Short Communication

Increased Resistance of *Pseudomonas aeruginosa* and *Streptococcus* species against Selective Antimicrobial Agents within a 2-Year Interval in Babylon, Iraq

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Abstract

Background: The occurrence of antibiotic resistance was observed quickly following the introduction of novel antibacterial agents. Antibiotic resistance can arise through natural selection when bacteria are endowed by nature with varying degrees of inherent low-level resistance. **Objectives:** We aimed 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 2 years, and to compare the extent of antibacterial resistance during this period for the demographic population of interest. **Materials and Methods:** The study was designed as a retrospective study. Data of (195) patients in 2018 and of (315) patients in 2020 were collected; antimicrobial resistance was considered by the culture and sensitivity tests. **Results:** There is a significant increase in the proportion of resistance of *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. **Conclusion:** 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 short timeframe.

Keywords: Antimicrobial resistance, Iraq, *Pseudomonas aeruginosa*, *Streptococcus*

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 70 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 ability of bacteria to resist the effects of antibiotics. This resistance is mainly characterized by drug insensitivity, persistence, the creation of biofilms, and the reduced ability of antibiotics

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to enter the bacteria or their higher removal from the bacterium.[4]

The present study aims to address a significant worldwide health issue regarding the loss of effectiveness of our defense mechanisms 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.

MATERIALS AND METHODS

Study design and patients

The study was conducted retrospectively, utilizing patient records to gather data on their infections and the antibiotic regimen. A total of 195 patients' data were collected from Al-Sadiq Teaching Hospital in Babylon, Iraq, in 2018, and 315 patients' data were collected in 2020. The data encompassed primary compliance, the infection, the bacteria, the resistance status, and the antibacterial agent utilized. The antimicrobial resistance was assessed by culture and sensitivity tests. Bacterial strains were isolated from various tissue samples and incubated under appropriate conditions. The sensitivity of these strains to specific antimicrobial agents was then examined using the VITEK 2 system (Marcy-l'Étoile, Lyon, France).

Statistical analysis

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 value below 0.05.

Ethical approval

Ethical considerations during research: the study requires patients' data from their health files, and the approval of the institution that holds this data was obtained to precede the data collection.

RESULTS

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

Table 1 presents the resistance of *P. aeruginosa* to various antibacterial drugs. It is noteworthy that the resistance percentage against the selected antibacterial agents is often significant, with rates of 71% against amikacin, 80% against piperacillin, 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 shown in Table 2.

Table 2 shows *Streptococcus* species resistance against different antibacterial agents, in which there is a 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

Table 1: Resistance of *P. aeruginosa* against different antibacterial agents during two different periods

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

TMS: trimethoprim–sulfa methoxazole

Table 2: Resistance of *Streptococcus* spp. against different antibacterial agents during two different periods

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

TMS: trimethoprim – sulfa methoxazole

between these two periods. It is worth mentioning that the resistance percentage against selected antibacterial agents is generally high (71% against ciprofloxacin and 74% against piperacillin).

DISCUSSION

The findings of the present investigation indicate a notable rise in the proportion of antibacterial resistance toward numerous antimicrobial agents, as well as an increase in this proportion over a span of 2 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.

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. *P. aeruginosa* limited membrane permeability makes it resistant to numerous antibiotics.[5-7] The antibiotics that successfully penetrate the *P. aeruginosa* cells 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.[8-11]

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. Furthermore, there are additional inherent mechanisms of resistance, such as efflux pumps, as well as enzymes that modify aminoglycosides, including aminoglycoside phosphotransferases, acetyltransferases, and nucleotidyltransferases.[12-14]

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.[15]

In spite of the limitations of this study, there were several strengths. This is a comprehensive study that sheds light on the extent and rate of antibacterial resistance. There were also some limitations, including a relatively small sample size, since the sample was distributed to many subgroups.

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 2 years. Enhancing scientific collaboration is necessary to address the global health issue of antibiotic resistance and to enable the effective application of new antibacterial therapies. The development of new drug combinations, antibiotic regimens, and novel antimicrobial substances, along with a deeper understanding of the molecular origins of resistance and the mechanisms of its spread, will surely aid in addressing the issue of antibiotic resistance.

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Conflicts of interest

There are no conflicts of interest.

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