Journal of Shahrekord University of Medical Sciences
doi: 10.34172/jsums.1053 2025;27(4):169-174 http://j.skums.ac.ir

Original Article

Investigation of Antibiotic Resistance Patterns and the Prevalence of Virulence Genes in the Clinical Strains of Carbapenem-Resistant *Escherichia coli*

Sara Gholami Dizicheh[1], Fereshte Ghandehari[1*], Mozhgan Ghiasian[1]

[1]Department of Microbiology, Fal. C., Islamic Azad University, Isfahan, Iran

***Corresponding Author:** Fereshte Ghandehari, Emails: fe_gh_2010@yahoo.com, Fe.ghandehari@iau.ac.ir

Abstract

Background and aims: The emergence of resistance to antibiotics in *Escherichia coli* has raised significant concerns in the medical community. This study evaluated the antibiotic resistance pattern and prevalence of virulence genes (*pap, fimA,* and *aer*) in carbapenem-resistant *E. coli* clinical isolates.

Methods: A total of 96 *E. coli* isolates were collected from clinical samples from various hospital departments in Isfahan. The isolates were confirmed using biochemical and molecular tests. Antibiotic susceptibility patterns were determined based on the CLSI guidelines. The presence of virulence genes underwent investigation.

Results: Among the isolates, 61% were obtained from male patients, and 39% were from female patients. The highest frequency was observed in the age groups of 41–50, 51–60, and 81–90 years old. The majority of antibiotic-resistant isolates (41%), multidrug-resistant (MDR) isolates (43.3%), and carbapenem-resistant isolates (41.7%) were collected from the emergency department (41%). The isolates showed the highest resistance to ampicillin (92%), while they exhibited the highest sensitivity to amikacin (96%). The MDR isolates were most resistant to ampicillin (93%), cotrimoxazole (88%), cefixime (80%), cefotaxime (67%), and ceftriaxone (50%). In general, 12 carbapenem-resistant isolates were confirmed to carry the *OXA-48* gene, among which 100% harbored the *aer* gene and 75% had the *pap* gene, whereas none overcame the *fimA* gene.

Conclusion: The highest rates of antibiotic resistance were in the emergency department, and urinary tract infections were the most common carbapenem-resistant infections. The high prevalence of virulence genes (*aer* and *pap*) should also be considered by the medical community to control strains carrying these genes.

Keywords: *Escherichia coli*, Antibiotic resistance, MDR, Virulence genes

Received: March 5, 2025, **Revised:** July 13, 2025, **Accepted:** July 14, 2025, **ePublished:** December 29, 2025

Introduction

Antibiotic resistance is recognized as one of the most critical global health threats undermining our ability to treat bacterial infections effectively. *Escherichia coli*, a major cause of urinary tract and bloodstream infections, plays a critical role in this tissue (1). In recent years, the rise of carbapenem-resistant *E. coli* has become a significant concern in effectively managing infections caused by this pathogen (1).

Carbapenems are a class of β-lactam antibiotics considered the first-line treatment for infections caused by Gram-negative bacteria resistant to other antibiotics, such as penicillins or cephalosporins. They exert their antibacterial effects by inhibiting bacterial cell wall synthesis, increasing the permeability of the outer membrane, and affecting the efflux pump system. Resistance to carbapenems arises through multiple mechanisms, including reduced expression of outer membrane proteins, enhanced activity of efflux pump systems, and the production of carbapenemase enzymes, which hydrolyze carbapenems. The gene-encoding carbapenemase is plasmid-borne, facilitating rapid horizontal transfer between bacterial species and promoting the dissemination of resistance (2). The increasing prevalence of carbapenem-resistant *E. coli* poses a significant challenge in treating bacterial infections (2).

In addition to antibiotic resistance, virulence factors are key to the pathogenicity of *E. coli*. Genes like *aer*, *fim*, and *pap* produce factors that help the bacteria attach to host cells, colonize, and evade the immune system. The *pap* gene encodes proteins that bind to glycolipid receptors on urinary tract epithelial cells. This allows the bacteria to invade deeper tissues, causing inflammation and damage. Similarly, the *fim* gene encodes proteins that aid in bacterial adhesion. It plays a significant role in urinary tract infections (UTIs), wound infections, and sepsis (3). The *aer* gene encodes the siderophore aerobactin, which helps the bacteria take up iron from the environment. This promotes bacterial growth and infection (4). The coexistence of virulence genes and antibiotic resistance genes in a bacterial strain greatly increases its ability to cause infections. These infections are often hard or even impossible to treat. As a result, they pose a serious threat to public health. This study analyzes

the antibiotic resistance profiles of carbapenem-resistant *E. coli* strains. It also investigates the correlation between the presence of virulence genes (*aer*, *fim*, and *pap*) and antibiotic resistance.

