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CHARACTERIZATION OF INTEGRON GENES OF CLINICAL ISOLATES OF *PSEUDOMONAS AERUGINOSA* WHICH PERFORM RESISTANCE TO ANTIBIOTICS AND BIOFILM FORMATION BY THESE STRAINS

Pseudomonas aeruginosa is a bacterium that holds significant clinical and epidemiological significance. It serves as the principal etiological cause of opportunistic infections in individuals with impaired immune systems. Integrons are known to have a notable impact on Gram-negative bacteria, particularly in the context of P. aeruginosa, a bacterium recognized for its ability to develop resistance to antimicrobial drugs. ***Aim.*** *To systematically characterize and detect integron genes (intI, intII, intIII) with antibiotic-resistant and biofilm-forming capabilities in isolated P. aeruginosa.* ***Methods.*** *A total of 209 samples were collected from Al Yarmouk Teaching Hospital in Baghdad City, Iraq to isolate P. aeruginosa. The process of bacterial identification was carried out phenotypically and by biochemical tests. Antibiotic susceptibility was measured using the Vitek2 system. Biofilm quantification was done by the microtiter method. The PCR approach was employed to assess the presence of class 1, 2, and 3 integrons.* ***Results.*** *P. aeruginosa was identified in 83 isolates by using a combination of morphological and biochemical examinations where all isolates showed the ability to grow a selective medium on cetrimide agar for P. aeruginosa. The results also showed significant variances ($p < 0.05$) among the percentage of a number of samples and isolated P. aeruginosa. The burn and wound infection scored the highest percentages (25% and 19%) based on the positivity of P. aeruginosa, whereas burn and ear sites scored the highest percentage (58% and 50%). Also, the isolates show the ability to form biofilm at a percentage of 68.7% with resistance to a high number of antibiotics. The multidrug-resistant and sensitive P. aeruginosa isolates scored high percentages (49.4% and 34.9%) whereas potentially pan drug-resistant and extensively drug-resistant isolates scored low percentages (2.4% and 13.3%). PCR results showed that integron I scored the highest percentage (100%) compared to integron 2 found in 3 (10%) isolates, and no intI3 gene was detected in any of the P. aeruginosa isolates.* ***Conclusions.*** *Overall, the findings of the present investigation indicate that integrons and biofilm development are recognized as significant factors contribut-*

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ing to antibiotic resistance in P. aeruginosa. The prevalence of class 1 integrons is shown to be significantly high in all bacterial isolates, with a complete occurrence rate of 100%. This high incidence of class 1 integrons is associated with the development of resistance to crucial antibiotics, including β-lactams, aminoglycosides, and cephalosporins.

