Research Article

Prevalence of Pseudomonas Aeruginosa and Its Antibiotic Susceptibility Pattern Isolated from Various Clinical Samples at a Tertiary Care Hospital in North India

Anjali Kumari[1]*, Dr. Nikhil Payal[2], Sandhiya[3], Dr. M. Swarnalatha (PT)[4], Prashant Kumar[5], Shristi Tiwari[6]

[1]Assistant Professor, Vivekananda Global University, Jaipur, India, ORCID: 0009-0001-1443-012X
[2]Associate Professor, Department of Microbiology, Faculty of Medicine and Health Sciences, SGT University, Gurugram, Haryana, India, ORCID: 0009-0008-6910-5624
[3]Assistant Professor, GD Goenka Healthcare Academy, Nangloi, Delhi, India, ORCID: 0009-0006-5873-8229
[4]Phd Scholar, Assistant Professor, Vivekananda Global University, Jaipur, India, ORCID: 0009-0000-4494-7173
[5]Former PG Scholar, Asian International University, Manipur, India
[6]Former PG Scholar, SGT University, Gurugram, Haryana, India
Corresponding author: Anjali Kumari; Email: anjalirgsc@gmail.com

Abstract

Introduction: Pseudomonas is an aerobic, motile, opportunistic gram negative bacterium causes healthcare associated infections (HAI) such as Ear infections, Bacterimia, UTI, Burn infections, Skin and Soft Tissue infections. Pseudomonas exhibits a strong intrinsic resistance to antimicrobial drugs and the ability to evolve into increased resistance to drugs. [3]It shows resistance to many antibiotics including aminoglycosides, fluroquinolomas and β – lactams.
Result: A total of 6673 samples were received between January 2023 to December 2023 out of which 595 were positive isolates. Pseudomonas aeruginosa were isolated from 76 samples. Antibiotics such as Amikacin and cefepime shows increasing resistivity pattern. The antibiotic resistance shown by gentamicin [21%], tobramycin [25%] and meropenem were [13.5%]. Resistance pattern shown by imipenem were [14%] and Ceftazidime were [27.6%]. Antibiotics such as Amikacin and cefepime shows increasing resistivity pattern. **Conclusion:** Present studies shows that Pseudomonas aeruginosa is a rising cause of nosocomial infections. It is unavoidable that the antibiotic susceptibility pattern of bacterial pathogens like P. aeruginosa in specialized clinical units should be regularly monitored so as to minimize the resistance to in use routine antibiotics as amikacin, cefepime is increasingly become resistant.

Keywords: Pseudomonas aeruginosa, Amikacin, healthcare associated infections, Ear infections, Bacterimia, UTI, Burn infections, Skin and Soft Tissue infections.

Introduction

Pseudomonas is an aerobic, motile, opportunistic gram – negative bacterium causes healthcare associated infections (HAI) such as Ear infections, Bacterimia, UTI, Burn infections, Skin and Soft Tissue infections.[1,2] The rate of prevalence of Pseudomonas aeruginosa infection ranges from 10-30% in India.[2]According to the report of centre for disease control and prevention of noscomical infection survilience system, Pseudomonas aeruginosa is the third most common bacterium causing noscomial urinary tract infections[3] and eighth most common cause of nosocomial bacteraemia.[4]More than 5% of infectious exacerbations in individuals with chronic obstructive pulmonary disease (COPD) are caused by P. aeruginosa.[5]P.aeruginosa has been able to live in both community and hospital settings due to its capacity to withstand a wide range of physical conditions and to survive on minimum nutritional requirements.[6]

It is the most recent gram-negative bacteria, which releases its toxins to cause tissue damage and death (27–48%) to individuals whose immune systems are weakened.[7]

Since Pseudomonas species normally inhabit soil, water, and vegetation and can be isolated from the skin, throat, and stool of healthy persons.[8] Additionally, P. aeruginosa can colonize through failure of immune system or the administration of broad-spectrum antibiotics that disrupt normal flora balance.[8]

