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Urinary Tract Infections Amongst Youths of a University Community and Antimicrobial Resistance

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Abstract
Urinary tract infections are severe public health problem, which are caused by a range of pathogens, but most common are Escherichia coli, Klebsiella pneumoniae, Proteus mirabilis, Enterococcus faecalis and Staphylococcus saprophyticus. High incidence rate and increasing antimicrobial resistance among uropathogens threaten to greatly increase the morbidity and economic burden of these infections. In this research, detection of urinary tract infections (UTIs) among youths in the university community of Ikwo was carried out using standard microbiological methods. Fifty midstream urine samples were collected and cultured on MacConkey and CLED agar, and the resulting colonies enumerated and identified by biochemical tests. Antibiotic susceptibility testing was performed using the disk diffusion method following CLSI 2021 guidelines, and the Multiple Antibiotic Resistance Index (MARI) determined.Total bacterial Counts greater than 100,000 colony forming unit CFU/mL (10^5 CFU/mL) of a single organism typically indicated a urinary tract infection. Eleven bacterial isolates were identified Viz. Escherichia coli (36.3 %), Klebsiella pneumoniae (27.3%), Proteus mirabilis and Pseudomonas aeruginosa (18.2%) each. Antibiotic susceptibility testing revealed high resistance rates among Pseudomonas aeruginosa and Proteus mirabilis, whereas Escherichia coli and some Klebsiella pneumoniae isolates retained notable sensitivity to fluoroquinolones and aminoglycosides. The multiple antibiotic resistance index (MARI) ranged from 0.1to 0.9, with 73% of the isolates recording MARI ≥ 0.2, indicating exposure to environments with high antibiotic pressure. The high MARI values underscore the urgent need for regular surveillance, rational antibiotic use, and public health education to mitigate the spread of resistant uropathogens in the community.

Keyword: *Youths, Urinary Tract Infections and Antimicrobial Resistance*

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I. INTRODUCTION

Urinary tract infections (UTIs) are common bacterial infections that can affect any part of the urinary tract (urethra, bladder, ureters, kidneys) and are a frequent cause of morbidity worldwide. (Barola, 2024).

The burden of UTIs is substantial in low and middle-income regions, a systematic review of studies from sub-Saharan Africa reported a pooled prevalence that highlights a high and heterogeneous burden across countries, with *Escherichia* coli and other *Enterobacteriaceae* being the predominant pathogens. (Mwang'onde & Mchami, 2022).

Youths, particularly sexually active adolescents and young adults (15–24 years) and university students, represent an important population for UTI surveillance because behavioral, hygienic and sexual-risk factors influence UTI risk in this group; recent cross-sectional studies and meta-analyses among students show measurable prevalence rates that necessitates targeted detection and control efforts. (Fetene, 2024).

Management of UTIs is being increasingly complicated by antimicrobial resistance, recent facility-based studies report high rates of resistance and considerable proportions of multidrug-resistant (MDR) uropathogens, which undermines empirical therapy and makes culture-based detection and susceptibility testing essential for appropriate treatment. (Mlugu et al., 2023; Gajdács, 2020).

Given the high and variable prevalence of UTIs in sub-Saharan Africa, the documented occurrence among young people and the growing problem of antibiotic resistance, localized detection and microbiological characterization of UTI among youths is necessary to generate up-to-date data for clinical management and public-health interventions. This study therefore focuses on detecting UTIs among youths (15–24 years) in Ikwo,

identifying the causative organisms, and determining their antibiotic susceptibility patterns to inform local empirical treatment and surveillance.

Urinary tract infections (UTIs) are among the most prevalent bacterial infections worldwide, affecting individuals across all age groups, with a notable impact on young adults and adolescents. They occur when pathogenic microorganisms, particularly bacteria, invade and colonize any part of the urinary tract, including the urethra, bladder, ureters, or kidneys. Globally, UTIs rank second only to respiratory tract infections as the most common type of infection encountered in primary health care settings, posing a significant public health burden (Lüthje & Brauner, 2021).

UTIs are often classified based on the site of infection as lower UTIs (cystitis and urethritis) or upper UTIs (pyelonephritis), with the latter being associated with more severe complications. The majority of cases are uncomplicated and occur in otherwise healthy individuals, but complicated UTIs may arise in the presence of factors such as urinary obstruction, catheterization, or underlying immunosuppression (Köves & Wullt, 2022).

