Pseudomonas aeruginosa Epidemiology and Antibiotic Resistance: A Five Years Retrospective Study in Iraq.

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دراسة استرجاعية لمدة خمس سنوات عن وبائية بكتريا (*P. aeruginosa*) و توجهات مقاومة المضادات الحيوية في العزلات السريرية في بغداد \ العراق

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Abstract

One of the leading causes of diseases and deaths across the world are Bacterial infections, and the situation is only going to grow worse as antibiotic resistance spreads. Antimicrobial resistance must be closely monitored so as to control the spread of multiantibiotic-resistant microorganisms. As a result, the goal for the study was to estimate the prevalence of *Pseudomonas aeruginosa* infection on top of that to look into the antibacterial pattern over the last five years. This retrospective investigation was carried out in various hospitals in Iraq like Central Children's Teaching Hospital for Children, Al Kindi Teaching Hospital, Al-Numan Hospital, Yarmouk Hospital (Baghdad), Babylon Women's and Children's Hospital Diyala Teaching Hospital. The data were collected from January 2018 through December 2022. A total of 36,790 clinical isolates were collected from different samples, with *P. aeruginosa* accounting was 12.4% (n = 4,562).During the period of the study, antibiotic susceptibility patterns in *P. aeruginosa* exhibited a considerable elevation in a majority of the tested antibiotics. Tobramycin and piperacillin resistance rates were augmented dramatically, 48.99% and 86.98% in 2018 to 64.92% and 90.98% in 2022, respectively. Resistance rates for ceftazidime, cefixime, ceftriaxone, and cefepime went from 81%, 10.03%, 75.99% and 86.04% in 2018 to 91.07%, 9.92%, 90.98 and 90.09 in 2022, respectively, and resistance rates in carbopenimes between imipenem and meropenem grew dramatically. Imipenem and meropenem rates grew from 56.99 % and 2.03%, respectively, in 2018 to 72.95% and 4.96.2% in 2022. The current investigation found that *P. aeruginosa* drug resistance and has increased during study period. As a result, it is critical to regulate and reduce antibiotic resistance through nosocomial infection prevention and antibiotic stewardship.

Keywords: *Pseudomonas aeruginosa*, Antimicrobial resistance, AMR, Epidemiology

المستخلص

تعد الالتهابات البكتيرية أحد الأسباب الرئيسية للأمراض والوفيات في جميع أنحاء العالم، و يزداد الوضع سوءًا مع انتشار مقاومة المضادات الحيوية. من المهم جدا مراقبة مقاومة مضادات الميكروبات عن كثب من أجل السيطرة على انتشار الكائنات الحية الدقيقة المقاومة للمضادات الحيوية المتعددة. ونتيجة لذلك، كان الهدف من الدراسة هو تقدير مدى انتشار عدوى الزائفة الزنجارية للنظر في النمط المضاد للبكتيريا على مدى السنوات الخمس الماضية. تم إجراء هذا التحقيق بأثر رجعي في مستشفيات مختلفة في بغداد، العراق. تم جمع البيانات من يناير 2018 حتى ديسمبر 2022. وتم جمع ما مجموعه 36,790 عينة معزولة سريريا من مستشفيات مختلفة (مثل مستشفى الطفل المركزي التعليمي للأطفال، مستشفى الكندي التعليمي، مستشفى النعمان، مستشفى اليرموك (بغداد)، مستشفى بابل للنسائية والأطفال و مستشفى ديالى العام)، تمثل *P. aeruginosa* (12.4%) اي بعدد = 4,562.

