Available online at www.worldnewsnaturalsciences.com

World News of Natural Sciences

An International Scientific Journal

WNOFNS 63(2) (2025) 369-384 EISSN 2543-5426

Antimicrobial resistance profile of uropathogens: A comparative study in people living with HIV and Non-HIV individuals

Akubuo Chigaemezu Remmy-Martin*, Obasi Chikaodinaka Vivian, Akabogu Cynthia Chidera, Mejuru Christopher Chidiebere

Department of Microbiology, Faculty of Biological Science, Imo State University, Owerri, Imo State, Nigeria

*E-mail address: martinakubuo@gmail.com

ABSTRACT

Urinary tract infections (UTIs) represent a significant portion of the most commonly encountered bacterial infections globally, with the intricacies of this issue being exacerbated by the phenomenon of antimicrobial resistance (AMR), particularly within susceptible populations such as individuals living with HIV (PLHIV). The objective of this investigation was to evaluate the prevalence, categorization of bacterial agents, and patterns of antimicrobial susceptibility among uropathogens in both HIV-positive and HIV-negative cohorts in Owerri, Nigeria. A croaa sectional study was executed comprising 150 participants, evenly distributed with 75 HIV-positive and 75 HIV-negative individuals, all of whom were receiving care at the Federal University Teaching Hospital in Owerri. Midstream urine specimens were collected, cultured on standard bacteriological media, and the resulting isolates were identified via biochemical analysis. In order to evaluate antimicrobial susceptibility, Kirby–Bauer disk diffusion methodology was employed in accordance with CLSI (2017) standards. The data were subjected to analysis using Chi-square tests, with a significance threshold set at $p < 0.05$. The cumulative prevalence of UTIs was identified as 66.0%, with a markedly elevated occurrence among HIV-positive individuals (74.7%) in comparison to their HIV-negative counterparts (57.3%) ($\chi^2 = 4.92$, $p = 0.027$). The demographic cohort aged 30-39 years exhibited the highest rates of infection, and a greater prevalence was observed among females in both groups ($p = 0.008$). *Escherichia coli* (32.3%) was identified as the predominant isolate, followed by *Staphylococcus aureus* (24.1%) and *Klebsiella* spp. (14.1%). The highest levels of susceptibility were noted for fluoroquinolones and amoxicillin–clavulanate, whereas amoxicillin and cotrimoxazole demonstrated suboptimal effectiveness. Resistance profiles remained comparable across both cohorts ($p > 0.05$). This research underscores the fact that HIV infection

(Received 25 September 2025; Accepted 25 October 2025; Date of Publication 27 October 2025)

significantly elevates the likelihood of UTIs and that the escalating challenge posed by antimicrobial resistance represents a formidable barrier to effective treatment. Continuous surveillance, culture-guided therapeutic interventions, and judicious use of antimicrobials are imperative for addressing resistance. The integration of microbiological surveillance within HIV management programs is highly advocated.

Keywords: Urinary tract infection, HIV-positive patients, Antimicrobial resistance; Uropathogens, *Escherichia coli*, Fluoroquinolones, Cotrimoxazole resistance, Nigeria, Public health, Antimicrobial stewardship

1. INTRODUCTION

Urinary tract infections (UTIs) are among the most widespread bacterial infections globally and constitute a significant determinant of antibiotic utilization in both community and clinical settings. The challenge of antimicrobial resistance (AMR) in pathogens responsible for UTIs has been escalating: contemporary worldwide estimates suggest that in 2019, approximately 4.95 million fatalities were associated with bacterial AMR, with persistently elevated resistance rates observed in critical uropathogens such as *Escherichia coli* and *Klebsiella pneumoniae*, which account for the majority of UTIs in both community and healthcare contexts (Murray et al., 2022). Concurrently, the World Health Organization (WHO) has reported a substantial reduction in the efficacy of first-line therapeutic agents (ampicillin, co-trimoxazole, and fluoroquinolones) in treating *E. coli* infections, thus complicating the provision of effective empirical treatment and heightening the likelihood of therapeutic failure (WHO, 2023). Individuals living with HIV (PLHIV) exhibit an augmented susceptibility to bacterial infections, including UTIs, attributable to factors such as alterations in immune system function associated with HIV, modifications in the urogenital mucosa, frequent healthcare engagements, and the administration of prophylactic antibiotics. Recent investigations from sub-Saharan Africa and other locales underline a significant prevalence of UTIs among PLHIV, with pathogens including *E. coli, Klebsiella* spp., and non-fermenters being prevalent in more complex cases.

Lower CD4 T-cell counts and elevated viral loads have been consistently correlated with an increased incidence and severity of UTIs (Kahsay et al., 2024; Hantalo et al., 2024). It is imperative to acknowledge that co-trimoxazole prophylaxis (TMP-SMX), a pivotal strategy in the prevention of opportunistic infections, may precipitate the emergence of TMP-SMX-resistant Enterobacterales within the gastrointestinal and urinary tracts. This raises significant concerns regarding the diminished efficacy of this therapeutic intervention when UTIs manifest. Evidence from meta-analyses and cohort studies indicates a high overall resistance to co-trimoxazole among infections in PLHIV, accompanied by a rapid selection for resistant E. coli subsequent to prophylactic treatment (Morpeth et al., 2008; Assefa & Girmay, 2024).

In various healthcare contexts, the patterns of antimicrobial resistance (AMR) exhibit pronounced disparities between individuals living with HIV (PLHIV) and their HIV-negative counterparts. Investigations from both primary care and hospital cohorts indicate that PLHIV are at an increased risk of encountering Extended-Spectrum β-Lactamase producing Enterobacterales (ESBL-E). This phenomenon is likely attributed to factors such as recurrent antibiotic exposure, frequent healthcare interactions, and the pressures associated with colonization. A study undertaken in Harare in 2021 identified a correlation between HIV infection and the presence of ESBL-producing *E. coli* in symptomatic individuals. More recent analyses suggest that the prevalence of ESBL carriage and infections among PLHIV is considerable on a global scale, which bears significant implications for therapeutic strategies (Olaru et al., 2021; Tigabie et al., 2025). Data pertaining to gut colonization further substantiates this trend, revealing heightened levels of multidrug-resistant Enterobacterales and ESBL genes (including blaCTX-M and blaTEM) in PLHIV, thereby creating an ecological reservoir that could potentially lead to urinary tract infections (Dimani et al., 2023).

