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PREVALENCE AND ANTIMICROBIAL SUSCEPTIBILITY PATTERN OF Pseudomonas aeruginosa STRAINS ISOLATED FROM VARIOUS CLINICAL SAMPLES IN TERTIARY CARE HOSPITAL, MIRAJ

Clinical Microbiology

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ABSTRACT

Background: Pseudomonas aeruginosa are responsible for different healthcare-associated infections and are intrinsically resistant to many commonly used antibiotics. Hospital antibiograms are either not prepared or not regularly updated in most healthcare facilities. The aim of the present study was to determine the antimicrobial susceptibility pattern of P. aeruginosa isolates from various clinical samples in a tertiary care centre in order to guide antibiotic prescription for better patient safety in the hospital. **Methods:** Total 161 isolates were recovered from various specimens for a period of 12 months from January 2024 to December 2024 and the disc diffusion method was used for antibiotic susceptibility testing as per CLSI guidelines. **Results:** Prevalence of P. aeruginosa was 3.01%. Among the entire gram negative organisms (1571) isolated from different samples Pseudomonas aeruginosa isolates were around 10.24%. male patients accounted for 59% and female patients 41%. majority of the patients (44.09%) belonged to the age group 45-65 years .Out of the 161 Pseudomonas aeruginosa isolates studied, 71% were susceptible to Imipenem, 71% to Aztreonam , 63% to Amikacin,, 70% to Piperacillin-Tazobactum, 53% to Ceftazidime, 59% to Tobramycin & 42% to Ciprofloxacin respectively. **Conclusions:** Due to rise in Multi Drug resistant strains of P. aeruginosa , Infection control procedures and surveillance programmes for MDR organisms have to be implemented. Antimicrobial susceptibility pattern of P. aeruginosa in Clinical wards and Intensive care Units has to monitored strictly and the results should be readily made available to clinicians so as to help them in making clinical judgement in therapy to reduce development of drug resistance and associated comorbities.

KEYWORDS

Prevalence, Drug Resistance, Disc diffusion method, Pseudomonas aeruginosa

INTRODUCTION

Pseudomonas aeruginosa is a non-fermentative, aerobic, Gram-negative bacillus and is one of the leading causes of severe healthcare-associated infections, especially in critically ill and immunocompromised patients.[1,2] It has broad ecological adaptability, ubiquitous in nature and ability to acquire and disseminate drug resistance. It remains viable on inanimate and animate objects. It also survives in antiseptic solutions. It can survive in wide range of temperature.The adaptive nature makes the bacilli an excellent opportunistic pathogen.[3]

The prevalence rate of P.aeruginosa infection varies from one region to other. In a multicentric study conducted by Ling JM and Cheng AF, it was 3%-16%.[4] In India, prevalence rate of P.aeruginosa infection varies from 2.5%-30% .[5,6]

The resistance produced by Pseudomonas is complex and has varied mechanisms. P.aeruginosa is notorious as it is resistant to many structurally unrelated antimicrobial drugs, this property may be attributed to low permeability of its outer membrane, acquired resistance through gene from other organism via the plasmids, transposons, bacteriophages, and biofilm production.[7,8] Despite the advances in medical and surgical care and availability of wide range of antipseudomonal agents, treating the infections have become a challenge. Infections produced by ESBL(Extended spectrum beta lactamases), MDR (Multi drug resistance), MBL(Metallo beta lactamases).[9]

The growing threat of multidrug-resistant (MDR) Pseudomonas aeruginosa is exacerbated by the limited development of new antimicrobial agents.[10]

This study aims to assess the prevalence and resistance patterns of Pseudomonas aeruginosa strains to improve therapies and develop antibiotic policies.

METHODS

A retrospective analysis was done of the total samples received in the Department of Microbiology, Government Medical College and Hospital, Miraj.

Total 161 Pseudomonas aeruginosa strains were isolated from various clinical samples such as pus, urine, sputum, blood, swab, endotracheal aspirate, sterile body fluids (pleural, ascitic, peritoneal fluid) and Endotracheal Tip.The study period was 12 months starting from January 2024 to December 2024.