خلال فترة الدراسة، أظهرت أنماط الحساسية للمضادات الحيوية في *P. aeruginosa* ارتفاعًا كبيرًا في غالبية المضادات الحيوية التي تم اختبارها. وارتفعت معدلات مقاومة التوبراميسين والبيبيراسيلين بشكل كبير، 48.99% و86.98% في عام 2018 إلى 64.92% و90.98% في عام 2022 على التوالي. ارتفعت معدلات المقاومة للسيفتازيديم والسيفيكسيم والسيفترياكسون والسيفيبيم من 81% و10.03% و75.99% و86.04% في عام 2018 إلى 91.07% و9.92% و90.98 و90.09 في عام 2022 على التوالي، ومعدلات المقاومة في الكاربونيم بين الإيميبينيم والميروبينيم. لوحظت بشكل كبير. ارتفعت معدلات الإيميبينيم والميروبينيم من 56.99% و2.03% على التوالي في عام 2018 إلى 72.95% و4.96.2% في عام 2022. ووجد البحث الحالي أن مقاومة *P. aeruginosa* للأدوية زادت خلال فترة الدراسة. ونتيجة لذلك، فمن الأهمية بمكان تنظيم وتقليل مقاومة المضادات الحيوية من خلال الوقاية من عدوى المستشفيات والإشراف على المضادات الحيوية.

الكلمات المفتاحية: الزائفة الزنجارية، مقاومة مضادات الميكروبات، علم الأوبئة

Introduction

P. aeruginosa is a commonly occurring opportunistic pathogenic bacterium which causes severe infections, particularly in immunocompromized patients. This organism's spread in healthcare facilities is extremely harmful because it has the capacity to infiltrates the host's first line of defense, causing nosocomial infections, especially in intensive care units (ICUs). Given the availability of numerous resistance mechanisms to most antibiotics, *P. aeruginosa* pathogenesis dependent on a number of factors, As a result, a range of cellular structures and extracellular compounds are formed, which play an important role in enhancing pathogenicity [Al-Mayali, *et al*., 2020]. Eight to ten present of all health-care related infections in the United States are associated with *P. aeruginosa* (51,000 cases in 2013). While 13% of these patients were found to have Multidrug-resistant strains [Wagner, *et al*., 2016]. Up to 13.8% of nosocomial infections are caused by *P. aeruginosa* which is considered as common cause [Lizioli, *et al*., 2003]. On the other hand it is considered the second most common cause of infection, although trends differ by institution, *P. aeruginosa* has been identified as the second most prevalent cause of hospital-acquired pneumonia (HAP), healthcare-associated pneumonia (HCAP), and ventilator-associated pneumonia (VAP), only *S. aureus* surpasses it in frequency. *P. aeruginosa* was found to be the most prevalent infectious isolate in PAH after 4 days in the ICU, VAP after 4 days of mechanical ventilation, and VAP following ostomy [Kollef, *et al*., 2005]. According to microbiological observations has been identified as a significant pathogen in burn patients in several investigations, the colonization rate of burns increases dramatically after the first week of hospitalization [Erol, *et al*., 2004]. It is the most prevalent infectious isolate

in burn wards, accounting for a considerable proportion of wound infections, bacteremia, and VAP. A substantial number of surgical wound infections were discovered throughout the hospital. *P. aeruginosa* is responsible for around 6% of all cases and 9.5% of postoperative wound infections in ICU patients reported to the National Infection Surveillance System (NNIS) between 1986 and 2003. A study gathered the data from pediatric intensive care units showed that 16% of surgical site infections are caused by *P. aeruginosa* and also the main cause of surgical site infection after gastrointestinal surgery [Driscoll *et al*., 2007].

It is considered one of the primary reasons of antibiotic resistance and relapses, along with bacterial persistence. Many patients, however, reported a surge in dangerous infections caused by recurring bacteria. Pseudomonas aeruginosa, for example, is a prevalent bacterium that frequently causes infections in immunocompromised patients [Mulcahy, *et al*., 2010]. Antibiotic usage and abuse, combined with a resistant microbe's ability to move from person to person, has increased the problem of antibiotic resistance [CDC, 2017, Nicolle *et al*., 2014, Venier, *et al.*, 2012]. The growth of multidrug-resistant P. aeruginosa, for example, has been directly linked to the incorrect and excessive use of antibiotics in the treatment of hospitalized patients [Elgohari, *et al*., 2017]. It poses a considerable therapeutic challenge in the management of nosocomial infections and the selection of suitable antimicrobial therapy due to its potential to rapidly develop resistance to several types of antibiotics. Antibiotic resistance has become a serious worry in the medical community around the world because bacteria can be resistant to both old and novel antibiotics in diverse ways [Solano-Gálvez, *et al*., 2021, Swapna, *et al*., 2022]. As a result, thorough global monitoring of antimicrobial

