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Original Research Article

Characterization of Uropathogenic *Escherichia coli* by Phylogenetic Grouping, Integron, and Antibiotic Resistance Properties

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ABSTRACT

Multidrug-resistant phenotypes in clinically important Gram-negative bacteria are a major medical issue worldwide. The presence of integrons from classes 1 and 2 (*intl*1 and *intl*2) and their phylogenetic correlations with antibiotic resistance in UPEC clinical isolates were examined in this investigation. Midstream urine samples from urinary tract infection outpatients in multiple Baghdad hospitals yielded 100 highly resistant *E. coli* bacteria. The automated VITEK system recognized typical *E. coli* colonies. Disk diffusion was used to investigate antibiotic susceptibility for the most frequent phylogroups. PCR was utilized to detect and characterize integrons and antibiotic resistance genes. The most common phylogroups were F (36.66%) and C (23.33%). UPEC isolates were detected in all phylogroups except six untyped ones. Integrons were found in 74.4% of isolates (61.4% *intI*1 and 13.3% *intI*2). The highest integron rate (85.71%) was in phylogroup C isolates. Integrons were linked to multidrug resistance in 60% of phylogroup F and C isolates. Nearly half of these isolates had multidrug resistance. This study found that phylogroup F dominates *E. coli* isolates due to a complex set of variables that support its expansion and persistence. Enhanced fitness, pathogenicity, and antibiotic resistance make these strains a public health threat. This study shows that clinically mobile Class 1 integrons attract more mobile genomic components. This may affect the establishment of complex, horizontally moving multidrug-resistant units, complicating antibiotic therapy.

***Keywords*:** *Escherichia coli*, Extensively-drug resistant, Integrons, Phylogenetic group, Urinary tract infections.

Introduction

Urinary tract infection (UTI) is one of the most common infections in humans, and it can be acquired in the hospital or in the community.[1] The majority of UTI cases are caused by Gram-negative bacteria, especially uropathogenic *Escherichia coli* (UPEC), which accounts for 80% of infections,[2] and *Proteus mirabilis.*[3] *Escherichia coli* populations are divided into eight primary phylogenetic groups, which include A, B1, B2, C, D, E, F (belonging to *E. coli* sensu stricto), and clade I (belonging to *Escherichia* clade), based on the presence of specific genes or DNA fragments that can be identified using a new method developed by Clermont *et al*.[4]

One of the major challenges facing the global medical community is the rapid rise of multidrug-resistant phenotypes in clinically important Gram-negative bacteria. In this context, horizontal gene transfer mediated by transposons and plasmids is one of the main mechanisms for the transmission of antimicrobial resistance, and integrons are important mobile genetic elements involved in this dissemination, primarily in Gram-negative bacteria.

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Three elements are necessary for integrons to function: the gene *intI*, which encodes an integron integrase that catalyzes the excision and integration of the gene cassettes containing the antibiotic resistance gene, an associated recombination site (attl), and a promoter (Pc), which controls the transcription of the captured gene.[5] Integrons are divided into five classes based on the sequence of their integrase. Class I integron includes the ones that are most frequently detected in isolated clinical strains. It contains the 59-CS area, gene cassettes in a variable region, and then a conserved region known as the 39-CS, which contains two fixed genes: the quaternary ammonium resistance gene (*qacEDI*) and the sulphonamide resistance gene (*sul1*). A Class 1 integron would therefore have the structure *IntI* – attI [R11, R21]-qacED1-sul1.[6]

The present study was conducted to identify the dominant phylogenetic grouping, determine antimicrobial resistance profiles, and the prevalence and diversity of integrons. The potential association between the presence of integrons and multidrug resistance in UPEC isolates was also investigated.

