

Antibiotic Resistance Pattern to *Pseudomonas Aeruginosa* Isolated from Different Sample

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Abstract

Aim: The *P. aeruginosa* has become an important and frequent opportunistic nosocomial pathogen. Antimicrobial managers are often classified according to their principal mechanism of action. This study analysis the infections caused by *Ps. aeruginosa* and try to reveal the antimicrobial agents susceptibility against *Ps. aeruginosa*.

Material and Method: A cross-sectional study was carried out in different specimens (urine, sputum, tooth) were collected from Public Health Laboratory and private clinic lab, which transferred by using media or swab media between (October 2020 to 30 march 2021).

A total 50 *P. aeruginosa* isolates were obtained from 157 clinical samples.. Were (29, 58%) from urine ,(19, 38%) from sputum and (2, 4%) from tooth. These isolates were identified according to the traditional and molecular technique, such as culture and microscopic examination, biochemical tests, API 20E kit, Vitek2 system, and PCR

Result: In present study, isolates of *Ps. aeruginosa* isolated from various samples (29, 58%) urine ,(19, 38%) sputum and (2, 4%) from tooth. It was found out that (24.14% male and 75.86% female in urine sample) , (36.85% male and 63.15% female in sputum sample) and (50% male and 50% female in tooth sample) , For *Pseudomonas aeruginosa* the highest resistance percentages were found to Ampicillin, ceftriaxone, Imipenem, ,Gentamicin, norfloxacin, levofloxacin, Ciproflaxin, Amikacin, cefoxitin, and the lowest level of antibiotics was piperacillin .

Conclusion: Steady educational programs on infection control for all healthcare workers to stop the range of nosocomial infections. the antidrug resistance will continue to be a problem with *Pseudomonas spp.* infections, there is an immediate need to replace these antibiotics with developing treatment strategies, to avoid and to exclude the infections.

Introduction

Infections with *Pseudomonas aeruginosa* have become a real concern in hospital-acquired infections, especially in critically ill and immunocompromised patients. The major problem leading to high mortality lies in the appearance of drug-resistant strains [1]. *Pseudomonas aeruginosa* is one of the six bacterial pathogens, *Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter spp.*, which are commonly associated with antimicrobial resistance, and denoted by their acronym ESKAPE. Several virulence's may cause pathogenicity that facilitates adhesion and/or disrupt host cell signaling pathways while targeting the extracellular matrix . Among the pathogenicity caused by virulence factors, can be cited Lipopolysaccharide, Flagellum, Type IV Pili, Type III Secretion

System, Exotoxin A, Proteases, Alginate, Quorum Sensing, Biofilm Formation, Type VI Secretion Systems, Oxidant Generation in the Airspace. These are major virulence factors acting in different manners in the immune system [2].

MATERIALS AND METHODS

Isolation and identification of *P aeruginosa*

A total 50 *P. aeruginosa* isolates were obtained from 157 clinical samples. The sources of *P. aeruginosa* were (29, 58%) from urine, (19, 38%) from sputum and (2, 4%) from tooth, as summarized in the Table (1). Identification of causative microorganisms was performed by classic microbiological methods.

It was found out that (24.14% male and 75.86% female in urine sample), (36.85% male and 63.15% female in sputum sample) and (50% male and 50% female in tooth sample), Fig. (1). Table (2).

These isolates were identified according to the traditional and molecular technique, such as culture and microscopic examination, biochemical tests, API 20E kit, Vitek2 system Fig. (2)(3), and PCR.

Antimicrobial susceptibility test

The modified Kirby-Bauer method [3] was used for Antibiotic Susceptibility Testing. A total (50) *P aeruginosa* isolates were exposed to susceptibility testing using different antibiotics such as, Ciproflaxin (cip), levofloxacin (levo), norfloxacin (norf), Ampicillin (Am), piperacillin (pip), ceftriaxone (cro), Imipenem (imip), Amikacin (Ak), ceftazidime (fox), Gentamicin (GN).