resistance trends is critical. With an expected 32,600 cases and 2,700 deaths in 2019, P. aeruginosa (*P. aeruginosa*) multidrug resistance (MDR) is one of the top risks assessed by the CDC [CDC, 2019]. This is mostly owing to intrinsic (congenital), acquired (horizontal gene transfer), and/or adaptive resistance (biofilm formation and persistence) [Streeter, *et al*., 2016]. In various investigations, MDR *P. aeruginosa* infection has been linked to prolonged hospital admissions as well as greater morbidity and fatality rates (Akingbade, *et al*., 2012). *P. aeruginosa* exhibits a high level of intrinsic antibiotic resistance due to reduced outer membrane permeability, active efflux mechanisms, and the production of antibiotic-inactivating enzymes (Breidenstein, *et al*., 2011). *P. aeruginosa* is considered multidrug resistant if it is resistant to at least one of the three antimicrobial classes; XDR (extreme-drug resistance) is considered highly drug resistant if it is resistant to at least one antimicrobial agent in all but two classes; and drug-resistant PDRs are resistant to all of the listed antimicrobials (Magiorakos, *et al*., 2012). Fluoroquinolone resistance has evolved as a result of mutations in the chromosomal gene encoding DNA gyrase, which affects fluoroquinolones, topoisomerase II, the permeability barrier, and/or multidrug efflux pumps (Smith, *et al*., 2022). Resistance to beta-lactams is typically generated by beta-lactam enzymes that hydrolyze lactamases, cleaving the amide link in the lactam ring and rendering the antibiotic useless (Fatima *et al*., 2021). Drug inactivation/modification, rerouting, and reduced accumulation due to decreased permeability and/or greater concentration may result in resistance (Juan *et al*., 2005). Aminoglycoside resistance in *P. aeruginosa* is mediated by aminoglycoside-modifying enzymes, decreased outer membrane permeability, and an active efflux pump (Streeter, *et al*., 2016, Seupt *et al*., 2020).

Understanding the exact cost of resistance is a critical difficulty in treating anti-microbial resistance (AMR), especially in countries where surveillance is low and data is scarce. There is a substantial body of work evaluating the consequences of antimicrobial resistance on incidence, mortality, length of hospital stay, and healthcare expenditures for certain pathogen-drug combinations in specific locales (O'Neill, 2016. O'Neill, 2014. CDC, 2019. Naylor *et al*., *et al*., 2018. Cassini, *et al*., 2019, Lim *et al*., 2016), There have been no published complete estimates spanning all sites and a wide range of infections, pathogen families, and medicines. In the U.S, for example, the Centers for Disease Control and Prevention (CDC) produced a 2019 report on AMR diseases and deaths based on surveillance data for 18 AMR risks [CDC, 2019]. while Cassini and colleagues [Cassini, *et al*., 2019,] determined the prevalence of eight infectious agents and 16 pathogen-drug combinations in the European Union and European Economic Area from 2007 to 2015. Similarly, in 2010 a study [Lim *et al*., 2016] estimated the burden of multiantibiotic resistance in six pathogenic bacteria in Thailand, while another study [Temkin *et al*., 2018] stated the incidence of resistance to third-generation cephalosporins and carbapenems in 193 countries in 2014. While these publications make a substantial contribution to the work of the Task Force on Antibiotic Resistance, they are insufficient to comprehend the global burden of antibiotic resistance and to detect and control high-priority diseases in a range of situations.

Antibiotic resistance is a major worldwide health issue by any measure [Temkin, *et al*., 2018]. In 2019, the global burden of drug-resistant infections caused by 88 drug-pathogen combinations was expected to be approximately 4.95 million deaths (95% UI 3·62–6·57), with drug resistance being directly

responsible for 1.27 million (0.911-1.71) fatalities. To put it another way, More than a million deaths may have been prevented in 2019 if antibiotics have been handled properly over the world [Kitagawa, *et al*., 2019]. Antimicrobial resistance was the tenth cause of mortality from the third global burden of illness level, ahead of both HIV and malaria. AMR could be the third leading cause of death globally [Vos, *et al*., 2020].