From a therapeutic perspective, guideline organizations are currently emphasizing the significance of localized antimicrobial resistance (AMR) surveillance to inform the empirical management of urinary tract infections (UTIs). They further warn of the constraints associated with certain oral pharmacological agents in the context of extended-spectrum beta-lactamase-producing Enterobacteriaceae (ESBL-E) and intricate infections.

The Infectious Diseases Society of America (IDSA) AMR Guidance (v4.0, 2024) recommends refraining from reliance on fosfomycin or nitrofurantoin for upper urinary tract ailments and underscores the imperative of tailoring treatment according to resistance profiles and the anatomical site of infection, thus accentuating the essential role of precise resistance characterization (Tamma et al., 2024). Nonetheless, in numerous low- and middle-income nations characterized by elevated rates of both HIV and UTIs, comprehensive comparative data regarding uropathogen classifications and resistance trends contingent upon HIV status is frequently deficient, outdated, or restricted to singular healthcare facilities. This deficiency in extensive data obstructs the formulation of context-specific empirical treatment guidelines. This shortcoming is particularly significant for three primary reasons. Firstly, individuals living with HIV (PLHIV) encounter distinct risk determinants, including immunosuppression, particular prophylactic regimens, and trends in hospitalization that may affect both the pathogen ecology and the emergence of resistance. These determinants may vary from those present in HIV-negative cohorts within the same geographical region (Hantalo et al., 2024).

This phenomenon significantly constrains our options for oral pharmacotherapy, prolonging the duration required to identify effective treatment modalities and escalating costs due to the necessity for broad-spectrum agents and extended hospitalization periods. These difficulties are exacerbated in areas where access to susceptibility testing is restricted (Mareș et al., 2024). Conversely, possessing up-to-date, HIV-specific resistance profiles can substantially enhance the customization of our treatment strategies. This entails recognizing the appropriate juncture to transition from trimethoprim-sulfamethoxazole (TMP-SMX) or ciprofloxacin, improving our antimicrobial stewardship, and instituting preventive strategies such as optimized catheter management and prophylaxis protocols that are congruent with local epidemiological data and international guidelines (Tamma et al., 2024).

In light of these considerations, it is evident that a comparative investigation of antimicrobial resistance profiles in uropathogens among HIV-positive and HIV-negative patients is not only opportune but also essential for informed policy-making. By delineating the disparities in organism distribution and resistance patterns such as those associated with ESBL and fluoroquinolone resistance we can (i) enhance our empirical treatment approaches, (ii) refine our diagnostic stewardship (including the judicious timing of urine cultures prior to the initiation of treatment), and (iii) strengthen our contributions to AMR surveillance within national frameworks and the World Health Organization's Global Antimicrobial Resistance and Use Surveillance System (WHO GLASS), particularly in regions significantly burdened by these challenges (WHO, 2024). Ultimately, addressing these knowledge deficits is crucial to mitigate unnecessary treatment failures, curtail the reliance on last-resort agents, and alleviate the overall AMR burden highlighted in recent global evaluations (Tamma et al., 2024).

2. MATERIALS AND METHODS

2. 1. Study Design and Area

A comparative cross-sectional investigation was carried out between January and May 2017 at the General Hospital located in Mbieri, which is situated within the Mbaitoli Local Government Area (LGA) of Imo State, Nigeria. This healthcare institution serves as a pivotal secondary health facility in Imo State, providing an extensive array of medical services, including specialized care for patients living with HIV/AIDS through its Heart-to-Heart Antiretroviral Therapy Clinic (ARTC).

2. 2. Study Population

The study population encompassed both HIV-positive and HIV-negative individuals presenting clinical manifestations indicative of a urinary tract infection (UTI) at the medical facility.

HIV-positive group: This cohort comprised individuals attending the Antiretroviral Therapy Clinic (ARTC) who possessed a confirmed HIV diagnosis based on the national testing protocol (Determine™, Uni-Gold™, and Stat-Pak™) and had abstained from antibiotic use in the two weeks preceding sample collection**.**

HIV-negative group (control): This group consisted of patients visiting the Outpatient Department (OPD) exhibiting analogous UTI symptoms but who were verified as HIV-negative through voluntary counseling and testing.

2. 3. Sample Size Determination

A total of 150 participants were recruited, with 75 individuals assigned to the HIV-positive group and 75 to the HIV-negative group. The determination of sample size was accomplished utilizing the Araoye (2004) formula for comparative studies, targeting a 95% confidence interval and 80% statistical power, thereby ensuring sufficient precision for detecting disparities in antimicrobial resistance patterns between the cohorts.

2. 4. Sampling Technique and Data Collection

Participants were selected through a systematic random sampling method during their routine clinic visits. After securing written informed consent, each participant was interviewed using a structured, pre-validated questionnaire designed to gather demographic, clinical, and treatment-related information. Confidentiality for all participants was ensured, and personal identifiers were removed from the datasets.

2. 5. Ethical Considerations

Ethical approval was granted by the Imo State Hospital Management Board Ethics Committee, facilitated by the Medical Director of General Hospital Mbieri (Approval No: HMB/EC/2017/012). Each participant provided written informed consent, and all procedures were conducted in accordance with the principles set forth in the Declaration of Helsinki (2013). Participants diagnosed with bacteriuria were referred to their attending physicians for appropriate management.

2. 6. Specimen Collection

Approximately 5 mL of midstream urine was collected aseptically from each participant using sterile, wide-mouth universal containers.

- **Males** were instructed to wash their hands, retract the foreskin, and collect midstream urine.
- **Females** were advised to cleanse the vulva and perineum, separate the labia, and collect midstream urine to reduce contamination.

All samples were transported to the Microbiology Laboratory within one hour of collection for culture and analysis.

2. 7. Bacteriological Investigation

Culture and Isolation

Urine samples were mixed gently and inoculated onto Cystine Lactose Electrolyte-Deficient (CLED) agar and MacConkey agar (Oxoid Ltd., UK) using a standard calibrated inoculating loop (0.001 mL). Plates were incubated aerobically at 37 °C for 24 hours. Growth yielding $\geq 10^5$ colony-forming units (CFU)/mL was regarded as significant bacteriuria, while mixed growths were excluded as contamination.

Identification of Isolates

Distinct colonies were subcultured for purity and identified based on:

- Colony morphology
- Gram staining
- Biochemical characterization (oxidase, catalase, indole, citrate, urease, triple sugar iron, and motility tests) following standard procedures described by Cheesbrough (2005).