Young people, especially females, are at higher risk of UTIs due to anatomical and behavioral factors such as shorter urethra, sexual activity, and poor personal hygiene practices. Males, although less frequently affected, may also experience UTIs due to risk factors like unprotected sexual intercourse and poor toilet hygiene (Nielubowicz & Mobley, 2020).

The burden of UTIs is further compounded by the rise of antimicrobial resistance among uropathogens. This has made treatment increasingly challenging, leading to recurrent infections and higher rates of hospitalization (Khawcharoenporn & Vasoo, 2020).

Bacteria predominantly cause urinary tract infections (UTIs), although fungi and viruses may occasionally be implicated. The majority of UTIs are due to organisms originating from the gastrointestinal tract that colonize the periurethral area and ascend into the urinary tract (Mireles et al., 2021)

The most common etiological agent is *Escherichia coli*, responsible for about 70–90% of community-acquired UTIs. Its success as uropathogen is attributed to virulence factors such as fimbriae, adhesins, toxins, and biofilm formation, which enable colonization and persistence in the urinary tract (Terlizzi et al., 2021). Other important bacterial pathogens include *Klebsiella pneumoniae*, *Proteus mirabilis, Enterococcus faecalis*, *Staphylococcus saprophyticus*, *Enterobacter cloacae*, and *Pseudomonas aeruginosa* (Kline & Lewis, 2020). These organisms are more often associated with complicated or recurrent UTIs and may exhibit significant antimicrobial resistance.

In young females, *Staphylococcus saprophyticus* is a notable pathogen, often linked to sexual activity. *Proteus mirabilis* is frequently associated with urinary stones due to its urease activity, which alkalinizes urine and promotes crystal formation (Musher et al., 2021). *Klebsiella pneumoniae* and *Pseudomonas aeruginosa,* on the other hand, are more commonly implicated in nosocomial infections and in patients with underlying health conditions or catheterization (Manzoor et al., 2022). Although rare, fungal UTIs, especially those caused by *Candida albicans*, may occur in immunocompromised individuals or patients undergoing prolonged antibiotic therapy (Achkar & Fries, 2020). Viral UTIs are uncommon but have been reported in severely immunosuppressed patients.

The clinical presentation of urinary tract infections (UTIs) varies depending on the site of infection, the host's immune status, and whether the infection is uncomplicated or complicated. UTIs can involve the lower urinary tract (cystitis, urethritis) or the upper urinary tract (pyelonephritis). Lower urinary tract infections (cystitis and urethritis) are typically characterized by dysuria (painful or burning urination), increased frequency and urgency of urination, suprapubic discomfort or pain hematuria (blood in urine) in some cases (Colgan & Williams, 2020).

Upper urinary tract infections (pyelonephritis) often present with more severe systemic symptoms, including: flank pain or costovertebral angle tenderness, fever, chills, and malaise, nausea and vomiting. Sometimes associated with bacteremia and sepsis if untreated (Bonkat et al., 2021).

In young women, acute uncomplicated cystitis is the most common manifestation, often presenting suddenly with classic symptoms like dysuria and urinary urgency. Men are less frequently affected, but when they develop UTIs, it is often associated with anatomical abnormalities or instrumentation (Klein & Hultgren, 2020).

Asymptomatic bacteriuria (ASB) defined, as the presence of bacteria in urine without symptoms, is common in certain groups such as pregnant women and individuals with diabetes. While ASB generally does not require treatment, in pregnancy it is clinically significant due to the risk of progression to pyelonephritis and adverse pregnancy outcomes (Grigoryan et al., 2020).

Complicated UTIs, which occur in the presence of risk factors such as obstruction, catheterization, or immunosuppression, may present atypically and require more aggressive management (Murray et al., 2021). Overall, the clinical manifestations of UTIs in youths may range from mild lower tract symptoms to severe systemic illness. Recognizing these symptoms early is crucial for prompt diagnosis and effective treatment.

Antibiotic resistance among urinary tract infection (UTI) pathogens has emerged as a major global health concern, significantly complicating treatment outcomes and leading to recurrent infections. The widespread

misuse and overuse of antibiotics in both clinical and community settings have accelerated the development of resistant strains (Klein et al., 2021).