Keywords: *integron, antibiotic resistance, Pseudomonas aeruginosa, biofilm.*

Pseudomonas aeruginosa may typically be found in various environments, including soil, plants, and mammal tissue, where it can be isolated as a mobile, Gram-negative, and aerobic bacterium with a rod-shaped morphology (Botelho et al., 2019). It is an opportunistic bacterium that causes numerous infections in humans due to its high resistance to different classes of antibiotics. It has been identified as one of the globe's leading causes of hospital-acquired infections and is commonly associated with clinical treatment difficulties (Al-Mayyahi et al., 2018; Azam & Khan, 2019). A major worry around the world is an increase in *P. aeruginosa* antibiotic resistance (Abd El-Baky et al., 2020; Al-Daraghi & Al-Badrwi, 2020). The rise of antibiotic-resistant *P. aeruginosa* represents a serious threat to public health since it can delay or prevent the use of antibiotics, which elevates mortality rates (Safaei et al., 2017), and this contributes to causing a wide range of diseases by infections that are extremely difficult to treat (Tuon et al., 2022). *P. aeruginosa* is an interesting human pathogen that can adapt to a hostile environment in hosts by producing a variety of virulence factors that contribute to infection and disease (Al-Shamaa et al., 2016; Vidaillac & Chotirmall, 2021). Genomic variation of *P. aeruginosa* has a significant influence on its capacity to induce infection (Al-Shimmary, 2020). According to Wells & Feschotte (2020), transposable elements (TEs) are ubiquitously present in almost all organisms studied. They represent a significant component of certain genomes and have a notable influence on the evolution of genome structure (Lisch & Bennetzen, 2011). In order to enable the acquisition and differential expression of additional genes, integrons, «transposable genetic elements», are unique genetic elements that can cluster and express drug-resistant genes. They are formed of a succession of «cassettes» containing antibiotic-resistant genes. This plays a significant role in the development of multiple antibiotic resistance in bacteria that can capture mobile gene cassettes and act as platforms for genetic recombination that enhance bacterial plasticity (Khudair & Mahmood, 2021; Al-Daraghi et al., 2020). They can capture and express resistance genes, allowing bacteria to adapt and survive in the presence of antibiotics (Ghaly et al., 2021). A combination site (attI), a promoter (PC), and an integron-integrase gene (IntI) are the three fundamental components that all integrons share. IntI encodes an integrase (IntI) from the tyrosine recombinase family. As a result of the activity of integrase enzyme encoded by intI, recombination between the attI and/or attC sites, which is catalyzed by intI, results in the insertion or excision of cassettes, allowing external genes to be expressed and captured as a part of gene sequences that are rearranged at the attI site (Sabbagh et al., 2021). Based on the integrase gene's amino acid sequences, integrons are categorized into distinct classes: those containing intI1 refer to «class 1,» intI2 — to «class 2,» and intI3 — to «class 3» (Guangchao et al., 2013). The correlation between integrons and multidrug resistance in *P. aeruginosa* is a matter of significant concern because to its clinical consequences. The presence of multidrug-resistant strains of *P. aeruginosa* presents a substantial obstacle within healthcare environments, as it limits the available treatment choices and increases the possibility of therapy ineffectiveness (Khorshidi et al., 2022). Numerous investigations have been conducted to explore the correlation between antibiotic susceptibility, biofilm-forming capacity, and the presence of integrons.

In some cases, bacteria harboring positive class 1 integrons showed notable resistance to specific antibiotics, despite their capacity for biofilm formation (Babosan et al., 2022).

The **aim** of this study was to systematically characterize and detect Integron genes (intI, intII, intIII) with antibiotic-resistant and biofilm-forming in isolated *P. aeruginosa.*

Materials and Methods. S*amples collection and identification.* This study included a total of two hundred and nine (209) samples from patients suffering from moderate to severe burn (53), wound infections (40), UTI infection (35), blood (30) ear infections (28), and sputum (23), for both sexes of different ages. All the isolates were identified based on conventional biochemical and microbiological tests, and the positive result for biochemical test was considered an elementary criterion for *P. aeruginosa* recognition (Najafi et al., 2015).

Biofilm quantitation. The microtiter plate (MTP) is a quantitative technique applied to assess biofilm formation using a microtiter plate reader, as outlined by (O'Toole, 2010). The biofilm of *P. aeruginosa* cultivated in 96-well plates was assessed using biomass indicator crystal violet. The strains were classified into four distinct categories based on their biofilm production capabilities: no-biofilm producers, weak biofilm producers, moderate biofilm producers, and strong biofilm producers. All isolates exhibited a statistically significant disparity in the optical density of biofilm formation when compared to the control group (wells with broth media only), which was measured by assessing the absorbance at a wavelength of 570 nm using ELISA reader equipment.

Antimicrobial susceptibility. The automated microbiology compact system VITEK 2 uses growth-based technologies. It is used to ascertain the presence of microorganisms, perform antibiotic susceptibility testing, and determine resistance mechanisms by using colorimetric reagent cards that are incubated and interpreted automatically. Lists of antimicrobial categories proposed for antimicrobial susceptibility testing were created using documents and breakpoints from the Clinical Laboratory Standards Institute (CLSI), where we used 17 agents from six various antimicrobial categories used in *P. aeruginosa* elimination.