Pseudomonas exhibits a strong intrinsic resistance to antimicrobial drugs and the ability to evolve into increased resistance to drugs as a result of synthesis of ESBL enzymes, hyperexpression of AmpC inhibition or Inaction of OprD, overexpression of efflux pumps and limited permeability of its outer membrane.[1]It shows resistance to many antibiotics including aminoglycosides, fluroquinolomas and β – lactams.[1] The treatment landscape is further complicated by acquired resistance from mutation and horizontal gene transfer as well as adaptive resistance exhibited by the development of biofilms and persister cell appearance.[9]Also multidrug resistant pseudo is linked with increased mortality as there is no adequate treatment option exists. Hence there is a requirement to conduct monitoring studies for pseudomonas spp for its resistance pattern.[10] The

objective of the present studies was to determine the pattern of antibiotic susceptibility and drug resistance in Pseudomonas spp that were isolated from various clinical samples at a tertiary care hospital in Haryana.[12]

Materials And Methods

This is the retrospective study. The clinical isolates of Pseudomonas species that were isolated from different wards such as OPD, IPD, ICU from Jan 2023 to Dec 2023 are taken to study. Demographic details including gender, age, ward, of patients recorded from laboratory maintained computerized database. The isolates were collected from different clinical samples like blood, pus, tracheal aspirate, urine and sputum. Seventysix non – duplicate P. aeruginosa were recovered from various departments of SGT Hospital. The clinical samples were inoculated by streak plate method on blood agar and macconkey agar. Blood was inoculated on Bac t alert and the positive cultures were plated on blood agar and macconkey agar. The isolated colonies were identified based on morphology of the colony, gram staining, oxidase test and biochemical test like TSI, Agar, Indole, Citrate, Urease, Mannitol motility agar. Antibiotic susceptibility test was done by disc diffusion method on Muller – Hinton agar medium (MHA) a\c latest CLSI guidelines. Antibiotics such as Amikacin, Gentamicin, Tobramicin, Ciprofloxacin, Levofloxacin, Ceftazidime, Cefepime, Aztreonam, Piperacilin + Tazobactum, Ertapenem, Meropenem, Netilmicin Sulphate, Doripenem were placed. Plates were examined after 24 hours of incubation at 37°C.

Result

A total of 6673 samples were received in microbiology laboratory of SGT hospital out of which 595 were the positive isolates. 76 Pseudomonas aeruginosa were isolated from 595 different samples which is 12.9%.[9] Clinical samples were received from all wards including OPD[55.2%], ICU[5.2%], General surgery[10.5%], General medicine[15.7%], Post operative[3.9%], BICU[1.3%], Dermatology[1.3%], Dormitory[1.3%], pediatrics[1.3%], Pulmonary medicine[1.3%], RICU[1.3%], SICU[1.3%]. The maximum number of samples were obtained from OPD.

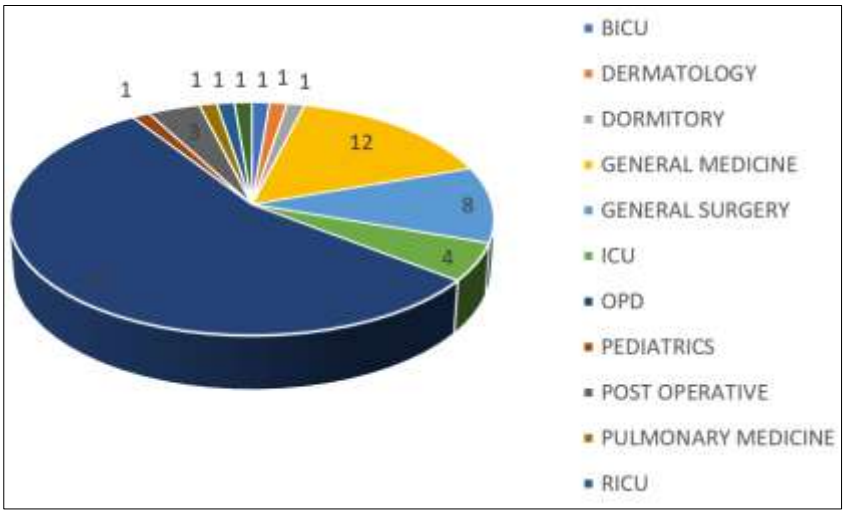
Table No 1: Distribution of bacterial species isolated from various wards