WHO recognized all six key pathogens contributing to the burden of antibiotic resistance in 2019 (*E. coli, S. aureus, K. pneumoniae, S. pneumoniae, A. baumannii, and P. aeruginosa*) have been listed as priority pathogens globally. In the political arena, this is accomplished through the Global Action Plan on Antimicrobial Resistance [WHO, 2015], the United Nations Inter-Agency Coordination Group [UN, 2017], the One Global Health Leaders Group [WHO, 2021], and numerous other organizations.

Materials and Methods

Designing the Study

This five-year study aimed to investigate the drug susceptibility trends of all *P. aeruginosa* isolates from hospitals. The samples were collected between January 2018 and December 2022. The total number of isolates throughout this time period was 36,790. Urine, sputum, ear swabs, and wound samples were obtained from various locations. All samples were cultured for 24-48 hours at 37 °C in two media: McConkey and sheep blood agar, using standard microbiological procedures. After 24-48 hours, use the Vitek-2 automated system to identify bacteria and antibiotic susceptibility patterns. Amikacin, Tobramycin, Gentamicin, Kanamycin, Cefixime,

Ceftazidime, Ceftriaxone, Cefepime, Levofloxacin, Aztreonam, Amoxicillin/clavulanic acid, Piperacillin, Amoxicillin, Ampicillin, Ampicillin+sulbactam, Meropenem, Imipenem, Norfloxacine, Clindamycin, and Trimethoprim / sulfamethoxazole were among the antibiotics studied in this study. The MIC data were interpreted using standard institute clinical laboratory guidelines [Ferraro, 2001].

Statistics

The database is updated with the total number of patients and sample kinds. All variables' frequencies and distributions were determined using descriptive analyses. The chi-square test was used to compare antibiotic susceptibility across time. Statistical significance was defined as a p-value less than 0.05.

Results

Patient prevalence and samples

The goal of this retrospective study was to evaluate the *P. aeruginosa* infection burden during a five-year period, from January 2018 to December 2022. 4,562 (12.4%) of the 36,790 isolates identified during the research period were *P. aeruginosa* isolates. *P. aeruginosa* isolates grew year after year, ranging from 612 to 1109 isolates per year, with an average of (912.4±85.1) isolates. The detection of *P. aeruginosa* jumped from 912 in 2018 to 1,109 in 2022. Infections with *P. aeruginosa* isolates, on the other hand, declined considerably from 892 cases in 2019 to 612 cases in 2020, presumably because of the strict adaptation of infection control released be the WHO through of the COVID-19 pandemic (Fig. 1).

During the study period, there was a substantially greater incidence of *P. aeruginosa* isolates from inpatients (mean: 749.2 ± 71.2) compared to outpatients (mean: 163.2 ± 27.2) (Table 1). Furthermore, male exhibited a greater *P. aeruginosa* isolation rate than female (p-value< 0.05) (Table 1).

Table 1. The demographic distribution of *Pseudomonas aeruginosa*.

Year	Total Isolates	Inpatient		Outpatient		p-value	Male		Female		p-value
		No.	%	No.	%		No.	%	No.	%	
2018	1037	855	82.45%	182	19.96%	<0.05*	633	61%	404	39%	<0.05*
2019	912	820	89.9%	92	10.09%	<0.05*	520	57.1%	392	42.9%	<0.05*
2020	612	477	77.94%	135	22.06%	<0.05*	404	66%	208	34%	<0.05*
2021	892	740	82.96%	152	17.04%	<0.05*	573	64.2%	319	35.8%	<0.05*
2022	1109	854	77.01%	255	22.99%	<0.05*	619	55.8%	490	44.2%	<0.05*

During the study period, *P. aeruginosa* isolates were found in urine (62%), ear infections (36%), wounds (1%), and sputum (1%) (Fig. 2). In general, the detection rate of *P. aeruginosa* isolated from diverse samples increased gradually over time (Table 2). Regardless of sample source, male patients samples had significantly more *P. aeruginosa* isolates (mean: 549.8 ± 41.5) than female patients samples (mean: 362.6 ± 47.2).