2. 8. Antimicrobial Susceptibility Testing

Antibiotic susceptibility was determined by the Kirby–Bauer disk diffusion method on Mueller–Hinton agar in accordance with Clinical and Laboratory Standards Institute (CLSI) guidelines, 2017 (M100, 33rd ed.).

The antibiotics tested reflected local prescribing patterns for UTIs and included: Ampicillin (10 µg), Amoxicillin-clavulanate (20/10 µg), Ceftriaxone (30 µg), Cloxacillin (5 µg), Ciprofloxacin (5 µg), Gentamicin (10 µg), Streptomycin (10 µg), Tetracycline (30 µg), Chloramphenicol (30 µg), Co-trimoxazole (25 µg), Nalidixic acid (30 µg), Ofloxacin (10 µg), and Nitrofurantoin (300 µg).

Plates were incubated at 37 °C for 18–24 hours, and zones of inhibition were measured using a calibrated ruler. Interpretations were made as Sensitive (S), Intermediate (I), or Resistant (R) per CLSI breakpoints. Isolates resistant to three or more antibiotic classes were classified as multidrug resistant (MDR).

2. 9. Data Management and Statistical Analysis

Laboratory and questionnaire data were entered into Microsoft Excel and analyzed using IBM SPSS Statistics version 26.0 (IBM Corp., Armonk, NY, USA). Descriptive statistics (means, frequencies, and percentages) summarized demographic and bacteriological data.

Associations between categorical variables were evaluated using the Chi-square (χ^2) test, while Student's t-test compared mean values between groups. Statistical significance was accepted at $p < 0.05$.

3. RESULT

3. 1. Prevalence of Urinary Tract Infection among HIV and Non-HIV Individuals

Out of 150 urine samples analyzed (75 HIV-positive and 75 HIV-negative), 99 (66.0%) yielded significant bacterial growth. The prevalence of urinary tract infection (UTI) was notably higher among HIV-positive patients (74.7%) compared to HIV-negative individuals (57.3%).

A Chi-square test revealed a statistically significant association between HIV status and UTI occurrence ($\chi^2 = 4.92$, df = 1, $p = 0.027$), indicating that HIV infection was a significant risk factor for urinary tract infection (Figure 1).

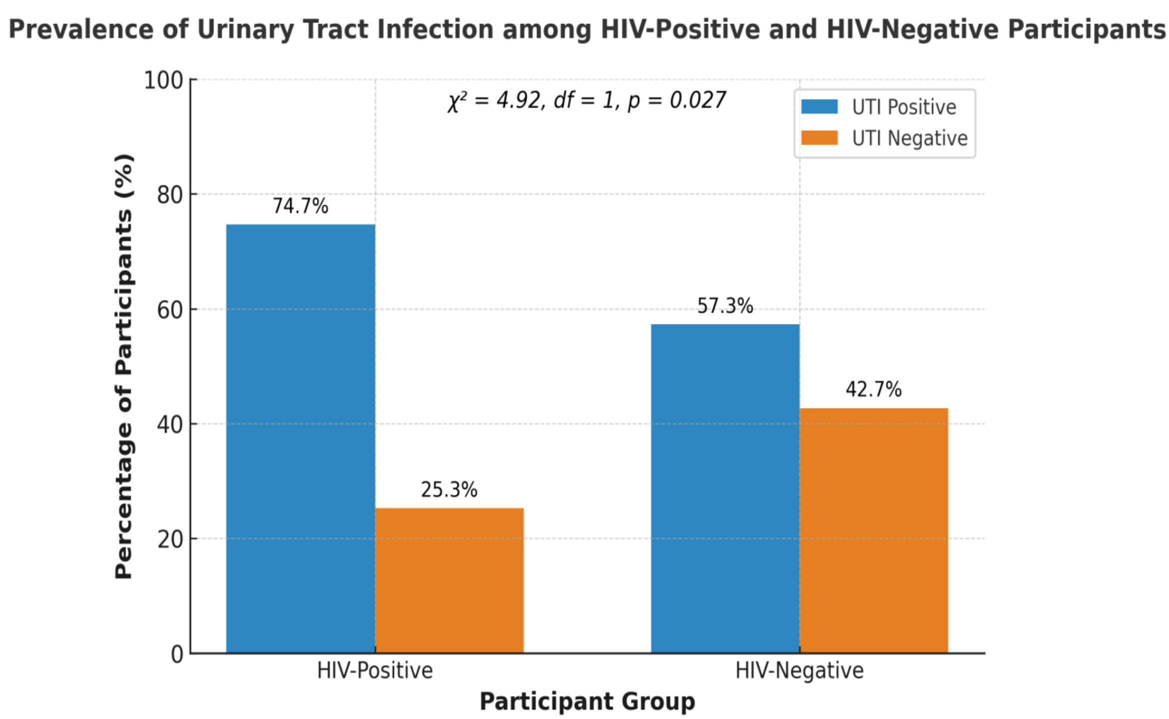

Fig. 1. Prevalence of Urinary Tract Infection among HIV and Non-HIV Individuals.

3. 2. Age Distribution of UTI in HIV and Non-HIV Participants

The 30–39 years age group recorded the highest frequency of UTI in both HIV-positive (39.3%) and HIV-negative (28.0%) participants. In contrast, the 70-79 years group exhibited the lowest infection rate (2.0%). Statistical analysis demonstrated a significant association between age and UTI prevalence ($\chi^2 = 11.48$, df = 6, p = 0.042), suggesting that UTI occurrence varied significantly across age categories (Figure 2).