Escherichia coli, the predominant uropathogen, has developed high levels of resistance to commonly prescribed antibiotics such as ampicillin, trimethoprim-sulfamethoxazole, fluoroquinolones, and certain cephalosporins. Extended-spectrum beta-lactamase (ESBL)-producing *E. coli* strains are increasingly reported, limiting therapeutic options (Jean et al., 2020). Similarly*, Klebsiella pneumoniae* and other *Enterobacteriaceae* often harbor multidrug resistance genes, including carbapenemases, making them more difficult to manage (Codjoe & Donkor, 2020).

Pseudomonas aeruginosa and *Proteus mirabilis*, although less frequent in community-acquired infections, frequently show intrinsic resistance to multiple classes of antibiotics, including cephalosporins and aminoglycosides. Their ability to form biofilms within the urinary tract further enhances resistance, protecting bacteria from both antibiotics and host immune defenses (Mulani et al., 2020).

Resistance trends differ geographically. In many low and middle-income countries, indiscriminate antibiotic use, self-medication, and poor infection control practices have contributed to higher resistance rates compared to high-income regions (Tadesse et al., 2021). Youths, particularly students and young adults, are also at risk due to high antibiotic misuse without prescriptions, leading to recurrent and resistant UTIs.

The clinical implications of antimicrobial resistance in UTIs include: increased treatment failures, higher rates of recurrent infections, longer duration of illness and hospitalization. Limited available treatment options, often requiring more expensive or toxic drugs such as carbapenems (Gupta et al., 2021).

Urinary tract infections (UTIs) remain among the most common bacterial infections worldwide, affecting individuals across all age groups and genders. Globally, it is estimated that more than 150 million people suffer from UTIs each year, making them a significant cause of morbidity and healthcare burden (Murray et al., 2022).

In terms of age distribution, UTIs occur more frequently in young women due to anatomical predisposition, sexual activity, and hormonal influences. However, studies show that UTIs are also prevalent among youths, particularly students and young adults, who are prone to self-medication and poor personal hygiene practices, thereby increasing their risk (Ayinde et al., 2021).

The global epidemiological trend indicates that *Escherichia coli* remains the leading cause of UTIs, accounting for 70–90% of community-acquired infections. Other pathogens such as *Klebsiella pneumoniae*, *Proteus mirabilis, Pseudomonas aeruginosa*, and *Enterococcus faecalis* contribute to a smaller but clinically significant proportion (Lee et al., 2021). In many African settings, the spectrum of pathogens is broader, with a higher prevalence of multidrug-resistant strains (Okoche et al., 2020).

Epidemiological studies also show that antimicrobial resistance is rising among UTI pathogens, particularly in low and middle-income countries where antibiotics are easily accessible without prescription. For instance, a study in Nigeria reported resistance rates of over 50% to commonly prescribed antibiotics among uropathogens (Onoh et al., 2022). This trend underscores the urgent need for continuous local surveillance to guide effective empirical treatment.

From a public health perspective, UTIs contribute to school and work absenteeism, reduced productivity, recurrent health facility visits, and high treatment costs. In resource-limited areas, these infections often go underdiagnosed or undertreated, leading to recurrent infections and potential complications such as pyelonephritis, sepsis, and renal damage (Taye et al., 2022).

A study among university students that employed standard urine culture reported a prevalence of symptomatic UTI of about 23.6% in female students, with *Escherichia coli* predominating among isolates (Fetene et al., 2024). Similarly, institutional surveys of female undergraduates have reported prevalence estimates in the range of approximate 10–15%, where culture-confirmed bacteriuria was used alongside symptom questionnaires, these studies also identified *E. coli* as the leading uropathogen and noted associations with sexual activity and hygiene practices (Ajani et al., 2020; Jelly et al., 2022).

Several regional studies in sub-Saharan Africa and other low and middle-income settings confirm this pattern but report variable prevalence: community and facility based studies among adolescents and young adults commonly find prevalence estimates from under 5% up to 25%, depending on whether asymptomatic bacteriuria is included and on local risk factors (Ezo et al., 2024).