Materials and Methods

Collection of specimens

In this cross-sectional study, one hundred midstream urine specimens (MUS) were collected in sterile screw-capped containers from UTI patients. The samples were collected from outpatients (males and females) younger than 18 years old, who suffered from UTIs. Between October 2021 and January 2022, the patients were attended to in the Centric Kids Technical Department of Medical City Hospital, Iskan Hospital for Children, and Al-Yarmuk Hospital. The urine specimens were plated immediately on blood agar, MacConkey agar, and Eosin methylene blue plates by direct streaking method, and then examined for bacterial growth as described by Atlas *et al*.[7] Typica *E. coli* colonies were identified using the automated VITEK system (BioMérieux,

France). The isolation and identification were carried out in the microbiology laboratories at Centric Kids Technical Department of Medical City Hospitals, Iskan Hospital for Kids, and Al-Yarmuk Hospital.

Ethical approval
Ethical approval for this study was obtained from the Ministry of Health and Environment in Iraq under the approval numbered 556 issued in March 3 2022. Informed consent was obtained from the participants for socio-demographic data to be collected, samples to be analyzed, and patient privacy to be maintained.

Antimicrobial susceptibility testing
The disk diffusion method was used to investigate antimicrobial susceptibility in clinical isolates of UPEC, according to the Clinical and Laboratory Standard Institute.[8] Sixteen antibiotic discs were used, which included amikacin (30 µg), ampicillin (10 µg), ceftazidime (30 µg), impenem (10 µg), tetracycline (30 µg), levofloxacin (5 µg), ciprofloxacin (5 µg), nalidixic acid (30 µg), nitrofurantoin (300 µg), co-trimoxazole (25 µg), gentamicin (10 µg), piperacillin/tazobactum (100 µg), cefepime, (10 µg), cefotaxime (10 µg), ceftriaxone (10 µg), augmentain (100 µg), piperacillin (10 µg), and colistin (10µg). The assay was carried out using Muller-Hinton agar. Bacterial isolates were classified according to the resistance profiles as indicated by the ECDC and the US Centers for Disease Control and Prevention.[9] Particularly, group 1 (low resistant bacteria) comprised those without resistance to any class or with resistance to one molecule in ≤2 classes; group 2 (highly resistant bacteria) included MDR bacteria with resistance to ≥1 molecule in ≥3 different classes and extensively drug-resistant (XDR) bacteria with resistance to ≥1 molecule in all, but 2 or fewer classes; and group 3 (pandrug-resistant bacteria, PDR) consisted of those with resistance to all drugs and classes of antibiotics.[10]

Molecular detection of classes 1, 2, and 3 integrons
Genomic DNA was extracted according to the method described by Ali and Khudhair.[11] Briefly, 3 to 5 colonies of an overnight culture of *E. coli* on brain heart infusion agar were suspended in 300 µL of sterile distilled water and boiled at 95°C for 10 minutes. Then cell debris was removed by centrifugation for 10 minutes at 13,000 rpm, and 200 µL of the supernatant was stored at −20˚ C for DNA amplification. The presence of classes 1, 2, and 3 integrons in *E. coli* was investigated by amplification of integrase genes with *intI*1, *intI*2, and *intI*3 specific primers, respectively, as described by Mobasseri *et al*,[12] with slight modifications. The PCR was prepared in a total volume of 25 µL and the amplification PCR solution contained a DNA template (5 µL), master mix (12.5 µL), distilled water (5.5 µL), and forward and reverse primers (1 µL). The PCR amplifications were performed on a thermocycler. Following the amplification, the PCR products were resolved on 1% agarose gel electrophoresis alongside a DNA ladder (100 bp). After staining with ethidium bromide, the bands were visualized by a UV-gel documentation system.

Detection of the integron I structure
The architecture of class 1 integron was assessed according to Vignoli *et al*.[13] The gene cassette regions (5` CS/ 3` CS), as well as the 30 conserved segments, corresponding to *qacED1* and *sulI* genes (*qacED1-F/Sul1-B)* were amplified.

Phylogenic grouping by a quadruplex polymerase chain reaction
This method targeted seven encoding genes: *chuA, yjaA, TspE4.C2, arpA, arpAgpEh, trpA, and trpBA* including the controls, to group *E. coli* into phylogroups A, B1, B2, C, D, E, F, and clade I. The quadruplex PCR was performed using primer sequences, and PCR reaction conditions as described by Clermont *et al*.[3,14] The amplified PCR products were analyzed for phylogrouping of *E. coli*.