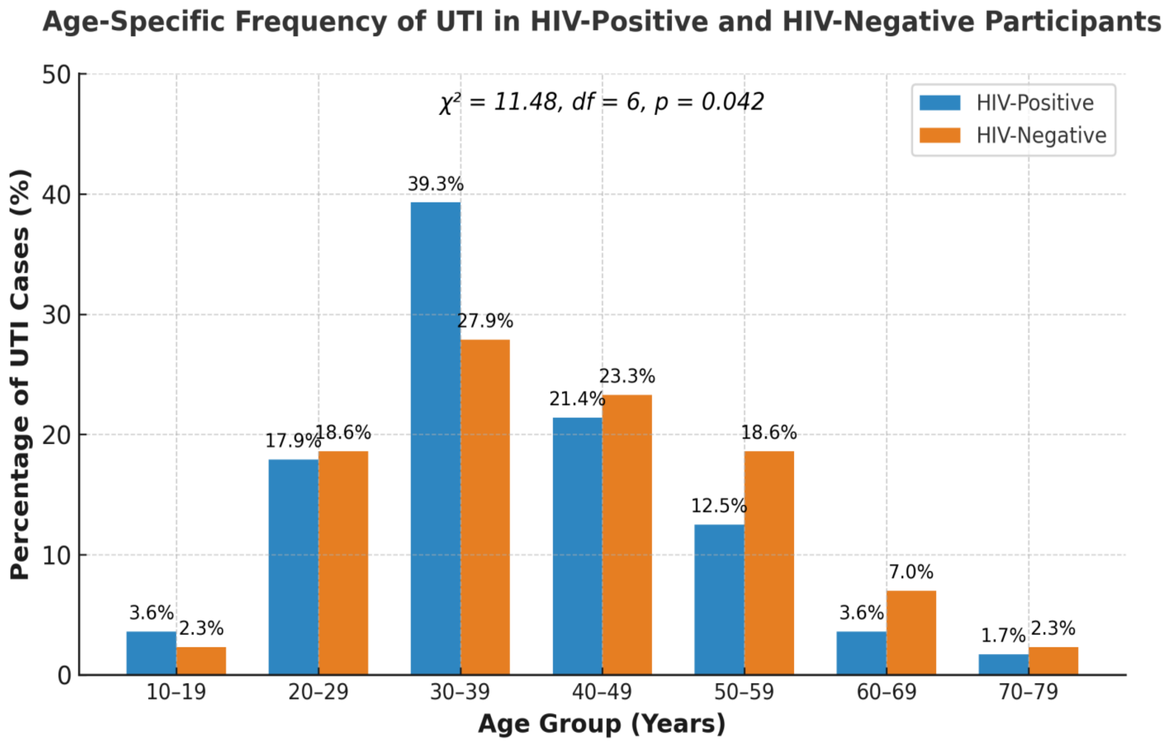

Fig. 2. Age Distribution of UTI in HIV and Non-HIV Participants.

3. 3. Sex Distribution of UTI among HIV and Non-HIV Participants

Of the 150 participants, 90 (60%) were females and 60 (40%) were males. The prevalence of UTI was higher among females across both groups 71.4% in HIV-positive females and 62.5% in HIV-negative females compared to 28.6% and 37.5% among their male counterparts, respectively.A Chi-square test showed that sex had a significant effect on UTI occurrence ($\chi^2 = 7.21$, df = 1, p = 0.008), indicating higher susceptibility among females (Table 1, Figure 3 and Figure 4).

Table 1. Sex Distribution of UTI among HIV and Non-HIV Participants.

Sex	HIV-Positive Infected n (%)	HIV-Negative Infected n (%)	Total n (%)
Male	16 (28.6)	16 (37.5)	32 (32.3)
Female	40 (71.4)	27 (62.5)	67 (67.7)
Total	56 (100)	43 (100)	99 (100)

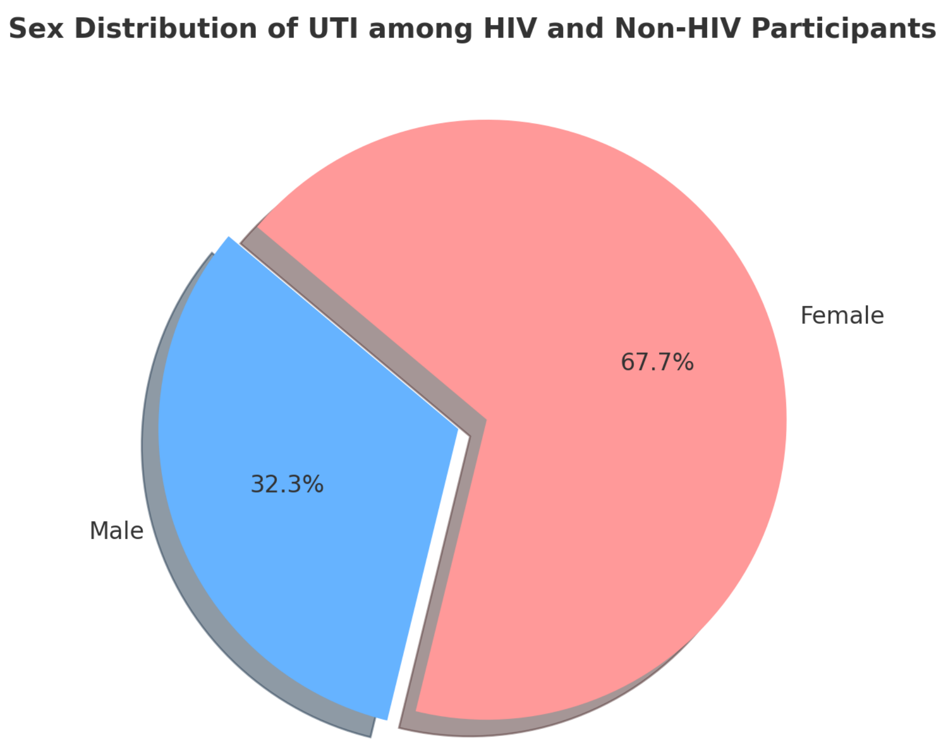

Fig. 3. Sex distribution of UTI among HIV and non-HIV participants.