DNA extraction and amplification. DNA was extracted from *P. aeruginosa* isolates using a commercial extraction kit (Presto™ Mini gDNA Bacteria Kit, Taiwan), following the manufacturer's instructions, The designed primers shown in Table 1 were supplied from Macrogene Company (Republic of Korea) and used to detect *IntI, IntII,* and *intIII* genes of *P. aeruginosa* according to the manufacturer's instructions, mixture of PCR for each primer with final volume 20 µL/reaction, and the protocol used depending on the Master Mix AccuPower® PCR PreMix (Bioneer, Republic of Korea) instructions. Each PCR reaction mixture consisted of 10 µL master mix, 1µL Forward Primer (10 picomole), 1µL Reverse Primer (10 picomole), 5µL De-ionized water, and 3µL the DNA. The following conditions were used for DNA amplification in a thermal cycler with a temperature gradient: initial DNA denaturation at 95 ^{0}C for 5 min, followed by annealing at temperatures of 58 ^{0}C (intI1), 58 ^{0}C (intI2), and 59 °C (intI3) for 30 sec, with an extension at 72 ^{0}C for 30 secand a final extension at 72 °C for 7 min. The PCR products were resolved by electrophoresis in a 1.5 % W/V agarose gel in TBE buffer and then visualized by Gel Documentation.

Statistical analysis. Levels of integrons were shown as Mean ± SD with an F test that was employed to compare more than two groups. Other parameters were noted as frequencies and percentages, and the Pethearson-Chi-square test was used to reveal significant differences within frequencies. $P \leq 0.05$ was detected as significant. The present data were programmed by the SPSS v. 24.0 statistical software program.

Results. *P. aeruginosa* was identified in 83 isolates from all the considered samples (209) collected from different clinical samples. The findings of the current study revealed statistically significant variances ($p < 0.05$) among the percentages of some samples and isolated *P. aeruginosa.* The burn and wound infection scored the highest percentages (25% and 19%) whereas ear and sputum scored the lowest frequency (13% and 11%). Based on the positivity of *P. aeruginosa*, burn and ear sites scored higher percentages (58% and 50%) than UTI and blood, which scored the lowest percentage (23%). Pronounced statistics can be observed in Table 2. All 83 isolates were Gram-negative, rod-shaped, and red-colored under the microscope**,** and the corresponding biochemical examinations on the addressed isolates were identical to those described previously by (Jalil et al., 2018).

Biofilm formation. The findings of the study indicated that the *P. aeruginosa* isolates (83 isolates) exhibited adherence and demonstrated the ability to create biofilms with positive characteristics. The results were categorized as follows: 18.1% exhibited strong-biofilm development, 21.7% — moderate-biofilm formation, 28.9% — weak-biofilm formation, and 31.3% were classified as non-biofilm producers. The findings of the current investigation revealed that the *P. aeruginosa* isolates that produce biofilm scored the highest percentage (68.7%) against non-producing biofilm isolates (31.3%) with significant differences ($p < 0.05$).

Table 1. **Compilation of primers for PCR amplification, each characterized by respective sequences, sizes, and annealing temperatures**

Target gene	Primer name	Oligonucleotide primer sequence (5'-3')	Amplicon size (bp)	Annealing temperature °C
IntII	F	GGGATGCGAACCACTTCAT	311	58
	R	CGCATACGCTACTTGCATTACA		
IntIII	F	GATTTTGATAATGGCTGCATCA	433	58
	R	GCCCTAAGAGTTCTTGCACAGT		
IntIIII	F	GTGCATGAGGCAGATACACG	575	59
	R	CAGCCTACAGACCGAGAAGG		
References	This study			

bp — base pair, F — forward sequence, R — reverse sequence

Table 2. **Frequency and percentage of *P. aeruginosa* isolates in different sites of the body**