Methods

Sample Collection

Overall, 200 clinical blood and urine samples were obtained from patients admitted to different hospital wards in Isfahan from February to May 2024. These samples were analyzed at the Microbiology Laboratory and the Cellular and Molecular Research Center of Islamic Azad University, Falavarjan Branch, leading to the isolation of 96 *E. coli* strains. Bacterial identification was performed using phenotypic assays, including the oxidase test, lysine decarboxylase activity, triple sugar iron reactions, Indole, Methyl Red, Voges-Proskauer, and Citrate tests, urease hydrolysis, and molecular methods.

Deoxyribonucleic Acid Extraction

DNA was extracted using a two-step precipitation kit (Cell Avand Pars Company). Initially, a few bacterial colonies were suspended in 100 µL of lysis buffer in a 1.5 mL microtube, vortexed for 10–15 seconds, and incubated at 70˚C for 30 minutes, followed by an additional incubation at 95˚C for 10 minutes. Subsequently, 200 µL of buffer and 400 µL of absolute ethanol were added, vortexed for 10–15 seconds, and centrifuged at 10,000 rpm for 10 minutes. The supernatant was discarded, and the pellet was washed with 600 µL of wash buffer, followed by centrifugation at 5,000 rpm for 5 minutes. After removing the supernatant, the pellet was dried at 90˚C for 2–5 minutes. Finally, 150 µL of sterile double-distilled water was added to the pellet, incubated at 95˚C for 10 minutes, and centrifuged at 14,000 rpm for 1 minute. The extracted DNA was stored at -20˚C. The presence of genomic DNA and successful amplification of the *16S rRNA* gene were confirmed using agarose gel electrophoresis.

Polymerase Chain Reaction Amplification

Primers 27F (5'-AGAGTTTGATCMTGGCTCAG-3') and 1492R (5'-GGTTACCTTGTTACGACTT-3') were used for *E. coli* identification (5).

PCRs were performed in a total volume of 50 µL containing 2.5 µL of each primer, 1.5 µL of magnesium chloride, 1 µL of deoxynucleoside triphosphate mix, 0.2 µL of Thermus aquaticus DNA polymerase, 5 µL of buffer, 3 µL of extracted DNA, and 34.8 µL of PCR-grade water. The PCR cycling program consisted of an initial denaturation at 94˚C for 3 minutes, followed by 30 cycles of denaturation at 94˚C for 30 seconds, annealing at 55˚C for 30 seconds, extension at 72˚C for 1 minute, and a final extension at 72˚C for 10 minutes. The amplification of the target sequences was confirmed using horizontal gel electrophoresis. Eventually, PCR products were sent to Macrogen (South Korea) for sequencing.

Antibiotic Susceptibility Testing

This test was conducted using the disc diffusion method on Mueller-Hinton agar, following the Clinical and Laboratory Standards Institute guidelines (2022). The antibiotic discs used included amikacin (30 µg), meropenem (10 µg), cefepime (30 µg), cotrimoxazole (25 µg), gentamicin (10 µg), cefixime (10 µg), ampicillin (10 µg), cefotaxime (30 µg), and ceftriaxone (30 µg) (6). All antibiotic discs were obtained from PadTan Teb Company. *E. coli* ATCC 25922 and *Klebsiella pneumoniae* ATCC 70063 strains were used as reference strains for quality control. These standard strains were obtained in lyophilized form from the microbial collection of Ideal Gostar Company. Isolates demonstrating resistance to two or more antibiotic classes were categorized as multidrug-resistant (MDR). Strains resistant to meropenem were selected for further analysis.

Detection of the OXA-48 Resistance Gene

The presence of the *OXA-48* resistance gene was detected using PCR with forward (5′-GCGTGGTTAAGGATGAACAC-3′) and reverse (5′-CATCAAGTTCAACCCAACCG-3′) primers (7). The PCR cycling conditions included an initial denaturation at 94˚C for 5 minutes, followed by 30 cycles of 94˚C for 1 minute, 52.5˚C for 1 minute, and 72˚C for 1 minute. A final extension step was performed at 72˚C for 5 minutes.