WARD	Number of isolates	Percentages (%)
IPD	293	49.24%
OPD	200	33.61%
ICU	35	5.88%
RICU	18	3.03%
SICU	17	2.86%
ICCU	12	2.02%
NICU	8	1.34%
HDU	5	0.84%
BICU	4	0.67%
PICU	3	0.50%
Total	**595**	**100%**

Table No 2: Distribution of Pseudomonas aeruginosa isolated from various wards

WARD	Number of isolates of Pseudomonas aeruginosa	Percentages (%)
OPD	42	55.2%
ICU	4	5.2%
RICU	1	1.3%
SICU	1	1.3%
Dermatology	1	1.3%
Dormitory	1	1.3%
BICU	1	1.3%
General medicine	12	15.7%
General surgery	8	10.5%
Pediatrics	1	1.3%
Post operative	3	3.9%
Pulmonary medicine	1	1.3%
Total	**76**	**100%**

Figure 1: Pie chart showing distribution of Pseudomonas aeruginosa isolated from various wards



From all wards of SGT University, Budhera, Gurugram; 595 were the positive isolates for any bacteria including Urine (233), Pus (200), Blood (91), Sputum (19),Endotracheal (18), BAL (7), Stool (7), Tracheal aspirates (7), Vaginal swabs (6), Tissue (5), Catheter (3), CSF (3) Ear (2), Plueral fluid (2), Drain (1) and Eyes (1).

Table No 3: Distribution of Pseudomonas aeruginosa isolated from various speciemen

Type of specimen	Total no. Of specimens
Urine	233
Pus	200
Blood	91
Sputum	19
E.T.	18
Bal	7
Stool	7
Tracheal aspirates	7
Vagina	6
Tissue	5
Catheter	3
CSF	3
Ear	2
Plueral fluid	2
Drain	1
Eyes	1
Total	**595**

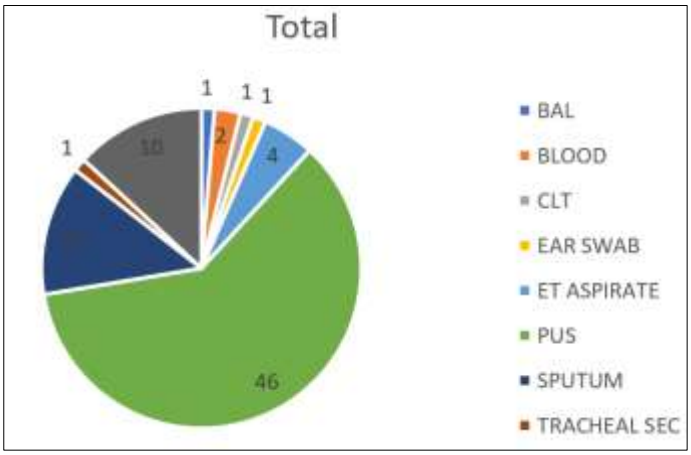
Out of 595,76 isolates were identified as Psuedomonas aeruginosa in different clinical samples like pus[60.5%], BAL[1.21%], Blood[2.63%], clt[1.31%], Ear swab [1.31%], ET aspirate[5.26%], Sputum[13.5%], Tracheal secretion[1.31%], Urine[13.5%]

Table No 4: Distribution of no. of positive isolates for Psuedomonas aeruginosa

Speciemen type	No. Of positive isolates for Psuedomonas aeruginosa	Percentage (%)
Pus	46	60.5%
Blood	2	2.6%
Tracheal secretion	1	1.3%
BAL	1	1.3%
ET aspirate	1	1.3%
Clt	1	1.3%

