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Prevalence and Antimicrobial Resistance Patterns of *Pseudomonas aeruginosa* Isolated from Sputum samples of Patients with Lower Respiratory Tract Infections in Amassoma, Nigeria

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ABSTRACT

Background: *Pseudomonas aeruginosa* are Gram -negative bacteria capable of causing a wide range of infections. They often exhibit high levels of resistance to multiple antibiotics, which can lead to significant morbidity and mortality, particularly in immune-compromised individuals.
Methods: Three hundred and seventy- eight (378) sputum samples were obtained from patients with Lower respiratory tract infection. The samples were inoculated onto blood agar and MacConkey agar plates and incubated at 37°C for 24 hours. The isolates obtained were identified based on colony morphology, Gram staining and standard biochemical tests. Pure isolates were subsequently sub cultured on Cetrimide agar for confirmatory identification. Antimicrobial susceptibility testing was carried out on Mueller-Hinton agar using Kirby-Bauer disc diffusion method.
Results: Out of the 378 sputum samples examined, 53 *Pseudomonas aeruginosa* isolates were recovered. Of these, 29(54.7%) were obtained from females while 24(45.2%) were obtained from males. The highest frequency of isolation was observed in the 45-54 age group with 18(33.9%) isolates, followed by the 35-44 years age group which accounted for 15(28.3%).Antimicrobial susceptibility testing showed that the isolates exhibited resistance to tetracycline (94.3%), Co-trimoxazole (90.4%), Ceftriaxone (79.2%), nitrofurantoin (73.5%) and amoxicillin/ clavulanic acid (64.1%).
Conclusion: This research has demonstrated the presence of *Pseudomonas aeruginosa* among analyzed sputum samples of patients attending medical facilities, with antibiotic resistance. The research emphasized the need for continuous monitoring of antimicrobial resistance pattern and the judicious antibiotics use.

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INTRODUCTION

Pseudomonas aeruginosa is a Gram-negative bacterium that can be found alone, in pairs, or sometimes in short chains. As an opportunistic nosocomial pathogen, *Pseudomonas aeruginosa*, causes a variety of infections and significantly impairs the immune system of patients. *Pseudomonas aeruginosa*, regrettably, exhibits resistance to several antibiotics, endangering the choice of the best course of action (Arora *et al*., 2011).

Increasing numbers of *Pseudomonas aeruginosa* isolates are being recovered from the respiratory tract (Gellatly *et al*., 2013). Although, the organism may colonize the respiratory system without necessarily causing disease, its presence can still pose a potential risk. This is largely due to its high level of resistance to many antibiotics; and even the drugs that remain effective may be associated with adverse effects, making treatment more challenging (Lee, *et al*., 2015). In chronic, progressive infectious and inflammatory pulmonary condition, such as severe pneumonia in individuals with weakened immune systems, the lung is a primary site for bacterial colonization and infection (Gibson *et al*., 2003; Sadikot *et al*., 2005). Isolation of *P. aeruginosa* from sputum holds important clinical significance, especially in patients with chronic respiratory diseases or compromised immune systems. Its detection often reflects both colonization and active infection, which can adversely affect lung function, increased morbidity and mortality, and reduce overall quality of life. (WHO, 2017).

A poor host defense system and antibiotic-resistant bacteria are the two main causes of the high mortality rate linked to these diseases. Since there are few antimicrobial medicines that have consistent efficacy against this infamous bacterium, resistance to widely used antimicrobial drugs is becoming a recognized public health concern and a growing clinical issue. *Pseudomonas aeruginosa* is naturally resistant to a variety of antimicrobial treatments (Thornton *et al*., 2004).

Multidrug-resistant (MDR) *Pseudomonas aeruginosa* has emerged as a significant issue. The production of chromosomally encoded beta-lactamases, aminoglycoside-modifying enzymes via horizontal gene transfer, and chromosomal gene mutations (target site, efflux mutations), which are the target of fluoroquinolones, especially ciprofloxacin, are some of the mechanisms that may contribute to *Pseudomonas aeruginosa*'s microbial resistance (Liverrmore, 2000; Arora *et al*., 2011).

This study aimed to determine the prevalence and antibiotic resistance pattern of *Pseudomonas aeruginosa* among lower respiratory tract infection patients in Amassoma, Nigeria.

MATERIALS AND METHOD

Study Area/ Population

A cross- sectional research was carried out on patients age groups 15-54 who were clinically diagnosed with lower respiratory tract infection, with symptoms of chest pain, cough, fever and other associated symptoms from selected hospitals in Amassoma, Bayelsa State (General Hospital Amassoma, Tantua Hospital Amassoma and Health Clinic situated at the Niger Delta University Campus, Amassoma). About 5% of those who participated in the research have used antibiotics prior to attending the medical facilities where samples were obtained. Ethical approval was obtained and consent forms were signed by participants prior to sample collection. Samples were obtained within a period of one (1) year, from October, 2024-October 2025 and the research was completed in January 2026. Participants were selected using random Sampling.