The amplification of the target sequence was confirmed using horizontal agarose gel electrophoresis. A single, distinct band at 438 base pairs indicated the presence of the *OXA-48* gene (Figure 1).

Detection of fimA, pap, and aer Genes

The forward primer (5′-GTTGTTCTGTCGGCTCTGTC-3′) and reverse primer (5′-ATGGTGTTGGTTCCGTTATTC-3′) were utilized to detect the *fimA* gene (1). The PCR program included an initial denaturation at 94˚C for 5 minutes, followed by 30 cycles of 94˚C for 1 minute, 52.5˚C for 1 minute, and 72˚C for 1 minute. A final extension was performed at 72˚C for 5 minutes. A single sharp band at 447 base pairs confirmed the presence of the *fimA* gene (Figure 2).

The *pap* gene was detected using the forward primer (5′-GCAACAGCAACGCTGGTTGCATCAT-3′) and reverse primer (5′-AGAGAGAGCACTCTTATACGGACA-3′). The PCR program involved initial denaturation at 95˚C for 5 minutes, followed by 30 cycles of 94˚C for 1 minute, 58.5˚C for 1 minute, and 72˚C for 1 minute. The final extension step was conducted at 72˚C for 5 minutes. The presence of the *pap* gene was confirmed by a distinct band at 336 base pairs (Figure 2).

The forward primer (5′-TACCGGATTGTCATATGCAGACCG-3′) and reverse primer (5′-AATATCTTCCTCCAGTCCGGAG-3′) were

employed for the *aer* gene (1). The PCR conditions were similar to those for *pap*, with annealing at 58˚C. A sharp band at 602 base pairs confirmed the presence of the *aer* gene (Figure 2).

Statistical Analysis

All experiments were conducted in duplicate. The obtained data were analyzed using SPSS software (version 20; SPSS Inc., Chicago, USA) and Excel 2010 (Microsoft Corporation, USA).

Results

Among 200 clinical samples collected from various hospitals in Isfahan, 96 *E. coli* strains were identified using phenotypic and molecular methods. Among the identified isolates, 61% were derived from male patients, and 39% were obtained from female patients. The highest contamination rate was observed in urine samples (91%), while blood samples exhibited the lowest contamination rate (9%) (Figure 3).

Furthermore, the distribution of isolates across hospital wards revealed that the majority of them were obtained from the emergency department (41%) and the intensive care unit (24%). In contrast, the lowest frequency was reported in gastroenterology, operating room, and neurology wards, contributing to only 1% of the total isolates. Based on the antibiotic resistance pattern analysis, the highest resistance rates were observed against ampicillin (92%), trimethoprim-sulfamethoxazole (68%), and cefixime (55%) (Figure 4a). Conversely, susceptibility rates were recorded for amikacin (96%), gentamicin (85%), meropenem (83%), and cefepime (68%), respectively (Figure 4b).

Notably, among the studied strains, the prevalence of MDR strains was 62.5%. The highest resistance rates were found for ampicillin (93%), cotrimoxazole (88%), cefixime (80%), cefotaxime (67%), and ceftriaxone (50%) (Figure 5a). Contrarily, the highest susceptibility rates were recorded for amikacin (98%), gentamicin (92%), and cefepime (90%), respectively (Figure 5b).

The prevalence of carbapenem-resistant strains was reported to be 12.5%. Additionally, the highest frequency of MDR and carbapenem-resistant strains was observed in urine isolates, with 88% and 92%, respectively (Figure 6).

PCR analysis confirmed the presence of the *OXA-48* gene in 12 carbapenem-resistant strains. In the investigation of virulence gene prevalence among 12 carbapenem-resistant strains, the *aer*, *pap*, and *fimA* genes were present in all (100%), 9 (75%), and none (0%) of them, respectively (Figure 7).