Type of infection	Number of samples %		Frequency of *P. aeruginosa*	%	P value
Burn	53	25	31	58	$P > 0.05$
Wound	40	19	14	35	$P < 0.05^{*}$
UTI	35	17	8	23	$P < 0.01^{**}$
Blood	30	14	7	23	$P < 0.01^{**}$
Ear	28	13	14	50	1.00
Sputum	23	11	9	39	$P < 0.05^{*}$
Total	209	100	83	40	$P < 0.05^{*}$
P value	$P < 0.01^{**}$		$P < 0.001^{***}$		

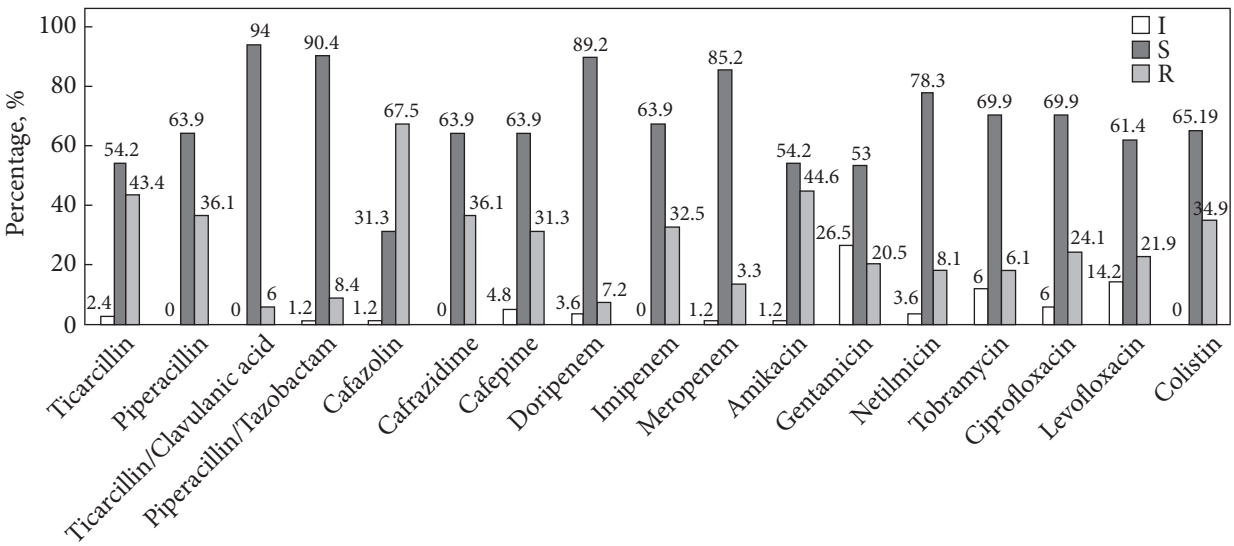

Fig. 1. Sensitivity of clinical *P. aeruginosa* to 17 antibiotics, where S: Sensitive; I: Intermediate; R: Resistant

Antibiotic susceptibility. Out of a total of 83 clinical isolates of *P. aeruginosa*, 49.4% (41) were identified as multidrug-resistant (MDR), 34.9% (29) as sensitive, 13.3% (11) as extensively drug-resistant (XDR), and approximately 2.4% (2) as potentially pan drug-resistant (PDR). The results of the study indicated that MDR and sensitive *P. aeruginosa* isolates exhibited the highest percentage, while the PDR and XDR isolates demonstrated the lowest percentages. These differences were found to be statistically significant ($p < 0.05$). We established that the majority of *P. aeruginosa* isolates were resistant to several antibiotics and were MDR. Fig. 1 summarizes that among all 17 tested antibiotics, ticarcillin/clavulanic acid was shown to be the most potent antimicrobial drug, with a susceptibility rate of 94%, followed by piperacillin/tazobactam (90%), doripenem (89%), and meropenem (85%), where the highest resistance was found against cefazolin (67.50%), amikacin (44.60%), and ticarcillin (43.40%).