Table 2. The prevalence of different sample type of *P. aeruginosa*

Infection site	No. of isolates / % of isolates	Years					p-value
		2018	2019	2020	2021	2022	
Sputum	No.	13	5	4	9	21	<0.05*
	%	25%	9.6%	7.7%	17.3%	40.4%	
Wound	No.	16	7	5	7	19	<0.05*
	%	0.3	0.13	0.09	0.129	0.35	
Urine	No.	683	552	307	575	714	<0.05*
	%	0.24	0.2	0.11	0.20	0.25	
Ear swabs	No.	325	348	297	301	354	<0.05
	%	0.2	0.21	0.18	0.19	0.22	

Pseudomonas aeruginosa antibiotic resistance profile

The analysis of *P. aeruginosa* antimicrobial susceptibility patterns revealed a considerable increase in resistance to the majority of the tested drugs (Table 3). Ampicillin had one of the highest prevalence of resistance (98.02%) during the study period, while Meropenem had the lowest rate (0.98%) (Table 3). Resistance rates to β-lactam/-lactamase antibiotic combinations (Amoxicillin/ Clavulanic acid and Ampicillin/Sulbactam) had no significant change over the five years (Table 3). Similarly, resistance to 3rd and 4th generation Cephalosporins (Ceftazidime, Ceftriaxon, and Cefepime) had no significant change (Table 3), except Cefexime which had the lowest resistance rate (9.20%).

During the first two years of the investigation, Aztreonam was the most sensitive antibiotic in the β-lactam antibiotic family. However, Aztreonam resistance is gradually raised to reach 56% and is expected to reach 70% by 2027 (Table 3). Resistance rates to aminoglycosides (Amikacin Kanamycin, Tobramycin and Gentamicin), increased significantly over the research period. Over a five-year period, the average rate of Amikacin resistance was 68.88%, while the rate of Gentamicin resistance was 59.79% (Table 3). Similarly, Ciprofloxacin and Co-trimoxazole (Trimethoprim-Sulfamethoxazole) resistance rates increased dramatically over time, with average resistance rates of 29.4% and 34.59%, respectively (Table 3).

Discussion

Antimicrobial resistance (AMR), which happens when bacteria adapt and make antibiotics used to treat infections less effective, in the 21st century the AMR emerged as a public health problems of the twenty-first century. Several studies in The United Kingdom estimated that antimicrobial resistance

might kill about 10 million people per year by the year of 2050 [O'Neill, 2016. O'Neill, 2014], although this projection has been questioned by some [de Kraker *et al*., 2016, NOAH, 2016]. The World Health Organization and many other organizations and researchers believe that the rise of antibiotic resistance is an important issue that requires a coordinated global action plan [Wagner, *et al*.. 2016; WHO, 2015; WHO,2023; Prestinaci, *et al*., 2015].

It is vital to have information on the current situation of the bacterial antibiotic-resistant, trends in different parts of the world, and the primary pathogens and medication combinations responsible for the antibiotic-resistant bacterial burden. Antimicrobial resistance, if unregulated, has the potential to make many bacterial infections more lethal than they are now.

Only a few studies have been undertaken in Iraq to track trends in *P. aeruginosa* antibiotic resistance. As a result, we investigated the prevalence and trends of antibiotic resistance in *P. aeruginosa* in this study. Over a 5-year period, the frequency of *P. aeruginosa* was 12.4% (n = 4562). *P. aeruginosa* frequency is lower than previously reported in other locations of Iraq. In Basrah and Baghdad, for example, the prevalence of *P. aeruginosa* infection was 38% and 37.7%, respectively [Alkhulaifi and Mohammed, 2023, Shaker and Al-Musawi 2022]. However, the prevalence of *P. aeruginosa* infection in Iraq is comparable to what has been reported elsewhere 9.9% in Qatar [Ahmed, *et al*., 2022], 70.6% in South Africa [Hosu *et al*., 2021], and in 2020, 29 EU/EEA nations reported 20,675 isolates of *P. aeruginosa* [CDC, 2022]. According to the findings of this study, the majority of *P. aeruginosa* isolates are significantly higher in male patients, with an average of 60.82%. This conclusion is similar to a prior study in which the majority of *P. aeruginosa* isolates were from male patients [Shaker and Al-Musawi 2022]. When *P.*