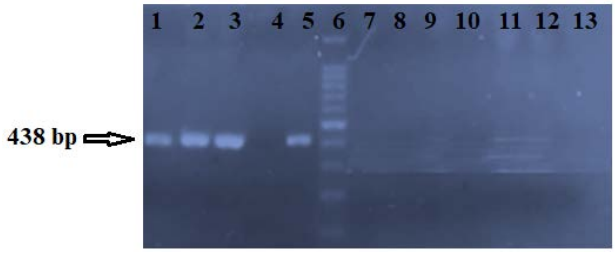

Figure 1. Results of the Agarose Gel Electrophoresis of the PCR Product
Note. PCR: Polymerase chain reaction. Wells 1–5 show the presence of the *OXA-48* gene, and wells 6 and 7 display the 100 base pair marker and the negative control, respectively

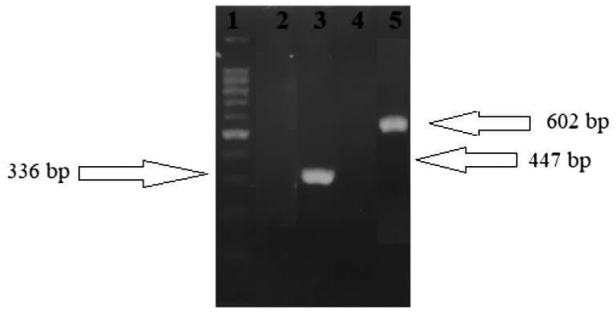

Figure 2. Results of the Agarose Gel Electrophoresis of the PCR Product
Note. PCR: Polymerase chain reaction. Wells 1 and 2 depict the 100 base pair marker and the negative control, respectively. Wells 3, 4, and 5 show the *pap*, *aer*, and *fimA* genes, respectively

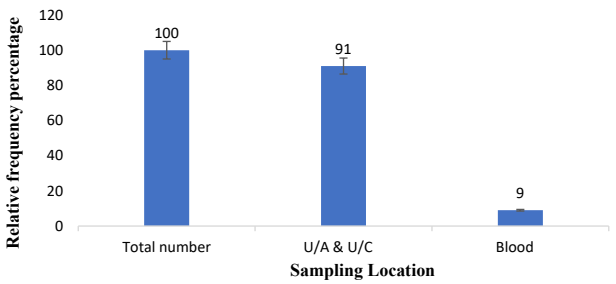

Figure 3. Frequency Distribution of *Escherichia coli* Strains Based on Clinical Samples

Discussion

E. coli is a prominent and widespread pathogen responsible for nosocomial infections, particularly UTIs. In the

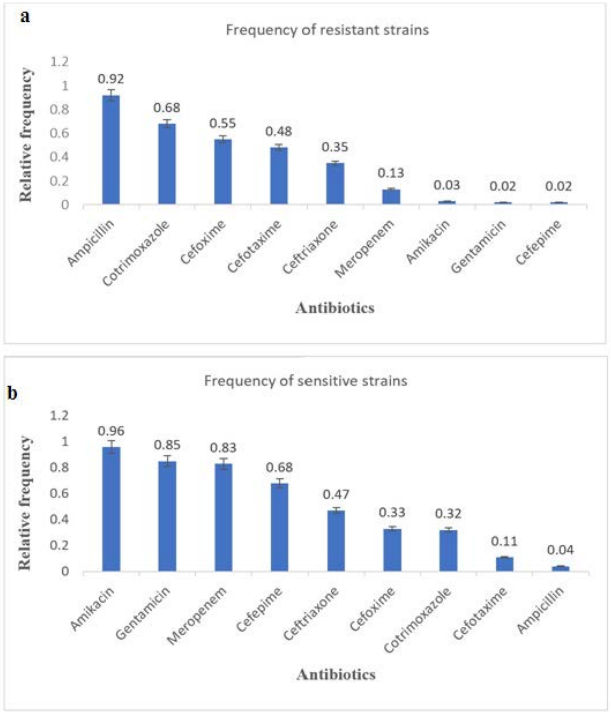

Figure 4. Frequency Distribution of Resistance **(a)** and Sensitivity of Strains **(b)** to Various Antibiotics