Beyond prevalence, these studies consistently show that culture remains the gold standard for UTI detection in youth populations and is necessary to distinguish true infection from contamination or asymptomatic bacteriuria. Many investigators used the midstream clean-catch technique combined with semi-quantitative colony counting to define significant bacteriuria: commonly $\geq 10^5$ CFU/mL for midstream specimens and then proceeded to organism identification and antibiotic susceptibility testing. The reliance on culture enables both accurate detection and the generation of antibiograms necessary for guiding therapy (Fetene et al., 2024; Ajani et al., 2020).

On pathogen distribution, the reviewed studies uniformly report *Enterobacteriaceae* (particularly *E. coli* and *Klebsiella* spp.) as the most frequent isolates among youths, with *Proteus, Pseudomonas* and occasional Gram-positive organisms (e.g., *Staphylococcus saprophyticus, Enterococcus* spp.) occurring less often. These

organism patterns are consistent across community and university settings and reflect both fecal-perineal contamination routes and local epidemiology (Fetene et al., 2024; Jelly et al., 2022).

A concerning and recurrent finding across recent studies is elevated levels of antimicrobial resistance among uropathogens isolated from youths. Reports document resistance to commonly prescribed oral agents (trimethoprim-sulfamethoxazole, ampicillin) and rising resistance to fluoroquinolones and some third-generation cephalosporins; pockets of ESBL-producing *Enterobacteriaceae* have been documented in community isolates, reducing empirical options (Ezo et al., 2024; Fetene et al., 2024).

II. MATERIALS AND METHOD

The study was conducted in Ikwo Local Government Area, Ebonyi State, Nigeria, a semi-urban university community with youthful population. Microbial analysis of the urine samples was carried out in the Department of Microbiology of Alex Ekwueme Federal University Ndufu-Alike (AE-FUNAI). Fifty (50) urine samples were collected from youths aged 15–24 years. Samples were collected using the midstream clean-catch method to reduce contamination. Each participant was provided with a sterile urine sample bottle with clear instructions on proper collection procedure.

Culture media used

CLED agar plates – used to culture urine and support growth of both Gram-positive and Gram-negative bacteria while differentiating lactose fermenters.

MacConkey agar plates – used to selectively isolate Gram-negative bacteria and differentiate lactose fermenters from non-fermenters.

Mueller-Hinton agar plates – used to perform antibiotic susceptibility testing using the Kirby-Bauer method.

Urine culture using calibrated loop

The colony-forming units (CFU) of bacteria in urine samples were determined using a calibrated loop method (Karah et al., 2020). A sterile calibrated loop (holding 1 microliter of urine) was dipped vertically into an uncentrifuged urine sample and streaked across the agar plates (CLED agar and MacConkey agar). The inoculated agar plates were incubated at 37°C for 24 hours.

Calculation and interpretation of result

After 24 hours incubation, the number of discrete visible bacterial colonies that grew on the agar plates were counted .To obtain the colony forming unit per milliliter (CFU/mL) , the counted number of colonies were multiplied by the dilution factor of the inoculation loop. Since 1-microliter (10^{-3} mL) inoculation loop was used, the colony count was multiplied by 1,000 to get CFU/mL. For example 50 count i.e. 50 multiplied by 1000 CFU/mLgave 50 000 CFU/mL etc.

In freshly voided urine, the culture of ≥ 100 colonies of one type (number of bacteria is $\geq 10^5$ CFU/mL) has usually been regarded as a cutoff for UTI (Simões et al., 2019; CDC, 2020). Though bacterial numbers of 10^3 CFU/mL might be significant, especially in men, depending on the implicated pathogen (Tabibian et al.,2008). Primary uropathogens, even in low amounts, could be more significant than less pathogenic bacteria in higher amounts (Kornfält et al., 2019).

