

Increased Resistance of *Pseudomonas Aeruginosa* and *Streptococcus* species against Selective Antimicrobial Agents within two Years Interval

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Abstract— Background: Antimicrobial resistance is the phenomenon where a medication loses its efficacy in inhibiting bacterial growth. Bacteria develop resistance and proliferate in the presence of therapeutic concentrations of antibiotics. Bacteria that continue to reproduce in the presence of antibiotics are referred to as resistant bacteria.

The occurrence of antibiotic resistance was noted quickly following the introduction of novel antibacterial agents. Antibiotic resistance can arise by natural selection, when bacteria are endowed by nature with varying degrees of inherent low-level resistance.

Aim: To compare the bacterial resistance toward selective antimicrobial agents between two different occasions with two years interval.

Objectives: To assess antibacterial resistance toward certain antibacterial agents in specified types of infections, to assess antibacterial resistance toward certain antibacterial agents in the same specified types of infections after two years and compare the extent of antibacterial resistance during this period for the demographic population of interest.

Design and Methods: The study was designed as a retrospective study, Data of (195) patients in 2018 and of (315) patients in 2020 were taken, the antimicrobial resistance was considered by the culture and sensitivity tests.

Results: There is significant decrease in the percentage of resistance of the *Pseudomonas Aeruginosa* against vancomycin in 2020 compared to the cases taken in 2018 ($P < 0.05$), there is significant increase in the percentage of resistance of the *Streptococcus* species against vancomycin in 2020 ($P < 0.05$), against azithromycin ($P < 0.05$) and against ampicillin ($P < 0.05$) compared to the cases taken in 2018.

Conclusions: The current investigation reveals a significant level of antibacterial resistance among the agents examined, as evidenced by their resistance to antibacterial drugs from several pharmacological categories. The rate of resistance has significantly increased due to a rapid surge in resistance within a relatively little timeframe.

Index Terms— Antimicrobial agent, Antimicrobial resistance, Percentage of resistance, *Pseudomonas aeruginosa*, *Streptococcus* species.

I. INTRODUCTION

Antibiotics are regarded as a pivotal breakthrough in the field of medicine, since they have enabled the successful treatment of infectious diseases, ultimately saving countless human lives over a span of almost seventy years. Nevertheless, the improper utilization of antibiotics in both human medicine and agriculture, coupled with the emergence and dissemination of mobile genetic components that confer resistance, has precipitated the surge in multidrug resistance (MDR) and extensively drug-resistant strains in recent decades (1).

Antibiotic resistance is the phenomenon where a medication loses its efficacy in inhibiting bacterial growth. Bacteria develop resistance and persistently reproduce in the presence of therapeutic concentrations of antibiotics. Bacteria that are able to reproduce even in the presence of antibiotics are referred to as resistant bacteria (2). Bacteria acquire genetic resistance to drugs through various pathways as an adaptive response driven by evolution (3). Phenotypic antibiotic resistance (PAR) refers to the temporary and non-inheritable capacity of bacteria to withstand antibiotics. This resistance is mainly characterized by drug insensitivity, persistence, the creation of biofilms, and the reduced ability of antibiotics to enter the bacteria or their greater removal from the bacterium (4).

In underdeveloped countries, the majority of antibiotics are accessible without a medical prescription, leading to a significant component in the development of antibiotic resistance (5). The high pathogenicity level of these priority bacteria, coupled with their resistance to the majority of current antibiotic therapies, underscores the need for a robust scientific collaboration across all disciplines and fields to effectively combat this resistance phenomena (6).

The present study aims to address a significant worldwide health issue about the loss of effectiveness of our defenses against bacterial infections. It seeks to identify a potential

temporal pattern in the development of resistance to antibiotics and determine the magnitude of this problem among these microorganisms.

II. DESIGN AND METHODS

The study was conducted retrospectively, utilizing patient records to gather data on their infections and the antibiotic regimen.

A total of 195 patients' data was collected from Al-Sadiq Teaching Hospital in Babylon, Iraq in 2018, and 315 patients' data was collected in 2020. The data encompassed the primary compliance, the infection kind, the bacteria type, the resistance status, and the antibacterial agent type utilized.

The antimicrobial resistance was assessed by culture and sensitivity tests. Bacterial strains were isolated from various tissue samples and incubated in appropriate conditions. The sensitivity of these strains to specific antimicrobial agents was then examined using the VITEK 2 system.

The statistical analyses were conducted using the Statistical Package for the Social Sciences (SPSS), version 22. The study examined two nominal variables: antimicrobial resistance and antimicrobial agents. A Chi-square (χ^2) test was conducted on these variables. Significance will be attributed to P values below 0.05.

III. RESULTS

The resistance percentage of *Pseudomonas Aeruginosa* was compared between two sample collection periods (2018 and 2020) for each antibacterial agent. The statistical significance of any changes in resistance between the two periods was determined using Chi square analysis. The results are presented in table 1.

