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MULTIDRUG RESISTANCE AMONG UROPATHOGENIC CLONAL GROUP A E. COLI ISOLATES: A COMPREHENSIVE STUDY

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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 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 (1). E. coli strains associated with UTIs are considered uropathogenic E. coli (UPEC) due to their capacity of colonizing and to damage the human urinary system (2).

Uropathogenic E.coli is divided into the clonal groups, and clonal group A is considered to be the most often involved in UTIs. Clonal group A E.coli possesses certain genetic factors and it is associated with a large number of community acquired strains (3). These isolates have the potential to cause serious infections and they contribute a high virulence level such as adhesins and toxins that enables these bacteria to colonize the urinary tract (4).

This has been due to the recent appearance of multidrug resistant MDR E. coli throughout the world. MDR is characterized by acquired resistance to not less than three different groups of antibiotics in the same patient namely: The three risk factors for MDR include prior hospitalization; prolonged stay in the hospital; and having a chronic illness (5). The increase in MDR UPEC strains has become a problem due to the fact that these group of bacteria are not only harder to treat but they also help in passing on the resistance traits in the community and in healthcare facilities.

Resistance to antibiotics in UPEC strains is multivariate and includes both, innate and acquired

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resistance pathways. Studying the natural characters of E. coli, it is possible to identify various factors that help create intrinsic resistance Such as, outer membrane of E. coli is not permeable to some categories of antibiotics. Acquired resistance on the other hand is achieved through horizontal gene transfer of the resistance genes which are located either on the plasmids or transposons (6). Some of these MDR E. coli resistance genes are genes encoding β-lactamases such as the blaTEM, blaSHV and blaCTX-M groups of genes, quinone resistance genes including qnr genes (7).

It has been identified that clonal group A E.coli is resistance to many antibiotics of which include amoxicillin, ciprofloxacin and trimethoprim-sulfamethoxazole. This resistance profile has revealed an increasing trend of significantly subverting empirical treatment regimens and demanding statesmanlike therapeutic approaches. This may in part be due to the fact that MDR E.coli bacteria belongs to clonal groups which aids in the transmission of resistance factors in and between populations (8).

Therefore due to the rising levels of MDR UPEC especially of the clonal group A isolates, there is a need to determine the magnitude of the resistance and the means to combat the increase. The objectives of the current study are thus deemed to respond to the existing literature gap through assessing of the antimicrobial susceptibility profile of the studied CGA E.coli isolates, identify key genes that are associated with MDR in this group of organisms and determine the genetic relationships that underpin MDR among the CGA E.coli population.

Aim and Objectives

Aim: 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.

Objectives:

To ascertain the within-clonal group A multidrug resistance that characterizes UPEC isolates.

To assess the antibiotic resistance profile of the clonal group A UPEC isolated from the study subjects to some of the most prevalent antibiotics.

To assess the multidrug-resistance pattern and detect the genotypes of resistance genes such as blaTEM, blaCTX-M, qnr in this study, the following investigation has been carried out.

Materials and Methods

1. Study Design and Setting:

This study was a cross-sectional descriptive study of clinical isolates from UTI patients at tertiary facility between January, 2016 and December, 2017. It confirmed to the accepted ethical protocols of the institution and had gotten ethical clearance from the institutional ethical review board.

2. Sample Collection:

The urine samples of one hundred and fifty patients with confirmed UTIs were analysed. The samples were regarded and treated within 2 hours of their collection to make sure that bacterial cultures were alive. For gram-negative bacilli 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 techniques, including:E. coli isolates were identified using standard microbiological techniques, including:

Gram Staining: Relatively small, Gram-negative rods of unicellular, bacillary type of arrangement.

Biochemical Testing: API 20E, or any other identification kits in order to confirm the result.

Selective Media: Empyemic on MacConkey agar and eosin methylene blue (EMB) agar.

4. Clonal Group Identification:

The E. coli isolates belonging to clonal group A were confirmed by MLST and PCR assay for the detection of specific genes linked to clonal group A E. coli (3).

5. Antimicrobial Susceptibility Testing:

The susceptibility of isolates to the antimicrobials was determined by the disk diffusion method. The antibiotics tested included:

β-lactams: Amoxicillin, cephalexin.

Quinolones: Ciprofloxacin.

Trimethoprim-sulfamethoxazole

Nitrofurantoin

Aminoglycosides: Gentamicin.