Statistical analysis
The data were analyzed using Stata software (version 14.0). The Chi-square test was used to determine the association between the phylogenetic groups, the presence of integrons in both research groups, and the antimicrobial resistance profile. The significance level was chosen at $p < 0.05$.

Results and Discussion

In this study, 100 patients with *E. coli* isolates from 150 individuals suspected of having a UTI were documented. Sixty-four (66%) of the isolates were recovered from female patients, and 36 (36%) were obtained from male patients. The age range of the patents was from 1 month to 18 years. Majority of UTI cases were in females, with the age range of 12 to 18 years old, which accounts for 38%. Table 1 summarizes the social-demographic information and symptoms.

Antimicrobial properties
According to the results of the sensitivity test, it was observed that 65% of the isolates had extensively multiple antibiotic resistance (XDR) to the test antibiotics (Table 2). The resistance of the isolates to the quinolounes antibiotics, which include nalidixic acid, flouroquinolounes such as ciprofloxacin, and levofloxacin, was found to be 86.6 %, 66.6 %, and 50 %, respectively. Cephalosporins I, II, III, and IV, which include cefoxitin, ceftazidime, cefepime, and ceftriaxone, had resistance rates of 63.3, 73.3, 43.3, and 63.3%, respectively. Meropenem and impenem are two carbapenems that the isolates were resistant to at 20 and 30%, respectively. The resistance was observed to be 18.8 and 20% for β-lactam combinations, which include augmentin and piperacillin-tazobactum. Also, the resistance was found to be 45.6% for the penicillin group of antibiotics, which includes piperacillin. Chloramphenicol from the antibiotic group, phenicol and tetracycline from the same antibiotic group both showed a 46.6% resistance rate. Colistin, an antibiotic belonging to the lipopeptide class, had a 23% resistance rate.

Integron typing of uropathogenic Escherichia coli
The presence of integrons in clinical pathogenic isolates is also highly related to antibiotic resistance. Class 1-integron was highly prevalent in these pathogenic isolates. Fifty-five isolates were positive for the *int1* gene and harboring class 1-integron, whereas eleven isolates were positive for the *intI*2 gene and harboring class 2-integron, and class 3-integron was not detected in any of the isolates due to the absence of the *intI*3 gene.

Table 1: Socio-demographic characteristics and symptoms of the sample

Characteristics	Description	Number (%)
Age Groups	< 1 - 6	24(24%)
	6 - 12	31(31 %)
	12 - 18	45(45 %)
Gender	Female	66(66 %)
	Male	34(34 %)
Attendance	Outpatient	24(24%)
	Ward	76(76 %)
UTI Recurrence	New infection	52(52 %)
	Recurrent infection	48(48%)
Clinical Symptoms	Symptomatic	61(61 %)
	Asymptomatic	39(39 %)
Hospitals	Medical City	32(32%)
	Alyarmok	24(24%)
	Iskan Teaching for kids	44(44%)

Architecture of integron classes

As presented in Table 3, G0 contained 18 isolates that have only the *IntI gene* and showed 7 resistance patterns to antibiotics AUG, CO, CFM, GN, AK, PIP, and FOX. Class I (GI) revealed 11 isolates with *intI* and *sull genes* and have only 4 resistance patterns of antibiotics, which included AUG, CO, CFM, and GN.

On the other hand, *intI, sull, and qace1* genes were observed in Class II (GII) integron and included 8 isolates that showed 6 resistance patterns to AUG, FOX, CFM, FEP, AK, and LEV antibiotics. Class III (GIII) integron showed 7 isolates that are resistant to AUG, FEP, PIP, AK, GN, and CO, as well as having integron structures *intI, sull, qace1* and *gene cassette*, while the last class of integron has a complete structure *intI, sull, qace1*, gene cassette, and the *orf* gene, which demonstrated 2 resistance patterns. Only 8 isolates were observed to be resistant to AUG and FEP.

