**MULTI-DRUG RESISTANCE PROFILE OF BACTERIA ISOLATES FROM URINARY TRACT INFECTIONS AMONGST HOSPITALIZED MALE PATIENTS IN BENIN CITY.**

**ABSTRACT**

**Background:** Urinary tract infection (UTI) is prevalent among hospitalized male patients and is often complicated by multidrug resistance (MDR). **Aim:** This study determined the MDR profile of bacterial isolates from UTIs in hospitalized male patients at Faith Mediplex Hospital, Benin City. **Methods:** A cross-sectional study using randomized sampling was conducted on 50 urine samples. The samples were transported to the Medical Microbiology Laboratory at Benson Idahosa University. They were cultured on CLED and MacConkey agar and incubated aerobically for 24 hours. Bacterial isolates were identified using standard microbiological techniques, and antibiotic susceptibility testing was performed using the Kirby-Bauer disc diffusion method against nine antibiotics. MDR isolates were subjected to molecular analysis. Data were analyzed using SPSS (IBM) version 27 with chi-square. **Results:** Among the 50 samples, 27 bacterial isolates from five genera were identified, revealing a 60% UTI prevalence. *Staphylococcus aureus* (44%) was the most common, followed by *Escherichia coli* (26%), *Klebsiella pneumoniae* (15%), *Proteus mirabilis* (11%), and *Pseudomonas aeruginosa* (4%). Gram-negative bacteria were more prevalent than Gram-positive bacteria. Imipenem (27.2%) and Ciprofloxacin (26.9%) showed the highest sensitivity. Most Gram-negative bacteria exhibited high resistance to cephalosporins (cefuroxime, ceftriaxone) and penicillins (Augmentin, oxacillin). Molecular analysis revealed that isolates resistant to Augmentin harboured the TEM-resistant gene at 1000bp, confirming the molecular basis of resistance. **Conclusion:** These findings underscore the need for urgent monitoring and tailored antibiotic regimens to combat MDR in hospitalized male patients with UTIs at Faith Mediplex Hospital.

**Keywords:** Analysis, Antibiotics, Bacteria, Infection, Patients, Resistance

**INTRODUCTION**

Urinary tract infections (UTIs) are among the most common infections in clinical practice, affecting approximately 150 million people globally each year (Mancuso *et al*., 2023). Accurate diagnosis and evidence-based treatment improve clinical management and reduce unnecessary antibiotic use. Urinalysis and urine culture are key diagnostic tools, though they have limitations. Differentiating between asymptomatic bacteriuria (ASB) and true UTI is crucial, as antibiotics are generally unnecessary for ASB in non-pregnant individuals and may cause harm if misused (Lawati *et al*., 2024). The urinary system consists of the kidneys, ureters, bladder, and urethra, primarily functioning to filter blood, remove metabolic waste, regulate ion concentration, and maintain blood volume and pressure. In healthy individuals, urine is sterile or contains few microorganisms capable of causing infections. UTIs can occur in the urethra (urethritis), bladder (cystitis), or kidneys (pyelonephritis). They are classified as uncomplicated (uUTIs) or complicated (cUTIs). uUTIs occur in healthy individuals without structural or neurological urinary tract abnormalities, while cUTIs involve conditions such as urinary retention, neurogenic bladder, renal failure, pregnancy, and catheterization (Baimakhanova *et al*., 2025).

UTIs commonly result from bacterial infections, primarily by uropathogenic *Escherichia coli* (UPEC), with Enterobacteriaceae dominating both community and hospital infections. Antibiotic-resistant Gram-negative bacteria, such as carbapenemase-resistant Enterobacteriaceae, are more frequent in hospitals. Fungal and viral UTIs are rare, with *Candida albicans* being the most common fungal cause, while viral UTIs may be due to cytomegalovirus, human poliovirus type 1, and herpes simplex virus (Mancuso *et al*., 2023).

Women have a higher UTI incidence due to their anatomy, with increased prevalence during pregnancy. Symptoms vary based on the site of infection, with cystitis causing painful and frequent urination, while pyelonephritis presents with high fever and flank pain. Both symptomatic and asymptomatic UTIs pose significant public health risks, affecting quality of life and increasing absenteeism from work. Misdiagnosis can contribute to UTIs being one of the most common nosocomial infections, varying in epidemiology, etiology, severity, and risk of recurrence (Vasudevan, 2014; Odoki *et al*., 2019).