Isolation and identification of P. aeruginosa was done using standard biochemical tests and were subjected to antibiotic susceptibility testing by Kirby - Bauer disk diffusion method. The results were interpreted according to Clinical Laboratory Standards Institute (CLSI) guidelines. P. aeruginosa ATCC 27853 was used as control strain.

The antimicrobial susceptibility testing was carried out against the following antibiotic disks procured from Himedia, and tested according to the standard guidelines.(Table No.1)

Table No.1 : List of Antimicrobial agents tested

Code	Antibiotic name
TZP_ND100	Piperacillin/Tazobactam
CAZ_ND30	Ceftazidime
FEP_ND30	Cefepime
ATM_ND30	Aztreonam
IPM_ND10	Imipenem
AMK_ND30	Amikacin
TOB_ND10	Tobramycin
CIP_ND5	Ciprofloxacin
NOR_ND10	Norfloxacin
NIT_ND300	Nitrofurantoin

RESULTS

A Total of 161 P. aeruginosa strains were isolated during the study period from the various samples received to the laboratory.

Prevalence rate amongst the culture positive samples (5338) was found to be 3.01%.

Among the Total Gram Negative Organisms (1571) isolated from different samples Pseudomonas aeruginosa isolates were around 10.24%(161).

Out of the total 161 isolates, male patients accounted for 59% and female patients 41%.

The majority of the patients (44.09%) belonged to the age group 45-65 years followed by 18-45 years age group(26.08%) followed by 1-18 years age group (14.28%).

Among the male population, the majority of the isolates were from the 45-65 age group (30.43%), whereas the majority of the isolates among the female population were from the 18-45 age group (14.90%) (Table No.2)

Out of 161 isolates, the majority of isolates were from General Surgery(39.75%) followed by General Medicine (21.11%) followed by Paediatric Intensive care Unit (7.45%) (Fig. No. 1).

Out of the 161 isolates, majority of isolates were from pus samples(47.2%) followed by Urine (27.32%) followed by Sputum (9.93%) and Blood (4.96%). (Table No.3)

Table No. 2 : Age and Gender wise distribution of P.aeruginosa isolates

Age Group (yrs)	Male	Female	Total	Percentage
0-1	5	2	7	4.34
1 to 18	11	12	23	14.28
18 to 45	18	24	42	26.08
45 to 65	49	22	71	44.09
> 65	12	6	18	11.18
Total	95(59%)	66(41%)	161	100

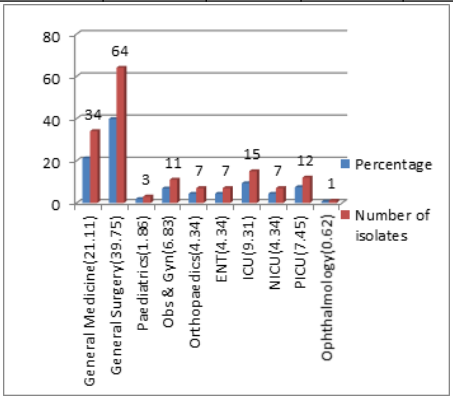

Fig. No.1 : Frequency of P. aeruginosa isolates from different Departments

ICU- Intensive Care Unit, NICU- Neonatal Intensive Care Unit, PICU- Paediatric Intensive Care Unit, ENT- Ear, Nose and Throat Department, OBS & GYN- Obstetrics & Gynaecology

Table No. 3: Distribution of P. aeruginosa isolates in different specimens

Specimen type	Number of isolates	Percentage(%)
Blood	8	4.96
Sterile Body Fluids	4	2.48
Pus	76	47.2
Swab	7	4.34
Sputum	16	9.93
Endotracheal aspirate	5	3.1
ET Tip	1	0.62
Urine	44	27.32

The Antiobiotic Susceptibility Profile Of Psedomonas Aeruginosa Isolates Is As Shown In Table No.4.

