the spectrum of activity of beta-lactams, making the combination drug the preferred treatment for P.aeruginosa. Because certain drug resistance genes are more common in some regions than others, P. aeruginosa's susceptibility pattern varies. [23]

V. CONCLUSION(S)

To stop the emergence of P. aeruginosa that is resistant to antibiotics, strict antibiotic policies and a frequent surveillance program of antimicrobial resistance should be implemented. Even today, Colistin and Polymyxin B are highly sensitive to MDR P. aeruginosa phenotypes. All bacterial isolates of Pseudomonas aeruginosa should undergo routine early detection of beta-lactamases in order to inform antibiotic choice and improve the management of serious illness in ICU patients.

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