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Original Research

Prevalence of P. aeruginosa and antibiotic sensitivity from respiratory samples

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ABSTRACT:

Background: Because of the bacteria's ability to quickly acquire antibiotic resistance, particularly when patients are receiving antibiotic treatment, Pseudomonas aeruginosa respiratory infections are generating significant rates of morbidity and mortality. The present study was conducted to assess prevalence of P. aeruginosa and antibiotic sensitivity from respiratory samples. **Materials & Methods:** 94 respiratory samples of both genders were selected. After processing each sample, isolates were examined for colony shape, microscopic analysis, and pertinent biochemical testing. As Pseudomonas species were tested, isolates were identified by gram staining, motility, oxidase testing, colony morphology for size, shape, and pigmentation on various culture media, color of colonies on MacConkey agar, and failure to ferment glucose. The indole test was used to identify Pseudomonas aeruginosa. Using the disk diffusion method, antimicrobial susceptibility testing was conducted. **Results:** Out of 94 patients, 54 were males and 40 were females. Out of 94 respiratory samples, 23 (24.4%) had P. aeruginosa. Antibiotic sensitivity pattern of Pseudomonas isolates was seen 58% to Ceftriaxone, 64% to Ceftazidime, 71% to Ciprofloxacin, 87% to Ofloxacin, 85% to Amikacin, 82% to Meropenem and 65% to Imipenem. The difference was significant (P< 0.05). **Conclusion:** Pseudomonas aeruginosa was found in respiratory samples at significant concentrations. Pseudomonas aeruginosa's growing resistance necessitates ongoing monitoring of trends in antibiotic resistance and the use of the right medications.

Keywords: Ciprofloxacin, Pseudomonas aeruginosa, respiratory

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INTRODUCTION

Because of the bacteria's ability to quickly acquire antibiotic resistance, particularly when patients are receiving antibiotic treatment, Pseudomonas aeruginosa respiratory infections are generating significant rates of morbidity and mortality.[1] Numerous possible virulence factors that are tightly regulated by cell-to-cell communication systems may be present in the organism.[2] Pseudomonas aeruginosa develops resistance to nearly all antibiotics by a variety of processes, including mutations in several chromosomal genes, biofilm development, resistance genes, multi-drug resistance efflux pumps, and enzymes that alter aminoglycosides. Additionally, patient-to-patient transmission and exposure to wide spectrum antibiotics have contributed to the sharp rise in the isolation of resistant strains.[3] Life-threatening infections brought on by Pseudomonas aeruginosa are still regarded as one of the main health issues, even with the diversity of antipseudomonal medications and medical advancements.[4]

Multidrug-resistant (MDR) P. aeruginosa infections are challenging to treat and can have a high fatality rate, particularly in patients with weakened immune systems or chronic lung conditions.[5] Plasmid-mediated AmpC βlactamase, various extended-spectrum βlactamases (ESBLs), and metallo-β-lactamases (MBLs) are the main ways that P. aeruginosa develops resistance. Exotoxin A (toxA), the most lethal virulence factor found in P. aeruginosa, is one of several possible virulence factors released by this bacterium that are crucial to its pathogenicity.[6] The present study was conducted to assess prevalence of P. aeruginosa and antibiotic sensitivity from respiratory samples.

MATERIALS &METHODS

The present study consisted of 94respiratory samples of both genders. Patients were well informed regarding the study and a valid written consent was obtained.

Data such as name, age, gender etc. was recorded. After processing each sample, isolates were examined for colony shape, microscopic analysis, and pertinent biochemical testing. As Pseudomonas species were tested, isolates were identified by gram staining, motility, oxidase testing, colony morphology for size, shape, and pigmentation on various culture media, color of colonies on MacConkey agar, and failure to ferment glucose. The indole test was used to identify Pseudomonas aeruginosa. Using the disk diffusion method, antimicrobial susceptibility testing was conducted.The results were compiled and subjected for statistical analysis. P value less than 0.05 was considered significant.

RESULTS

Table I Distribution of patients

Total- 94		
Gender	**Male**	**Female**
Number	54	40

Table I shows that out of 94 patients, 54 were males and 40 were females.

Table II Prevalence of P. aeruginosa

Total	Prevalence	Percentage
94	23	24.4%

Table II shows that out of 94 respiratory samples, 23 (24.4%) had P. aeruginosa.

Table III Antibiotic sensitivity pattern of Pseudomonas isolates

Antimicrobial agents	Percentage	P value
Ceftriaxone	58%	0.05
Ceftazidime	64%	
Ciprofloxacin	71%	
Ofloxacin	87%	
Amikacin	85%	
Meropenem	82%	
Imipenem	65%	

Table III, graph I shows that antibiotic sensitivity pattern of Pseudomonas isolates was seen 58% to Ceftriaxone, 64% to Ceftazidime, 71% to Ciprofloxacin, 87% to Ofloxacin, 85% to Amikacin, 82% to Meropenem and 65% to Imipenem. The difference was significant (P< 0.05).