Selection of isolates for molecular detection. According to the findings illustrated in Table 3, we selected 30 isolates for molecular profiles of integrons. We selected 5 isolates sensitive to antibiotics (3 strong biofilm producers and 2 moderate biofilm producers), with 15 MDR isolates (6 strong biofilm producers, 5 moderate biofilm producers, 3 weak biofilm producers and 1 no biofilm producer), from XDR we selected 8 isolates (2 strong biofilm producers, 4 moderate biofilm producers, 1 weak biofilm producer, and 1 no biofilm producer), and two PDR isolates (1moderate biofilm producer and 1 no biofilm producer). The procedure of selecting these isolates was based on antibiotic sensitivity, the frequency of isolates in each group (sensitive, MDR, XDR, and PDR), as well as taking into consideration the variety in the selected isolates' ability to form a biofilm.

DNA extraction and integron detection. Whole-genome DNA from overnight cultures for selected isolates (30 isolates) of *P. aeruginosa* were extracted efficiently by the PrestoTMMini gDNA Bacteria Kit Quick Protocol (Geneaid). PCR technique was performed on extracted DNAs to detect intI and intII genes using the set of primers listed in Table 1. The findings of the current investigation indicate the presence of a statistically significant disparity ($p < 0.05$). Among percentages of integrons, where integron

I scored the highest percentage (100%) (Table 4), of which 6.6% were PDR, 20% XDR, 46.6% MDR, and 16.6% were sensitive to tested antibiotics, was found in 3 (10 %) *P. aeruginosa* isolates (Fig. 2), all of which (100 %) were XDR, and 3 (10 %) strains had both intI and intII genes. No intIII gene was detected in any of the isolates.

Discussion. *P. aeruginosa* is categorized as an opportunistic pathogen, often associated with infectious diseases that contribute to a substantial global burden of diseases. The results of this study are consistent with the findings published in prior investigations, including the study conducted by (Shawkat, 2022; Al-Bayati et al., 2021) concerning the distribution of *P. aeruginosa* isolates associated with different patient infections. Furthermore, the statistical analysis revealed substantial disparities with a high level of significance (P < 0.01). Upon comparing the results of this investigation with those of previous studies, it becomes evident that there exist variations and similarities in the proportions of

Table 3. **Comparison of biofilm intensity and antibiotic sensitivity of *P. aeruginosa* isolates**

Sensitive MDR			Antibiotic sensitivity				Total	P value
			PDR	XDR				
Biofilm intensity	Absent	n	11	13	1	2	27	$P < 0.05$*
		%	37.9%	31.7%	50.0%	18.2%	32.5 %	
	Weak	n	12	8	0	3	23	$P < 0.01$**
		%	41.4%	19.5%	0.0%	27.3%	27.7 %	
	Moderate	n	3	11	1	3	18	$P < 0.01$**
		%	10.3%	26.8%	50.0%	27.3%	21.7 %	
	Strong	n	3	9 0		3	15	$P < 0.05$*
		%	10.3%	22.0%	0.0%	27.3%	18.1%	
Total %		n	29	41	2	11	83	$P < 0.01$**
		100.0%	100.0%	100.0%	100.0%	100.0%		
P value			$P < 0.05$*	$P > 0.05$	$P > 0.05$	$P > 0.05$	$P < 0.01$**	

Table 4. **Frequency and percentage of integron-positive samples for *P. aeruginosa* isolates based on clinical samples**

