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Research Article

HIGH PREVALENCE OF TRANSFERABLE INTEGRON-ASSOCIATED DRUG RESISTANCE IN ESCHERICHIA COLI STRAINS ISOLATED FROM BLOOD CULTURES IN A UNIVERSITY HOSPITAL IN TRABZON, TURKEY

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ABSTRACT

Objective: This study aimed to determine the carriage of transferable integron-associated drug resistance in Escherichia coli (E. coli) strains isolated from blood cultures.

Materials and Methods: A total of 111 E. coli isolates were included in this study. Antimicrobial susceptibility testing of the isolates against 17 antibiotics was performed using an automated microbiology system. Integron-specific polymerase chain reactions (PCR) were used to detect the presence of integrons. The antibiotic resistance gene cassettes in the variable regions of integrons were analyzed by DNA sequencing. Plasmid transfer assays were performed using the broth mating method. The clonal relationships among integron-carrying strains were evaluated by pulsed-field gel electrophoresis (PFGE).

Results: Resistance rates to antibiotics ranged from 0.9% to 63%. Thirty-eight strains carried gene cassettes encoding dfrA7, dfr17-aadA5, dfrV, dfrA1-aadA1, and dfrA12-aadA2. Seven strains possessed class 2 integrons with gene arrays dfrA1-sat2-aadA1 and dfrA1-sat2-aadA30. Twenty-two integron-carrying isolates harbored conjugative resistance plasmids, three of which were identified as belonging to the IncN group. Two strains with class 1 integrons, isolated from different clinics, exhibited similar patterns in the PFGE analysis.

Conclusion: Approximately 50% of E. coli isolates from blood cultures at our hospital were found to carry integron-associated transferable drug resistance, suggesting their potential role in the horizontal dissemination of resistance genes. Further research is needed to understand the prevalence of E. coli strains of blood origin and the role of integrons and gene cassette arrays in the spread of resistance.

Keywords: Escherichia coli, Gene Cassette, Integron, Conjugation, Plasmid

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INTRODUCTION

Bloodstream infections (BSIs) are among the most significant nosocomial infections, contributing to increased mortality and morbidity due to rising antimicrobial resistance (1). Escherichia coli, an opportunistic pathogen, is capable of causing a wide range of infections, from from those in the gastrointestinal tract to extraintestinal infections, such as those affecting the central nervous system, urinary tract, and bloodstream. Globally, it is a leading cause of bloodstream infections and exhibits resistant to many drugs (2). While most bacterial infections are treatable with antibiotics, E. coli and other pathogens can rapidly develop antibiotic resistance, making infections more difficult to manage and potentially life-threatening (3). The excessive and inappropriate use of antimicrobials accelerates the emergence and spread of resistance. Therefore, the timely and effective use of antimicrobial drugs is essential in preventing resistance (4). Bacteria can develop resistance to antibiotics through genetic mechanisms involving mobile genetic elements (MGEs), such as plasmids, transposons (Tn), insertion sequences (IS), and integrons. Integrons, especially those located on plasmids or transposons, play a critical role in disseminating antimicrobial resistance genes, particularly in gram-negative bacteria. These integrons carry drug-resistant genes and facilitate the exchange of genetic elements. They are classified based on the sequence of intI gene, with classes 1 and 2 being the most prevalent (5).

The class 1 integrons consist of two conserved regions namely 5' (5'CS) and 3' (3'CS), and a variable region (VR) containing gene cassettes. The 5'CS includes the integrase gene (intI), which encodes the tyrosine recombinase enzyme, the recombination site (attI), and a promoter (P) region involved in the expression of inserted genes or gene cassettes. The 3'CS contains the defective quaternary ammonium resistance gene (qacEΔ1) and the sulI gene, which mediates resistance to sulfonamides. The variable region, located between these two conserved regions, contains the attC site, where various antibiotic resistance cassettes are integrated via recombination. Unlike class 1 integrons, class 2 integrons lack sul genes and typically include resistance gene cassettes such as dfrA1, sat2, and aadA1, which confer resistance to aminoglycosides and sulfamethoxazole (6).

