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Research Article

Phenotypic and Genotypic Analysis of Multidrug-Resistant Uropathogenic Escherichia coli

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Abstract

Background: Escherichia coli (E. coli) is the most common causative agent of urinary tract infections (UTIs), and the emergence of multidrug-resistant (MDR) strains of uropathogenic E. coli (UPEC) has become a significant public health concern. MDR UPEC strains are resistant to multiple classes of antibiotics, leading to treatment failure and increased morbidity.

Aim: This study aims to analyze the phenotypic and genotypic characteristics of MDR UPEC strains isolated from clinical urine samples.

Methods: A cross-sectional study was conducted over 12 months in a tertiary care hospital. A total of 150 clinical isolates of E. coli from UTI patients were collected and tested for antimicrobial susceptibility using disk diffusion method. Genotypic analysis for the presence of resistance genes was performed using polymerase chain reaction (PCR) for common resistance genes, including extended-spectrum beta-lactamases (ESBLs), carbapenemases, and aminoglycoside-modifying enzymes.

Results: Out of 150 isolates, 70% were found to be multidrug-resistant. The majority of MDR strains showed resistance to ampicillin, cephalosporins, and trimethoprim-sulfamethoxazole. PCR analysis revealed the presence of common resistance genes, including blaTEM, blaCTX-M, and aac(3)-II. High prevalence of ESBL-producing strains was also noted.

Conclusion: The study highlights the significant prevalence of MDR UPEC in UTI patients, with resistance linked to specific genotypic markers. This underscores the importance of molecular surveillance and the need for alternative therapeutic strategies.

Keywords: Multidrug-resistant, Uropathogenic Escherichia coli, phenotypic analysis, genotypic analysis, resistance genes, urinary tract infections.

Introduction

Urinary tract infections (UTIs) are one of the most common infectious diseases worldwide, affecting both adults and children. Among the various pathogens causing UTIs, *Escherichia coli* (E. coli) remains the leading etiological agent, responsible for up to 90% of uncomplicated UTIs (1). *Uropathogenic E. coli* (UPEC) is a particular strain of *E. coli* that is adapted to infect the urinary tract and has evolved mechanisms to cause both acute and recurrent infections (2). The emergence of multidrug-resistant (MDR) strains of UPEC has become an alarming global issue, complicating the treatment of UTIs and leading to higher rates of morbidity, prolonged hospital stays, and increased healthcare costs (3).

The resistance of UPEC to commonly prescribed antibiotics, such as beta-lactams,

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aminoglycosides, and fluoroquinolones, has been steadily increasing. Infections caused by MDR UPEC strains often fail to respond to conventional antimicrobial treatments, forcing clinicians to resort to second-line antibiotics, which may have more significant side effects or be less effective (4). MDR strains are typically defined as those resistant to at least three or more classes of antibiotics, and their emergence is driven by factors such as the overuse and misuse of antibiotics, horizontal gene transfer, and selective pressure from antimicrobial agents in clinical settings (5).

Resistance mechanisms in MDR UPEC are multifactorial and involve both phenotypic and genotypic changes. Phenotypically, these bacteria can exhibit various mechanisms of resistance, such as the production of extended-spectrum beta-lactamases (ESBLs), carbapenemases, and aminoglycoside-modifying enzymes. Genotypically, the presence of resistance genes, including *blaTEM*, *blaCTX-M*, *aac(3)-II*, and others, contributes to the resistance phenotype (6). The identification of these resistance genes is crucial for understanding the molecular basis of resistance and for implementing effective control measures.

This study aims to perform a phenotypic and genotypic analysis of MDR UPEC strains isolated from UTI patients, investigating the resistance profiles and identifying key resistance genes responsible for the MDR phenotype.

Aim and Objectives

Aim:

To analyze the phenotypic and genotypic characteristics of multidrug-resistant uropathogenic *Escherichia coli* strains isolated from urinary tract infection patients.

Objectives:

1. To determine the prevalence of multidrug resistance among *E. coli* strains isolated from UTI patients.
2. To identify the phenotypic resistance patterns and the presence of resistance genes in these multidrug-resistant strains.

Materials and Methods

Study Design:

This was a cross-sectional, laboratory-based study conducted at a tertiary care hospital over a 12-month period.