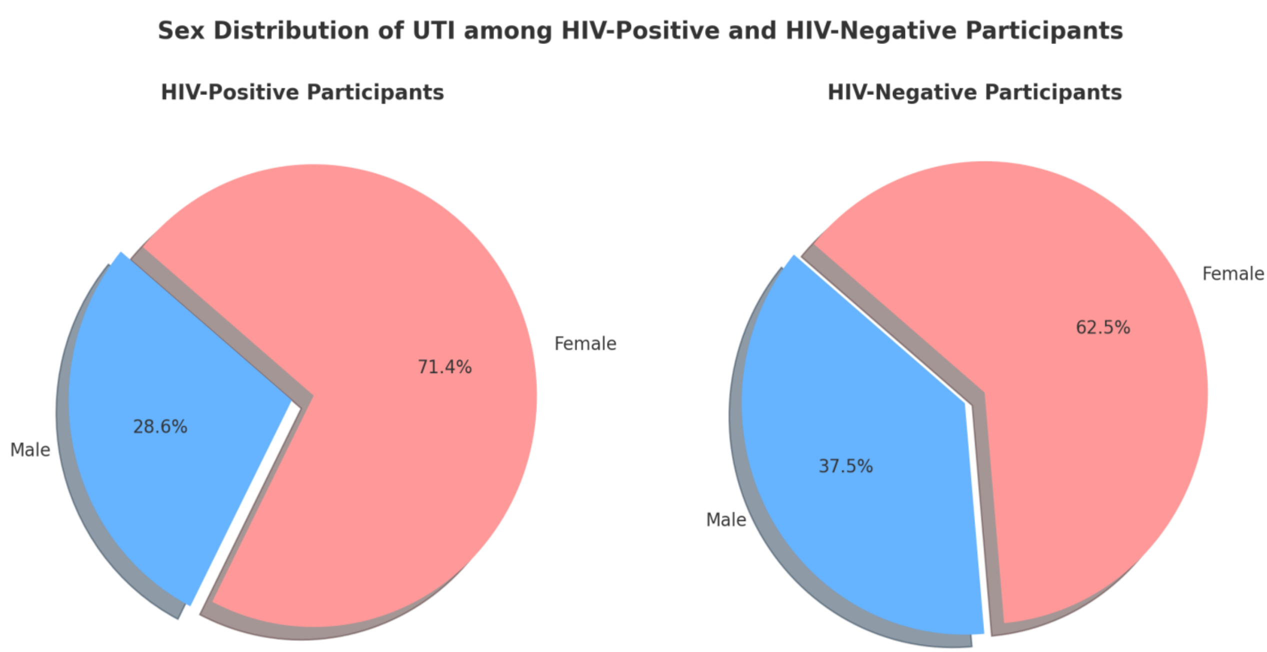

Fig. 4. Sex distribution of UTI among HIV-Positive Participants" and "HIV-Negative Participants.

3. 4. Distribution of Bacterial Isolates

A total of 99 bacterial isolates were recovered, comprising Gram-negative organisms (61.6%) and Gram-positive organisms (38.4%). *Escherichia coli* was the predominant isolate (32.3%), followed by *Staphylococcus aureus* (24.1%), *Klebsiella* spp. (14.1%), and *Enterococcus* spp. (11.1%). No statistically significant difference was observed in the distribution of bacterial species between HIV-positive and HIV-negative groups ($p > 0.05$) (Table 2).

Table 2. Distribution of Uropathogens among HIV-Positive and HIV-Negative Participants.

Organism	Total Isolated n (%)	HIV-Positive n (%)	HIV-Negative n (%)
Escherichia coli	32 (32.3)	24 (42.9)	8 (18.6)
Klebsiella spp.	14 (14.1)	8 (14.3)	6 (13.9)
Pseudomonas spp.	10 (10.1)	6 (10.7)	4 (9.3)
Proteus spp.	5 (5.0)	4 (8.9)	1 (2.3)
Staphylococcus spp.	24 (24.1)	15 (26.8)	9 (20.9)
Enterococcus spp.	11 (11.1)	8 (14.3)	3 (7.0)
Streptococcus spp.	3 (3.0)	3 (5.4)	0 (0.0)
Total	**99 (100)**	**56 (100)**	**43 (100)**

3. 5. Antibiotic Susceptibility Pattern of Uropathogens in HIV-Positive Participants

Among HIV-positive participants, fluoroquinolones (Ofloxacin, Ciprofloxacin) and Augmentin showed the highest sensitivity (60-80%). Amoxicillin and Sulfamethoxazole displayed the lowest activity (< 20%). A Chi-square analysis indicated significant variation in resistance rates among antibiotics ($\chi^2 = 14.03$, df = 7, $p = 0.049$) (Table 3).

Table 3. Antibiotic Susceptibility of Uropathogens from HIV-Positive Participants.

Organism	No. Tested	OFX %	PEF %	CN %	AU %	S %	SXT %	PN %	CPX %
Pseudomonas spp.	6	67	50	33	70	0	10	40	60
E. coli	24	63	54	33	58	0	13	46	54
Klebsiella spp.	8	56	44	31	50	13	19	44	50
Proteus spp.	4	75	50	38	63	25	25	50	63

Staphylococcus spp.	15	80	60	30	87	10	0	50	70
Enterococcus spp.	8	50	50	38	60	10	10	40	50
Streptococcus spp.	3	50	50	50	50	0	0	50	50

Key: OFX = Ofloxacin (10 µg); PEF = Pefloxacin (5-10 µg); CN = Gentamicin (10 µg); AU = Amoxicillin–clavulanate (Augmentin, 20/10 µg); S = Amoxicillin (10 µg); SXT = Trimethoprim–sulfamethoxazole (25 µg; 1.25/23.75 µg); PN = Nitrofurantoin (300 µg); CPX = Ciprofloxacin (5 µg) Results interpreted according to CLSI (2017) guidelines.

3. 6. Antibiotic Susceptibility Pattern of Uropathogens in HIV-Negative Participants

In HIV-negative participants, fluoroquinolones and Augmentin also showed the highest activity (55–70%), while Amoxicillin and Sulfamethoxazole remained the least effective.

The overall pattern of antibiotic susceptibility between HIV-positive and HIV-negative groups showed no statistically significant difference ($p > 0.05$) (Table 4).

Table 4. Antibiotic Susceptibility of Uropathogens from HIV-Negative Participants.

Organism	No. Tested	OFX %	PEF %	CN %	AU %	S %	SXT %	PN %	CPX %
Pseudomonas spp.	4	56	44	33	67	0	11	44	56
E. coli	8	60	50	35	55	0	10	40	50
Klebsiella spp.	6	53	47	33	47	7	20	40	53
Proteus spp.	3	71	43	29	57	14	14	43	57
Staphylococcus spp.	9	80	60	33	87	13	0	53	73
Enterococcus spp.	3	50	50	40	60	10	10	40	50

Key: OFX = Ofloxacin (10 µg); PEF = Pefloxacin (5-10 µg); CN = Gentamicin (10 µg); AU = Amoxicillin–clavulanate (Augmentin, 20/10 µg); S = Amoxicillin (10 µg); SXT = Trimethoprim–sulfamethoxazole (25 µg; 1.25/23.75 µg); PN = Nitrofurantoin (300 µg); CPX = Ciprofloxacin (5 µg).