aeruginosa was discovered in a variety of samples, the greatest levels were observed in urine samples, followed by ear swabs. *P. aeruginosa* is a prevalent cause of urinary tract infections (UTIs), specially catheter-associated UTIs (CAUTIs). It occurs for 10% of all CAUTIs and 16% of UTIs in ICU patients [Rosenthal, *et al*., 2015, Mittal, *et al*., 2009], and bloodstream infections (BSIs) are associated with increased morbidity and mortality rates ranging from 43.2% to 58.8%. [Kang, *et al*., 2005; Micek, *et al*.,2011; Thaden, *et al*., 2017]

P. aeruginosa is a well-known problem and infection in burn patients, where the moist environment is hypothesized to contribute to burn susceptibility [Norbury, *et al*., 2016]. *P. aeruginosa* is the most prevalent Gram-negative bacterium in burn victims, and it is linked to sepsis and death [Norbury, *et al*., 2016; Williams, *et al*., 2009; Mayhall, 2003; Azzopardi, *et al*., 2014]. *P. aeruginosa* multidrug resistance (MDR) is an increasing cause of death in burn patients, accounting for 86% of Sepsis deaths in children intensive care units, with *P. aeruginosa* being the causative agent in 64% of cases between 1999 and 2009. [Williams, *et al*., 2009]. Current knowledge is that *P. aeruginosa* is the causal agent of otitis media, and this must be considered when diagnosing otitis media. Bacteria produce 98% of acute otitis externa patients in North America [Rosenfeld, *et al*., 2006]. *P. aeruginosa* and *Staphylococcus aureus* are the most prevalent isolates. Many other aerobic and anaerobic bacteria, however, have been discovered [Ninkovic *et al*.. 2008, Roland and Stroman, 2002], Mixed bacterial infections account for approximately one-third of all cases [Rosenfeld, *et al*., 2006]. Our findings support national and international concerns that antimicrobial resistance is on the rise, especially with *P. aeruginosa* resistant to the most commonly prescribed antibiotics. [Sala, *et al*., 2019, Mirzaei *et al*.. 2020]. Among the studied antibiotics,

Ampicillin + sulbactam exhibited the highest resistance rate over the study period, with an average resistance rate of 98.26%. Previous investigations in Iraq yielded similar results. Ampicillin resistance rates in Iran and Basra\Iraq, for example, were 93% and 100%, respectively [Ahmadi *et al*., 2016, Alkhulaifi and Mohammed, 2023]. *P. aeruginosa* resistance to third and fourth generation cephalosporins was also shown to be slightly higher, Ceftriaxone, cefexim, Ceftazidime, and cefepim was shown to be effective in 83.18% (n = 3816), 8.8% (n = 434), 86.43% (n = 3941), and 88.83% (n = 4067) of patients respectively. This observation is consistent with earlier Iraqi findings of a rise in *P. aeruginosa* on cephalosporin medicines [Alkhulaifi and Mohammed, 2023]. The similar observation has been reported in China and other nations throughout the world, demonstrating that *P. aeruginosa* resistance to third and fourth generation cephalosporins is increasing globally [Lyu, *et al*., 2023. Ibrahim, 2018., de Oliveira Santos, *et al*., 2019]. Due to their function in generating resistance, the widespread use of fluoroquinolones has led to their being implicated as a "smoking gun." This increase in resistance indicates that great caution should be given when selecting to use them [Trautner, 2018]. This increase in fluoroquinolone (FQs)-resistance among UTI isolates of E. coli is now resulting in calls to combat their use as first choice agents [Stewardson, *et al*., 2018]. Treatment regimens with FQs being highly inappropriate and the medications are growing resistance to them. Levofloxacin is not advised even in cases where the isolated microorganism is drug-sensitive if there are acceptable alternatives (such as fosfomycin, co-trimoxazole, or nitrofurantoin) due to the frequent and potentially serious adverse events associated with the use of FQs [Bientinesi, *et al*., 2020]. Carbapenem is an efficient antibiotic used to treat

Gram-negative bacterial infections. Imipenem enhanced the strength index against *P. aeruginosa*. In the early years of study, imipenem was shown to be one of the effective antibiotics, with a resistance rate of 56.9%. It's sad to say that the resistance began to rise during the research period, reaching 72.9% in 2022. A similar outcome was reported in Brazil, where *P. aeruginosa* resistance to amikacin is anticipated to reach 63.6% in the 2022 [de Oliveira Santos, *et al*., 2019]. Our study found a low rate of meropenem resistance of 6.88% across the five-year study period; however meropenem showed resistance in Saudi Arabia [Ibrahim, 2018].