The prevalence, etiology, risk factors, and antimicrobial susceptibility patterns of bacterial isolates associated with urinary tract infections (UTIs) among hospitalized male patients in Faith Mediplex Hospital have posed significant challenges, leading to a high prevalence of multidrug-resistant (MDR) isolates in Benin City. This study aims to isolate and employ phenotypic methods to identify MDR bacterial isolates from UTIs in Faith Mediplex Hospital, Benin City, Edo State. Specifically, the study seeks to isolate and phenotypically identify bacterial isolates from UTIs, determine the prevalence of UTIs among hospitalized male patients, assess the antibiogram of the bacterial isolates, and identify resistance genes associated with MDR bacterial isolates.

**MATERIALS AND METHODS**

**Study Design**

This study was conducted in Faith Mediplex Hospital, Benin City, on hospitalized male patients presenting with signs of urinary tract infections (UTIs). The research, including sample collection, laboratory analysis, and data compilation, was carried out between April 2024 and June 2024.

**Inclusion and Exclusion Criteria**

Only urine samples from hospitalized male patients were used, while samples from non-hospitalized male and female patients were excluded from the study.

**Ethical Considerations**

Ethical approval was obtained from the ethical committee of Faith Mediplex Hospital, Benin City, Edo State, via letter referenced FMH 004. Written informed consent was obtained from all participants or their guardians/relatives before sample collection.

**Sample Collection and Preservation**

A total of fifty (50) urine specimens were collected from both symptomatic and asymptomatic hospitalized male patients in sterile universal bottles under strict aseptic conditions. The samples were immediately transported to the Medical Microbiology Laboratory in the Department of Medical Laboratory Science, Benson Idahosa University, Benin City, for analysis. Midstream urine specimens were collected in sterile universal containers containing boric acid crystals (0.2g per 20ml of urine) and stored at 4°C until processing to prevent bacterial multiplication.

**Cultural Methods**

Specimens were aseptically inoculated onto freshly prepared sterile MacConkey agar and Cysteine Lactose Electrolyte Deficient (CLED) agar in Petri dishes, then incubated aerobically at 37°C for 24 hours. Materials used in the study included a standard wire loop, MacConkey agar plates, CLED agar, Muellar Hinton agar, biochemical test sugars, clean grease-free slides, cover slips, a centrifuge, and sterile universal containers. All culture media were prepared according to the manufacturer’s instructions.

**Microscopy of Centrifuged Urine**

Urine samples (10ml) were centrifuged at 3,000 rpm for 10 minutes, with the supernatant discarded and the deposit resuspended. A drop of the unstained deposit was examined under ×10 and ×40 objective lenses to identify pus cells, epithelial cells, crystals, yeast cells, and other elements.

**Bacterial Identification/ Biochemical Tests**

Bacterial isolates were identified using standard procedures such as Gram staining technique to grouped the bacteria into gram positive and gram-negative bacteria, and were further analysed biochemically at Benson Idahosa University laboratory, Benin City according to(Cowan and steel, 1974).

**Antimicrobial Susceptibility Testing**

Antimicrobial susceptibility testing was carried out on each isolate by the disc diffusion method using the Kirby- Bauer disc diffusion method in accordance with the National Committee for Clinical Laboratory Standards (NCCL) guideline to evaluate the sensitivity of the test organisms to the various antibiotics. Test isolates were grown on Nutrient agar and incubated at 37°C for 24 hours. Colonies were suspended into sterile normal saline and the inocula density was adjusted to 0.5 McFarland turbidity standards. A sterile cotton wool swab was inserted into each test tube containing the standardized inocula suspension, rotated with firm pressure on the inside wall of the test tube to remove excess fluid and then used to swab the surface of a freshly prepared dried Mueller-Hinton agar plate. The antimicrobial disc used included Ceftriaxone (CRX 5ug), Imipenem (Imp, 30µg), Gentamycin (GM, 30µg), Oxacillin (OX 5µg), Ciprofloxacin (CPR, 5µg), Erythromycin (ERY, 10ug), Cefuroxime (CRX, 30ug), Cefepime (Cro, 5ug), and Augmentin (Aug, 30ug). The disc was placed on the surface of the inoculated Muller Hinton agar plate and incubated at 37°C for 24 hours. After incubation, diameters of zones of inhibition were measured to the nearest millimetre using a transparent meter rule.