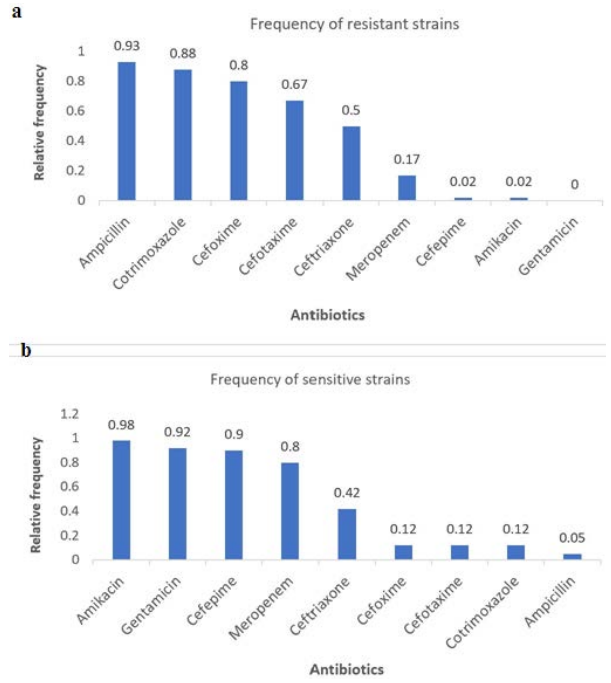

Figure 5. Frequency of Resistance **(a)** and Sensitivity of Isolated MDR Strains **(b)** to Various Antibiotics
Note. MDR: Multidrug-resistant

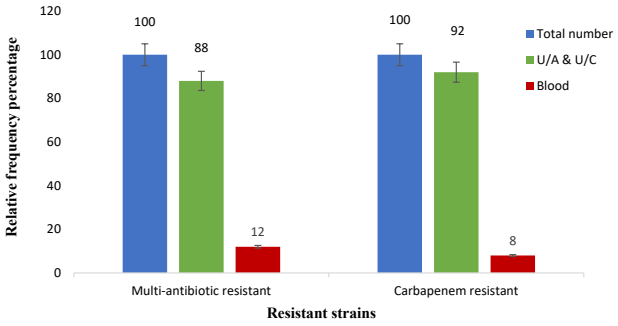

Figure 6. Frequency of Carbapenem-Resistant and Multi-Antibiotic-Resistant Strains Based on Clinical Samples

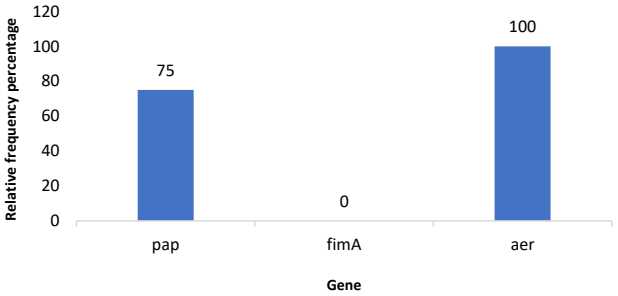

Figure 7. Distribution of Relative Abundance of Different Genes in Carbapenem-Resistant Strains

present study, the rate of UTIs was reported to be higher in men than in women. Although UTI is more common in the general female population, the high prevalence of male isolates in this study may be due to sampling from a hospital setting and specific risk factors in hospitalized patients. The emergence of MDR and carbapenem-resistant strains creates significant challenges when choosing effective treatments. Epidemiological studies that examine antibiotic resistance patterns in different regions and compare them with global data are essential. These studies help us understand how resistance genes spread among bacterial strains in various areas. They also provide a basis for developing strategies to combat, control, and prevent the global spread of resistant strains. Research on the prevalence of carbapenem-resistant bacteria is crucial. It helps select proper antibiotic therapies and reduce the rise of resistant strains and their transmission to other bacterial species.

Furthermore, these studies contribute to developing novel antibiotics and vaccines targeting carbapenem-resistant strains. Due to their broad-spectrum antimicrobial activity against a wide range of bacteria, carbapenems are frequently prescribed for treating various infections. However, their overuse has played a significant role in the growing resistance of bacteria to these antibiotics (8).

Given the high incidence of infections caused by *E. coli* and the increasing rates of antibiotic resistance, this study evaluated the antibiotic resistance patterns in clinical *E. coli* isolates and the prevalence of virulence genes in these strains. The results underscore the concerning occurrence of MDR and carbapenem-resistant strains in various hospital settings, particularly in emergency departments and urinary tract samples. Currently, *E. coli* is one of the most common causes of nosocomial infections. Humans are the main reservoir for this bacterium. The hands of healthcare workers and patients' gastrointestinal tracts are significant sources of *Enterobacteriaceae* transmission. This leads to higher hospital infection rates than in community settings (9). Excessive antibiotic use in hospitals is the main factor behind this high prevalence. Some studies have detected *E. coli* in up to 77% of stool samples from hospitalized patients (10). Hospital emergency departments are complex healthcare settings. Their main focus is to provide rapid and urgent medical care. Poor management in these departments can harm the quality of patient care. It may also increase the risk of nosocomial infections and medical errors. This is especially critical for vulnerable patients, such as those with cardiac conditions or on mechanical ventilation. Therefore, implementing infection control programs in emergency departments is essential for improving overall hospital performance (11). The results of this study also indicated an increasing resistance to ampicillin, trimethoprim-sulfamethoxazole, and cefixime compared to other antibiotics. Based on the findings, antibiotics, such as imipenem, gentamicin, and amikacin, which showed higher sensitivity among the isolates, should be prioritized for treating *E. coli* infections. However, it is crucial to note the emergence of carbapenem-resistant *Enterobacteriaceae* strains, as the misuse of these drugs may contribute to the further spread of resistance, potentially rendering these antibiotics ineffective. The pathogenic potential of *E. coli* isolates is associated with the presence of virulence factors. Understanding the relationship between virulence factors and the type of infection can influence the management