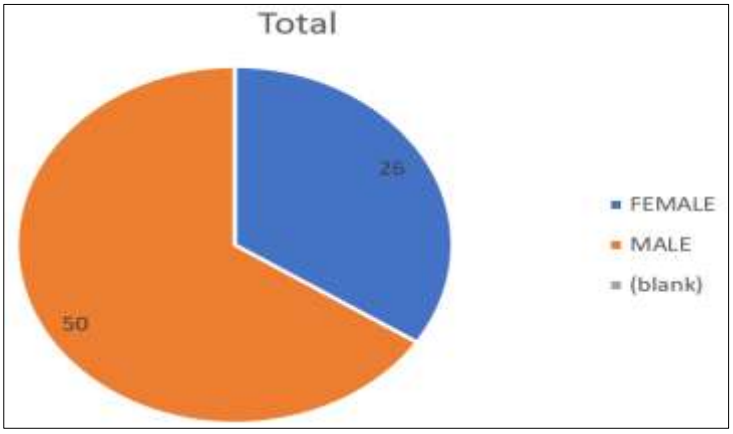
Ear Swab	1	1.3%
Urine	10	13.5%
Sputum	10	13.5%

Figure 2: Pie chart showing no. of positive isolates for Pseudomonas aeruginosa



Out of all 76 isolates of Pseudomonas aeruginosa 50 were males and 26 were females.

Figure 3: Pie chart showing gender wise distribution of Pseudomonas aeruginosa isolated from different samples



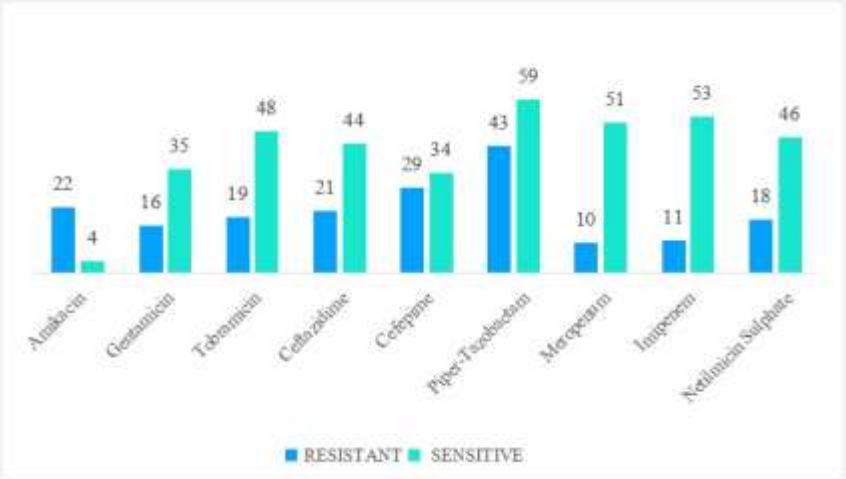
Antibiotic susceptibility pattern

Antibiotic susceptibility test was done by disc diffusion method on Muller – Hinton agar medium (MHA) a\c latest CLSI guidelines. The antibiotic resistance shown by gentamicin [21%], tobramycin [25%] and meropenem were [13.5%]. Resistance pattern shown by imipenem were [14%] and Ceftazidime were [27.6%].

