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Multidrug Resistance in Uropathogenic Clonal Group A E. coli Isolates

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Abstract

Bacterial infections especially in women and the aged group are some of the most common infections in the world they include urinary tract infections. Of all the causative organisms in UTI, Escherichia coli species accounts for about 70-95% of the cases. This study aimed at understanding the extend and pattern of multidrug resistance (MDR) among uropathogenic Escherichia coli (UPEC) that are belonging to clonal group A, in order to identify key resistant genes and explain their distribution and effects towards treatment outcomes. The increasing prevalence of multidrug-resistant Escherichia coli (UPEC) strains especially those of clonal group A predispose UTI management to a lot of challenges. They found that the rate of MDR in clonal group A isolates was very high, with overall resistance to at least three antimicrobial classes noted in 80 percent of isolates. This present work also focuses on the high level of antibiotic resistance in clonal group A E. coli isolates. The high level of resistance to important antibiotic classes, coupled with the description of important resistance, suggest that approaching UTIs by MDR UPECs that are emerging is a complicate affair.

Keywords: multidrug resistance, urinary tract infections, Escherichia coli, Bacterial infections, uropathogenic Escherichia coli

Introduction

Bacterial infections, particularly among women and the elderly, are some of the most common infections globally, with urinary tract infections (UTIs) being a major contributor. Among the various causative organisms of UTIs, *Escherichia coli* (E. coli) is responsible for approximately 70-95% of cases (1). The E. coli strains associated with UTIs are classified as uropathogenic *E. coli* (UPEC) due to their ability to colonize and cause damage to the human urinary system (2).

Uropathogenic *E. coli* is further categorized into clonal groups, with clonal group A being the most frequently involved in UTIs. Clonal group A *E. coli* strains are characterized by specific genetic factors, and many of these are associated with community-acquired infections (3). These isolates are capable of causing severe infections, owing to their high virulence factors such as adhesins and toxins, which enable the bacteria to adhere to and colonize the urinary tract (4).

A significant concern in recent years has been the emergence of multidrug-resistant (MDR) *E. coli* strains globally. MDR is defined as the acquired resistance to at least three different classes of antibiotics. The key risk factors for MDR include prior hospitalization, prolonged stays in healthcare facilities, and chronic illnesses (5). The rise of MDR UPEC strains presents a serious challenge, as these bacteria are not only more difficult to treat but also contribute to the spread

of resistance traits in both community settings and healthcare environments.

Antibiotic resistance in UPEC strains is complex, involving both innate and acquired mechanisms. The outer membrane of *E. coli* is naturally impermeable to certain antibiotics, which contributes to intrinsic resistance. Acquired resistance, however, arises through horizontal gene transfer of resistance genes located on plasmids or transposons (6). Some of the key resistance genes in MDR *E. coli* include those encoding β-lactamases, such as blaTEM, blaSHV, and blaCTX-M, as well as quinolone resistance genes like qnr (7).

Clonal group A *E. coli* strains are known to exhibit resistance to several antibiotics, including amoxicillin, ciprofloxacin, and trimethoprim-sulfamethoxazole. This increasing resistance has led to challenges in empirical treatment regimens, necessitating more nuanced therapeutic strategies. The fact that MDR *E. coli* strains belong to clonal groups, which facilitates the transmission of resistance factors, underscores the need for targeted interventions (8).

Given the rising levels of MDR UPEC, particularly from clonal group A isolates, it is essential to assess the extent of resistance and develop strategies to counteract this issue. The objectives of the current study are to fill the existing gap in the literature by evaluating the antimicrobial susceptibility profile of CGA *E. coli* isolates, identifying key genes associated with MDR in this group, and understanding the genetic relationships driving MDR within the CGA *E. coli* population.

Aim and Objectives

Aim:

This study aims to understand the extent and patterns of multidrug resistance (MDR) among uropathogenic *E. coli* (UPEC) strains belonging to clonal group A. The study will focus on identifying key resistance genes and exploring their distribution and effects on treatment outcomes.

Objectives:

1. To evaluate the multidrug resistance patterns within clonal group A *E. coli* isolates.
2. To assess the antibiotic resistance profile of clonal group A UPEC isolates from the study population against commonly used antibiotics.
3. To examine the MDR patterns and identify resistance genes (such as blaTEM, blaCTX-M, qnr) in the study isolates.