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Although several studies in Turkey have investigated integron-associated drug resistance in E. coli isolates from urine samples (7, 11), very few reports are available (12) on the E. coli isolates from blood samples. This study aimed to identify transferable integron-associated drug resistance in E. coli strains isolated from patients in various clinics.

MATERIALS AND METHODS

Sampling, isolation and identification of bacterial strains

A total of 111 E. coli strains were isolated from hospitalized patients at Karadeniz Technical University's Medical Microbiology Laboratory between January and December 2014. The bacterial strains were cultured using 5% sheep blood agar and EMB agar. Conventional biochemical methods and MALDI-TOF MS (Microflex™, Bruker, Germany) were employed to confirm species-level identification.

Antimicrobial susceptibility testing

Antimicrobial susceptibility testing was performed using the Phoenix ID/AST automated microbiology system (Becton Dickinson Diagnostic Instrument Systems, Sparks, MD, USA), following the manufacturer's instructions. Antibiotic susceptibility test results were interpreted according to Clinical and Laboratory Standards Institute (CLSI) criteria. The isolates were tested for the following antibiotics: amikacin (AK), ampicillin/sulbactam (SAM), aztreonam (ATM), cefazolin (CZ), cefepime (FEP), cefoperazone/sulbactam (CES), cefoksitin (FOX), ceftazidime (CAZ), ceftriaxone (CRO), ciprofloxacin (CIP), ertapenem (ERT), gentamicin (CN), imipenem (IPM), levofloxacin (LEV), meropenem (MEM), piperacillin tazobactam (TZP) and trimethoprim/sulfamethoxazole (SXT). The susceptibility of isolates containing class 1 and class 2 integrons was determined using the disc diffusion method in accordance with CLSI criteria (13). Antibiotic discs (Oxoid, UK) containing ampicillin (10 μg), streptomycin (10 μg), tetracycline (30 μg), nalidixic acid (30 μg), and chloramphenicol (30 μg) were used for this purpose.

DNA isolation

DNA templates for polymerase chain reaction (PCR) were prepared using a modified boiling method based on the protocol by Perez et al (14). After washing, the supernatant was used as the DNA template for PCR analyses.

Detection of integron gene cassettes and integrase genes

To detect integron gene cassettes in E. coli isolates, specific primers were used: For class 1 integrons: intI-1F (GGTCAAGGATCTGGATTTGG) and intI-1R (ACATGCGTGTAAATCATCGTC). For class 2 integrons: intI-2F (CACGGATATGCGACAAAAAGGT) and intI-2R (GTAGCAAACGAGTGACGAAATG). To amplify the variable regions of the integrons, the following primers were used: For class 1 integrons: 5'-CS (GGCATCCAAGCAGCAAG) and 3'-CS (AAGCAGACTTGACCTGA). For class 2 integrons: hep51 (GATGCCATCGCAAGTACGAG) and hep74 (CGGGATCCCGGACGGATGCACGATTTGTA). PCR reaction conditions and compositions followed previously described methods (15).

DNA sequencing and data analysis

PCR products from class 1 and class 2 integrons were purified using the High Pure PCR Clean-up Micro Kit (Roche, Germany). Cloning was performed with the pGEM-T Easy Vector System (Promega, USA) and T4 DNA Ligase enzyme, following the manufacturer's guidelines as described by Sambrook et al. (16). After incubation, blue-white colony screening was used for selection. Plasmid DNA from selected white colonies was isolated using the alkaline lysis method (17). Recombinant plasmids carrying amplicons of class 1 and class 2 integrons were sequenced on an ABI 3130 Genetic Analyzer (Applied Biosystems, USA) using SP6 and T7 promoter primers. DNA sequence data were analyzed using BLAST (http://www.ncbi.nlm.nih.gov/BLAST) and CLUSTALW2 (http://www.ebi.ac.uk/Tools/msa/clustalw2) for sequence alignment and comparisons (18).

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Conjugation experiment

Transfer experiments of plasmids from integron-containing isolates were performed based on the broth mating principle, which was previously described (19). Escherichia coli isolates containing integrons were used as donors, and E. coli J53-2 (met pro RifR) as the recipient cells. Broth cultures of both donor and recipient were mixed in equal volumes (1:1) and incubated for 20 hours at 37°C without shaking. Transconjugants were selected on LB agar supplemented with rifampicin (300 µg/mL), to which the recipient cells are resistant, and either trimethoprim (25 µg/mL) or streptomycin (100 µg/mL) to which the donor cells are resistant.