Sample Size

The determination of sample size was done using Yamane's formula as modified and described by Adzani *et al*. (2021).

$$N = \frac{N}{K+N\,(e)^2}$$

Where: N=Population of Study
K=Constant (1)
E=degree of error expected
N=Sample size

With a population of 6,970 according to the 2016 census and a 5% error margin, the sample size calculated was 378 participants.

Sample Collection/Identification

A total of 378 sputum samples were obtained from patients who were clinically diagnosed with Lower respiratory tract infection. Early morning sputum was used for the research. Patients were asked to cough deeply into sterile containers. With the aid of sterile swab, sputum samples were inoculated onto blood and Mac-Conkey agar, incubated at 37°C for 24 hours. Identification was made with Basic Microbiological methods which includes colony morphology, Gram staining, oxidase, Indole, catalase and coagulase tests .Pure isolates were sub cultured on Cetrimide agar for production of blue green pigment pyocyanin which served as confirmatory test.

Gram staining

Gram staining was performed following protocol by Cheesbrough (2006) .Addition of crystal violet to a

prepared smear on a slide for 60 second was done and the stain was rinsed with water. Iodine was added for 60 seconds and rinsed with water. Alcohol which serves as the decolorizer was added. It was rinsed with water for 5 minutes. The next stage was the addition of neutral red stain for 2 minutes. It was rinsed water and allowed to dry. The smear was viewed under the microscope using 40x and 100 x magnification**.**

Oxidase test

A piece of filter paper was soaked in kovac's reagent and allowed to dry. A colony of 16-24 culture was picked with an inoculating loop and rubbed on the filter paper and color change was observed.

Indole Test

Small quantity of microbial culture was introduced into tryptone broth in a test tube and incubated for 24-48 hours at 35^0C. Five (5) drops of Kovac's reagent was added to the tube and observation was made.

Catalase Test

With an inoculating loop, small amount of an 18-24 hour test organism was placed on a microscopic glass slide. A drop of 3% hydrogen peroxide was added to the slide. Observation of bubble as positive result was done.

Coagulase Test

Zero point five (0.5) ml of plasma was transferred to test tube. Two colonies of the isolates were emulsified in the plasma and incubated. Agglutination was checked for at intervals within the next 4 hours for positive result.

Antibiotic susceptibility test

Antimicrobial susceptibility testing was performed according to the guidelines of the clinical and Laboratory standard institute (CLSI, 2021). The inoculum for antimicrobial susceptibility testing was prepared by selecting 3-5 well isolated colonies of each pure bacterial isolate from an overnight culture. The colonies were aseptically transferred into a sterile tube containing 5ml of 0.9% normal saline and mixed to form a homogenous suspension. The turbidity was adjusted to match that of a 0.5 McFarland standard, corresponding to approximately 1×10^8 CFU/ml, to ensure a consistent inoculum. Sterile swabs were then used to evenly inoculate Mueller- Hinton agar plates, which were allowed to dry before placing antibiotic discs (tetracycline, co-trimoxazole, ceftriaxone, nitrofurantoin, amoxicillin/clavulinic acid, tazobactam/piperacillin, clindamycin, ciprofloxacin, gentamicin, levofloxacin, and ofloxacin). The quality control strain *Pseudomonas aeruginosa* ATCC 27853 was used to validate the antimicrobial sensitivity test. All plates were then incubated for 24 hours at 37 °C. Inhibitory zones were measured in millimeters (mm).

Statistical Analysis

Statistical analysis was performed with SPSS 21. Data was analyzed using descriptive analysis. The chi square test was used to assess the association between sexes.

RESULTS

A total of fifty-three (53) isolates were obtained from the three hundred and seventy eight (378) sputum samples examined. Chi square analysis showed no significant association between the sexes and the occurrence of isolates. Females accounted for 29(54.7%) isolates while males had 24(45.2%). The difference was not statistically significant ($X^2 = 0.47$, df = 1, $p \geq 0.05$). Age group 45-54 had the highest isolation of *Pseudomonas aeruginosa* with a total of 18(33.96%), followed by age group 35-44, 15(28.30%) as shown in Figure 1.