Phylogenic grouping of uropathogenic Escherichia coli

As shown in Tables 4 and 5, uropathogenic *E. coli* isolates from groups F and C had the largest integron containers in the present study. The results revealed significant differences in integron class 1 and 2 distributions among phylogenetic groups, with the highest distribution of the *Intl1* gene among phylogenetic groups recorded in group F (33 isolates, 72.7%), followed by group C (21 isolates, 85.71%), and group B2 (12 isolates, 83.33%). Meanwhile, the *IntI1* gene was mainly observed in group B2 (12 isolates, 16.67%). Furthermore, *IntI*2 (1 isolate; 20%) of group D had both classes of integron, followed by 20% (1 isolate) each for groups D and B1. This study found that females (66 %) were more likely than males (34 %) to have UTIs. This observation is consistent with the findings of other studies,[15] which showed that women are more likely to develop UTIs than men. Some patients develop recurrent urinary tract infections.[16] Recurrent UTI is defined as two or more recurrences within six months and three or more UTIs during a 12-month period.

According to Nuutinen and Uhari's research,[17] approximately 20–30% of adult women with an initial UTI will experience a recurrence within 3–4 months, while in children, roughly one-third of those who experience a UTI before the age of one will experience a recurrence within 3 years, and 18% will experience a recurrence within a few months. About 50% of UTIs are misdiagnosed, although recurrent UTIs can be caused by a variety of factors, including the same or different strains of UTI-causing bacteria in the stomach that can (re) inoculate the bladder. The findings of this study are in agreement with those of Silverman *et al*.,[18] who found that bacteria present in the bladder epithelium can periodically reappear and trigger UTI recurrence.

The main risk factors for UTI development and recurrence are having experienced a UTI before the age of 15, engaging in sexual activity three or more times per week, the use of spermicides, having new or multiple sexual partners, and having experienced a UTI in the past. Systemic hormonal therapy is ineffective as a preventative measure in menopausal women, and most cases of asymptomatic bacteriuria during this time do not require treatment. This is in line with the findings of the study by Milart *et al*.,[19] which showed that in postmenopausal women, the risk is primarily increased by the aftereffects of low estrogen levels, which are frequently linked to vaginal atrophy.[20] However, the majority of research on this topic has been conducted in the two districts of Baghdad's capital, Karkh, and Rusafa, which differ from one another in terms of population, social conditions, and economic standing. As a result, UTIs are much more prevalent, complicated, and poorly documented, with results that are similar to those of another study conducted in Iraq but with a different percentage.[21]

The present study discovered resistance to the antibiotics nalidixic acid, ceftazidime, and augmentin (amoxillin/clavulanic acid) at 80, 85, and 52%, respectively. Ali *et al*.,[22] also reported resistance to these three antibiotics in his isolates. In contrast, resistance to cefotazidime and cefepime was found to be 78%, resistance to levofloxacin was observed to be 55.5%, and resistance to levofloxacin and impineme was shown to be 73%.

Table 2: The antibiotic-resistant patterns of *Escherichia coli* isolates measured by disk diffusion method.

Antibiotic group	Antibiotics	No. of resistant isolates	Resistance percentage
β-lactam carabapenem	Meropenem	18	20%
	Impenem	27	30%
χ^2 (df.), P-value	1.8 (df. = 1), 0.17 NS		
β-lactam combinations	Amoxillin-clavulnate	17	18.8%
	Piperacillin-tazobactam	18	20 %
χ^2 (df.), P-value	6.4 (df. = 1), 0.011*		
Lipopiptide	Colistin	20	23%
Cephems (including	Cefotaxime	66	73.3%
cephalosporins I, II, III, IV)	Cefoxitin	57	63.3%
	Ceftazidime	78	86.6%
	Cefepime	39	43.3%
	Ceftriaxone	57	63.3%
χ^2 (df.), P-value	4.79 (df. = 5), 0.4 NS		
Fluroquinolones	Levofloxacin	57	50%
	Nalidixic acid	25	86.6%
	Cirpofloaxacin	60	66.6%
χ^2 (df.), P-value	15.9 (df. = 2), 0.003**		
Tetracyclines	Tetracycline	42	46.6%
Pencillin	Piperacillin	41	45.6%
Phenicols	Chloramphenicol	78	46.6%
χ^2 (df.), P-value	16.5 (df. = 2), 0.002**		

χ2: Chi-square; df: Degree of freedom; P: Probability; **: $p < 0.01$; *: $p < 0.05$; NS: Non-significant.