Results and Discussion

The patterns of antimicrobial resistance were as follows: the highest resistance percentages were found to Ampicillin (98%), ceftriaxone (62%), Imipenem (58%), Gentamicin (56%), norfloxacin (56%), levofloxacin (56%), Ciproflaxin (54%), Amikacin (42%), ceftazidime (42%), and the lowest level of antibiotics was piperacillin (18%), as summarized in the Table (3). Fig (4).

In local study done by [4] mentioned that isolate of *P. aeruginosa* were resistance rate Ampicillin (81.1%), Ceftriaxone and Amoxicillin-Clavulanic acid were (78.4%), Ampicillin – Sulbactam (75.6%), Cefepime (72.9%), Trimethoprim-Sulphamethoxazole (70.2%), Nitrofurantoin (64.8%), Cefazolin and Tobromycin (62.2%) then moderate resistance to Ciproflaxin (56.7%), Ceftazidime (51.4%), Imipenem (45.9%) and the lowest level of antibiotics was Amikacin (40.5%), which agreed with the results of the current study.

While another study, disagreed with this results and showed that level resist to Ciproflaxin (14%), Amikcin (2%) and Imipenem (0%) [5].

The high antibiotic resistance of the *P. aeruginosa* bacterium might contribute to many different factors including: the widespread use of a broad spectrum antibiotics leading to the selective survival advantage of the bacteria [6]. and another study [7] making this bacterium is difficult to treat as well as the serious biofilm formation by *P. aeruginosa*. In addition to the

capability of the bacterium to form a biofilm, which provides the physical protection to the bacterium, hence the biofilm formations retard the penetration of the antimicrobial agents [8]. A concerning trend towards multi-drug resistance is emerging worldwide, which has given implications for the capacity of current therapies to eradicate *P.aeruginosa* infections in the future [9]. Infections by *P. aeruginosa* are notoriously difficult to treat due to its intrinsic ability to resist many classes of antibiotics as well as its ability to acquire resistance. All known mechanisms of antibiotic resistance can be displayed by this bacterium (intrinsic, acquired, and adaptive); sometimes all within the same isolate [10].

Table (1): Prevalence of *P. aeruginosa* among Different Clinical Samples

Isolate	Urine	Sputum	Tooth	Number	
<i>Pseudomonas aeruginosa</i>	29 (58%)	19 (38%)	2 (4%)	50	12.06 **
** (P≤0.01).					

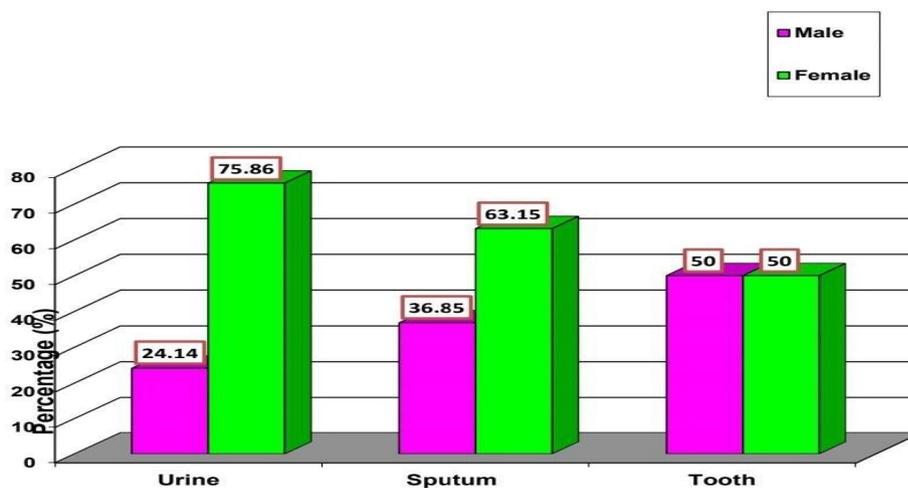


Figure (1).Distribution of *Pseudomonas aeruginosa* according to gender

Table (2) : Distribution of *Pseudomonas aeruginosa* according to gender

Sex	Urine NO(%)	Sputum NO(%)	Tooth NO(%)	Chi-Square (χ^2)
Male	7 (24.14%)	7 (36.85%)	1 (50.00%)	9.33 **
Female	22 (75.86%)	12 (63.15%)	1 (50.00%)	9.33 **
Total	29	19	2	---
Chi-Square (χ^2)	12.502 **	8.966 **	0.00 NS	----
** (P≤0.01), NS: Non-Significant.				