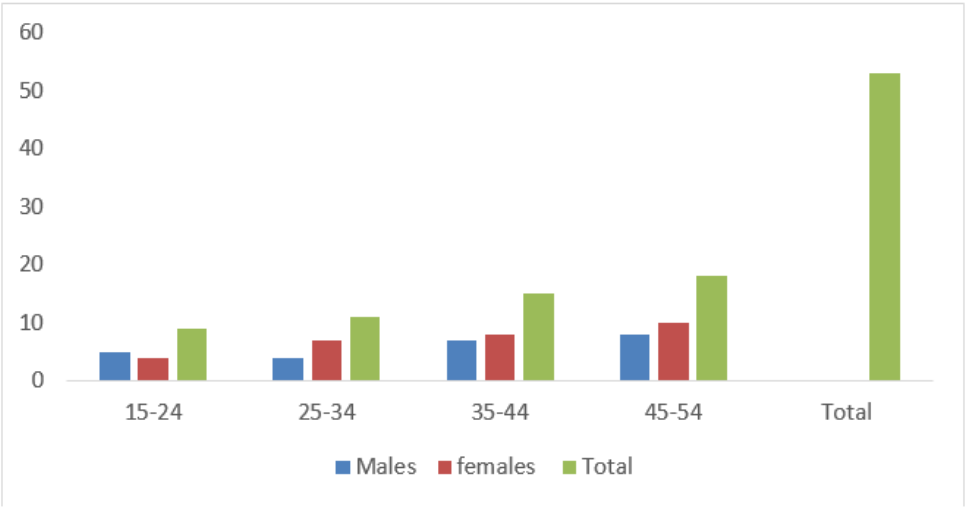

Figure 1: Distribution of *Pseudomonas aeruginosa* isolates by Age and Sex

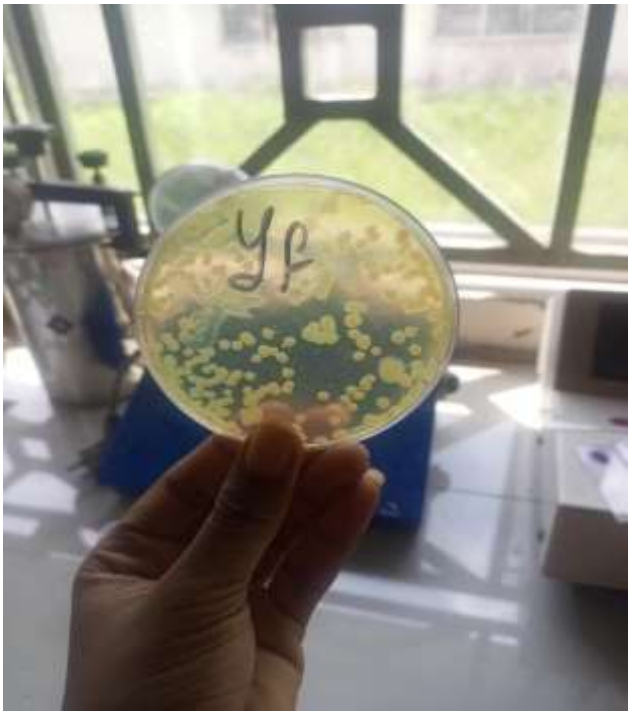

Plate 1: Colonies of *Pseudomonas aeruginosa* on Cetrimide agar

Plate 2: Colonies of *Pseudomonas aeruginosa* on Cetrimide agar

The susceptibility test results of *P. aeruginosa* in this study revealed resistance of the isolates to tetracycline (94.3%), Co-trimoxazole (90.4%), Ceftriaxone (79.2%), nitrofurantoin (73.5%) and amoxicillin/ clavulanic acid (64.1%); moderate resistance to tazobactam/ piperacillin (54.7%) and clindamycin (56.6%). However, there was high susceptibility to ciprofloxacin (100%), gentamicin (94.3%), levofloxacin (90.4%) and ofloxacin (84.9%) as shown in table 1.

Table 1: Antibiotic resistance pattern of *Pseudomonas aeruginosa* isolates

S/N	Antimicrobial Agent	Number Resistance (%)	Number Susceptible (%)
1	Co-trimoxazole	48(90.4)	5 (9.4)
2	Ofloxacin	8(15.0)	45(84.9)
3	Tetracycline	50(94.3)	3(5.6)
4	Amoxicilin/Clavunic acid	34(64.1)	19(35.8)
5	Gentamicin	3(5.6)	50(94.3)
6	Levofloxacin	5(9.4)	48(90.4)
7	Ceftriaxone	42(79.2)	11(20.7)
8	Nitrofurantoin	39(73.5)	14(26.4)
9	Clindamycin	30(56.6)	23(43.3)
10	Ciprofloxacin	0(0.0)	53(100.0)
11	Tazobactam/piperacillin	29(54.7)	24(45.2)

DISCUSSION

The present study revealed a total of fifty-three (53) *Pseudomonas aeruginosa* isolation from clinical sputum. Isolation was higher in females (54.7%) than males (45.2%). This does not agree with research by Saroj *et al*. (2016), Ali *et al*. (2018) and Ahmed *et al*. (2012) where males had the highest occurrence. Increased exposure to healthcare may be the cause of the higher percentage among women. Compared to men, women appear to seek medical attention more frequently and earlier (Thompson *et al*., 2016).