The findings of this study differ from what was reported by Maleki *et al*.,[23] where the resistance to ceftazidim had reached 26.1% in Iran, and the resistance to cefotaxime was 30%. They reported that the efflux pumps were responsible for the rise in antibiotic resistance. The findings of the current study are consistent with what Shah *et al*.,[24] reported.

Meropeneme resistance was found to be 26%, whereas cefotriaxone resistance was discovered to be 49%. The rise in β-lactam antibiotic resistance is due to the production of β-lactamse, which includes cephalosporinase and pencillinase that act on breaking the β-lactam ring, inhibiting antibiotics belonging to the group's penicillins and cephalosporins.[25] All the isolates were resistant to at least one of the tested antibiotics in terms of susceptibility to antimicrobial agents, with 97 isolates displaying MDR. Third-generation cephalosporins "cefotaxime/ceftazidime" were reported to be resistant to *E. coli* isolates from urine samples obtained from hospitalized patients in England (13.8% - 21.3%).[26] The percentage of UPEC susceptible to the third generation cephalosporins in Romania was 87%, according to the findings of Ciontea *et al*.[27]

The molecule technique applied in different topic of medicine, included identification of pathogens [28, 29]. However, Genetic testing revealed class 1 and class 2-integron-integrase genes in 55 and 2% of isolates, respectively. These findings agree with those of Khoramrooz *et al*.,[30] who found the presence of integrons in clinical isolates of *E. coli* from a variety of countries and locations around the world. Several studies generally indicated a higher prevalence of class 1-integron. There were, however, some differences depending on the source of the infection and regional dissemination. Class 1 and Class 2 integrons were found in 52 and 2.5% of UPEC isolates, respectively, in a study conducted by Yasuj in southwest Iran, in 2018.[31] Another study from China discovered that only 22% of isolates had the Class 1-integron gene, which is consistent with the results in the present findings. The incidence of integrons appears to vary between the general public and medical facilities. Classes 1 and 2 integrons were found in 6.25 and 10.41%, respectively, of the community-acquired *E. coli* isolates by Sütterlin *et al*.[32] Class 1-integron (c1-integron), a main source of antibiotic resistance genes, may significantly affect how *E. coli* isolates behave.[31] Bacterial strains with c1-integrons are more likely to develop antibiotic resistance than strains without c1-integrons, and c1-integrons also play a role in multidrug resistance (MDR).[33]

The distribution of integron Classes 1 and 2 among phylogenetic groups was significantly different according to the results obtained. It was found that group B2 had the highest distribution of the *IntI1* gene, with 10 isolates (83.33%), followed by group E (6 isolates; 85.71%), and group A (3 isolates; 75%). In addition, five isolates from groups E, D, C, B1, and B2 (20% total) exhibit both types of integrons. Among all the phylogenetic groups studied, *E. coli* isolates from groups F and C had the highest frequency of integrons. In the current study, the quaternary ammonium resistance gene (*qacE*) 1 was carried by 61.4% of the Class 1 integron, which is less than the percentage reported by Gaze *et al*.,[34] who found 95% of the Class I integron in the United Kingdom. Selection for *qacE1* gene resistance may result in co-selection for antibiotic resistance since the Class I integron represents a well-known mechanism for the horizontal transfer of antibiotic resistance genes.[34]