**Molecular Analysis**

The molecular analysis was carried out on isolates that were resistant to more two class of antimicrobial agents. This analysis was conducted at Iykenson Medical and Diagnostic Centre, Awka in Anambra state.

**Genomic DNA Extraction using Thermo Scientific Gene jet**

A single colony of each isolate from Nutrient agar plate was inoculated into 3 ml of Luria broth and incubated at 37°C overnight with constant agitation at 120 rpm. One point five milliliters of the overnight culture were transferred into a micro centrifuge tube. The overnight culture was centrifuged at 13000rpm for 10 minutes and the supernatant was discarded. The pellet was resuspended in 180µl digestion Solution. Two hundred micro litres of proteinase K solution were added and mixed thoroughly by vortexing to obtain a uniform suspension. The sample was incubated at 56°C in a thermomixer until the cells are completely lysed. Twenty microlitres of RNaseA solution was added to the mixture and incubated for 10 minutes at room temperature. Two hundred micro litres of Lysis Solution was added to the sample and mixed thoroughly by vortexing for about 15 seconds to obtain a homogeneous mixture. Four hundred micro litres of 50% ethanol were added to the mixture and mixed by vortexing. The resultant lysate was transferred to a Gene JET Genomic DNA Purification Column inserted in a collection tube and centrifuged at 6000 x g for 1 minute. The resultant flow-through solution was discarded. The Gene JET Genomic DNA Purification Column was placed inside a new 2ml collection tube. Five hundred micro litres of Wash Buffer I was added to the column and centrifuged at 8000 x g for 1 minute. The flow-through was discarded. Five hundred micro litre of Wash Buffer II was added to the Gene JET Genomic DNA Purification Column Centrifuged at 12000 x g for 3 minutes. Two hundred micro litres of the Elution Buffer was added to the center of the Gene JET Genomic DNA purification column membrane and incubated at 2 minutes. The column was centrifuged at 8000 x g for 1 minute to elute genomic DNA for PCR amplification.

**Polymerase chain reaction detection (PCR)**

The multidrug resistant isolates underwent molecular techniques against some selected resistant genes primers. The resistant gene primer was targeted against the multidrug resistant bacteria isolate to know the resistant genes associated with the MDR bacteria, to ascertained the sequences of their nucleotides. This was purchased from Inqaba Biotech industries, Harfield, South Africa.

**Primer used for the Study.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Gene Symbol** | **Primers 5I-3I (forward, reverse)** | **n moles (mg)** | **Molecular weight** | **Melting temperature (TM) (0C)** |
| TEM | F- ATGAGTATTCAACATTTCCG  R- CTGACAGTTACCAATGCT | 38.98  32.02 | 6090.7  5458.3 | 54.25  55.34 |

(Ehiaghe *et al.,* 2024).

**Quick load One Taq One Step Polymerase Chain Reaction (Resistance Genes Detection)** Quick load One Taq one step PCR master (2X) with catalog number NEB MO486S was purchased from lnqaba Biotech Hartfield South Africa incorporated and used according to the manufacturer’s instruction. Above are the sequence of the primer used. The system components were thaw and mixed by inverting ten times. The PCR was performed in 50µl reaction mixture containing 25µl Quick load One Taq one- step PCR master mix (2x), 1µL of each gene-specific forward primer (10µM), 1µL of each specific reverse primer(10µM), 13ml of nuclease free water and 10µl of DNA template was added last. The PCR was started immediately as follows: Initial denaturation at 94°c for 1 minute, denaturation at 94°c for 30secs, annealing at Tm-5 for 30secs, extension at 72°C for 1 minute, go to the denaturation step for 39 cycles, final extension at 72°C for 15mins and final holding at 40°C.

