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Short Communication **Open Access**

Integron-mediated multidrug resistance in uropathogenic *Escherichia coli* isolates from intensive care unit: Molecular evidence from Iran within a Global Surveillance Framework

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Abstract:

Background: Integrons are genetic platforms that facilitate acquisition and expression of antimicrobial resistance gene cassettes. Their contribution to multidrug resistance (MDR) among intensive care unit (ICU) uropathogenic *Escherichia coli* (UPEC) is of increasing concern. This study determined the prevalence of class 1 and class 2 integrons among ICU UPEC isolates and examined their association with resistance phenotypes.
Methodology: A total of 100 UPEC isolated from ICU patients were identified using standard microbiological techniques. Antimicrobial susceptibility testing against ampicillin, ciprofloxacin and trimethoprim-sulfamethoxazole was performed according to CLSI guidelines. MDR was defined as resistance to the 3 antimicrobial classes. Polymerase chain reaction (PCR) assays targeted *intI1* and *intI2* genes. Association of MDR with integron carriage was analyzed using Chi-square test with $p<0.05$ considered significant.
Results: Resistance rates were highest for ampicillin (40.0%, n=40) and trimethoprim-sulfamethoxazole (40.0%, n=40), while ciprofloxacin resistance was 32.0%. MDR was observed in 56.0% of the isolates. Class 1 integrons were detected in 62.0% and class 2 integrons in 18.0% of the isolates. Class 1 integron carriage was significantly associated with MDR phenotype ($p<0.05$).
Conclusion: These findings underscore the importance of molecular surveillance in ICU settings to guide infection control and antimicrobial stewardship.

Keywords: Integrons; multidrug resistance; uropathogenic *Escherichia coli*; ICU

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Résistance aux médicaments multiples par les intégrons chez des isolats d'*Escherichia coli* uropathogènes provenant d'unités de soins intensifs: données moléculaires iraniennes dans le cadre d'une surveillance mondiale

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Résumé:

Contexte: Les intégrons sont des plateformes génétiques qui facilitent l'acquisition et l'expression de cassettes de gènes de résistance aux antimicrobiens. Leur contribution à la multirésistance (MDR) chez *Escherichia coli* uropathogène (UPEC) en unités de soins intensifs (USI) est une préoccupation croissante. Cette étude a déterminé la prévalence des intégrons de classe 1 et de classe 2 parmi les isolats d'UPEC en USI et a examiné leur association avec les phénotypes de résistance.
Méthodologie: Au total, 100 isolats d'UPEC provenant de patients en USI ont été identifiés à l'aide de techniques microbiologiques standard. Des tests de sensibilité aux antimicrobiens (ampicilline, ciprofloxacine et triméthoprime-sulfaméthoxazole) ont été réalisés conformément aux recommandations du CLSI. La multirésistance (MDR) a été

définie comme une résistance aux trois classes d'antimicrobiens. Les tests de réaction en chaîne par polymérase (PCR) ont ciblé les gènes *intI1* et *intI2*. L'association entre la MDR et le portage d'intégrons a été analysée par le test du χ^2 (p<0,05 étant considéré comme significatif).
Résultats: Les taux de résistance les plus élevés ont été observés pour l'ampicilline (40,0%, n=40) et le triméthoprime-sulfaméthoxazole (40,0%, n=40), tandis que la résistance à la ciprofloxacine était de 32,0%. Une MDR a été observée chez 56,0% des isolats. Des intégrons de classe 1 ont été détectés chez 62,0% des isolats et des intégrons de classe 2 chez 18,0% d'entre eux. Le portage d'intégrons de classe 1 était significativement associé au phénotype MDR (p<0,05).
Conclusion: Ces résultats soulignent l'importance de la surveillance moléculaire en soins intensifs pour orienter la lutte contre les infections et l'utilisation judicieuse des antibiotiques.

Mots-clés: Intégrines; multirésistance; *Escherichia coli* uropathogène; soins intensifs

Introduction:

Urinary tract infections (UTIs) are among the most common healthcare-associated infections, particularly in intensive care units (ICUs). Uropathogenic *Escherichia coli* (UPEC) remains the leading causative agent. The global rise of antimicrobial resistance represents a major public health concern (1-3).

Integrons, particularly class 1 integrons, play a crucial role in capturing and disseminating resistance gene cassettes, contributing significantly to the emergence of multidrug-resistant organisms (4). The objective of this study is to determine the prevalence of class 1 and class 2 integrons among ICU UPEC isolates and examined their association with resistance phenotypes.

Materials and method:

Study setting and design:

This laboratory-based study was conducted at Alzahra Hospital, Isfahan, Iran, between January and June 2023.

Clinical samples, bacterial isolation and identification:

A total of 100 non-duplicate ICU isolates were collected after urine samples were cultured on MacConkey and CLED agar, and isolates were identified using standard biochemical tests.

Antimicrobial susceptibility testing:

The Kirby–Bauer disk diffusion method was performed on each isolate according to the 2022 Clinical and Laboratory Standards Institute (CLSI) guidelines (5). The antibiotics tested included ampicillin, ciprofloxacin, and trimethoprim–sulfamethoxazole.

Multidrug resistance (MDR) was defined as resistance to at least one agent in three or more antimicrobial classes.