of UTIs. Adhesins, toxins, and iron-chelating factors (siderophores) are considered the primary virulence factors of *E. coli* (12, 13). Our findings confirmed a significant correlation between the examined virulence genes and carbapenem resistance in *E. coli* isolates. Among the virulence genes, *aer* and *pap* were the most prevalent. A study conducted in Egypt determined the prevalence of biofilm-producing and non-biofilm-producing *E. coli* isolates and evaluated their antibiotic resistance patterns in catheterized hospitalized patients. The expression of bla_{CTX-M} and *fimH* genes was also analyzed. The *E. coli* isolates exhibited resistance rates of 75%, 72%, 71%, 71%, 61%, and 53% to nitrofurantoin, ceftazidime, cephalexin, amikacin, piperacillin-tazobactam, and cefepime, respectively. Biofilm formation and the presence of bla-*CTX-M* and *fimH* genes were observed in all isolates. These findings emphasize the serious nature of infections in catheterized patients and underscore the importance of proper aseptic techniques during catheter insertion and maintenance to prevent catheter-associated UTIs (14).

Another study investigated the role of the *fimH* adhesin in promoting kidney infections caused by *E. coli* and its interaction with the *pap* adhesin. The study compared the prevalence of adhesive genes and their coexistence patterns between upper and lower UTI strains. The results indicated that strains with only the *fimH* genotype were predominantly associated with lower UTIs. In contrast, strains with the *fimH/papGII* genotype were significantly linked to upper UTIs. These findings emphasize the critical role of these adhesins in kidney infections (15).

Abdolahzadeh et al reported the prevalence of the virulence genes *papC, aer*, and *fim* in *E. coli* isolates from UTI patients in Yazd as 6.9%, 85.6%, and 87%, respectively (16). In a separate study by Khoshbakht et al 75 (31.9%) *E. coli* strains were isolated from 235 urinary samples, and 47 strains (62.7%) were resistant to imipenem. The *fim*, *papEF*, and *sfaD* genes were detected in 59.6%, 17%, and 42.4% of the isolates, respectively (17).

The high prevalence of the *fim* gene observed in this study is likely associated with the pathogenicity of the isolates, as bacterial adhesion to uroepithelial surfaces is a crucial factor in initiating infection (4). The *pap* gene, one of the most prevalent genes encoding fimbriae in *E. coli* strains isolated from UTIs, has been found to have a higher prevalence in cases of acute pyelonephritis than cystitis (18-19). Geographic variability and the region from which the bacterial isolates are obtained may significantly influence the frequency of this gene. Identifying the presence of P fimbriae in *E. coli* isolates from UTIs can assist in selecting appropriate treatment strategies.

Aerobactin, an iron-chelating factor, facilitates bacterial colonization in iron-deficient environments, such as dilute urine. The *aer* gene operon becomes activated under iron scarcity, enabling bacterial survival by secreting Fe^{3+} from host cells (20). The high prevalence of this gene in the present study highlights its crucial role in the bacterial colonization of the urinary tract, which aligns with the findings of Raeispour et al (21).

Similar virulence gene findings between this study and other studies suggest shared pathogenic mechanisms. At the same time, observed differences may be attributed to variations in sampling methods, geographic regions, sample sizes, and genetic diversity among isolates. Furthermore, antibiotic sensitivity and resistance profiles may influence the frequency of virulence genes (22). Overall, findings from various studies highlight the role of fimbrial genes in the pathogenicity of uropathogenic *E. coli*. Understanding these genes is key to developing effective vaccines against such infections. However, more extensive research on other virulence factors, such as toxin production, is still necessary. This would help control and treat infections better. The comparative analysis of infection-related factors can also offer a more complete view of the disease process.