**Preparation of Agarose Gel (1.5% Agarose Gel used for Genomic DNA Detection)**

One point five percent agarose gel was prepared by dissolving 1.5g in 100ml Tris EDTA Buffer. The mixture was then heated in a microwave for 5 minutes to dissolve completely. It was then allowed to cool at 56°C and 6µl of ethidium bromide was added to it. The agarose gel was poured into the electrophoresis chambers with gel comb, and allowed to solidify.

**Electrophoresis**

Five microlitres of the amplified PCR products was analyzed on 1.5% agarose gel containing ethidium bromide in Tris EDTA buffer. Electrophoresis was performed at 90v for 60 minutes. After electrophoresis the PCR products were visualized by Wealth Dolphin Doc UV transilluminator and photographed. Molecular weights were calculated using molecular weight standard of the maker.

**RESULTS**

Out of the fifty (50) urine samples cultured from hospitalized male patients, twenty-seven had growth of bacteria of different genera which gave a total prevalence rate of 54% (Figure 1). Bacteria isolates recovered from the urine sampled were *E. coli* 7 (26 %), *Klebsiella pneumonia* (15%), *Staphylococcus aureus* (44%), *Proteus mirabilis* (11%) and *P. aeruginosa* (4%) (Table 1). Table 2 summarizes the Gram stain characteristics, biochemical reactions, and motility of *Escherichia coli, Klebsiella, Proteus mirabilis, Pseudomonas aeruginosa and Staphylococcus aureus.*

|  |  |  |
| --- | --- | --- |
| **Figure 1. Prevalence of Urinary tract infection among participants**  **Table 1. Percentage of Bacteria Isolated** | | |
| **Organism** | **Frequency** | **Percentage** |
| *Escherichia coli* | 7 | 26% |
| *Klebsiella pneumonia* | 4 | 15% |
| *Staphylococcus aureus* | 12 | 44% |
| *Proteus mirabilis* | 3 | 11% |
| *Pseudomonas aeruginosa* | 1 | 4% |

**Table 2: Phenotypic Identification of bacteria isolates from urine**

| **Bacteria** | **Gram** | **Oxidase** | **Catalase** | **VP** | **MR** | **Indole** | **Citrate** | **Motility** | **Urease** |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| ***Escherichia coli*** | -ve bacilli | -ve | +ve | -ve | +ve | +ve | -ve | Yes | -ve |
| ***Klebsiella pneumoniae*** | -ve bacilli | -ve | +ve | +ve | -ve | -ve | +ve | No | +ve |
| ***Proteus mirabilis*** | -ve bacilli | -ve | +ve | +ve | +ve | +ve | +ve | Yes | +ve |
| ***Pseudomonas*** | -ve bacilli | +ve | +ve | -ve | -ve | -ve | +ve | Yes | -ve |
| ***Staphylococcus aureus*** | +ve cocci | -ve | +ve | +ve | -ve | -ve | +ve | No | -ve |

Keys: -Ve = Negative, +Ve = Positive, VP: Voges-Proskauer test, MR: Methyl Red test, Indole: Indole test

The antibiogram patterns of bacterial isolates against various antibiotics revealed significant variations in susceptibility and resistance. Ciprofloxacin showed moderate effectiveness, with *Klebsiella pneumoniae* (100%) being the most susceptible, while *E. coli* (57.1%) exhibited the highest resistance. *P. aeruginosa* was completely resistant to cefuroxime, followed by *E. coli* (57.1%) and *Klebsiella pneumoniae* (50.0%). Oxacillin showed no efficacy, as all tested bacterial isolates were 100% resistant. Resistance to Augmentin was highest in *P. aeruginosa* (100%), followed by *Klebsiella pneumoniae* (75.0%) and *E. coli* (71.4%), though *Proteus mirabilis* displayed higher sensitivity. Erythromycin resistance was prominent, with *Klebsiella pneumoniae*, *Proteus mirabilis*, and *P. aeruginosa* (100%) showing complete resistance, while *E. coli* (85.7%) and *S. aureus* (83.3%) were also highly resistant. Imipenem exhibited strong efficacy, with all bacterial isolates being 100% susceptible except for *E. coli* (28.6%). Ceftriaxone resistance was observed in *Klebsiella pneumoniae*, *S. aureus*, and *P. aeruginosa* (50%), while *E. coli* (57.1%) and *Proteus mirabilis* (66.7%) were more resistant. Similarly, *Proteus mirabilis* (66.7%), *E. coli* (57.1%), and *Klebsiella pneumoniae* (50.0%) displayed high resistance to Cefepime, whereas *S. aureus* was highly sensitive. Gentamicin was most effective against *P. aeruginosa* (100%) and *S. aureus* (83.3%), while *Proteus mirabilis* (66.7%) and *Klebsiella pneumoniae* (57.1%) exhibited the highest resistance (Table 3).