Isolation of plasmid DNA

A colony was picked from transconjugant plates and sub-cultured in 3 mL of LB broth at 150 rpm shaking at 37°C for 16-18 hours. A 1.5-ml aliquot of the overnight culture was centrifuged at 12,000 rpm to pellet the bacteria. The cells were lysed, and plasmid DNA was isolated using the standard alkali-lysis method. Finally, the pellet was dried at 37oC and resuspended in 30-40 µl of 1X TE buffer containing 0.5-1 µg/mL of RNase. Plasmid DNA was analyzed by electrophoresis, and visualized under a UV transilluminator (20).

PCR-based replicon typing

To identify the incompatibility (Inc) groups that contribute significantly to the dissemination of resistance genes, plasmids isolated from transconjugants were subjected to replicon typing using specific primers as described by Götz et al. (21).

Pulsed-field gel electrophoresis (PFGE)

Clonal relationship among 58 E. coli isolates containing integrase genes (intI-1 and intI-2) belonging to class 1 and class 2 integrons were determined using the PFGE method, with modifications based on the studies of Durmaz et al. (22). PFGE was performed with the CHEF DR-III (Bio-Rad, USA) system using a 1% ultrapure agarose gel in 2L of 0.5X TBE. The gel was stained in a solution containing 10 mg/mL ethidium bromide for 30

minutes. Gel visualization and photography were conducted using the VersaDocTM system, and images were analyzed with GelJ software, version 2.

Statistical analysis

Statistical analyses were performed using Pearson's Chi-square test and Fisher's Exact test with the Statistical Package for the Social Sciences (SPSS) version 23 for Windows. A p-value of < 0.05 was considered statistically significant.

RESULTS

Antimicrobial resistance phenotypes of E. coli isolates

Antimicrobial susceptibility tests for 111 E. coli isolates from blood cultures were performed using the Phoenix™ 100 device. The resistance rates of the isolates to 17 antibiotics are shown in Figure 1.

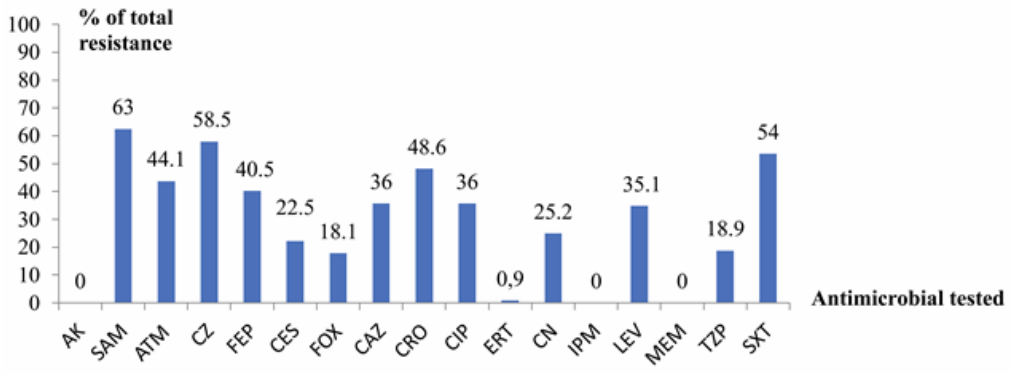

Figure 1. Total antimicrobial resistance rates of 111 clinical Escherichia coli isolates.

The highest resistance percentage was observed for SAM 63% (n=70), while the lowest was for ERT 0.9% (n=1). Resistance rates to other antibiotics were as follows: ATM 44.1% (n=49), CZ 58.5% (n=65), FEP 40.5% (n=45), CES 22.5% (n=25), FOX 18.1% (n=20), CAZ 36% (n=40), CRO 48.6% (n=54), CIP 36% (n=40), CN 25.2% (n=28), LEV 35.1% (n=39), TZP 18.9% (n=21), and SXT 54% (n=60). None of the isolates was resistant to AK, IPM, and MEM (Fig. 1). In a subset of 45 E. coli isolates with class 1 and class 2 integron gene cassettes, tested using the disc diffusion method, resistance to ampicillin, streptomycin, and tetracycline was found to be 66.6% (n=30),

while resistance to nalidixic acid was 64.4% (n=29). The lowest resistance rate was 26.6% (n=12) for chloramphenicol (Figure 2).