Sulfamethoxazole resistance genes were found to be less prevalent than previously reported by Phongpaichit *et al*.,[35] and Momtaz *et al*.,[36] who observed that 35.8 and 45.5% of the isolates, respectively, were positive for the presence of the *sul1* gene. Only six isolates (5.6%) had all three of the conserved genes (*intI1*, *qacE*, and *sul1*) linked to Class I integron, compared to the 59 and 27.8% reported by Phongpaichit *et al*.[35] A Class 1 integron in a human commensal or pathogen cannot be known with certainty. However, circumstantial evidence strongly points to a role for *qac* gene cassette. These genes encode versatile efflux pumps that confer resistance to toxic cationic molecules such as quaternary ammonium compounds and may have a role in protecting cells against toxins found in natural ecosystems.[33] Class 1 integron recovered from natural habitats typically carry them in about half of their cassette arrays, and in freshwater biofilms, qac cassettes are dynamically transferred between integrons. Hence, any Class 1 integron placed into a Tn402 backbone has a 50% chance of carrying a *qac* cassette. Such an integron would confer resistance to quaternary ammonium compounds, providing a significant advantage to cells carrying the Tn*402*-integron and driving them to fixation in human-associated bacteria exposed to these disinfectants. Quaternary ammonium compounds were first used as hospital disinfectants in the early 1930s, predating the clinical use of antibiotics. This would explain why the possession of the *qacE* gene appears to be ancestral in clinical Class 1 integron.[37] The first true antibiotics were the sulfonamides, introduced during the mid-to-late 1930s. Selection for antibiotic resistance begins from this point, so it is not surprising that the next event in the evolution of clinical Class 1 integron involves a gene for sulfonamide resistance. The *sul1* gene encodes a drug-resistant variant of the sulfonamide target enzyme, dihydropteroate synthase. This gene was inserted into the Tn*402*-Class 1 integron, deleting the end of the *qacE* gene and its attendant *attC* generating the 3′ conserved segment (3′-CS) that is characteristic of much extant clinical Class 1 integron. The loss of transposition functions was caused by additional deletions to the Tn402 element, which also produced diversity in the 3′ ends of the Tn402-Class 1 integron. [30]

Table 3: Structural groups of Class I integrin

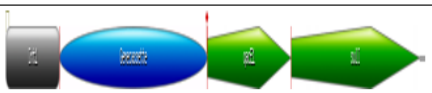
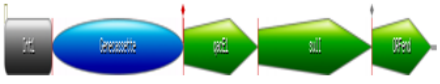
Structural groups of class I integrons	Integron structure	Isolate	Isolate no.	Resistant pattern
G0		E1,E3,E5,E6,E7,E10,E12,E21,E22,E23,E26,E31,E37,E41,E45,E48,E50,E53	18	AUG,CO,CFM,GN,AK,PIP,FOX
GI		E9,E11,E18,E20,E28,E32,E36,E40,E43,E47,E51	11	AUG, CO.CFM , GN
GII		E2,E14,E19,E25,E30,E33,E35,E42	8	AUG,FOX,CFM,FEP,AK,LEV
GIII		E4,E16,E30,E34,E38,E52,E55	7	AUG,FEP,PIP,AK,GN,CO
GIV		E8,E13,E15,E17,E29,E39,E44,E49	8	AUG,FEP

Table 4: Antibiotic susceptibility pattern of Class I integron positive and integron-negative of *Escherichia coli isolates.*