Table No. 4 : Antibiotic Susceptibility Profile of Pseudomonas aeruginosa isolates

Antibiotic name	%Susceptible	%Intermediate	%Resistance
Piperacillin/Tazobactam	69.81	5.03	25.15
Ceftazidime	52.56	1.28	46.15
Cefepime	55.7	0	44.29
Aztreonam	71.06	3.14	25.78
Imipenem	71.15	1.92	26.92
Amikacin	62.73	1.24	36.024
Tobramycin	59.31	6.89	33.79
Ciprofloxacin	42.67	15.92	41.4
Norfloxacin	46.34	0	53.65
Nitrofurantoin	28.2	0	71.79

The isolates showed maximum susceptibility to Imipenem (71.15%), followed by Aztreonam (71.06%) followed by Piperacilin-Tazobactam (69.81%) and Amikacin (62.73%).

On the other side, the isolates showed maximum resistance to to Nitrofurantoin (71.79%), followed by Norfloxacin (53.65%), and Ciprofloxacin (41.4%). (Fig. No. 2)

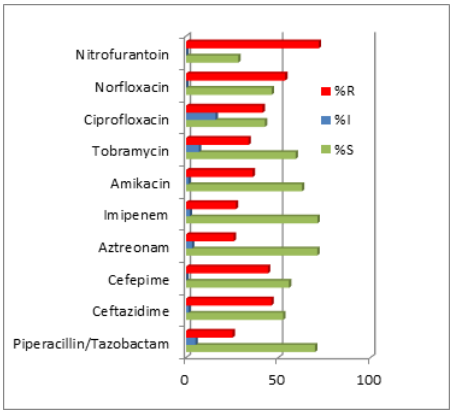

Fig. No. 2 : Antibiotic Susceptibility of P. aeruginosa isolates (S-Susceptible, I-Intermediate, R-Resistant)

Out of the Total 161 isolates, 60 isolates were found to be resistant to three or more classes of antibiotics. So, 37.26% of the isolates were found to be Multidrug resistant i.e. MDR strains. All the isolates which were resistant to Imipenem were also found to be Multi Drug Reistant strains.

DISCUSSION

A Total of 161 P. aeruginosa strains were isolated from 5338 culture positive samples so the prevalence was found to be 3.01% which is similar to the study conducted by Harshada V et al.[11] which was 3.1%. Prevalence of other studies in mentioned in table No.4..A higher prevalence rate was noted in study done by Pathi B et. al.[15](8.43%) and Raytekar N.A. et al. [16] (20.19%)which can be attributed to Infection Control Practices of the Hospital or the local population in the study

Out of the total 161 isolates, male patients accounted for 59% and female patients 41%, similar study by Nimbalkar et al reported 59.4% of isolates from male patients .[17] Other studies Khajuria et al (68%) and Pandya and Yagnesh (74%) also found a higher proportion of male isolates.[18,19] Andhale reported an even higher percentage (76%) of male isolates, exceeding the findings of this study.[20]

The majority of the patients (44.09%) belonged to the age group 45-65 years, similar findings were reported by Soni M. et al. where 49% of the isolates belonged to the same age group.[21]

Out of 161 isolates, the majority of isolates were from General Surgery accounting for 39.75% which is similar to the study conducted by Sreeshma et al. of 44% from the surgery ward.[22] This aligns with the studies of Jayanthi et al and Khajuria et al, which reported 32% of isolates from the surgery ward. [23,24] The prevalence of isolation was higher from surgical ward samples due to prolonged hospital stay after surgery resulting in colonization and infection.[25]

Out of the 161 isolates, majority of isolates were from pus samples(47.2%) followed by Urine (27.32%). Similar findings were reported from Sindhu Cugati et al with majority isolates from pus(63%) and then followed by Urine and other samples.[26] Similar findings were reported by Siguan SS et al and Massadeh HA et al.[27,28]

Our Study revealed highest susceptibility to Imipenem (71.15%), followed by Aztreonam (71.06%) followed by Piperacilin-Tazobactam (69.81%) and Amikacin(62.73%). Similar findings were reported by Sindhu Cugati et al with highest susceptibility to Imipenem(87%),Piperacillin-Tazobactam(82%) , Aztreonam(69%) and Amikacin(69%).