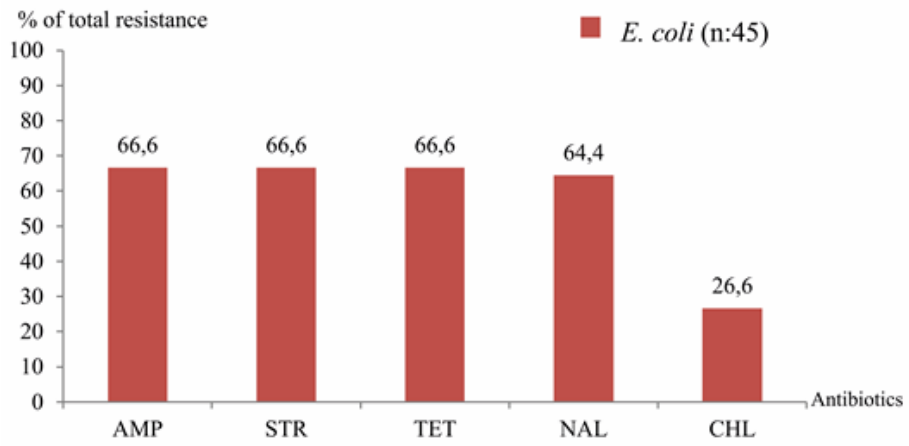

Figure 2. Total antimicrobial resistance rates of *E. coli* isolates containing class 1 and class 2 integrons.

Statistical analysis revealed significant differences in antimicrobial resistance between strains with and without class 1 and class 2 integrase genes for SAM, ATM, CZ, FEP, CAZ, CRO, CIP, and SXT ($p<0.05$). However, no significant differences were observed for CES, FOX, ERT, CN, LEV, and TZP antibiotics ($p>0.05$). Statistical analysis could not be conducted for AK, IPM, and MEM, as no resistant strains were found in either group.

PCR for integrons

A total of 111 E. coli isolates were screened for the presence of class 1 and class 2 integrase genes. Of these, 51 isolates (46%) were positive for class 1 integrase, and seven isolates (%6) were positive for class 2 integrase. PCR analysis of the variable region of class 1 integrons showed that 38 isolates (34%) contained class 1 integrons, while 13 isolates (11.7%) carried empty integrons. Class 2 integrons were detected in 7 isolates (6%) (Table 1). Gene cassette arrays of 45 E. coli isolates with integrons were determined by DNA sequencing. Among 27 of the 38 isolates with class 1 integrons, five gene cassette arrays were identified: dfrA7, dfr17-aadA5, dfrV, dfrA1-aadA1 ve dfrA12-aadA2, associated with trimethoprim and streptomycin-spectinomycin resistances. These arrays ranged from 800-1800 bp in length. Gene cassette arrays could not be sequenced for

11 class 1 integrons due to technical difficulties of the unknown nature (TEC002, TEC005, TEC010, TEC015, TEC020, TEC043, TEC055, TEC057, TEC072, TEC078 and TEC091). For the seven isolates with class 2 integrons, two gene cassette arrays were identified: dfrA1-sat2-aadA1 and dfrA1-sat2-aadA30, approximately 2500 bp in length. Sequencing was unsuccessful for three class 2 integrons (TEC012, TEC033, TEC081) (Table 1).

Conjugation experiments

Plasmid transfer studies were executed on 45 E. coli isolates with integrons. Among these, 22 isolates (48.8%) carried conjugative plasmids larger than 100 kb. Conjugation frequency ranged from 10-9 to 10-8. Transconjugants were validated genotypically using previously established PCR methods. PCR assays revealed that three plasmids (pTEC010, pTEC015 and pTEC075) belonged to the IncN group. No Inc P, IncQ, or IncW group plasmids were detected in any of the transconjugants (Table 1).