The highest number of isolates occurred in the 45–54 age group, which is in agreement with studies conducted by Saroj *et al*. (2016), Ali *et al*. (2018) and AL-Magrami *et al*. 2018 where age group ≥41, ≥ 60 and ≥ 50 respectively had the highest isolate. Reduced immunity, extended hospital stays, and other related comorbidities in these age groups may be the cause (Saroj *et al*., 2016).

The present study showed high resistance to tetracycline (94.3%), co-trimoxazole (90.4%), ceftriaxone (79.2%), nitrofurantoin (73.5%) and amoxicillin/ clavulinic acid (64.1%); moderate resistance to tazobactam/ piperacillin (54.7%) and clindamycin (56.6%). This is in agreement with Alyahawi *et al*. (2018) where there was 96.2 resistance to amoxicillin/ clavulinic acid, ceftriaxone 78%, nitrofurantoin 88%, cotrimoxzole 80.5%. However their research showed 77.2% susceptibility to piperacillin/tazobactam .Research by

AL-Magrami *et al* (2018) showed 100% resistance to ceftriaxone and ciprofloxacin. The study conducted by Abdulrasheed *et al.*(2020) on the antimicrobial susceptibility patterns and bacterial isolates in septicemia patients attending FMC Yenagoa reported that *Pseudomonas* isolates exhibited 100% resistance to tetracycline, ceftriaxone and amoxicillin-clavulanic acid.

The production of beta-lactamases, such as AmpC cephalosporinase or extended-spectrum beta-lactamases (ESBLs), which break down the beta-lactam rings and make the medication ineffective, is suggested by resistance to the beta-lactam antibiotics (amoxicillin/clavulinic acid, ceftriaxone) (Bush and Bradford, 2020).

The pressure on bacterial selection brought on by improper drug use and questionable quality sold may account for the concerning rates of bacterial resistance (Ndoutamia *et al*., 2017). *P. aeruginosa* has inherent resistance to beta-lactam antibiotics due to its low outer membrane permeability, efflux pumps, other genetic characteristics, and capacity to build biofilms (Karl and Lain, 2021).

Tetracycline resistance is likely caused by ribosomal protection proteins that prevent tetracycline binding or efflux pump-mediated drug ejection (Grossman, 2016). The isolates' resistance to clindamycin may indicate the presence of an active efflux mechanism or a change in the target ribosome. Because of its limited permeability and efflux pump function, *Pseudomonas aeruginosa* is inherently resistant to clindamycin (Nikaido, 2009). The observed resistance to nitrofurantoin is consistent with intrinsic resistance in *Pseudomonas aeruginosa* (Cunha *et al*., 2011).

An interesting part of the study is the fact that high susceptibility was observed in Ciprofloxacin (100%), gentamicin (94.3%), levofloxacin (90.4%) and ofloxacin (84.9%).These drugs proved to be the most effective in the current study. However, previous research by AL-Magrami *et al*. (2018) showed 100% resistance to ciprofloxacin, 85.7% to levofloxacin and 35.7% to gentamicin. On the other hand, Ali *et al*. (2018), had a susceptibility rate of 71.5%% to ciprofloxacin, 66% to Levofloxacin, and 56% to Gentamicin. Strong broad-spectrum antibiotics, fluoroquinolones mostly target Gram-negative bacteria but can also target some Gram-positive ones. One of their advantages is that they work well against bacteria that are resistant to many drugs (Cunha, 1994). All isolates' gentamicin sensitivity attests to the continued effectiveness of aminoglycosides against *Pseudomonas aeruginosa* (Ramirez and Tolmasky, 2017).

CONCLUSION

This research confirmed the occurrence of *Pseudomonas aeruginosa* in 378 sputum samples examined, with fifty-three (53) isolates recovered. A slightly higher prevalence was observed among females compared to males. The highest occurrence of isolates was recorded in individuals within the 45-54 age group. The antimicrobial susceptibility pattern showed resistance of *Pseudomonas aeruginosa* to commonly used antibiotics. This shows the challenge posed by *Pseudomonas aeruginosa* in lower respiratory infections .Thus, routine susceptibility testing and appropriate infections control measures are essential to ensure effective management and control of infections caused by *Pseudomonas aeruginosa*.

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Conflict of interest

The author declare no conflict of interest

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