Conclusion

The findings of this study revealed the significant prevalence of antibiotic resistance, including carbapenem resistance, in MDR *E. coli* isolates sourced from a range of clinical samples in Isfahan. The emergency department exhibited the highest rates of antibiotic resistance, with UTIs ranking as the most prevalent antibiotic-resistant and carbapenem-resistant infections. The significant prevalence of virulence genes ***aer*** and ***pap*** warrants attention from the medical and pharmaceutical communities to control strains carrying these genes. While the overall carbapenem resistance prevalence was 12.5%, its concentration in critical care settings and association with virulence genes make it a significant clinical concern. Healthcare professionals and infection control specialists should focus on the rational use of effective antibiotics. They must also implement proper infection control measures in hospital settings. Educating medical staff on infection control strategies is essential. This helps prevent and limit the spread of UTIs in hospitals and the community. Future research should explore the other pathogenic factors of *E. coli* in different regions of the country. These studies can provide more complete data on the prevention, treatment, and management of infections. Such insights are valuable for developing strategies to combat resistant *E. coli* strains.

Acknowledgments

The authors are grateful to the Faculty of Basic Sciences, Islamic Azad University, Falavarjan Branch, for their cooperation and supply of experimental equipment.

Authors' Contributions

Conceptualization: Fereshte Ghandehari, Mozhgan Ghiasian.
Data curation: Sara Gholami Dizicheh.
Formal analysis: Fereshte Ghandehari.
Funding acquisition: Sara Gholami Dizicheh.
Investigation: Mozhgan Ghiasian, Sara Gholami Dizicheh, Fereshte Ghandehari.
Methodology: Fereshte Ghandehari, Mozhgan Ghiasian.
Project administration: Fereshte Ghandehari, Mozhgan Ghiasian.

Resources: Fereshte Ghandehari.
Software: Sara Gholami Dizicheh.
Supervision: Fereshte Ghandehari.
Validation: Fereshte Ghandehari, Mozhgan Ghiasian.
Visualization: Fereshte Ghandehari, Mozhgan Ghiasian.
Writing–original draft: Sara Gholami Dizicheh.
Writing–review & editing: Sara Gholami Dizicheh.

Competing Interests
The authors declare no conflict of interests.

Ethical Approval
This study adhered to all ethical principles for human subject research and was approved by the Ethics Committee of Islamic Azad University, Falavarjan Branch (IR.IAU.FALA.REC.1401.023).

Funding
This study was self-funded by the authors and received no external financial support from any funding organization.