Pulsed-field gel electrophoresis analysis

PFGE dendrogram analysis of 50 E. coli strains with integrons, their antibiotic resistance patterns, and sources shown in Figure 3. These strains were divided into 39 distinct groups, some of which were further subdivided into subgroups (A, B, C). Eleven subgroups (4, 7, 9, 10, 12, 13, 14, 16, 25, 35, 37) showed similarity rates above 80%. Subgroups 13 showed similarity rates exceeding 90%. Notably, strains TEC010 and TEC015 all carrying class 1 integrons, demonstrated high clonal similarity despite significant differences in their clinical origins and antibiotic resistance patterns. Eight strains were excluded from the analysis because the DNA pattern quality obtained as a result of PFGE experiments was not sufficient for dendrogram analysis.

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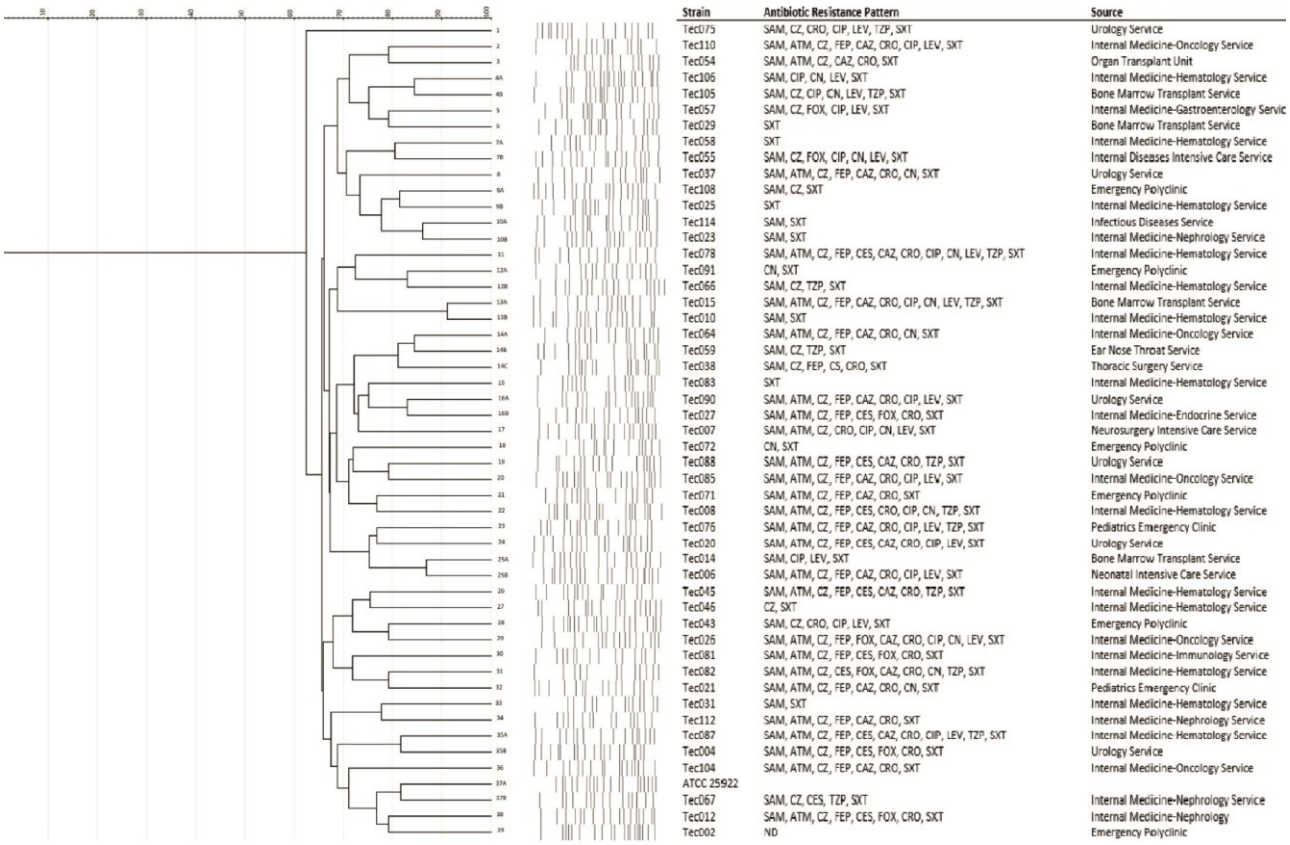