Sample Collection:

A total of 150 clinical urine samples were collected from patients diagnosed with UTIs. The samples were processed and cultured on selective media to isolate *E. coli*.

Phenotypic Analysis:

The antimicrobial susceptibility of the *E. coli* isolates was determined using the disk diffusion method, following the guidelines set by the Clinical and Laboratory Standards Institute (CLSI). The following antibiotics were tested: ampicillin, cephalosporins (ceftriaxone, cefotaxime), aminoglycosides (gentamicin, amikacin), fluoroquinolones (ciprofloxacin), trimethoprim-sulfamethoxazole, and carbapenems (imipenem).

Genotypic Analysis:

Genomic DNA was extracted from *E. coli* isolates using the standard phenol-chloroform method. Polymerase chain reaction (PCR) was performed to detect resistance genes associated with extended-spectrum beta-lactamases (ESBLs) (*blaTEM*, *blaCTX-M*), carbapenemases (*blaKPC*, *blaNDM*), and aminoglycoside-modifying enzymes (*aac(3)-II*). Specific primers were used for each gene based on known sequences.

Inclusion Criteria:

- Patients diagnosed with urinary tract infections.
- Children and adults with clinical signs of UTIs.
- *E. coli* strains isolated from urine samples.

Exclusion Criteria:

- Patients with other types of infections (e.g., respiratory infections).
- *E. coli* strains isolated from non-urinary specimens.

Results

Table 1: Antibiotic Resistance Patterns of Uropathogenic *Escherichia coli* Strains

Antibiotic	Resistance Rate (%)
Ampicillin	82
Ceftriaxone	65
Gentamicin	38
Ciprofloxacin	45
Trimethoprim-sulfamethoxazole	68
Imipenem	10

The highest resistance was observed to ampicillin (82%), followed by trimethoprim-sulfamethoxazole (68%) and ceftriaxone (65%). However, only 10% of the strains were resistant to imipenem, a carbapenem antibiotic.

Table 2: Prevalence of Resistance Genes in MDR Uropathogenic *E. coli* Strains

Resistance Gene	Frequency (%)
blaTEM	60
blaCTX-M	50
aac(3)-II	45
blaKPC	12
blaNDM	8

The most prevalent resistance genes were *blaTEM* (60%) and *blaCTX-M* (50%), followed by *aac(3)-II* (45%). The presence of carbapenemase genes (*blaKPC* and *blaNDM*) was less common.

Discussion

The prevalence of multidrug-resistant *E. coli* strains in UTIs is a growing concern, especially in hospital settings where patients are often exposed to multiple antibiotics. This study found that 70% of *E. coli* isolates were multidrug-resistant, consistent with previous reports of high MDR rates in UPEC (7). The highest resistance was observed to ampicillin, followed by trimethoprim-sulfamethoxazole, and ceftriaxone, which are commonly used antibiotics for UTIs (8). These findings emphasize the need for alternative therapeutic strategies, including the use of carbapenems, which showed the lowest resistance in this study.

Genotypic analysis revealed that *blaTEM* and *blaCTX-M* were the most prevalent resistance genes in the MDR isolates. These genes are associated with extended-spectrum beta-lactamase production, which confers resistance to a wide range of beta-lactam antibiotics, including third-generation cephalosporins (9). The presence of aminoglycoside-modifying enzymes, such as *aac(3)-II*, further complicates treatment options, as these enzymes deactivate aminoglycosides, which are often used to treat severe UTIs (10). The low prevalence of carbapenemase-producing genes (*blaKPC* and *blaNDM*) suggests that carbapenem resistance is still relatively rare in our study population, but continuous surveillance is necessary to monitor emerging resistance.

Our study also highlights the need for molecular surveillance to guide the choice of antibiotics in clinical practice. By identifying resistance genes in UPEC, clinicians can make informed decisions about treatment and reduce the inappropriate use of antibiotics, which is a key driver of resistance (11).

Conclusion

The high prevalence of multidrug-resistant *E. coli* in UTI patients underscores the need for vigilance in the management of these infections.

Phenotypic and genotypic analysis of MDR strains reveals that resistance is primarily due to the production of extended-spectrum beta-lactamases and aminoglycoside-modifying enzymes. Further research and continuous molecular surveillance are essential to better understand the mechanisms of resistance and to develop targeted therapeutic approaches to combat MDR uropathogenic *E. coli*.

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