References
1. Candan ED, Aksöz N. *Escherichia coli*: characteristics of carbapenem resistance and virulence factors. Braz Arch Biol Technol. 2017;60:e17160416. doi: 10.1590/1678-4324-2017160416.
2. Meletis G. Carbapenem resistance: overview of the problem and future perspectives. Ther Adv Infect Dis. 2016;3(1):15-21. doi: 10.1177/2049936115621709.
3. Habouria H, Bessaiah H, Pokharel P, Dhakal S, Maris S, Buron J, et al. A newly identified group of p-like (PL) fimbria genes from extraintestinal pathogenic *Escherichia coli* (ExPEC) encode distinct adhesin subunits and mediate adherence to host cells. Appl Environ Microbiol. 2022;88(13):e0142121. doi: 10.1128/aem.01421-21.
4. Kademane A, Dixit M, Vasundhara. A comprehensive review of the pathogenesis and virulence factors of *E. coli*. Salud Cienc Tecnol. 2023;3:411. doi: 10.56294/saludcyt2023411.
5. Lane DJ, Pace B, Olsen GJ, Stahl DA, Sogin ML, Pace NR. Rapid determination of 16S ribosomal RNA sequences for phylogenetic analyses. Proc Natl Acad Sci U S A. 1985;82(20):6955-9. doi: 10.1073/pnas.82.20.6955.
6. Exner M, Bhattacharya S, Christiansen B, Gebel J, Goroncy-Bermes P, Hartemann P, et al. Antibiotic resistance: what is so special about multidrug-resistant gram-negative bacteria? GMS Hyg Infect Control. 2017;12:Doc05. doi: 10.3205/dgkh000290.
7. Poirel L, Potron A, Nordmann P. OXA-48-like carbapenemases: the phantom menace. J Antimicrob Chemother. 2012;67(7):1597-606. doi: 10.1093/jac/dks121.
8. Zakavati M, Habibzadeh S, Sadeghieh S, Mohammadi P, Mostafalou S. The pattern of imipenem/cilastatin administration in Imam Khomeini hospital (Ardabil) in 2018. J Ardabil Univ Med Sci. 2019;19(1):100-9. doi: 10.29252/jarums.19.1.100. [Persian].
9. Jondle CN, Gupta K, Mishra BB, Sharma J. *Klebsiella pneumoniae* infection of murine neutrophils impairs their efferocytic clearance by modulating cell death machinery. PLoS Pathog. 2018;14(10):e1007338. doi: 10.1371/journal.ppat.1007338.
10. Tsereteli M, Sidamonidze K, Tsereteli D, Malania L, Vashakidze E. Epidemiology of carbapenem-resistant *Klebsiella pneumoniae* in intensive care units of multiprofile hospitals in Tbilisi, Georgia. Georgian Med News. 2018(280-281):164-8.
11. Asghari Mahforujaki M, Jamalli A, Golfiroozi S, Shahryari A. Evaluation of the implementation of the nosocomial infection control program in the emergency department of teaching hospitals of Gorgan, Iran. Iran J Health Environ. 2023;16(1):113-28. [Persian].
12. Ranjbar R, Farahani O. The prevalence of virulence genes and virulotypes of *Escherichia coli* strains isolated from hospital wastewaters in Tehran, Iran. Iran J Public Health. 2018;47(5):713-9.
13. Sora VM, Meroni G, Martino PA, Soggiu A, Bonizzi L, Zecconi A. Extraintestinal pathogenic *Escherichia coli*: virulence factors and antibiotic resistance. Pathogens. 2021;10(11):1355. doi: 10.3390/pathogens10111355.
14. Mousa WA, Omar NS, Riad OK, Omran ME. Expression of bla-CTX-M and fimH genes in uropathogenic *Escherichia coli* isolated from Egyptian catheterized patients. Azhar Int J Pharm Med Sci. 2022;2(2):94-104. doi: 10.21608/aijpms.2022.94662.1093.
15. Tseng CC, Lin WH, Wu AB, Wang MC, Teng CH, Wu JJ. *Escherichia coli* fimH adhesins act synergistically with PapGII adhesins for enhancing establishment and maintenance of kidney infection. J Microbiol Immunol Infect. 2022;55(1):44-50. doi: 10.1016/j.jmii.2020.09.001.
16. Abdolahzadeh Z, Astani A, Mosadegh A, Hosseini Mohammad Abadi SS, Vakili M. Frequency of fimH, papC, and aer in *E. coli* strains isolated from patients with urinary tract infection, and their antibiotic resistance pattern. J Shahid Sadoughi Univ Med Sci. 2021;29(3):3357-64. doi: 10.18502/ssu.v29i3.6200. [Persian].
17. Khoshbakht R, Panahi Z, Alizadeh F. Evaluation of the presence of pap, sfa, and fimH genes in imipenem-resistant *Escherichia coli* isolated from the patients with urinary tract infections from the laboratories of Amol in 2018-2019. Research in Medicine. 2021;45(4):96-101. [Persian].
18. Alishah M, Zahraei Salehi T, Amini K, Yahya-Rayat R. Evaluation of antibiotic resistance and detection of papC and papG genes in *Escherichia coli* strains isolated from patients with urinary tract infection. Qom Univ Med Sci J. 2016;10(8):80-7. [Persian].
19. Bien J, Sokolova O, Bozko P. Role of uropathogenic *Escherichia coli* virulence factors in development of urinary tract infection and kidney damage. Int J Nephrol. 2012;2012:681473. doi: 10.1155/2012/681473.
20. Ejrnæs K. Bacterial characteristics of importance for recurrent urinary tract infections caused by *Escherichia coli*. Dan Med Bull. 2011;58(4):B4187.
21. Raeispour M, Ranjbar R. Antibiotic resistance, virulence factors and genotyping of uropathogenic *Escherichia coli* strains. Antimicrob Resist Infect Control. 2018;7:118. doi: 10.1186/s13756-018-0411-4.
22. Asadi S, Kargar M, Solhjoo K, Najafi A, Ghorbani-Dalini S. The association of virulence determinants of uropathogenic *Escherichia coli* with antibiotic resistance. Jundishapur J Microbiol. 2014;7(5):e9936. doi: 10.5812/jjm.9936.