Strain	Antibiotic Resistance Pattern	Source
Tec075	SAM, CZ, CRO, CIP, LEV, TZP, SXT	Urology Service
Tec110	SAM, ATM, CZ, FEP, CAZ, CRO, CIP, LEV, SXT	Internal Medicine-Oncology Service
Tec054	SAM, ATM, CZ, CAZ, CRO, SXT	Organ Transplant Unit
Tec106	SAM, CIP, CN, LEV, SXT	Internal Medicine-Hematology Service
Tec105	SAM, CZ, CIP, CN, LEV, TZP, SXT	Bone Marrow Transplant Service
Tec057	SAM, CZ, FOX, CIP, LEV, SXT	Internal Medicine-Gastroenterology Servic
Tec029	SXT	Bone Marrow Transplant Service
Tec058	SXT	Internal Medicine-Hematology Service
Tec055	SAM, CZ, FOX, CIP, CN, LEV, SXT	Internal Diseases Intensive Care Service
Tec037	SAM, ATM, CZ, FEP, CAZ, CRO, CN, SXT	Urology Service
Tec108	SAM, CZ, SXT	Emergency Polyclinic
Tec025	SXT	Internal Medicine-Hematology Service
Tec114	SAM, SXT	Infectious Diseases Service
Tec023	SAM, SXT	Internal Medicine-Nephrology Service
Tec078	SAM, ATM, CZ, FEP, CES, CAZ, CRO, CIP, CN, LEV, TZP, SXT	Internal Medicine-Hematology Service
Tec091	CN, SXT	Emergency Polyclinic
Tec066	SAM, CZ, TZP, SXT	Internal Medicine-Hematology Service
Tec015	SAM, ATM, CZ, FEP, CAZ, CRO, CIP, CN, LEV, TZP, SXT	Bone Marrow Transplant Service
Tec010	SAM, SXT	Internal Medicine-Hematology Service
Tec064	SAM, ATM, CZ, FEP, CAZ, CRO, CN, SXT	Internal Medicine-Oncology Service
Tec059	SAM, CZ, TZP, SXT	Ear Nose Throat Service
Tec038	SAM, CZ, FEP, CS, CRO, SXT	Thoracic Surgery Service
Tec083	SXT	Internal Medicine-Hematology Service
Tec090	SAM, ATM, CZ, FEP, CAZ, CRO, CIP, LEV, SXT	Urology Service
Tec027	SAM, ATM, CZ, FEP, CES, FOX, CRO, SXT	Internal Medicine-Endocrine Service
Tec007	SAM, ATM, CZ, CRO, CIP, CN, LEV, SXT	Neurosurgery Intensive Care Service
Tec072	CN, SXT	Emergency Polyclinic
Tec088	SAM, ATM, CZ, FEP, CES, CAZ, CRO, TZP, SXT	Urology Service
Tec085	SAM, ATM, CZ, FEP, CAZ, CRO, CIP, LEV, SXT	Internal Medicine-Oncology Service
Tec071	SAM, ATM, CZ, FEP, CAZ, CRO, SXT	Emergency Polyclinic
Tec008	SAM, ATM, CZ, FEP, CES, CRO, CIP, CN, TZP, SXT	Internal Medicine-Hematology Service
Tec076	SAM, ATM, CZ, FEP, CAZ, CRO, CIP, LEV, TZP, SXT	Pediatrics Emergency Clinic
Tec020	SAM, ATM, CZ, FEP, CES, CAZ, CRO, CIP, LEV, SXT	Urology Service
Tec014	SAM, CIP, LEV, SXT	Bone Marrow Transplant Service
Tec006	SAM, ATM, CZ, FEP, CAZ, CRO, CIP, LEV, SXT	Neonatal Intensive Care Service
Tec045	SAM, ATM, CZ, FEP, CES, CAZ, CRO, TZP, SXT	Internal Medicine-Hematology Service
Tec046	CZ, SXT	Internal Medicine-Hematology Service
Tec043	SAM, CZ, CRO, CIP, LEV, SXT	Emergency Polyclinic
Tec026	SAM, ATM, CZ, FEP, FOX, CAZ, CRO, CIP, CN, LEV, SXT	Internal Medicine-Oncology Service
Tec081	SAM, ATM, CZ, FEP, CES, FOX, CRO, SXT	Internal Medicine-Immunology Service
Tec082	SAM, ATM, CZ, CES, FOX, CAZ, CRO, CN, TZP, SXT	Internal Medicine-Hematology Service
Tec021	SAM, ATM, CZ, FEP, CAZ, CRO, CN, SXT	Pediatrics Emergency Clinic
Tec031	SAM, SXT	Internal Medicine-Hematology Service
Tec112	SAM, ATM, CZ, FEP, CAZ, CRO, SXT	Internal Medicine-Nephrology Service
Tec087	SAM, ATM, CZ, FEP, CES, CAZ, CRO, CIP, LEV, TZP, SXT	Internal Medicine-Hematology Service
Tec004	SAM, ATM, CZ, FEP, CES, FOX, CRO, SXT	Urology Service
Tec104	SAM, ATM, CZ, FEP, CAZ, CRO, SXT	Internal Medicine-Oncology Service
ATCC 25922		
Tec067	SAM, CZ, CES, TZP, SXT	Internal Medicine-Nephrology Service
Tec012	SAM, ATM, CZ, FEP, CES, FOX, CRO, SXT	Internal Medicine-Nephrology
Tec002	ND	Emergency Polyclinic