Table No: 5 Antibiotic resistance profile of Pseudomonas aeruginosa isolated from different samples

Antibiotic	Sensitivity no.	Sensitivity %	Resistance No.	Resistivity %
Amikacin	54	71%	22	28.9%
Gentamicin	60	85%	16	21%
Tobramicin	57	74%	19	25%
Ceftazidime	55	72%	21	27%
Cefepime	47	61.8%	29	38%
Piperacillin/tazobactam	63	83%	13	17%
Meropenam	66	87%	10	13%
Imepenam	65	85.5%	11	14%
Netilmicin sulphate	58	76.3%	18	23.6%

Figure 4: Graph showing antibiotic resistance profile of Pseudomonas aeruginosa isolated from different samples



Discussion

P. aeruginosa is considered as a major cause of gram negative bacterial infections mainly in immunocompromised patients who require long duration of hospitalization.[1]

Virulence factors of Pseudomonas aeruginosa play a crucial role in lung infections. P. aeruginosa's quorum-sensing systems, as well as controlled virulence factors including rhamnolipids and elastase, have been found to play essential roles.[14]

Patients may develop severe and potentially fatal infections from P. aeruginosa, especially in light of the worldwide increase in antibiotic resistance. Effective control measures are required for managing the considerable public health threat caused by devloping resistance to Pseudomonas aeruginosa.[6]The main objectives of the research were to examine the epidemiological information of Pseudomonas species isolated from various clinical samples and to examine the patterns of antimicrobial resistance to commonly used antibiotics. Resistance to antimicrobial agents is an increasing public health threat.[7]Now a days, P. aeruginosa is becoming more and more resistant to beta-lactam antibiotics, especially to third and fourth generation cephalosporins. There are multiple molecular mechanisms by which resistance to these antibiotics can develop, including the production of extended-spectrum betalactamases (ESBL), integration of bla genes into integrons, inhibition of porin gene expression, and modification of antibiotic target sites.[8]

Most of the patients infected by Pseudomonas spp are male[65%]when compared to the females[35%], which is in close concordance with the study of Shampa Anupurba et al. , (208 males; 68.3%).[9]

In this study, the prevalence of P. aeruginosa was 12.9% which is similar to the study of Rehman et.al [12.9%].[10] The number of P. aeruginosa predominantly found in pus[60.5%][2,15]than other specimens followed by urine [13.5%][2] which is similar to the study of D.Bindu[2] and sputum [13.5%] which is in accordance with the study done by Chitralekha Saikumar[9] followed by sample from central line tip [1.3%] which is similar to the study of Viren et.al [16].In context with resistance to antibiotics, amikacin is 28.9%[9] and cefepime is [38%] resistance to pseudomonas aeruginosa which is close to the result of study conducted by Regha et al[3].

The antibiotic resistance shown by gentamicin [21%] similar to the study of sara et.al[5] and tobramycin[25%] which is related to the study of khilasa et.al[12], meropenem[13.5%] followed by imipenem [14%], ceftazidime[27%] close to the result shown by D.Bindu[2].

Resistance pattern shown by piperacillin+ tazobactum is 17% towards P. aeruginosa is similar to the result shown by Jaswinder et.al. However, our study had some limitations. First, relying on retrospective data from medical records definitely have the possibility of missing or insufficient data mainly in the aspect of sensitivity pattern of the colonised pathogens. Second, the study was conducted at a single tertiary care hospital in gurgaon, which may have limited the findings' applicability to other settings or populations.

The period was limited to one years, with no long-term patient monitoring. As a result, the study lacked the ability to assess the outcomes and long-term consequences of Pseudomonas infections.[5]

Conclusion

P. aeruginosa is one of the most commonly found pathogen from the specimens.[18] Present studies shows that Pseudomonas aeruginosa is a rising cause of nosocomial infections. It is unavoidable that the antibiotic susceptibility pattern of bacterial pathogens like P. aeruginosa in specialized clinical units should be regularly monitored so as to minimize the resistance to in use routine antibiotics as amikacin, cefepime is increasingly become resistant. The availability and affinity of a B-lactam antibiotic for the target enzyme or enzymes responsible for cell wall production determine its effectiveness against P. aeruginosa.[19]

Proper infection control measures and timely identification of resistant pathogen can help in reducing the spread of multidrug resistant strain.So In addition, regular antimicrobial susceptibility surveillance is essential for monitoring of the antibiogram patterns for better patient management.[20]

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