Clinical sample	No. of samples	IntI positive No. (%)	IntII positive No. (%)	IntII negative No. (%)	IntIII positive No. (%)	IntIII negative No. (%)
Burn	11	11 (100%)	3 (27.27%)	8 (72.72%)	0	11 (100%)
Wound	7	7 (100%)	0	7 (100%)	0	7 (100%)
UTI	3	3 (100%)	0	3 (100%)	0	3 (100%)
Blood	2	2 (100%)	0	2 (100%)	0	2 (100%)
Ear	4	4 (100%)	0	4 (100%)	0	4 (100%)
Sputum	3	3 (100%)	0	3 (100%)	0	3 (100%)
Total	30	30 (100%)	3 (10%)	27 (90%)	0	30 (100%)
P value	*P<0.01***					

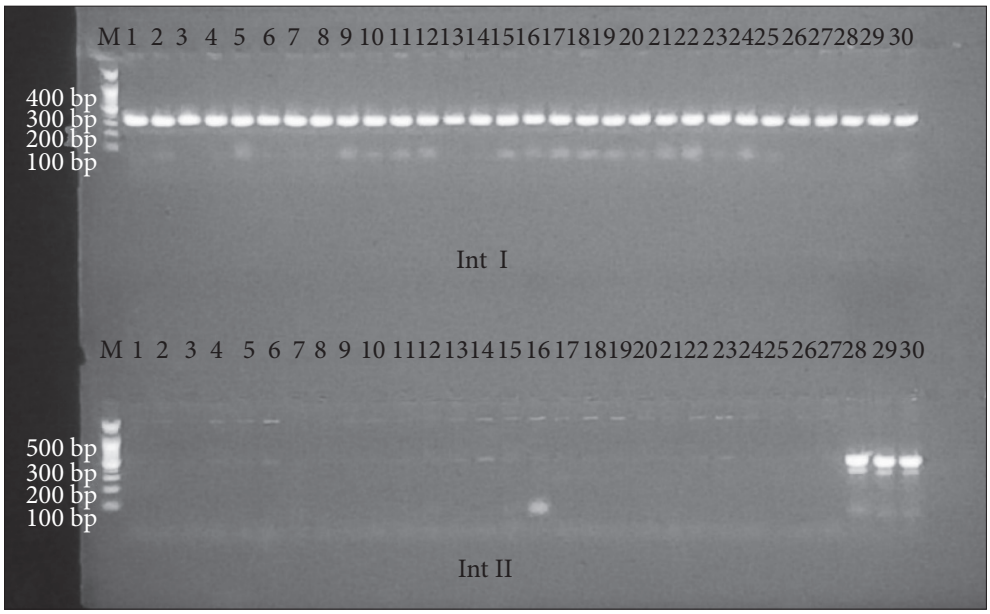

Fig. 2. Agarose gel electrophoresis of PCR assay of integron gene (IntI and IntII) cassette amplification, (M = DNA ladder 100bp, 1—30 selected *P. aeruginosa* isolates)

bacteria isolated from various samples. This is because *P. aeruginosa* bacteria are a major cause of acquired infections and are related to a variety of factors, such as resistance to a broad range of sterilization materials and antibiotics, the percentages of distributed isolates, and different antiseptics used in hospitals (Al-Mamari, 2019). Those results are consistent with our research, which indicates that *P. aeruginosa* was extensively present in burn wounds and pus samples. The presence of pus in burn and surgical wounds creates a favorable environment for the proliferation of pathogens and the subsequent transmission of infections. These circumstances collectively lead to the elevated incidence of *P. aeruginosa* (Procop et al., 2020). *Pseudomonas* species possess many important virulence factors using horizontal gene transfer to acquire novel resistant genes (i.e., integrons, plasmids, or transposons) and act on losing the effectiveness of the primary categories of anti-pseudomonal medications, namely pertinent carbapenems, cephalosporins (including cephalosporin/β-lactamase combos), aminoglycosides, respiratory fluoroquinolones (such as levofloxacin, ciprofloxacin, and moxifloxacin), and colistin (Gajdács et al., 2021). The increasing resistance of *P. aeruginosa* to numerous antibiotics is now leading to the accumulation of antibiotic resistance and cross-resistance between antibiotics and the appearance of MDR forms of *P. aeruginosa.* The term «multidrug-resistant» (MDR) was originally coined to describe the condition where a microorganism becomes resistant to at least one antimicrobial agent in three or more categories. «Extensively drug-resistant» (XDR) refers to the situation where the microorganism is resistant to at least one agent in all but two or fewer antimicrobial categories, meaning that the bacterial isolates remain susceptible to only one or two categories. «Pan drug-resistant» (PDR) is defined as the condition in which the microorganism is non-susceptible to all agents in all antimicrobial categories (Magiorakos et al., 2012). In the current research, we found that a significant proportion of *P. aeruginosa* isolates are resistant to several antibiotics and the majority of isolates were MDR. Fig. 1 summarizes that among all 17 tested antibiotics, Ticarcillin clavulanic acid was shown to be the most potent antimicrobial drug, and this finding of our research is very close to the previous observa-