Figure 3. Dendogram analysis of E. coli isolates containing class 1 and class 2 integrons

DISCUSSION

Infections caused by Gram-negative bacteria, such as septicemia, are significant contributors to mortality and morbidity. The isolation of bacteria, particularly from blood cultures, often indicates a severe invasive infection requiring immediate antimicrobial therapy. Among these, E. coli is one of the most commonly isolated pathogens from blood cultures. The World Health Organization (WHO) has identified E. coli as a priority pathogen of concern due to its role in the global development of antimicrobial resistance, especially infections affecting the blood and urinary tract. Antibiotic resistance presents a considerable challenge to public health. Accurate detection of resistant bacteria and determination of antimicrobial resistance, particularly in clinical laboratories, are therefore essential for enabling clinicians to administer effective antibiotic treatments (23, 24).

In our study, the antibiotic resistance patterns of E. coli from blood cultures were analyzed against 17 different antibiotics. Resistance rates were highest against SAM, CZ, CRO, and SXT, as also reported in the previous studies (25, 26). As a matter of fact, these antibiotics have historically been used extensively in the empirical treatment of sepsis and other infections (23). Our findings align with those of Kreidl et al. (27), who reported resistance rates of 71.8% against aminopenicillins and 37.5% against CIP. Furthermore, all E. coli isolates in our study were sensitive to AK and carbapenems (IPM and MEM), consistent with findings by Anvarinejad et al. (28).

Timely and accurate diagnosis and treatment are essential for mitigating the severe effects of sepsis and reducing mortality. Identifying common bacterial pathogens and their resistance patterns is crucial for guiding appropriate antimicrobial therapy. Ampicillin, nalidixic acid, SXT, and tetracyclines, widely used in both clinical and veterinary medicine (28), showed significant resistance in this study. Notably, strains with class 1 and class 2 integrons exhibited the highest resistance rates. These classes of integrons contain genes conferring resistance to trimethoprim and streptomycin. Class 1 integrons, in particular, harbor the sul1 gene encoding sulfonamide resistance adjacent to the 3'-conserved region (29). Integrons are genetic elements that facilitate the capture, insertion, and exchange of antibiotic resistance gene cassettes, thereby playing a significant role in the dissemination of resistance genes, particularly among Gram-negative bacteria (30). The high prevalence of trimethoprim and streptomycin resistance in this study are thought to be resulted in the integrons containing various antibiotic gene cassette arrays.