Conclusion

The prevalence of *P. aeruginosa* grew dramatically during the research period, according to our findings. Furthermore, we noticed a rise in resistance to practically all antibiotics tested over the course of the study. Unfortunately, none of the antibiotics studied demonstrated a significant reduction in resistance. To manage antimicrobial resistance in *P. aeruginosa* and other multidrug-resistant bacteria, proper antibiotic usage awareness, effective supervised educational programs for doctors and clinical pharmacists are required. This research was limited to a single center in Baghdad, Iraq. This study used a sample of 36,790 isolates obtained over a 5-year period. So it's reasonable to claim that this is a good representation of Baghdad. However, this figure does not rule out the necessity for similar studies to be conducted in other regions and in other cities and towns. However, such a study necessitates greater financial resources as well as more time. As a result, we urge that another study be conducted in this area, encompassing more cities and providing more extensive information on prescribing trends and patient characteristics.

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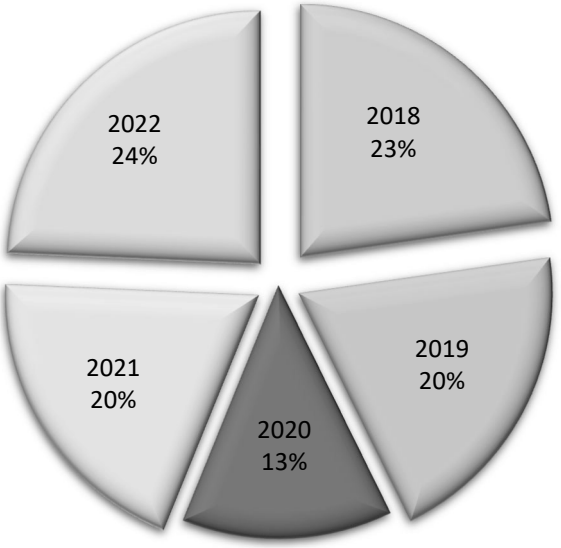