Class	Antibiotics	Integron-positive 1 n=55		Integron-negative n = 45		χ2, P-value
		Resistant N (%)	Sensitive N (%)	Resistant N (%)	Sensitive N (%)	
Carbapenems	Meropenem	12 (21.8%)	43 (78%)	43 (95.5%)	2 (4.4%)	χ2= 53.84, 0.001**
	Imipeneme	32 (58%)	23 (41.8%)	41 (91%)	4 (8.8%)	χ2= 30, 0.001**
Aminoglycosides	Amikacin	25 (47%)	30 (53%)	39 (86.6%)	6 (13.3%)	χ2= 23.28, 0.003**
Aminopenicillin	Ampicillin	49 (89%)	6 (10.9%)	36 (80%)	9 (20%)	χ2= 52.56, 0.001**
	Cefoxitin	54 (98.1%)	1 (1.8%)	43 (95.5%)	2 (4.4%)	χ2= 90.8, 0.001**
	Ceftriaxone	53 (96.3%)	2 (3.6%)	43 (95.5%)	2 (4.4%)	χ2= 86.64, 0.001**
Cephalosporin	Cefixime	37 (67.2%)	18 (32.7%)	35 (77.7%)	10 (22%)	χ2= 20.72, 0.001**
	Ceftazidim	6 (10.9%)	49 (89%)	39 (86.6%)	6 (13.3%)	χ2= 59.76, 0.001**
Phenicols	Choramphenical	26 (47.2%)	29 (52.7%)	41 (91.1%)	4 (8.8%)	χ2= 28.56, 0.0027**
Fluoroquinolons	Ciprofloxacin	38 (69%)	17 (30%)	37 (82.2%)	8 (17.7%)	χ2= 26.64, 0.007**
	piperacillin	49 (89%)	6 (11%)	40 86.6%)	5 (13.3%)	χ2= 62.48, 0.001**
	Nalidixicacid	45 (81.8%)	10 (18%)	40 (86.6 %)	5 (13.3%)	χ2= 50.00, 0.001**
β-lactames inhibitors	Amoxicillin Clavanate	46 (83.6%)	9 (16.3%)	43 (95.5%)	2 (4.4%)	χ2= 62.00, 0.001**
	Piperacillin tazobactm	6 (10.9%)	49 (89.0%)	45 (100%)	-	χ2= 33.86, 0.001**
Tetracyclines	Tetracycline	44 (80%)	11 (20%)	36 (80%)	9 (20%)	χ2= 37.36, 0.001**
Quinolons	Levofloxacin	41 (74.5%)	14 (25.4%)	41(91.1%)	4 (8.8%)	χ2= 42.96, 0.001**
Nitrofurans	Nitrofurantin	48 (88%)	7 (12%)	40 (86.6%)	5 (13%)	χ2= 59.12, 0.001**

χ2: Chi-square; df: Degree of freedom; P: Probability; **: p < 0.01; *: p < 0.05; NS: Non-significant.

Table 5: Prevalence of integron Classes 1 and 2 among phylogenetic groups of *Escherichia coli* isolates

E. coli Phylo-groups	Integron N (%)	Integron class 1 (n = 55)		Integron class 2 (n = 12)		Integron classes 1 and 2 (n = 5)		χ^2	p-value
		N	%	N	%	N	%		
A (N =3)	3 (100%)	3	5.45	0	0	0	0	NA	
B1 (N = 4)	3 (75%)	2	3.64	2	16.67	1	20	0.4	0.81 NS
B2 (N = 12)	10 (83.33%)	8	14.54	2	16.67	1	20	7.8	0.02*
C(N = 21)	18 (85.71%)	15	27.2	2	16.67	1	20	20.3	0.003**
D (N = 4)	3 (75%)	1	1.82	1	8.33	1	20	0	1 NS
E(N =7)	6 (85.71%)	3	5.45	3	25.0	1	20	1.1	0.56 NS
F (N = 33)	24 (72.7%)	22	40	2	16.67	0	0	16.6	0.004**
Phylogenetic UP (N=6)	1 (16.6%)	1	1.82	0	0	0	0	NA	
χ^2	57.17	-							
p-value	0.005**								

χ^2: Chi-square; N: Number; P: Probability; **: Significant at <0.01; *: Significant at < 0.05; NA: Not available; NS: Non-significant.

Conclusion

The study's findings reveal variations in integron gene composition influenced by distinct selective pressures across geographical locations. Notably, the identification of Class 1 integron in UPEC isolates from clinical settings in Baghdad is a novel contribution. Moving forward, future directions include global surveillance, functional studies for mechanistic understanding, development of targeted therapies, integration with clinical practice, and educational initiatives. These efforts aim to advance knowledge, inform interventions, and foster global collaboration to address antimicrobial resistance effectively.

Conflict of Interest

The authors declare no conflict of interest.

Authors' Declaration

The authors hereby declare that the work presented in this article is original and that any liability for claims relating to the content of this article will be borne by them.

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