Procedure for bacterial identification

Cultures were examined and the ability to grow on CLED agar and MacConkey agar plates recorded. The ability to ferment lactose on the standard CLED and MacConkey agar plate was noted. Gram-staining procedure was done on smears from the isolated colonies and examined microscopically. The bacterial isolates were subjected to a variety of biochemical identification tests to determine the species/genus of the implicated pathogen. Such tests as lactose fermentation, indole, citrate utilization, , Voges-Proskauer, urease, , hydrogen sulfide production, lysine decarboxylase; nitrates reduction, oxidase. (Cheesbrough, 2006;Shields and Cathcart, 2020)

Table 1 Biochemical identification of isolated uropathogens

Uropathogen				**biochemical test**								
Isolate	**Gram Reaction**	**No of Isolates**	**% of Isolate**	**Lac**	**Ind**	**Cit**	**VP**	**Ure**	**Oxi**	**H_2S**	**LDC**	**Nit**
Escherichia Coli	Gram -	4	36.3	+	+	-	-	-	-	-	+	+
Klebsiella pneumoniae	Gram -	3	27.3	+	-	+	+	+	-	-	+	+
Proteus mirabilis	Gram -	2	18.2	-	-	+	+	+	-	+	-	+
Pseudomonas aeruginosa	Gram -	2	18.2	-	-	+	-	-	+	-	-	+

Lac, lactose fermentation ; Ind, indole; Cit, citrate utilization; VP, Voges-Proskauer; Ure, urease; Oxi, Oxidase; H2S, hydrogen sulfide production; LDC, lysine decarboxylase; Nit, nitrates reduction; Oxi, oxidase. +, Positive; -, Negative.

Antibiotic susceptibility testing

The bacterial isolates were subjected to antibiotic susceptibility testing using the disk diffusion method on Mueller-Hinton agar according to CLSI 2021 guidelines.

Colonies of the 24-hour old isolate were picked with wire loop, transferred to sterile saline and emulsified. The suspension was adjusted to give a turbidity equivalent to O.5 McFarland. With sterile pipette, 50 µ of the O.5 McFarland suspension was transferred to 1O ml sterile saline and mixed thoroughly. After 100 µ of the suspension was transferred to Mueller Hinton agar. The suspension was plated out uniformly on the surface of the agar using sterile wire loop. Predetermined antibacterial discs were dispensed onto the surfaces of inoculated agar plates. Ten commonly used antibiotic discs were carefully placed on the inoculated agar surface using sterile forceps. The discs included: Ofloxacin, Augmentin (Amoxicillin-Clavulanic acid), peflacine, Ceftazidime, Ceftriaxone, Gentamicin, Ciprofloxacin, Ceporex, Streptomycin and Cefuroxime Each disc was pressed down to ensure complete contact with the agar. The agar plates were incubated at 37ºc for 24 hour. After incubation, the zones of inhibition around each disc were measured in millimeters using a caliper. The diameters were interpreted as sensitive (S), intermediate (I), or resistant (R) according to CLSI standards. The results were recorded (Table 2) for each isolate, providing information on the antibiotic resistance patterns of the uropathogens. (Kirby-Baur, 1966).

Multiple antibiotic resistance (MAR) index

The Multiple Antibiotic Resistance (MAR) index was determined for each bacterial isolate to assess the level of antibiotic resistance. The MAR index indicates the risk level associated with the source of the isolates, with higher values suggesting exposure to environments with frequent antibiotic use. The MAR index for each isolate was calculated using the formula:

$$\text{MAR Index} = \frac{\text{Number of Antibiotics to which the Isolates is resistant}}{\text{Total number of Antibiotics tested}}$$

In this study, each isolate was tested against ten (10) commonly used antibiotics, so the MAR index was obtained by dividing the number of antibiotics the isolate was resistant to by ten (10).

A MAR index ≥ 0.2 was considered to indicate that the isolate originated from a high-risk source with frequent antibiotic exposure pointing to strong selective pressure and potential multi-drug resistance , while a MAR index ≤ 0.2 indicates the bacteria come from an environment or source with little to no antibiotic usage (Pei Yee et al., 2023).

The calculated MAR indices were recorded for all the isolates to determine the resistance patterns of the uropathogens and provide insight into antibiotic usage practices in the community.

III. RESULTS

***Bacterial loads and colony forming units per milliliter* (CFU/mL)**

The bacterial loads in the urine samples were assessed by counting colonies on CLED and MacConkey agar plates. Out of the fifty (50) samples analyzed, eleven (22 ++++-%) showed significant bacterial growth. Colony counts were expressed in colony-forming units per milliliter (CFU/mL). The observed variation in bacterial load reflected differences in the level of urinary tract infection among the sampled youths.