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Table 3. Antibiogram Pattern of Antibiotics Against Tested Isolates.** | | | | | | | | | | |
|  | ***E. coli* (n=7)** | | ***K. pneumonia* (n=4)** | | ***S. aureus* (n=12)** | | ***P. mirabilis* (n=3)** | | ***P. aeruginosa* (n=1)** | |
| **Antibiotics** | **S (%)** | **R (%)** | **S (%)** | **R (%)** | **S (%)** | **R (%)** | **S (%)** | **R (%)** | **S (%)** | **R (%)** |
| Ciprofloxacin | 3 (42.9%) | 4 (57.1) | 4 (100 %) | 0 (0.0 %) | 8 (66.7%) | 4 (33.3%) | 2 (66.7%) | 1 (33.3%) | 1 (100%) | 0 (0.0 %) |
| Cefuroxime | 3 (42.9%) | 4 (57.1) | 2 (50.0%) | 2 (50.0%) | 9 (75.0 %) | 3 (25%) | 2 (66.7%) | 1 (33.3%) | 0 (0.0%) | 1 (100%) |
| Oxacillin | 0 (0.0%) | 7 (100) | 0 (0.0%) | 4 (100) | 0 (0.0%) | 12 (100) | 0 (0.0%) | 3 (100) | 0 (0.0%) | 1 (100) |
| Augmentin | 2 (28.6 %) | 5 (71.4 %) | 1 (25.0 %) | 3 (75.0%) | 7 (58.3%) | 5 (41.7%) | 2 (66.7%) | 1 (33.3%) | 0 (0.0%) | 1 (100%) |
| Erythromycin | 1 (14.3%) | 6 (85.7 %) | 0 (0.0 %) | 4 (100%) | 2 (16.7 %) | 10 (83.3 %) | 0 (0.0 %) | 3 (100.0 %) | 0 (0.0 %) | 1 (100%) |
| Imipenem | 5 (71.4%) | 2 (28.6%) | 4 (100%) | 0 (0.0%) | 12 (100.0 %) | 0 (0.0%) | 3 (100.0 %) | 0 (0.0%) | 1 (100%) | 0 (0.0%) |
| Ceftriaxone | 3 (42.9%) | 4 (57.1%) | 2 (50.0 %) | 2 (50.0%) | 6 (50.0%) | 6 (50.0%) | 1 (33.3%) | 2 (66.7%) | 1 (50.0%) | 1 (50.0%) |
| Cefepime | 5 (71.4%) | 2 (57.1%) | 2 (50.0 %) | 2 (50.0%) | 10 (83.3%) | 2 (16.7 %) | 1 (33.3%) | 2 (66.7%) | 1 (100%) | 0 (0.0%) |
| Gentamicin | 5 (71.4%) | 2 (57.1%) | 2 (50.0 %) | 2 (50.0%) | 10 (83.3%) | 2 (16.7 %) | 1 (33.3%) | 2 (66.7%) | 1 (100.0%) | 0 (0.0%) |

Key: S=Sensitive, R=Resistant.

The comparison of phenotypic and genotypic detections of multidrug resistant strains of *E*. *coli* with the presence of TEM, resistant genes. It was found that the samples number 2 and number 43 had strain of *E*. *coli* with 100% abundance of TEM resistant genes The comparison of phenotypic and genotypic detections of multidrug resistant strains of *E*. *coli* with the presence of TEM resistant genes revealed that *E*. *coli* isolated phenotypically from the patients ‘sample number 2 and number 43 were resistant to Amoxicillin-clavulanic acid, Oxacillin, Ciprofloxacin, Cefuroxime (CXM) and Ceftriaxone (CRO) respectively. Moreover, it was found to be susceptible to imipenem, cefepime (CPM) and gentamicin respectively (Plate 1).