3. 7. Summary of Findings

The composite summary chart presents the statistical significance of the major variables analyzed in the study. Each horizontal bar represents a variable tested, and the corresponding p-values indicate whether the differences were significant ($p < 0.05$).The red dashed line denotes the significance threshold ($p = 0.05$). Blue bars correspond to statistically significant associations, while the orange bar represents descriptive data (bacterial type). Significant associations were observed between HIV status, age, sex, and antibiotic response with UTI occurrence, whereas bacterial type was reported descriptively (Figure 5).

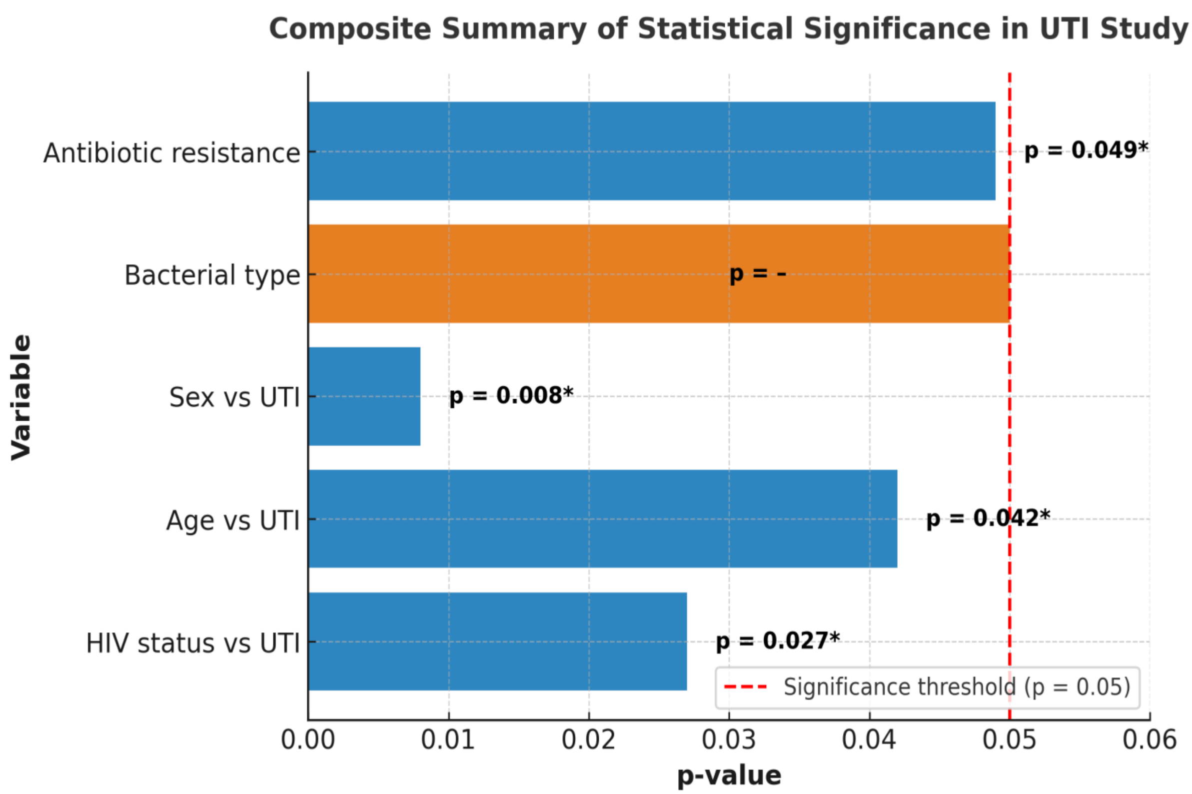

Fig. 5. Composite Summary of Statistical Significance in UTI Study.

4. DISCUSSION

This study revealed a significantly higher prevalence of urinary tract infection (UTI) among HIV-positive individuals than among HIV-negative participants, reinforcing the well-established link between immunosuppression and susceptibility to bacterial infections. The depletion of $CD4^+$ T-cells and impairment of mucosal immunity weaken local host defenses, promoting colonization by opportunistic and resistant uropathogens. Comparable findings have been reported across sub-Saharan Africa: Tilahun et al. (2024) in Northeast Ethiopia and Kahsay et al. (2024) in Tigray both documented significantly higher UTI rates among people living with HIV (PLHIV) relative to the general population.

Their studies identified recurrent hospital exposure, prophylactic antibiotic use, and catheterization as key predisposing factors. The association observed here between HIV infection and UTI prevalence aligns with results from Tessema et al. (2020) and Gebremedhin et al. (2025), who found that UTI risk remains elevated despite antiretroviral therapy (ART). Similarly, a pan-African meta-analysis by Shabohurira et al. (2025) estimated a pooled UTI prevalence of roughly 24% among PLHIV - lower than the rate recorded in this study, but still substantially above that of HIV-negative populations.

Differences in ART coverage, local antibiotic exposure, and population demographics may explain these discrepancies. Globally, Li et al. (2022) reported that HIV-associated immune suppression magnifies the burden of antimicrobial-resistant UTIs, underscoring the intersection of immunodeficiency and resistance dynamics.

The highest UTI prevalence was recorded in the 30–39-year age group, corresponding to the reproductive phase of adulthood. This age-related pattern mirrors findings by Tilahun et al. (2024) and Ejerssa et al. (2021), who identified mid-aged adults as the most affected demographic. Factors such as sexual activity, contraceptive use, and hormonal variation contribute to bacterial ascension and urinary colonization. The lower infection rate among elderly participants may reflect immune reconstitution with ART or reduced exposure to behavioral risk factors.

Contrastingly, Simeneh et al. (2022) observed increased UTI incidence among older HIV patients, attributing it to comorbidities, catheter use, and prolonged hospitalization. Keenan et al. (2024) further contextualized these trends by demonstrating that social and environmental determinants such as poor sanitation and antibiotic access modulate MDR-UTI risk across age categories.

Female participants exhibited a markedly higher prevalence of UTI across both HIV categories. This observation is consistent with Kahsay et al. (2024), Tessema et al. (2020), and Ejerssa et al. (2021), who reported similar female predominance. Anatomical predisposition, shorter urethral length, and proximity to the anal region facilitate ascending infections. In HIV-positive women, vaginal dysbiosis and mucosal inflammation intensify this vulnerability.

Shabohurira et al. (2025) also identified female sex as an independent risk factor among PLHIV across African cohorts. Interestingly, Nakandi et al. (2025) observed a narrowing of the sex gap in semi-urban Uganda, where instrumentation and prostate disorders increased male infection rates, suggesting that sex differences are context-dependent and influenced by healthcare access and comorbidity profiles.