The results showed that *Escherichia coli* was the most prevalent uropathogen Table 1, accounting for 36.3 % of the isolates, reflecting its known dominance in UTI, followed by *Klebsiella pneumoniae* representing 27.3% , suggesting significant involvement in urinary tract infections. *Proteus mirabilis* and *Pseudomonas aeruginosa occurred 18.2 % each.* This distribution highlighted the predominance of these organisms in the community and provided a foundation for analyzing antibiotic susceptibility patterns and resistance trend.

Antibiotic susceptibility of the bacterial isolates

The antibiotic susceptibility testing (AST) results show variable susceptibility patterns among the bacterial isolates, Table 2. *Escherichia coli* mostly exhibited high susceptibility to the antibiotics, with three of the four isolates displaying susceptibility (sensitive and intermediate sensitive) to 80% of the antibiotics, thus multiple antibiotic resistance index (MARI) of $\leq$, 0.2, it was only one isolate that showed noticeable resistance with MARI of 0.4.

Klebsiella pneumoniae on the other hand exhibited much remarkable resistance, with one of the three isolates having MARI of $\leq$, 0.2; the remaining two have multiple antibiotic resistance indices of 0.3 and 0.4 respectively.

Proteus mirabilis and *Pseudomonas aeruginosa* on the other hand displayed resistant to multiple antibiotics. One of the *Proteus mirabilis* isolate showed intermediate susceptibility to two of the tested antibiotics (ofloxacin and ciprofloxacin) and thus resistant to the remaimaning eight. , while the other exhibited also intermediate susceptibility to three (ofloxacin, peflacine and ciprofloxacin) and resistant to seven, thus MARI of $\geq$ 0.7 for both. . In the case of Pseudomonas *aeruginosa,* the trend of multi drug resistant was also apparent. One of the isolates showed susceptibility to one antibiotic (ceftriaxone), intermediate susceptibility to another (ceporex) and resistance to eight. Whereas the other was susceptibly to only ceftriaxone, thus MARI of $\geq$ 0.8 in this case.

The antibiotic susceptibility test finding reveals distinct resistance trends among the uropathogens. *Escherichia* coli displayed high susceptibility to most antibiotics reflecting their susceptible nature in community-urinary tract infections (UTIs). *Klebsiella pneumoniae Proteus mirabilis* and *Pseudomonas aeruginosa* were largely resistant, demonstrating multidrug resistance (MDR) patterns.

Overall, the isolates demonstrated variable antibiotic resistance, highlighting the presence of multidrug-resistant (MDR) pathogens and the importance of susceptibility-guided therapy.

Multiple antibiotic resistance index (MARI) of bacterial Isolates

Multiple Antibiotic Resistance Index (MARI) $\geq$ 0.2 indicates the isolate originates from an environment with high antibiotic exposure, suggesting potential selection pressure. While Low MARI values $\leq$ 0.2 indicatees susceptible isolates, often found in low antibiotic exposure environments. Therefore, high MARI values highlight multidrug-resistant (MDR) isolates, particularly *Pseudomonas aeruginosa* and *Proteus mirabilis*. Overall, the range of MARI values (0.1–0.9) shows significant variability in resistance, underlining the need for continuous antimicrobial surveillance and rational antibiotic use.

Table 2: Antibiotics susceptibility profile of the bacterial isolates

Bacteria Isolates	OFX	AUG	PEF	TRX	CN	CPX	CEP	CTZ	STR	CEF	%S	%I	%R	MAR Index
E. coli	S	S	S	I	S	S	S	R	S	S	80	10	10	0.1
E. coli	S	S	S	S	R	S	R	I	S	S	70	10	20	0.2
E. coli	S	S	S	I	S	S	S	I	R	I	60	30	10	0.1
E. coli	R	S	R	I	S	S	S	I	R	R	40	20	40	0.4
Klebsiella Pneumonia	S	I	I	R	S	S	I	I	I	I	30	60	10	0.1
Klebsiella Pneumonia	S	R	I	R	I	I	I	R	I	R	10	50	40	0.4
Klebsiella Pneumonia	S	R	I	R	I	I	I	I	I	R	10	60	30	0.3
Proteus mirabilis	I	R	R	R	R	I	R	R	R	R	0	20	80	0.8
Proteus mirabilis	I	R	I	R	R	I	R	R	R	R	0	30	70	0.7
Pseudomonas aeruginosa	R	R	R	S	R	R	R	R	R	R	10	0	90	0.9
Pseudomonas aeruginosa	R	R	R	S	R	R	I	R	R	R	10	10	80	0.8