L 2 7 12 20 26 30 38 39 43 47

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1000bp

100bp

Plate 1: Polymerase chain reaction results of TEM resistant genes detected in clinical isolates were analyzed on a 1.5% agarose gel electrophoresis stained with ethidium bromide. L is 100bp-1kb DNA ladder (molecular marker). Samples 2, 7, 12, 20, 26, 30, 38, 39, 43 and 47 are positive for Augmentin (TEM) resistant genes with bands at 1000bp.

**DISCUSSION**

This study was carried out to determine the multidrug resistance profile of Bacteria isolates from Urinary Tract Infection amongst hospitalized male patients in Benin City, Edo State. Out of the fifty (50) urine samples cultured from hospitalized male patients, twenty-seven had growth of bacteria of different genera of bacteria which gave overall total prevalence rate of 27 (54%) among the hospitalized male patients. The prevalence rate of 54% indicates that more than half of the urine samples from hospitalized male patients contained bacteria. This is a significant finding as it suggests a high likelihood of bacterial infections among this group. This high prevalence rate of UTIs among the Hospitalized patients that were vulnerable to infections could be due to factors such as invasive procedures, prolonged catheter use, compromised immunity, and exposure to antibiotic-resistant bacteria within healthcare environments. These factors contribute to the high prevalence observed in this study or the size of the study population. A higher prevalence rate was observed when compared to the report from Uganda 32.2% (Odoki *et al.,* 2019) South-Western Uganda 35% (Johnson *et al.,* 2021).

According to (Johnson *et al.,* 2021) this study was in accordance, due to more percentage of gram-negative bacteria isolated from the urine samples. The Phenotypic characterization of bacterial isolates in this study reveals the occurrence of Four Gram-negative isolates and One Gram positive isolate as shown in the pie chart in objective one with *Staphylococcus aureus* having the highest occurrence by (44%). followed by *Escherichia coli with* (26%), then *Klebsiella pneumonia* (15%), *Proteus mirabilis* (11%) and *Pseudomonas aeruginosa* (4%). The bacterial isolates produced a varied microbial landscape. *Staphylococcus aureus* is the leading pathogen isolated, representing 44% of all isolates (Idrees *et al*., 2021). *Escherichia coli,* which usually dominates in many areas, comprises 26% of the isolates, with some isolates of *Klebsiella pneumonia* (15%), *Proteus mirabilis* (11%), and *Pseudomonas aeruginosa* (4%). The high predominance of *Staphylococcus aureus* in this study population is most significant, as it might indicate the changing microbial etiology of UTIs within this population or may be indicative of hospital-acquired infections and contamination.

The high resistance observed in *E. coli*, *Klebsiella pneumoniae*, *P. aeruginosa*, and *Proteus mirabilis* aligns with the global trend of increasing multidrug-resistant (MDR) bacterial strains (Adekanmbi *et al*., 2022). The complete resistance of *P. aeruginosa* to cefuroxime and its 100% resistance to Augmentin are particularly concerning, as *P. aeruginosa* is a known opportunistic pathogen frequently implicated in hospital-acquired infections (HAIs) (Abban *et al*., 2023). This resistance could be attributed to its ability to produce β-lactamases, efflux pumps, and biofilms that enhance antibiotic resistance. Previous studies have documented similar trends, where *P. aeruginosa* demonstrated high resistance to β-lactam antibiotics, limiting treatment options (Glen and Lamont, 2021).