Materials and Methods

1. Study Design and Setting:

This study was a cross-sectional descriptive analysis of clinical isolates from UTI patients at a tertiary facility. Ethical approval was obtained from the institution's ethical review board.

2. Sample Collection:

Urine samples were collected from 150 patients diagnosed with UTIs. The samples were processed within 2 hours of collection to ensure bacterial viability. Each sample was streaked on selective media for the isolation and identification of *E. coli*.

3. Bacterial Identification:

E. coli isolates were identified using standard microbiological methods, including:

- **Gram Staining:** Small, Gram-negative rods.
- **Biochemical Testing:** API 20E or other identification kits.
- **Selective Media:** MacConkey agar and eosin methylene blue (EMB) agar.

4. Clonal Group Identification:

E. coli isolates belonging to clonal group A were identified using multilocus sequence typing (MLST) and PCR assays to detect specific genetic markers associated with clonal group A (3).

5. **Antimicrobial Susceptibility Testing:**

The antimicrobial susceptibility of isolates was tested using the disk diffusion method. Antibiotics tested included:

- β-lactams: Amoxicillin, Cephalexin
- Quinolones: Ciprofloxacin
- Trimethoprim-sulfamethoxazole
- Nitrofurantoin
- Aminoglycosides: Gentamicin

The isolates were classified as resistant, intermediate, or susceptible. MDR was defined as resistance to at least three different antibiotic classes.

6. **Data Analysis:**

Prevalence and resistance patterns of MDR among clonal group A isolates were assessed using descriptive statistics. Genetic correlations were analyzed using chi-square tests to examine the relationship between genetic factors and phenotypic resistance patterns.

Results

Table 1: Prevalence of Multidrug Resistance Among Clonal Group A UPEC Isolates

Total Isolates (n)	Clonal Group A Isolates (n)	Multidrug-Resistant Isolates (n)	Percentage of MDR Isolates (%)
150	90	72	80%

Out of 150 total isolates, 72 (80%) were multidrug-resistant, with clonal group A accounting for 90 isolates.

Table 2: Antimicrobial Susceptibility Profile of Clonal Group A UPEC Isolates

Antibiotic	Total Isolates Tested (n)	Resistant Isolates (n)	Percentage Resistant (%)
Amoxicillin	90	77	85%
Ciprofloxacin	90	63	70%
Nitrofurantoin	90	18	20%
Trimethoprim-sulfamethoxazole	90	59	65%
Cephalexin	90	27	30%
Gentamicin	90	11	12%

Table 3: Antimicrobial Resistance Patterns in Multidrug-Resistant Clonal Group A UPEC Isolates

Resistance Pattern	Number of Isolates (n)	Percentage (%)
Resistant to Amoxicillin, Ciprofloxacin, and Trimethoprim-sulfamethoxazole	30	42%
Resistant to Amoxicillin, Ciprofloxacin, and Cephalexin	15	21%
Resistant to Amoxicillin, Trimethoprim-sulfamethoxazole, and Nitrofurantoin	12	17%
Resistant to Ciprofloxacin, Trimethoprim-sulfamethoxazole, and Nitrofurantoin	10	14%
Resistant to all tested antibiotics	5	7%

Discussion

The prevalence of multidrug-resistant *E. coli* strains, particularly those belonging to clonal group A, presents significant challenges in UTI management. The study found that 80% of clonal group A isolates were MDR, with high resistance to commonly used antibiotics such as amoxicillin (85%), ciprofloxacin (70%), and trimethoprim-sulfamethoxazole (65%). This reinforces the growing concern regarding the ineffectiveness of empirical therapies and the need for more targeted treatment strategies.

The identification of specific resistance profiles, including resistance to multiple classes of antibiotics, underscores the need for continuous surveillance of *E. coli* resistance patterns and the development of alternative treatment approaches.

Conclusion

This study highlights the rising concern of multidrug resistance in clonal group A *E. coli* isolates, which complicates the treatment of UTIs. The findings emphasize the necessity of an integrated approach to managing MDR UPEC, including enhanced diagnostic tools, antibiotic stewardship programs, and research into alternative treatment options. Understanding the genetic basis of resistance and its dissemination pathways is essential to developing effective strategies to combat the growing threat of MDR bacteria.

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