OFX: Ofloxacin, AUG: Augmentin (Amoxicillin-Clavulanic acid), PEF: peflacine, TRX: Ceftriaxone, CN: Gentamicin, CPX: Ciprofloxacin, CEP: Ceporex, CTZ: Ceftazidime, STR:Streptomycin, CEF: Cefuroxime
S, Sensitive; I, Intermediate Sensitive; R, Resistant

IV. DISCUSSION

Bacterial load and implications of urinary tract infection

The bacterial load considered significant urinary tract infection in this study ranged from 1.0×10^5 CFU/mL upwards, which are consistent with the diagnostic threshold for significant bacteriuria (10^5 CFU/mL), as outlined by the Clinical and Laboratory Standards Institute, confirming that most isolates represent clinically significant infections rather than contamination (Kara et al., 2020;CLSI, 2021) . Likewise, Khan et al. (2024) observed that midstream urine samples in Pakistan had counts ranging from 1.5×10^4 to 3.2×10^4 CFU/mL, which falls within the same range as the present study. In contrast, Lee et al. (2022) reported higher loads ($\geq 10^5$ CFU/mL) in hospitalized patients, suggesting that community-acquired UTIs such as those in this study often have moderate bacterial loads, while hospital-acquired cases may exhibit higher densities due to recurrent infections and multidrug resistance.

In terms of bacterial type*, Escherichia coli* was the predominant isolate , accounting for 36.3 %, of the pathogens ,supporting the well-established role of *E. coli* as the leading uropathogen globally. This is in consonance with other studies elsewhere in Africa indicating 40 – 46% of isolates are *Escherichia coli* (Moges, A.F. et al., 2012; Wenyama, 2003; Mayanja,et al., 2005). The incidence of microorganisms associated with UTI showed variation in different countries*, Escherichia coli* remained the most prevalent uropathogens. In this study, the prevalence of Escherichia coli was 36.3 %, in comparison with other countries, Australian study (73%) (Aswan, et al., 2014) Pakistan (Faroqui, et al., 1989) and Kenyan study (40%) (Nabbugodi, et al., 2015). After *E. coli*, the next in rank was *Klebsiella pneumoniae* 27.3%, while *Proteus mirabilis* and *Pseudomonas aeruginosa* occurred 18.2 % each.

Antibiotic susceptibility profile of the isolates

The antibiotic susceptibility testing against ten antibiotics revealed marked variations in resistance and susceptibility status. *Escherichia coli* showed the highest susceptibility, with three of the four isolates having MARI of ≤ 0.2, while the fourth has MARI of 0.4. This demonstrates that *E. coli* remains largely treatable in the study area, which agrees with Srivastava et al. (2022), who reported that community-acquired *E. coli* isolates retained high sensitivity to fluoroquinolones and aminoglycosides. However, partial resistance in some isolates suggests an emerging resistance trend, a pattern also highlighted by Lee et al. (2024) in Asia.

In contrast*, Pseudomonas aeruginosa* displayed extensive resistance, one of the isolates was susceptible to only ceftriaxone out of the ten antibiotics tested thus MARI of 0.9, while another exhibited susceptibility to ceftriaxone and intermediate susceptibility to ceporex thereby showing MARI of 0.8. This extreme resistance profile reflects the intrinsic and adaptive resistance mechanisms of *Pseudomonas,* including efflux pumps and biofilm formation, as reported by Khan et al. (2024). Similar multidrug resistance in *Pseudomonas aeruginosa* was documented by Zhao et al. (2025), who emphasized the clinical difficulty in treating UTIs caused by this organism.