The resistance profile shown to Ceftazidme (46.15%), Cefepime (44.29%) and Ciprofloxacin (41.4%) was similar to the study

conducted by Reddy SG et al with Ceftazidime (53.18%), Cefepime (52.8%) and Ciprofloxacin (49.06%).[6]

The Pseudomonas aeruginosa isolates showed Maximum resistance to Norfloxacin(71.79%) and Nitrofurantoin(53.65%) which was similar to the study conducted by Belete et al which showed high resistance to Norfoxacin (66.7%) and Devi SS et al which also showed increased resistance to Nitrofurantoin (66.66%).[29,30]

The resistance shown to Imipenem and Piperacillin- Tazobactam is 26.92% and 25.15% respectively. The study conducted by Qayoom S et al also correlates with the present study findings with 24.4% resistance to Imipenem and 30% resistance to Piperacillin-Tazobactam. This shows the increasing trend of resistance patterns which may be attributed to the increasing usage of drugs for empirical management.[31]

Piperacillin tazobactam resistance among P. aeruginosa has become a threat, this may be attributed to the chromosomal β-lactamases of P.aeruginosa that show low effectiveness against tazobactam. The rate of resistance to both piperacillin and tazobactum is similar to that for piperacillin alone. [32]

Increase in use of carbapenems further increases resistance rates to carbapenems. A study by C. Plüss-Suard in 2013 confirmed a correlation between carbapenem use and carbapenem resistance rates at the hospital and regional levels.[33] Carbapenem resistance is also attributed to increased efflux pumps, MBL production, overuse and prolonged hospital stay of the patients.

Pseudomonas aeruginosa MDR strains are spreading around the globe these days. Over 10% of P. aeruginosa strains globally are multidrug resistant.[34] P. aeruginosa that is MDR can mediate a variety of methods, including altered target locations, bacterial efflux pumps, enzyme synthesis or inhibition, loss of membrane protein, etc.[35]

Currently, there is no standard definition for MDR Pseudomonas aeruginosa. Gill et al and Fatema et al defined MDR.[36,34]Pseudomonas aeruginosa as isolates that are resistant to an anti-microbial agent in three or more categories of anti-pseudomonal anti-microbials. XDR Pseudomonas aeruginosa refers to isolates that are resistant to at least one antimicrobial agent in six or more categories of anti-Pseudomonal antimicrobials. Pan-drug resistant (PDR) Pseudomonas aeruginosa refers to isolates that are resistant to all antimicrobial drugs effective against Pseudomonas aeruginosa.[37]

This investigation demonstrated the pattern of drug susceptibility and the prevalence of MDR P. aeruginosa, where 60 isolates, 37.26%, were found to be Multi Drug Resistant strains. Similar findings were reported by Bindu D et al.[38]

CONCLUSION

The development of resistance in P. aeruginosa is an increasing healthcare problem, which decreases future therapeutic choices and is also associated with high rates of mortality, morbidity and high costs. The prevalence and antimicrobial susceptibility of P. aeruginosa often varies between communities, hospitals in the same community and among different patient populations in the same hospital. Strict adherence to the Healthcare antibiotic policies like dosage and duration of antimicrobial administration has to be undertaken to prevent the emergence and spread of these resistant bacteria. Infection control procedures and surveillance programmes for MDR organisms have to be implemented. Antimicrobial susceptibility pattern of P. aeruginosa in Clinical wards and Intensive care Units has to monitored strictly and the results should be readily made available to clinicians so as to help them in making clinical judgement in therapy to reduce development of drug resistance and associated comorbities.

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Declarations

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Authors' Contribution

All the authors have made a substantial, direct and intellectual contribution to the work, and approved it for publication.

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