TABLE I
THE RESISTANCE OF *PSEUDOMONAS AERUGINOSA* AGAINST DIFFERENT ANTIBACTERIAL AGENTS BETWEEN TWO DIFFERENT PERIODS

P value	Percentage of resistance	Resistant cases	Sensitive cases	<i>Pseudomonas Aeruginosa</i>	
0.007	71%	24	10	2018	Amikacin
	32%	6	13	2020	
0.476	53%	9	8	2018	Azithromycin
	59%	13	9	2020	
0.541	58%	7	5	2018	Cefotaxime
	63%	12	7	2020	
0.091	68%	19	9	2018	Ciprofloxacin
	46%	12	14	2020	
0.283	50%	5	5	2018	Vancomycin
	68%	13	6	2020	
0.225	80%	24	6	2018	Pipracillin
	64%	9	5	2020	
0.471	64%	9	5	2018	TMS
	56%	9	7	2020	
0.350	63%	10	6	2018	Ampicillin
	73%	19	7	2020	
0.276	64%	9	5	2018	Nitrofurantoin
	47%	8	9	2020	

TMS: trimethoprim – sulfa methoxazole

Table 1 presents the resistance of *Pseudomonas Aeruginosa* to various antibacterial drugs. It demonstrates a noteworthy reduction in the percentage of *Pseudomonas Aeruginosa* resistance to vancomycin in 2020 compared to the cases examined in 2018 ($P < 0.05$). However, the susceptibility of *Pseudomonas Aeruginosa* to various antibiotic drugs remains relatively unchanged across these two time periods.

It is noteworthy that the resistance percentage against the selected antibacterial agents is often significant, with rates of 71% against amikacin, 80% against pipracilin, and 73% against ampicillin.

The resistance percentage of *Streptococcus* species was compared between the two sample collection periods (2018 and 2020) for each antibacterial agent. The statistical significance of the changes in resistance between the two periods was determined using Chi square analysis, as presented in table 2.

TABLE II
THE RESISTANCE OF STREPTOCOCCUS SPECIES AGAINST DIFFERENT ANTIBACTERIAL AGENTS BETWEEN TWO DIFFERENT PERIODS

P value	Percentage of resistance	Resistant cases	Sensitive cases	Streptococcus species	
0.316	45%	9	11	2018	Amikacin
	56%	20	16	2020	
0.049	56%	13	10	2018	Azithromycin
	80%	28	7	2020	
0.372	67%	10	5	2018	Cefotaxime
	56%	14	11	2020	
0.292	71%	17	7	2018	Ciprofloxacin
	61%	23	15	2020	
0.019	29%	6	15	2018	Vancomycin
	60%	24	16	2020	
0.597	74%	17	6	2018	Pipracillin
	73%	16	6	2020	
0.096	68%	27	13	2018	TMS
	43%	6	8	2020	
0.036	30%	8	19	2018	Ampicillin
	56%	19	15	2020	
0.358	40%	6	9	2018	Nitrofurantoin
	53%	8	7	2020	

TMS: trimethoprim – sulfa methoxazole

The table 2 shows *Streptococcus* species resistance against different antibacterial agents in which there is significant increase in the percentage of resistance of the *Streptococcus* species against vancomycin in 2020 ($P < 0.05$), against azithromycin ($P < 0.05$) and against ampicillin ($P < 0.05$) compared to the cases taken in 2018. However the resistance of *Streptococcus* species against other antibacterial agents is not significantly changed between these two periods.

It is worth to mention that the resistance percentage against selected antibacterial agents is generally high (71 % against ciprofloxacin and 74 % against pipracilin).

IV. DISCUSSION

The findings of the present investigation indicate a notable rise in the proportion of antibacterial resistance towards numerous antimicrobial agents, as well as an escalation in this proportion over a span of two years for several of these agents. Nevertheless, the purpose of the study is to examine the hypothesis that there is a significant and/or substantial rise in antibiotic resistance.

The extensive utilization of commercial antibiotics in both human medicine and agriculture, coupled with the emergence and dissemination of mobile genetic factors that confer resistance, may further facilitate the development of drug resistance and multidrug resistance (MDR) (7).

The sole reduction in resistance percentage observed in the present investigation was specifically in *Pseudomonas Aeruginosa*'s resistance to vancomycin. This decline can be largely attributed to the observation that vancomycin usage was discontinued for treating patients infected with *Pseudomonas Aeruginosa*.

Pseudomonas aeruginosa stands apart from other bacteria due to the fact that each of its intrinsic resistance mechanisms provides resistance to several antibiotics simultaneously, unlike other bacteria which have distinct intrinsic resistance mechanisms for various antibiotics. *Pseudomonas aeruginosa*'s limited membrane permeability makes it resistant to numerous antibiotics (8). The antibiotics that successfully penetrate the *P. aeruginosa* cell are susceptible to efflux pumps and antibiotic-inactivating enzymes. *Pseudomonas aeruginosa* possesses both inherent and acquired mechanisms of resistance to beta-lactam antibiotics. The intrinsic features comprise influx pumps and several beta-lactamases. More precisely, *P. aeruginosa* possesses AmpC beta-lactamases and extended-spectrum beta-lactamases (ESBLs) that are encoded in its chromosomes (9).

The resistance of *P. aeruginosa* to aminoglycosides is mostly due to its inherent impermeability, which prevents the antibiotics from entering its cell wall and achieving effective intracellular concentrations (10). Furthermore, there are additional inherent mechanisms of resistance, such as efflux pumps, as well as enzymes that change aminoglycosides, including aminoglycoside phosphotransferases, acetyltransferases, and nucleotidyltransferases (11).

Streptococcus species can become resistant to macrolide antibiotics, including azithromycin, by target modification caused by the acquisition of the *erm(B)* gene via horizontal transfer. This gene, when methylated by *ErmB*, affects the 23S rRNA (12).

CONCLUSION

The current investigation reveals a significant level of antibacterial resistance among the evaluated agents, as they demonstrate resistance to antibacterial drugs from several pharmacological categories. The rate of resistance has significantly increased within a relatively short period of two years.

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