Figure 1: percentage of Pseudomonas aeruginosa infection across 5 years of study

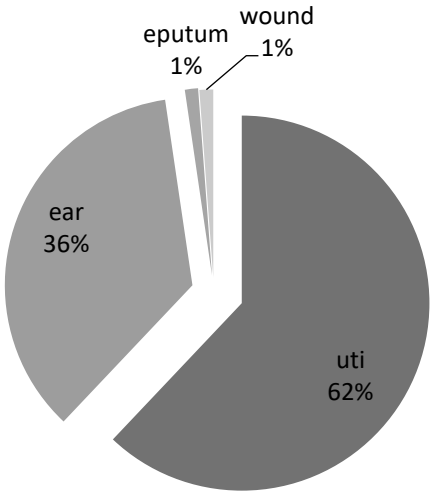

Figure 2: P. aeruginosa isolates percentage throughout the study period

Table 3. The prevalence of antibiotic over 5 years

antibiotic class	antibiotic name	%	2018		2019		2020		2021		2022		p-value
		No. of samples	R	S	R	S	R	S	R	S	R	S	
Aminoglycoside	Amikacin	%	64.92%	35.08%	77.24%	22.76%	62.01%	37.99%	68.30%	31.70%	71.93%	28.07%	<0.05*
		no	674	363	703	209	367	245	606	286	798	311	
	Tobramycin	%	48.99%	51.01%	52.96%	47.04%	59.97%	40.03%	53.03%	46.97%	64.92%	35.08%	<0.05*
		no	508	529	483	429	367	245	473	419	720	389	
	Gentamicin	%	56.03%	43.97%	68.97%	31.03%	50%	50%	64.01%	35.99%	59.96%	40.04%	<0.05*
		no	581	456	629	283	306	306	571	321	665	444	
	Kanamycin	%	23.05%	76.95%	13.93%	86.07%	25%	75%	25%	75%	19.03%	80.97%	<0.05*
		no	239	798	127	784	153	459	223	669	211	898	
third-generation cephalosporin	Cefixime	%	10.03%	89.97%	8.00%	92.00%	5.07%	94.93%	13.00%	87.00%	9.92%	90.08%	<0.05*
		no	104	933	73	839	31	581	116	776	110	999	
	Ceftazidime	%	81.00%	19.00%	88.05%	11.95%	88.07%	11.93%	83.97%	16.03%	91.07%	8.93%	<0.05
		no	840	197	803	109	539	73	749	143	1010	99	
	Ceftriaxone	%	75.99%	24.01%	83.00%	17.00%	77.94%	22.06%	88.00%	12.00%	90.98%	9.02%	<0.05
		no	788	249	757	155	477	135	785	107	1009	100	
fourth-generation cephalosporin	Cefepime	%	86.04%	13.96%	89.02%	10.98%	89.67%	10.33%	88.53%	11.47%	90.90%	9.10%	<0.05
		no	892	145	812	100	551	61	802	90	1010	99	
fluoroquinolone	Levofloxacin	%	26.04%	73.96%	25%	75%	18.95%	81.05%	42.04%	57.96%	34.99%	65.01%	<0.05*
		no	270	767	228	684	116	496	375	517	388	721	

beta-lactam	Aztreonam	%	43.01%	56.99%	51.97%	48.03%	66.99%	33.01%	59.98%	40.02%	56.00%	44.00%	<0.05*
		no	446	591	474	438	410	202	535	357	621	488	
	Amoxicillin + clavulanic acid	%	88.04%	11.96%	86.95%	13.05%	82.03%	17.97%	88.00%	12.00%	91.97%	8.03%	<0.05
		no	913	124	793	119	502	110	785	107	1020	89	
	Piperacillin	%	86.98%	13.02%	94.96%	5.04%	91.01%	8.99%	85.99%	14.01%	90.98%	9.02%	<0.05
		no	902	135	866	46	557	55	767	125	1009	100	
	Amoxicillin	%	73.00%	27.00%	75.99%	24.01%	61.93%	38.07%	78.03%	21.97%	78.09%	21.91%	<0.05
		no	757	280	693	219	379	233	696	196	866	243	
	Ampicillin	%	97.01%	2.99%	98.03%	1.97%	92.97%	7.03%	93.05%	6.95%	93.96%	6.04%	<0.05*
		no	1006	31	894	18	569	43	830	62	1042	67	
	Ampicillin + sulbactam	%	97.97%	2.03%	99.01%	0.99%	98.04%	1.96%	98.99%	1.01%	97.29%	2.71%	<0.05
		no	1016	21	903	9	600	12	883	9	1079	30	
carbopenimes	Meropenem	%	2.03%	97.97%	1.97%	98.03%	0.98%	99.02%	3.03%	96.97%	4.96%	95.04%	<0.05*
		no	21	1016	18	894	6	606	27	865	55	1054	
	Imipenem	%	56.99%	43.01%	60.96%	39.04%	56.05%	43.95%	63.00%	37.00%	72.95%	27.05%	<0.05*
		no	591	446	556	356	343	269	562	330	809	300	
quinolone	Norfloxacine	%	32.02%	67.98%	42.98%	57.02%	28.92%	71.08%	31.05%	68.95%	37.96%	62.04%	<0.05*
		no	332	705	392	520	177	435	277	615	421	688	
lincosamide	Clindamycin	%	59.98%	40.02%	53.95%	46.05%	56.05%	43.95%	59.98%	40.02%	63.93%	36.07%	<0.05
		no	622	415	492	420	343	269	535	357	709	400	
Sulfonamide	Trimethoprim / sulfamethoxazole	%	77.92%	22.08%	83.00%	17.00%	81.05%	18.95%	73.99%	26.01%	86.29%	13.71%	<0.05
		no	808	228	757	155	496	116	660	232	957	152	