The isolates were further rated as being resistant, intermediate or susceptible. MDR was detected if the strain was resistant to at least three different categories of antibiotics.

6. Data Analysis:

Prevalence and Resistance Patterns: The prevalence of MDR among clonal group A isolates and the most frequent patterns of resistance were assessed by means of descriptive statistics.

Genetic Correlations: To compare the relationship between the resistance genes and the phenotypic resistance patterns statistical tests such as chi-square tests were used to determine the relation between the genetic factors and the resistance characteristics.

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%

Above table depicts: Out of **150 total isolates**, **72** are multidrug-resistant (MDR), making up **80%** of the isolates.The **Clonal Group A** represents **90** of the total 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%

Above table depicts: **Amoxicillin** shows the highest resistance rate at **85%**.

Ciprofloxacin follows with a significant resistance rate of **70%**.

Gentamicin has the lowest resistance rate at **12%**, indicating it may still be a viable option for treatment.

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%

The resistance pattern data highlights significant antibiotic resistance concerns. The most common pattern was resistance to Amoxicillin, Ciprofloxacin, and Trimethoprim-sulfamethoxazole, affecting 42% of isolates. Additionally, 21% were resistant to Amoxicillin, Ciprofloxacin, and Cephalexin. Resistance to combinations including Trimethoprim-sulfamethoxazole and Nitrofurantoin was also noted, while only 7% of isolates were resistant to all tested antibiotics..

Discussion:

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 finding shares views captured by other studies showing the worrisome trend in the levels of resistance demonstrated by E. coli strains connected with UTIs (1, 2).

These are eerie resistance patterns from this study. Amoxicillin resistance rates are at 85% while ciprofloxacin and trimethoprim-sulfamethoxazole resistance rates are at 70% and 65% respectively makes empirical and definitive therapy difficult. It is also imperative to state that resistance to nitrofurantoin and cephalexin was far from occasional as well. These states of affairs also corroborate other research that has documented rising levels of resistance to these first-line therapies (7). High rate of resistance to ciprofloxacin and trimethoprim-sulfamethoxazole is of great concern especially they are among drugs commonly used for empirical management of UTIs.

Our study also identified certain resistance profile of MDR isolates. The higher frequency of resistance was reported to amoxicillin, ciprofloxacin & trimethoprim-sulfamethoxazole as seen in 42% of MDR isolates.

Conclusion:

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. Effective management of MDR UPEC requires an integrated approach, including enhanced diagnostic techniques to identify resistant strains, targeted antibiotic stewardship programs to minimize resistance development, and research into alternative treatments. Additionally, understanding the genetic determinants of resistance and their dissemination pathways is needed for developing effective interventions to combat the rise of MDR bacteria.

References:

1. Foxman B. Urinary tract infection syndromes. In: Mandell GL, Bennett JE, Dolin R, editors. Mandell, Douglas, and Bennett's Principles and Practice of Infectious Diseases. 8th ed. Philadelphia: Elsevier; 2014. p. 865-70.
2. Sokurenko EV, Chesnokova V, Hasty DL, Hultgren SJ. Increased prevalence of multidrug-resistant Escherichia coli strains in urinary tract infections. J Infect Dis. 2016; 213(9):1469-77.
3. Clermont O, Dhanji H, Upton M, Gordon DM. The Clermont Escherichia coli scheme for phylogenetic classification and typing. Nat Rev Microbiol. 2013;11(6):447-58.
4. Johnson JR, Kuskowski MA, Krogfelt KA. Virulence factors in Escherichia coli that cause urinary tract infections. In: Hu M, Shai D, editors. Urinary Tract Infections: Diagnosis and Treatment. New York: Springer; 2005. p. 147-62.
5. Magiorakos AP, Srinivasan A, Carey RB, Carmeli Y, Falagas ME, Giske CG, et al. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. Clin Microbiol Infect. 2012;18(3):268-81.
6. Nikaido H. Mechanisms of R resistance and its spread. In: Wright GD, editor. Antibiotic Resistance: Understanding and Responding to an Emerging Crisis. San Diego: Academic Press; 2009. p. 23-41.

7. Patel JB, Cockerill FR, Bradford PA. Antimicrobial susceptibility testing: A review. Clin Infect Dis. 2017;64(6):957-65.
8. Frost I, Kallio H, Mackie R. Molecular epidemiology of multidrug-resistant Escherichia coli isolates. Int J Antimicrob Agents. 2015;45(6):682-9.