Escherichia coli emerged as the predominant uropathogen, followed by *Klebsiella*, *Pseudomonas*, and *Proteus* among Gram-negatives, and *Staphylococcus* and *Enterococcus* among Gram-positives. This pattern is consistent with regional and international reports confirming *E. coli* as the leading etiologic agent of both community- and hospital-acquired UTIs (Tilahun et al., 2024; Nwokolo et al., 2022; Shabohurira et al., 2025).

The organism's virulence arsenal - including fimbrial adhesins, siderophores, and biofilm-forming capacity facilitates persistent colonization within the urinary tract. The relatively higher recovery of Gram-positive cocci among HIV-infected participants echoes the observations of Kahsay et al. (2024) and Gebremedhin et al. (2025), who linked this shift to antibiotic pressure and altered host immunity. Conversely, Nakandi et al. (2025) found a higher prevalence of *Klebsiella* spp. in Uganda, reflecting possible nosocomial influence and differing antibiotic use patterns.

Fluoroquinolones (Ofloxacin, Ciprofloxacin) and β-lactam/β-lactamase inhibitor combinations (Augmentin) demonstrated the highest susceptibility rates, whereas Amoxicillin and Cotrimoxazole showed minimal activity. This mirrors the resistance patterns documented by Tilahun et al. (2024), Kahsay et al. (2024), and Nwokolo et al. (2022), who associated low Cotrimoxazole sensitivity with its prophylactic use in HIV management. Similarly,

Simeneh et al. (2022) and Kasew et al. (2022) reported growing multidrug resistance (MDR) among *E. coli* and *Klebsiella* isolates driven by plasmid-mediated extended-spectrum β-lactamase (ESBL) genes.

The meta-analysis by Asmare et al. (2024) confirmed that ESBL-producing *E. coli* has become endemic in Ethiopian hospitals, whereas Assefa et al. (2024) estimated pooled MDR prevalence at ≈ 58% among HIV-positive individuals nationwide.

The present study's slightly higher fluoroquinolone susceptibility may reflect local prescribing habits or temporal variations in antibiotic exposure. Nonetheless, global surveillance data from Li et al. (2022) highlight the rapid emergence of fluoroquinolone and β-lactam resistance across all continents. Contrasting evidence from Gebremedhin et al. (2025) indicated increasing resistance among *Enterococcus* and *Staphylococcus* isolates, suggesting species-specific divergence in resistance evolution.

Importantly, the comparable resistance patterns between HIV-positive and HIV-negative participants support the hypothesis of a shared community reservoir of resistant uropathogens. This aligns with Nwokolo et al. (2022) and Keenan et al. (2024), who emphasized that antimicrobial misuse in humans, animals, and the environment collectively drives resistance dissemination. These findings reinforce the need for a coordinated One Health AMR surveillance framework integrating clinical, environmental, and agricultural data.

The coexistence of high UTI prevalence and widespread antimicrobial resistance presents a dual challenge for clinicians and policymakers. Empirical therapy guided by outdated antibiotic protocols risks treatment failure. Consistent with Kasew et al. (2022) and Tilahun et al. (2024), this study underscores the necessity of periodic local antibiogram review, routine urine culture diagnostics in HIV care, and stringent antimicrobial stewardship. Furthermore,

Keenan et al. (2024) highlighted that structural determinants such as sanitation infrastructure and antibiotic regulation are critical to reducing MDR-UTI incidence. Addressing these upstream drivers, alongside patient-level education and adherence support, will be essential to curbing the AMR burden in both HIV-infected and general populations.

5. CONCLUSIONS

The study revealed that urinary tract infection is significantly more prevalent among HIV-positive individuals than among HIV-negative counterparts, confirming HIV infection as an important predisposing factor. Adults in the 30-39-year age group and females were disproportionately affected, reflecting the influence of sexual behavior, hormonal factors, and anatomical predisposition.

Escherichia coli remained the predominant uropathogen, followed by *Staphylococcus aureus* and *Klebsiella* species, consistent with patterns reported in other sub-Saharan African studies.

Fluoroquinolones and amoxicillin-clavulanate retained comparatively high effectiveness, while amoxicillin and cotrimoxazole were largely ineffective, underscoring the need for routine culture-guided therapy. The similarity in resistance profiles between HIV-positive and HIV-negative groups suggests circulation of common resistant strains within the community.

These findings emphasize the urgency of antimicrobial stewardship, routine surveillance of resistance trends, and integration of microbiological screening into HIV care programs. Future studies incorporating molecular typing of resistance determinants and longitudinal monitoring of ART-related immune recovery are recommended to better understand the dynamics of urinary tract infections and antimicrobial resistance in immunocompromised populations.

References

[1] Asmare, Z., Erkihun, M., Abebe, W., & Tamrat, E. (2024). Antimicrobial resistance and ESBL production in uropathogenic Escherichia coli: a systematic review and meta-analysis in Ethiopia. *JAC-Antimicrobial Resistance* 6(3), dlae068

[2] Assefa, M., & Girmay, G. (2024). Prevalence of co-trimoxazole resistance among HIV-infected individuals in Ethiopia: a systematic review and meta-analysis. *Frontiers in Medicine*, 11, 1418954

[3] Assefa, M., Amare, A., Tigabie, M., Girmay, G., Setegn, A., Wondmagegn, Y. M., ... & Biset, S. (2024). Burden of multidrug-resistant bacteria among HIV-positive individuals in Ethiopia: A systematic review and meta-analysis. *PloS ONE* 19(8), e0309418

[4] Assefa, M., Amare, A., Tigabie, M., Girmay, G., Setegn, A., Wondmagegn, Y. M., ... & Biset, S. (2024). Burden of multidrug-resistant bacteria among HIV-positive individuals in Ethiopia: A systematic review and meta-analysis. *PloS ONE* 19(8), e0309418

[5] Cheesbrough, M. (2005). District laboratory practice in tropical countries, part 2. Cambridge University Press.