Detection of integrons by PCR assay:

DNA was extracted from each isolate using the boiling method. The integrase genes *intI1* (280 bp) and *intI2* (233 bp) were amplified by conventional PCR using *IntI1* (F 5′-CCTCCC GCACGATGATC-3′ and R 5-TCCACGCATCGTCA GGC-3′) and *IntI2* (F 5′-TTATTGCTGGGATTAG GC-3′ and R 5′-ACGGCTACCCTCTGTTATC-3′) primers (6).

The PCR conditions included initial denaturation at 95°C for 5 minutes, followed by 35 cycles of denaturation at 94°C for 30 seconds, annealing at 55°C for 30 seconds, extension at 72°C for 45 seconds, and a final extension at 72°C for 5 minutes. Amplified products were analyzed by agarose gel electrophoresis.

Statistical analysis:

Data were analyzed on SPSS and association of MDR with integron carriage was determined using Chi-square test, with p<0.05 considered statistically significant.

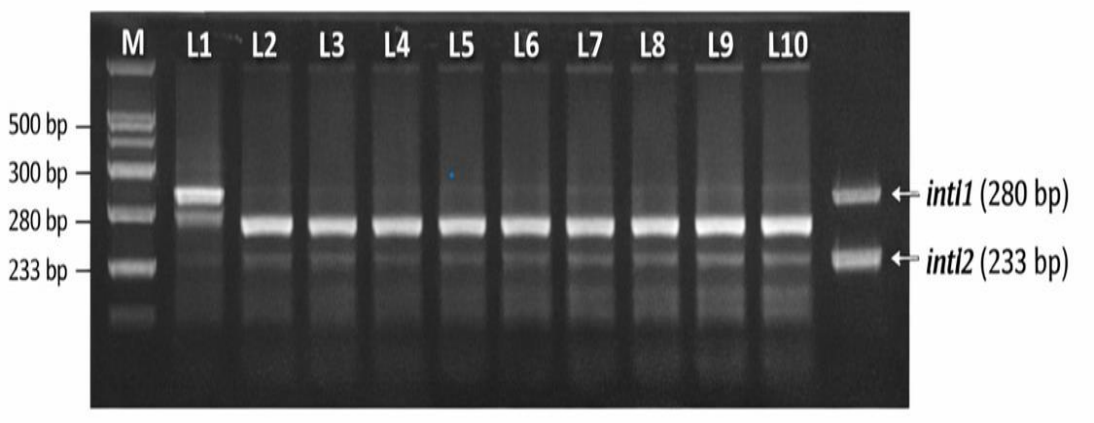
Results:

Of the 100 UPEC isolates, 40 (40.0%) were resistant to ampicillin, 40 (40.0%) to trimethoprim–sulfamethoxazole and 32 (32.0%) to ciprofloxacin. A total of 56 (56.0%) were multidrug resistant.

Class 1 integrons were identified in 62 (62.0%) isolates, while class 2 integrons were detected in 18 (18.0%) isolates. The prevalence of class 1 integrons was significantly associated with MDR isolates compared to non-MDR isolates (p<0.05).

Table 1: Antibiotic resistance among uropathogenic *Escherichia coli* isolates from ICU patients

Antibiotic	No of isolates	No resistant (%)
Ampicillin	100	40 (40.0)
Trimethoprim–sulfamethoxazole	100	40 (40.0)
Ciprofloxacin	100	32 (32.0)
All three antibiotics (MDR)	100	56 (56.0)



Lane M: DNA ladder; Lanes 1–10: ICU UPEC isolates

Fig 1: Agarose gel electrophoresis showing amplification of integron genes *intI1* (280 bp) and *intI2* (233 bp).

Discussion:

The present study demonstrates a high prevalence of class 1 integrons (62%) among ICU-associated UPEC isolates, highlighting their critical role in the acquisition and dissemination of antimicrobial resistance. Integrons function as efficient genetic platforms capable of capturing, integrating, and expressing gene cassettes, thereby facilitating rapid bacterial adaptation under antibiotic selective pressure (7,8, 9). The significant association observed between class 1 integrons and multidrug resistance (MDR) ($p<0.05$) further supports their contribution to the emergence of resistant phenotypes in clinical settings.

The MDR rate of 56% identified in this study is consistent with recent global reports indicating a rising burden of antimicrobial resistance among Enterobacteriaceae. This trend is driven by a combination of horizontal gene transfer and chromosomal mutations, often mediated by mobile genetic elements such as plasmids, transposons, and integrons (10,11,12). The ICU settings represent high-risk environments due to prolonged hospitalization, extensive antibiotic use, invasive procedures, and immunocompromised patients, all of which promote the selection of resistant strains.

Global surveillance reports indicate that integron-mediated resistance is widely distributed across healthcare settings worldwide (13, 14), highlighting the importance of molecular monitoring. The lower prevalence of class 2 integrons (18%) suggests a secondary but still relevant role in resistance dissemination. This finding reinforces the clinical significance of integron screening as part of routine antimicrobial resistance surveillance in high-risk hospital environments.

This study was limited to a single hospital and a defined sample size. Additionally, sequencing of integron gene cassettes was not performed. Future studies should include gene cassette sequencing and multi-centre surveillance to better understand resistance dissemination.

Conclusion:

Class 1 integrons are highly prevalent and significantly associated with multidrug resistance among ICU UPEC isolates. Continuous molecular surveillance is essential for effective infection control and antimicrobial stewardship.

Contributions of the author:

The author designed the study, collected and analysed the data, and wrote the manuscript for publication.

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Conflict of interest:

No conflict of interest is declared

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