Multidrug resistance in Enterobacterales is often associated with antimicrobial resistance genes carried by integrons (31). In Türkiye, numerous studies have focused on integrons in bacteria from clinical (32), animal (33), and aquatic (34) sources. Although there are some epidemiological studies in clinical bacteria, especially in urine samples (9), research on the molecular characterization of E. coli strains from blood samples remains limited. In this study, 46% (111/51) of isolates carried the intI1 gene, with 38 isolates (34%) containing class 1 integrons, and 13 isolates (11.7%) having empty integrons. Additionally, 6% (111/7) of isolates carried the intI2 gene, and all of these belong to class 2 integrons.

The frequency of the intI1 gene (34%) observed in this study is comparable to findings by Liu et al. (35) (41.33%) but lower than results reported byAbdel-Rhman et al. (36) (98.33%) and Liu et al. (35) (67.39 %). The lower prevalence of class 1 integrons may be attributed to alternative resistance mechanisms, such as of beta-lactamase enzyme production, efflux pumps overexpression, reduced bacterial outer membrane permeability, and intrinsic resistance factors (37). Class 2 integrons were identified at a rate of 6%, consistent with Ahumado-Santos et al. (38), who reported a low prevalence (1.4%).

The predominance of class 1 integrons over class 2 integrons in our isolates is consistent with another study (11). Empty integrons found in 13 isolates may represent bacteria containing empty integrons are probably due to the presence of a very large gene cassette and the inability to amplify these gene cassettes (39, 40) .We believe that the presence of empty integrons in bacteria could make these isolates have the potential to become multi-drug resistant by capturing antibiotic resistance genes from other bacteria in the hospital environment and spreading to the other bacteria of both commensal and clinical origin.

The presence of dfrA genes encoding trimethoprim resistance and aad/aac genes encoding aminoglycoside resistance has been widely reported (41, 42). Gene cassette arrays such as dfrA1, dfrA5, aadA1, and aadA5 are common in clinical bacteria, as reported by Cicek et al. (8) and Sandalli et al. (7). The dfrA17/aadA5 gene array, which confers resistance to trimethoprim and streptomycin, is often plasmid-mediated and associated with the proliferation of resistant bacterial isolates in clinical settings (43). In our study, 22 isolates (48.8%) containing class 1 and class 2 integrons harbored conjugative plasmids (>100 kb) confirmed through mating assays. These plasmids, particularly of the IncP and IncN groups, are known for their broad host range and role in spreading multidrug resistance in clinical settings (44).

The clonal relationships of integron-containing E. coli isolates were evaluated using PFGE. While PFGE effectively differentiated subgroups, it showed limited correlation with antibiotic resistance profiles, suggesting the influence of other genetic factors. Notably, isolates from different clinical origins and resistance profiles exhibited over 90% similarity in PFGE analyses, while clonally unrelated isolates from the same source displayed similar resistance profiles (Fig. 3). Also, TEC078 and TEC087 isolates, which were isolated from the same clinical source and had almost the same antibiotic resistance profiles, were determined as clonally

unrelated in different branches. As a result, PFGE patterns determined in E. coli isolates containing integrons and similar gene cassettes showed little clonal association.

CONCLUSION

This study is among the few to investigate the prevalence of integrons in E. coli isolates from blood samples in Türkiye. The transfer of antibiotic resistance genes via integrons and plasmids poses significant challenges for managing infectious diseases. Continuous surveillance of antimicrobial resistance in invasive E. coli isolates is essential to monitor trends and guide effective treatment strategies. Understanding the mechanisms of resistance, including the role of integrons, can inform the development of targeted antimicrobial therapies. Further research is needed to explore the interplay between integrons, gene cassette arrays, and resistance mechanisms in bloodstream infections.

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Authorship contributions

AR, OBÖ and AOK designed the study; AR, CKB and GB collected E. coli isolates and carried out phenotypic identification; AR, ER and İD performed the molecular assay; AR, OBÖ, ER and AOK prepared and revised the manuscript. All authors gave the final approval of the version to be published.

Data availibity statement

The authors state that the data supporting the study's results can be found in the article. Additionally, the raw data can be obtained from the corresponding author upon a reasonable request.

Declaration of competing interest

The authors declare that they have no conflict of interest.

Ethics

This study was approves by Karadeniz Technical University Faculty of Medicine Scientific Research Ethics Committee (Date: 12.10.2015, Decision no:3, Reference number 2015/117).

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