[6] Dimani, B. D., Founou, R. C., Zemtsa, J. R., Mbossi, A., Koudoum, P. L., Founou, L. L., ... & Sone, L. H. E. (2023). Faecal carriage of multidrug-resistant and extended-spectrum β-lactamase-producing Enterobacterales in people living with HIV in Yaoundé, Cameroon. *Journal of Global Antimicrobial Resistance*, 35, 26-34

[7] Ejerssa, A. W., Gadisa, D. A., & Orjino, T. A. (2021). Prevalence of bacterial uropathogens and their antimicrobial susceptibility patterns among pregnant women in Eastern Ethiopia: hospital-based cross-sectional study. *BMC Women's Health*, 21(1), 291

[8] Gebremedhin, K. B., Medhin, G., Alemayehu, H., Bopegamage, S., Amogne, W., & Eguale, T. (2025). Prevalence, Risk Factors and Antimicrobial Resistance of Enterococci caused Urinary Tract Infection among People Living with HIV in Addis Ababa, Ethiopia. *Nigerian Medical Journal*, 66(2), 657-668

[9] Hantalo, A. H., Shano, A. K., & Meja, T. I. (2024). Correlation of CD4+ count and viral load with urinary tract infection and antimicrobial resistance pattern of bacterial uropathogens among HIV patients in Wolaita Sodo, South Ethiopia. *Frontiers in Microbiology*, 15, 1363287

[10] Kahsay, T., Gebrehiwot, G. T., Gebreyohannes, G., Tilahun, M., Gessese, A., & Kahsay, A. (2024). Antimicrobial susceptibility patterns of urinary tract infections causing bacterial isolates and associated risk factors among HIV patients in Tigray, Northern Ethiopia. *BMC Microbiology*, 24(1), 148

[11] Kasew, D., Desalegn, B., Aynalem, M., Tila, S., Diriba, D., Afework, B., ... & Baynes, H. W. (2022). Antimicrobial resistance trend of bacterial uropathogens at the university of Gondar comprehensive specialized hospital, northwest Ethiopia: A 10 years retrospective study. *PloS One*, 17(4), e0266878

[12] Li, X., Fan, H., Zi, H., Hu, H., Li, B., Huang, J., ... & Zeng, X. (2022). Global and regional burden of bacterial antimicrobial resistance in urinary tract infections in 2019. *Journal of Clinical Medicine*, 11(10), 2817

[13] Keenan, K., Papathomas, M., Mshana, S.E. *et al.* (2024). Intersecting social and environmental determinants of multidrug-resistant urinary tract infections in East Africa beyond antibiotic use. *Nat Commun* 15, 9418. https://doi.org/10.1038/s41467-024-53253-x

[14] Mareș, C., Petca, R. C., Popescu, R. I., Petca, A., Mulțescu, R., Bulai, C. A., ... & Jinga, V. (2024). Update on urinary tract infection antibiotic resistance - a retrospective study in females in conjunction with clinical data. *Life*, 14(1), 106

[15] Morpeth, S. C., Thielman, N. M., Ramadhani, H. O., Hamilton, J. D., Ostermann, J., Kisenge, P. R., ... & Crump, J. A. (2008). Effect of trimethoprim-sulfamethoxazole prophylaxis on antimicrobial resistance of fecal Escherichia coli in HIV-infected patients in Tanzania. *JAIDS Journal of Acquired Immune Deficiency Syndromes*, 47(5), 585-591

[16] Murray, C. J., Ikuta, K. S., Sharara, F., Swetschinski, L., Aguilar, G. R., Gray, A., ... & Tasak, N. (2022). Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis. *The Lancet*, 399(10325), 629-655

[17] Nakandi, R. M., Kakeeto, P., Kihumuro, R. B., Kanyike, A. M., Nalunkuma, R., Lugwana, R. S., ... & Ssebuufu, R. (2025). Antibiotic susceptibility patterns of bacterial uropathogens at a private tertiary hospital in Uganda: a retrospective study. *BMC Infectious Diseases*, 25(1), 605

[18] Nwokolo, C. J., Ugwu, M. C., Ejikeugwu, C. P., Iroha, I. R., & Esimone, C. O. (2022). Incidence and antibiotic susceptibility profile of uropathogenic Escherichia coli positive for extended spectrum β-lactamase among HIV/AIDS patients in Awka metropolis, Nigeria. *Iranian Journal of Microbiology*, 14(3), 334

[19] Olaru, I. D., Ferrand, R. A., Chisenga, M., Yeung, S., Macrae, B., Chonzi, P., ... & Kranzer, K. (2021). Prevalence of ESBL-producing Escherichia coli in adults with and without HIV presenting with urinary tract infections to primary care clinics in Zimbabwe. *JAC-Antimicrobial Resistance*, 3(2), dlab082

[20] Simeneh, E., Gezimu, T., Woldemariam, M., & Alelign, D. (2022). Magnitude of multidrug-resistant bacterial uropathogens and associated factors in urinary tract infection suspected adult HIV-positive patients in southern Ethiopia. *The Open Microbiology Journal*, 16. https://doi.org/10.2174/18742858-v16-e2208180

[21] Shabohurira, A., Eilu, E., Sankarapandian, V., Muhwezi, R., & Makeri, D. (2025). Prevalence, bacterial profile and factors associated with urinary tract infections among people living with HIV in Africa: a systematic review and meta-analysis. *Discover Public Health*, 22(1), 50

[22] Tamma PD, Heil EL, Justo JA, Mathers AJ, Satlin MJ, Bonomo RA. (2024). Infectious Diseases Society of America 2024 Guidance on the Treatment of Antimicrobial-Resistant Gram-Negative Infections. *Clin Infect Dis.* ciae403. https://doi.org/10.1093/cid/ciae403

[23] Tessema, N. N., Ali, M. M., & Zenebe, M. H. (2020). Bacterial associated urinary tract infection, risk factors, and drug susceptibility profile among adult people living with HIV at Haswassa University Comprehensive Specialized Hospital, Hawassa, Southern Esthiopia. *Scientific Reports*, 10(1), 10790

[24] Tigabie, M., Birhanu, A., Assefa, M., Girmay, G., & Tadesse, K. (2025). Extended-spectrum β-lactamase-producing Enterobacterales among people living with human immunodeficiency virus across the globe: A systematic review and meta-analysis. *PLoS One*, 20(6), e0321873

[25] Tilahun, M., Fiseha, M., Alebachew, M., Gedefie, A., Ebrahim, E., Tesfaye, M., ... & Dessie, T. (2024). Uro-pathogens: Multidrug resistance and associated factors of community-acquired UTI among HIV patients attending antiretroviral therapy in Dessie Comprehensive Specialized Hospital, Northeast Ethiopia. *PloS One*, 19(5), e0296480