Klebsiella pneumoniae isolates exhibited variable resistance pattern. One out of the three isolates was very susceptible to the antibiotics with MARI of 0.1, the other two were quite different with MARI of 0.3 and 0.4 respectively

Proteus mirabilis on the other hand demonstrated significant resistance, with both isolates showing MARI of 0.7-0.8, confirming their capacity to withstand multiple drug classes. This observation is consistent with Chawla et al. (2023), who reported *Proteus* spp. as commonly resistant to cephalosporins and aminoglycosides in community-acquired UTIs. The resistance may be linked to urease production and plasmid-mediated resistance genes, which enhance survival in the urinary tract environment.

Overall, the antibiotic susceptibility data in this study reveal a clear divide between susceptible organisms (*E. coli*), moderately resistant *Klebsiella*, and highly resistant non-fermenters *Pseudomonas, Proteus*. This pattern is consistent with global reports indicating that first-line agents such as fluoroquinolones and aminoglycosides remain effective for many community isolates. (Yadav et al., 2021; Chawla et al., 2023).

The Multiple Antibiotic Resistance Index (MARI) is a useful epidemiological tool that indicates the extent of antibiotic exposure and misuse within a population. In this study, the MARI values ranged between 0.1 and 0.9, with *Proteus mirabilis* and *Pseudomonas aeruginosa* recording higher values *(≥0.7*), while some *E coli* and *Klebsiella Pneumonia* showed relatively lower values (≤0.2). A MARI value greater than 0.2 is generally considered significant, as it suggests that the isolates originated from environments where antibiotics are frequently used or misused (Khan et al., 2024; Akinola et al., 2021).

The MARI values observed in this study are consistent with the findings of Ojo et al. (2023), who reported MARI values of 0.25–0.75 between *E. coli* and *Klebsiella* spp. isolated from urinary samples in Nigeria. Similarly, Lee et al. (2024) demonstrated that over 60% of UTI pathogens in their cohort of young adults had MARI values above 0.3, reflecting widespread antimicrobial pressure. The implication of these findings is that

the uropathogens are likely derived from high-risk sources where antibiotics are commonly misused, such as self-medication etc.

Furthermore, the high MARI values underscore the risk of treatment failure. For example, *Pseudomonas aeruginosa* isolates with a MARI of 0.9 and 0.8 showed resistance to nine and eight out of ten tested antibiotics respectively , limiting therapeutic options. This observation is in line with Zhang et al. (2022), who emphasized that multidrug-resistant strains in UTIs are strongly associated with prolonged treatment duration and recurrent infections

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V. CONCLUSION

This study investigated the detection of urinary tract infections (UTIs) among the youths, emphasizing bacterial load, etiological agents, antibiotic susceptibility patterns, and multiple antibiotic resistance profiles. The findings revealed a significant bacterial burden among the studied population, with *Escherichia coli* emerging as the predominant uropathogen, followed by *Klebsiella pneumoniae*, while *Proteus mirabilis* and Pseudomonas *aeruginosa* have equal occurence. This aligns with global and regional reports identifying *E. coli* as the primary causative agent of UTIs.

The antibiotic susceptibility profile demonstrated variable responses, with some isolates remaining sensitive to fluoroquinolones (such as ciprofloxacin and ofloxacin). The high resistance levels observed were further reinforced by the Multiple Antibiotic Resistance Index (MARI) values, which ranged from 0.1 to 0.9, signifying that most isolates originated from environments with high antibiotic use or misuse.

These findings underscore the growing challenge of antimicrobial resistance in the management of UTIs, especially among young people who may be more prone to self-medication and incomplete treatment regimens. The study therefore highlights the urgent need for effective antibiotic stewardship, improved diagnostic surveillance, and increased public health awareness in order to curb the spread of multidrug-resistant uropathogens and ensure better management of UTIs.

Based on the findings of this study, the following recommendations are made: Antibiotic stewardship programs, health authorities should strengthen antibiotic stewardship to guide proper prescription.

Routine screening and surveillance: Regular microbiological monitoring of UTIs should be implemented among youths to detect emerging resistance trends and ensure timely interventions.

Public health education: Awareness campaigns should be intensified to discourage self-medication and incomplete antibiotic regimens, which contribute significantly to resistance.

Improved diagnostic facilities: Primary healthcare centers should be equipped with basic laboratory facilities to enable early and accurate detection of uropathogens.

Further research: Expanded studies with larger sample sizes and molecular characterization of resistant strains are recommended to provide deeper insights into resistance mechanisms and guide future treatment strategies.

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