DISCUSSION

Pseudomonas aeruginosa is the fifth most prevalent pathogen among the microorganisms that are prevalent in hospital settings and is responsible for around 10% of all hospital-acquired illnesses. In hospitalized and immunocompromised individuals, this bacterium is often identified as an opportunistic pathogen in recurrent infections.[7] Because of its adaptability to a wide range of environmental conditions and low nutritional needs, it is a pathogen that can survive on a wide range of living and non-living surfaces.[8]The present study was conducted to assess prevalence of P. aeruginosa and antibiotic sensitivity from respiratory samples.

We found thatout of 94 patients, 54 were males and 40 were females. Out of 94 respiratory samples, 23 (24.4%) had P. aeruginosa. Of the 3530 pus samples that were sent to Tam et al.[9], 775 (22%) had positive bacteriological culture results. Of the 71 (9.16%) isolates that were found to be Pseudomonas aeruginosa among the positive cultures, 29 (40.84%) were cultured from pus samples obtained from the outpatient department and 42 (59.16%) from the inpatient department. Of the patients, 24 (33.80%) were female and 47 (66.19%) were male. About 42.25% of the patients were under 25, while 7.05% were over 45. The majority of the patients (50.70%) were between the ages of 25 and 45.Only wound swabs were used to isolate 37 Pseudomonas aeruginosa isolates (52.11%), of which 16.21% came from outpatient departments, including surgical outpatient departments, and the remaining 35.90% were cultured from inpatient department wound swabs. About 20% of the IPD samples were from casualty wards, 8% from medical wards, and the remaining 9% came from other units (burn unit, etc.). 18 aural swabs (25.35%), 8 tracheal aspirates (11.26%), 5 sputum samples (7.04%), and 3 other samples (4.22%), such as pleural fluid and bed sores, were also included. Every ear swab was taken at an outpatient clinic.

We found that antibiotic sensitivity pattern of Pseudomonas isolates was seen 58% to Ceftriaxone, 64% to Ceftazidime, 71% to Ciprofloxacin, 87% to Ofloxacin, 85% to Amikacin, 82% to Meropenem and 65% to Imipenem. Obritsch MD et al[10]evaluated antimicrobial resistance among P. aeruginosa isolates from intensive care unit patients in the United States from 1993 to 2002 by using the Intensive Care Unit Surveillance Study database. Over the 10-year period, susceptibility of 13,999 nonduplicate isolates of P. aeruginosa was analyzed. From 1993 to 2002, nationwide increases in antimicrobial resistance were greatest for ciprofloxacin, imipenem, tobramycin, and aztreonam. Rates of multidrug resistance (resistance to > or =3 of the following drugs: ceftazidime, ciprofloxacin, tobramycin, and imipenem) increased from 4% in 1993 to 14% in 2002. The lowest dual resistance rates were observed between aminoglycosides or fluoroquinolones with piperacillin-tazobactam while the highest were for those that included beta-lactams and ciprofloxacin.

Rubin et al[11]in their study a wide range of susceptibility patterns were noted with some isolates being resistant to between 8 and 28 (mean 16) of the antimicrobials tested. Among the beta-lactams, all isolates were resistant to ampicillin, cefoxitin, cefpodoxime, cephalothin and cefazolin followed by amoxicillin/clavulanic acid (99%), ceftiofur (97%), ceftriaxone (39%), cefotaxime (26%), and cefotaxime/clavulanic acid (20%), whereas less than 7% of isolates were resistant to ceftazidime/clavulanic

acid, ceftazidime, piperacillin/tazobactam or cefepime. Two isolates were resistant to the carbapenems. Among the quinolones and fluoroquinolones, the most isolates were resistant to naladixic acid (96%), followed by orbifloxacin (52%), difloxacin (43%), enrofloxacin (31%), marbofloxacin (27%), gatifloxacin (23%), levofloxacin (21%), and ciprofloxacin (16%). Among the aminoglycosides, the most resistance was seen to kanamycin (90%), followed by streptomycin (69%), gentamicin (7%), and amikacin (3%). Of the remaining antimicrobials 100% of the isolates were resistant to chloramphenicol followed by tetracycline (98%), trimethoprim/sulfamethoxazole (57%), and sulfisoxazole (51%). Point mutations were present in gyrA, gyrB, parC, and/or parE genes among 34 of the 102 naladixicacid-resistant isolates. Two isolates contained class 1 integrons carrying aadA gene conferring streptomycin and spectinomycin resistance.

CONCLUSION

Pseudomonas aeruginosa was found in respiratory samples at significant concentrations. Pseudomonas aeruginosa's growing resistance necessitates ongoing monitoring of trends in antibiotic resistance and the use of the right medications.

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