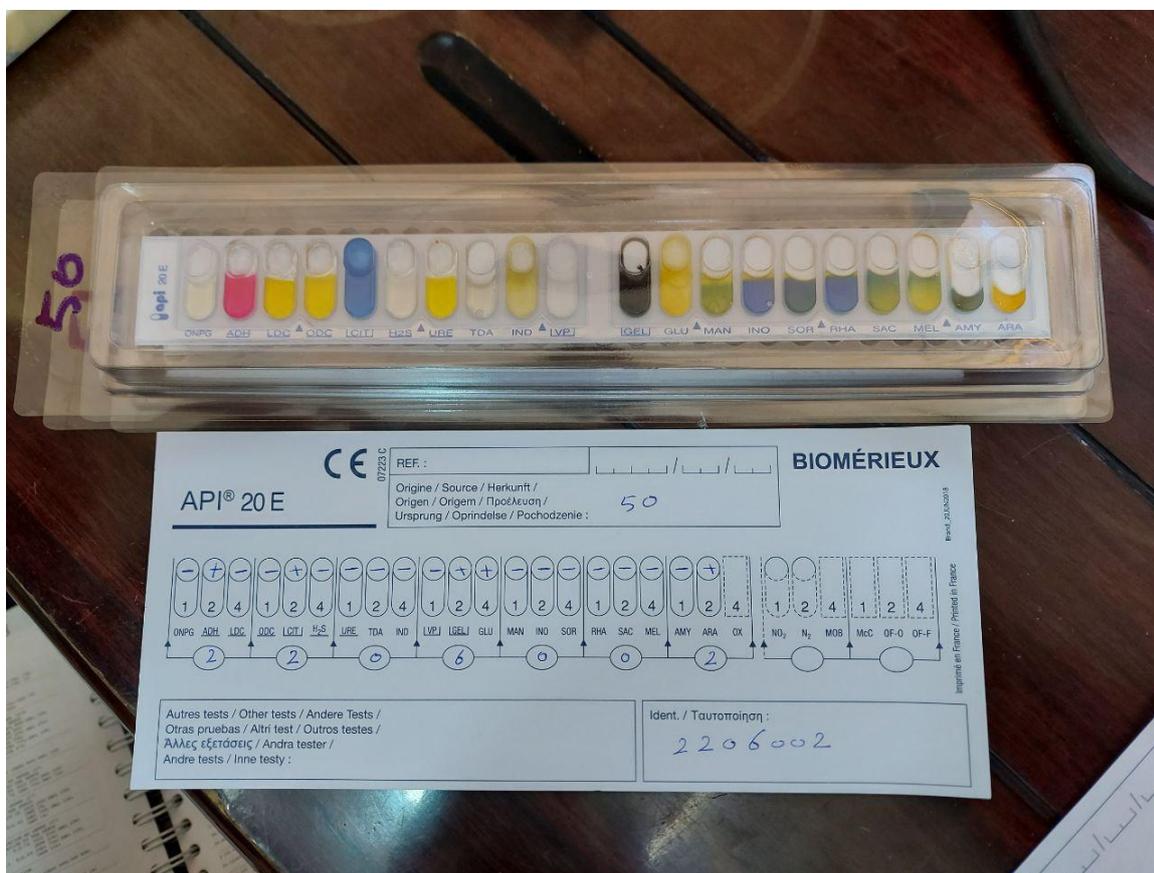


Figure (2): API 20E system Control for identification gram negative bacteria

bioMérieux Customer: Microbiology Chart Report Printed Nov 22, 2020 07:04 CST

Patient Name: Location: Lab ID: Muna Mohammed Patient ID: Physician: Isolate Number: 1

Organism Quantity: Selected Organism : *Pseudomonas aeruginosa*

Source: Collected:

Comments:

Identification Information	Analysis Time:	Status:
Selected Organism	5.35 hours	Final
ID Analysis Messages	<i>Pseudomonas aeruginosa</i>	

Susceptibility Information	Analysis Time:	Status:
Antimicrobial	14.62 hours	Final
ESBL		
Ampicillin		
Piperacillin/Tazobactam	8	S
Cefazolin	>= 64	R
Cefoxitin		
Ceftazidime	8	S
Ceftriaxone		
Cefepime	4	S
Ertapenem		
Imipenem	2	S
Amikacin	4	S
Gentamicin	8	I
Ciprofloxacin	<= 0.25	S
Levofloxacin	0.5	S
Tigecycline	>= 8	R
Nitrofurantoin		
Trimethoprim/Sulfamethoxazole		

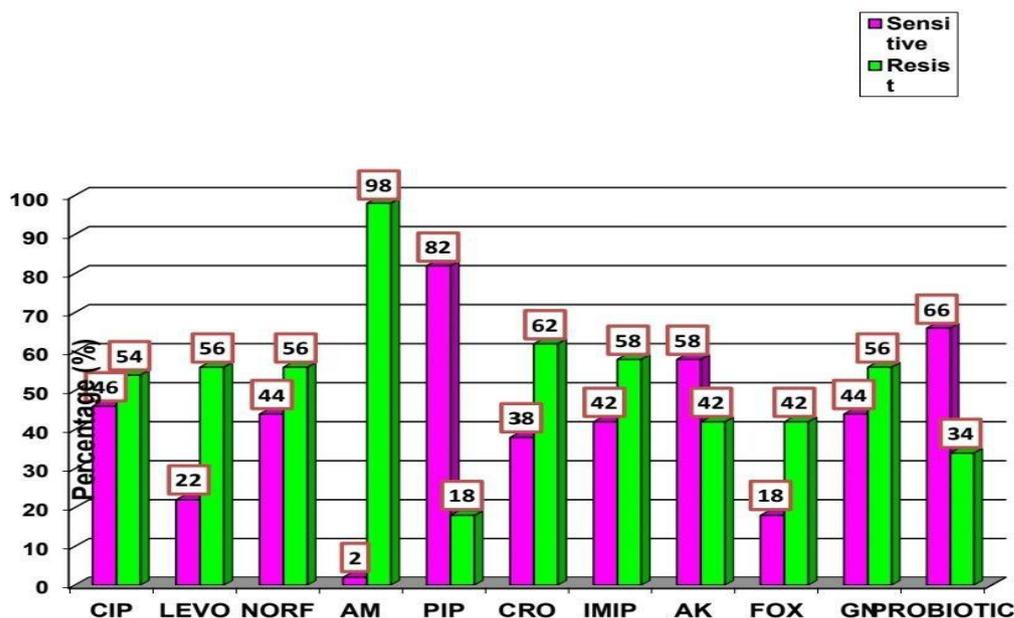
+= Deduced drug * = AES modified ** = User modified

AES Findings
Confidence: Consistent

Figure (3): Identification of *P.aeruginosa* by VITEK 2 System

Table(3) : Sensitivity test for *Pseudomonas aeruginosa*

Antibiotic	Sensitive	Resist	Total for isolate NO.	Chi-Square (χ^2)
CIP	23 (46%)	27 (54%)	50	2.96 NS
LEVO	22 (22%)	28 (56%)	50	9.52 **
NORF	22 (44%)	28 (56%)	50	4.75 *
AM	1 (2%)	49 (98%)	50	14.89 **
PIP	41 (82%)	9 (18%)	50	13.66 **
CRO	19 (38%)	31 (62%)	50	8.94 **
IMIP	21 (42%)	29 (58%)	50	0.921 NS
AK	29 (58%)	21 (42%)	50	6.02 **
FOX	9 (18%)	41 (42%)	50	10.46 **
GN	22 (44%)	28 (56%)	50	4.75 *

**Figure (4). The Antibiogram pattern of isolates towards antimicrobials used in this study.****References:**

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