tions (Karami et al., 2020). The results of the current study suggest that Ticarcillin clavulanic acid is the most effective antibiotic and could be a drug of choice. Most of the isolates were susceptible to Ticarcillin clavulanic acid, which may be explained by the limited utilization of this antibiotic in standard patient treatments. Biofilm production is recognized as a contributing factor to the development of resistance in *P. aeruginosa*. The presence of biofilm serves as a formidable obstacle for both the immune system and antibiotics, thus constituting a primary etiological factor in the development and progression of infectious diseases (Mohsenzadeh et al., 2021). The formation of a mucous layer and utilization of host proteins by biofilm contribute significantly to pathogenicity. These factors create an optimal environment for bacterial growth and enhance their resistance to treatment. The observed high prevalence of bacterial biofilm production in the present study may account for the elevated levels of bacterial resistance to all antibiotics (Al-Sheikhly et al., 2019; Shatti et al., 2022). Numerous investigations have been conducted to examine the correlation between antibiotic susceptibility, biofilm formation capacity, and the presence of integrons. Integrons are a section of dsDNA that are involved in bacterial evolution and versatility. Class I resistance integrons are the most prevalent, followed by class II and class III. Integrons have received attention recently for their potential contribution to the transmission and spread of resistance factors (Shilba et al., 2015; Deng et al., 2015). Findings close to ours for *P. aeruginosa* isolates have been obtained for 131 (100%) class 1 integron isolates. In contrast, only one of the five samples (equivalent to 3.81% of the total) was found to possess a class 2 integron. None of the isolates exhibited the presence of class 3 integron (Abdulla & Almuttairi, 2023). Another study indicated that the occurrence of class 1 and 2 integrons was observed in 55.5% and 29% of *P. aeruginosa* isolates obtained from clinical samples of wounds, blood, urine, and others (Faghri et al., 2018). Also, a total of 87 isolates (45.3%) were found to possess class 1 integrons, however no instances of class 2 or class 3 integrons were identified (Abd-Elmonsef & Maxwell, 2022). This difference can be attributed to several factors, including the geographic location under study, the total number of samples analyzed, the source of isolates, and the incorrect consumption of antibiotics. Integrons possess the capability to confer resistance to frequently administered therapeutic drugs, such as β-lactamases, fluoroquinolones, and even carbapenems. The emergence of a high frequency of intI1 represents serious future challenges and has the potential to increase and spread antibiotic resistance. To effectively combat antibiotic resistance in *P. aeruginosa*, it is crucial to comprehend the role of integrons in multidrug resistance.