The observed resistance of *E. coli* to cefuroxime, ceftriaxone, and cefepime suggests the possible presence of extended-spectrum β-lactamase (ESBL)-producing strains. ESBL production allows bacteria to hydrolyze and inactivate cephalosporins, making these antibiotics less effective (Padmini *et al*., 2017). Several studies have reported increasing ESBL prevalence among *E. coli* and *Klebsiella pneumoniae*, posing a significant challenge in empirical antibiotic therapy (Shakya *et al*., 2017; McDanel *et al*., 2017; Quan *et al*., 2016; Khanfar *et al*., 2009). The complete resistance of all tested isolates to oxacillin suggests the prevalence of methicillin-resistant *Staphylococcus aureus* (MRSA). MRSA infections are particularly difficult to treat due to resistance to β-lactam antibiotics, often necessitating the use of vancomycin or other last-resort antibiotics (Chanda *et al*., 2010). Similar findings have been reported in previous studies where MRSA strains exhibited high resistance to oxacillin and other penicillin derivatives (Harris *et al*., 2012).

Despite the widespread resistance to several antibiotics, imipenem demonstrated remarkable efficacy, with all isolates being completely susceptible except for *E. coli*. Carbapenems like imipenem are often reserved as last-line treatments for MDR infections, which could explain their high effectiveness. However, the emergence of carbapenem-resistant *E. coli* in this study is concerning, as carbapenem-resistant Enterobacteriaceae (CRE) pose a significant public health threat (Schwaber and Carmeli, 2008). This aligns with global reports of increasing carbapenem resistance due to carbapenemase-producing strains (Bonomo *et al*., 2018). The high resistance of *Klebsiella pneumoniae* and *Proteus mirabilis* to cefepime further suggests a growing problem with cephalosporin resistance. Cefepime, a fourth-generation cephalosporin, is typically used against MDR bacterial infections. The resistance observed in this study could be due to mutations in penicillin-binding proteins (PBPs) or the presence of AmpC β-lactamases, which confer resistance to cephalosporins (Sethuvel *et al*., 2023). Gentamicin remained effective against *P. aeruginosa* and *S. aureus*, suggesting that aminoglycosides may still be viable treatment options for certain bacterial infections. However, the resistance of *Proteus mirabilis* and *Klebsiella pneumoniae* to gentamicin indicates the need for continuous monitoring and susceptibility testing before administration.

The PCR findings corroborate the antibiotic sensitivity analysis data, particularly the high resistance rates to Augmentin (55.6%) and other antibiotics such as Ceftriaxone and Oxacillin. The identified bacteria, including *Escherichia coli, Klebsiella pneumonia, Proteus mirabilis, Pseudomonas aeruginosa, and Staphylococcus aureus,* exhibit varying resistance patterns to Augmentin (TEM) resistant genes. Notably, *Staphylococcus aureus* showed the highest incidence of TEM resistant genes, followed by *Escherichia coli* and *Proteus mirabilis.* This high prevalence of resistance, particularly in *Staphylococcus aureus,* highlights the pathogen's adaptive mechanisms and the role of horizontal gene transfer in spreading resistance, as discussed by Davies and Davies (2010). The detection of TEM-resistant genes in these isolates has critical clinical implications. TEM beta-lactamases are enzymes that confer resistance to beta-lactam antibiotics, including penicillins and cephalosporins. The high prevalence of such resistant genes among UTI pathogens indicates a significant challenge in treating these infections, necessitating the use of alternative or more potent antibiotics such as Imipenem, which showed the lowest resistance rate in the antibiogram data (Bush, 2018). The widespread presence of TEM-resistant genes among different bacterial species in hospitalized patients suggests a potential for horizontal gene transfer, which could exacerbate the spread of resistance within the hospital setting and the community at large. This finding highlights the urgent need for robust infection control practices, antibiotic stewardship programs, and continuous surveillance to monitor and mitigate the spread of resistant pathogens as discussed by Davies and Davies (2010).

**CONCLUSION**

This study revealed a significant prevalence of urinary tract infections (UTIs) among hospitalized male patients at Faith Mediplex Hospital, with 54% of urine samples yielding bacterial growth. *Staphylococcus aureus* was the most frequently isolated pathogen, followed by *Escherichia coli* and *Klebsiella pneumoniae*. Antibiotic susceptibility testing demonstrated high resistance patterns, particularly to Oxacillin and Augmentin, while Imipenem showed the highest efficacy across isolates. Furthermore, molecular analysis identified multidrug-resistant *E. coli* strains harbouring TEM-resistant genes.

Disclaimer (Artificial intelligence)

Option 1:

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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