Conclusions. The findings of the present investigation indicate that integrons and biofilm formation are key factors contributing to the development of antibiotic resistance in *P. aeruginosa*. Class 1 integrons were identified in all bacteria isolates (100%). The high prevalence of class 1 integrons can proliferate resistance to crucial antibiotics such as β-lactams, aminoglycosides, and cephalosporins. Integrons make it easier for bacteria to collect and rearrange gene cassettes, which enables them to quickly adapt and acquire multidrug resistance. These variables contribute to the complexity of treating infections caused by this bacterium and highlight the importance of constant monitoring of antibiotic resistance in clinical environments.

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ХАРАКТЕРИСТИКА ГЕНІВ ІНТЕГРОНІВ КЛІНІЧНИХ ІЗОЛЯТІВ *PSEUDOMONAS AERUGINOSA*, ЯКІ РЕАЛІЗУЮТЬ РЕЗИСТЕНТНІСТЬ ДО АНТИБІОТИКІВ ТА БІОПЛІВКОУТВОРЕННЯ ЦИМИ ШТАМАМИ

Pseudomonas aeruginosa — це бактерія, яка має важливе клінічне та епідеміологічне значення. Вона є основною етіологічною причиною опортуністичних інфекцій в осіб з ослабленим імунітетом. Відомо, що інтегрони мають помітний вплив на грамнегативні бактерії, особливо в контексті *P. aeruginosa*, бактерії, яка відома своєю здатністю розвивати резистентність до антимікробних препаратів. **Мета.** Системно охарактеризувати та виявити гени інтегронів (intI, intII, і intIII) з антибіотикорезистентністю та біоплівкоутворенням в клінічних ізолятах *P. aeruginosa*. **Методи.** В навчальній лікарні Аль-Ярмук, Багдад, Ірак, було відібрано 209 зразків, з яких було виділено ізоляти *P. aeruginosa*. Ідентифікацію бактерій проводили фенотипічно та за допомогою біохімічних тестів. Чутливість до антибіотиків визначали за допомогою системи Vitek2. Кількісне визначення утворення біоплівки проводили методом мікротитрування. Для оцінки присутності інтегронів класів 1, 2 і 3 використовували метод ПЛР. **Результати.** *P. aeruginosa* була ідентифікована у 83 зразках за допомогою комбінації морфологічних та біохімічних досліджень, де всі ізоляти показали здатність рости на цетримідному агарі, селективному середовищі для *P. aeruginosa*. Результати також показали значні відмінності ($p < 0,05$) між відсотковим співвідношенням кількості взятих зразків та виділених ізолятів *P. aeruginosa*. Найбільше було зразків з опікових поверхонь та інфікованих ран (25 % і 19 % відповідно), тоді як *P. aeruginosa* виявлялась найчастіше в зразках з опікових поверхонь та вух (58 % і 50 % відповідно). Крім того, було показано, що більшість ізолятів мали здатність утворювати біоплівку (68,7 %), з них мультирезистентні та чутливі ізоляти *P. aeruginosa* мали більший показник біоплівкоутворення (49,4 % і 34,9 % відповідно), ніж потенційно полірезистентні і помірнорезистентні ізоляти (2,4 % і 13,3 % відповідно). Результати ПЛР показали, що інтегрон класу 1 зустрічався частіше (100 %) порівняно з інтегроном класу 2, який був виявлений у 3 (10 %) ізолятів, тоді як ген intI3, не був виявлений у жодному з ізолятів *P. aeruginosa*. **Висновки.** В цілому, результати цього дослідження вказують на те, що інтегрони та здатність до утворення біоплівки є важливими факторами, що сприяють підвищенню антибіотикорезистентності *P. aeruginosa*. Поширеність інтегронів класу 1 є значно вищою у всіх бактеріальних ізолятах, причому в наших дослідженнях частота його виявлення склала 100 %. Така висока частота присутності інтегронів класу 1 пов'язана з розвитком резистентності до основних антибіотиків — β-лактамів, аміноглікозидів та цефалоспоринів.

Ключові слова: *інтегрон, антибіотикорезистентність, Pseudomonas aeruginosa, біоплівка.*