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Antibiotic Resistance Profile of Selected Uropathogenic Bacteria from Female Patients Attending Hospitals in Parts of Southern Taraba, Nigeria

Brown Samuel Tamuno Cockeye, Agwaranze Dawn Ify, James Samuel Pelentovun, Yusuf Precious Wama
Federal University Wukari, Taraba State, Nigeria
samuelpjames0@gmail.com

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Abstract

Urinary tract infections (UTIs) remain a major public health concern among women because of their high prevalence, recurrent occurrence, and rising antimicrobial resistance. This cross-sectional study assessed the prevalence, molecular characteristics, antibiotic susceptibility patterns, and associated risk factors of uropathogenic bacteria among 300 female patients aged 15–55 years in Wukari, Donga, and Ibi Local Government Areas of Southern Taraba. Midstream urine samples were collected and analyzed using standard microbiological procedures. Phenotypic identification was performed for all isolates, while molecular characterization using 16S rRNA gene sequencing was limited to *Staphylococcus aureus* (1%) and the opportunistic pathogens *Brucella intermedia* and *Alcaligenes faecalis* (0.3% each) because of the unusual phenotypic characteristics of the primary isolates. The prevalence of culture-positive UTIs was 13.6%, with *Escherichia coli* (6.3%) identified as the predominant pathogen, followed by *Klebsiella pneumoniae* (3%) and *Proteus* spp. (2.3%). Antibiotic susceptibility testing showed high resistance among Gram-negative isolates to ampicillin, gentamicin, ceftriaxone, and ciprofloxacin,

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while 12.6% of isolates exhibited multidrug resistance (MDR). Socio-demographic variables, including age, educational level, occupation, and residence, were significantly associated with UTIs ($p < 0.05$), whereas marital status and religion were not ($p > 0.05$). Sexual activity emerged as a significant behavioral risk factor, and the type of medication used, improper antibiotic use, and international travel were significantly associated with antibiotic resistance ($p < 0.05$). Clinically, hematuria and urinary pain or burning sensation were significantly associated with infection ($p < 0.05$). The study concludes that UTIs and multidrug-resistant uropathogens constitute an important health burden in this population. These findings contribute context-specific evidence on pathogen distribution, resistance patterns, and risk factors, and underscore the need for continuous surveillance, targeted health education, improved hygiene practices, and rational antibiotic stewardship.

Keywords: Urinary Tract Infections; Uropathogenic Bacteria; Antimicrobial Resistance; Multidrug Resistance; Women's Health

INTRODUCTION

Urinary tract infections (UTIs) occur when pathogenic bacteria invade any component of the urinary system, including the kidneys, ureters, bladder, or urethra, resulting in inflammatory conditions such as urethritis, cystitis, or pyelonephritis (Jenny and Kathryn, 2024). UTIs are among the most common infections affecting women across different stages of life. Their high prevalence in females is largely attributable to anatomical and physiological factors of the female lower urinary tract, as well as its close proximity to the reproductive organs. In particular, the relatively short length of the female urethra facilitates easier ascension of pathogenic microorganisms into the urinary tract, thereby increasing susceptibility to bacterial colonization and subsequent infection when compared to males (Krzysztof *et al.,* 2021). Globally, urinary tract infections affect approximately 150 million individuals each year, making them one of the most prevalent bacterial infections and a significant public health concern due to their high morbidity rates and substantial associated healthcare costs (Majumder *et al.,* 2022). According to available estimates, nearly 50% of women worldwide are expected to experience at least one episode of urinary tract infection during their lifetime, with the highest prevalence observed among women aged 16–64 years (Tandogdu *et al.,* 2016). Urinary tract infections can be caused by a wide range of bacterial pathogens, including both Gram-positive and Gram-negative organisms.

Among the Gram-positive bacteria, coagulase-positive staphylococci and *Staphylococcus aureus* are commonly implicated in UTIs (Navidinia *et al.,* 2021). *Staphylococcus aureus* is a well-established human pathogen responsible for diverse clinical infections. Although it accounts for only about 0.5-6% of reported UTI cases, infections caused by *S. aureus* can be severe and potentially life-threatening if not promptly and appropriately treated (Alshomrani *et al.,* 2023). Gram-negative uropathogens commonly implicated in urinary tract infections include *Escherichia coli, Klebsiella* species, *Pseudomonas* species, *Enterobacter* species, and *Proteus* species. These organisms are among the leading bacterial agents associated with UTIs (Saeed *et al.,* 2017). A study by Gessese *et al.* (2017) reported that Escherichia coli is the predominant Gram-negative pathogen causing urinary tract infections, accounting for approximately 60–70% of cases, followed by Klebsiella species (10%), Proteus species (5-10%), and Pseudomonas species (2-5%). Urinary tract infections can, although rarely, be caused by Brucella species, particularly Brucella intermedia. Genitourinary involvement is a recognized complication of brucellosis but is not among the most common clinical presentations. Nonetheless, the organism may be excreted in urine and can infect various components of the urogenital system, resulting in diverse urological manifestations (Ledwaba et al., 2020). Cases of urinary tract infections and cystitis caused by Alcaligenes faecalis have been reported in India, with many isolates demonstrating resistance to multiple classes of antibiotics (Momtaz *et al*., 2018).Though, *Alcaligenes faecalis* is considered an opportunistic pathogen, and managing infections caused by this organism can be challenging because it frequently exhibits resistance to multiple antibiotic groups, including antipseudomonal penicillins, cephalosporins, carbapenems, aminoglycosides, and quinolones (Moscoso, 2023).

Urinary tract infections commonly occur among hospitalized patients, individuals with diabetes, those with anatomical abnormalities of the urinary tract, and patients with underlying neurological conditions, as these factors can impair normal urine flow (Rezia et al., 2020). Several predisposing factors have been identified, including female gender, chronic kidney disease, advanced age, prolonged hospitalization, debilitating underlying illnesses, prior antibiotic use, and repeated urinary catheterization (Ibrahim et al., 2020; Rezia et al., 2020). Women are particularly susceptible to UTIs compared to men, largely due to their shorter urethra, which allows pathogens easier access to the bladder, and because sexual activity increases exposure to uropathogenic microorganisms (Ibrahim et al., 2020).

Although antibiotics remain the cornerstone of treatment for bacterial infections, their overuse, misuse, prolonged administration, or empirical application has significantly driven the growing emergence of antibiotics resistance. As a result, uropathogens resistant to commonly prescribed antibiotics are increasingly being reported worldwide (Oparaugo *et al.,* 2021). Gaining insight into patterns of antimicrobial resistance of bacterial pathogens is crucial for selecting appropriate antibiotics and ensuring effective treatment outcomes. When bacteria are able to resist medications meant to combat them, a condition known as antimicrobial resistance develops, rendering treatment useless (Limmathurotsakul *et al.,* 2019; Nuhu *et al.,* 2020).

Multidrug-resistant (MDR) uropathogenic bacteria have been reported as etiological agents of urinary tract infections worldwide, and the challenge is worsening due to the limited development of new antibiotics. Multiple drug resistance (MDR) is a prevalent feature of uropathogenic bacteria like *Klebsiella pneumoniae* and *Escherichia coli*, which presents a global health risk. Multidrug resistance occurs when a bacterial organism exhibits resistance to two or more antimicrobial agents (Nuhu *et al.,* 2020).

The emergence of antibiotic resistance has been linked to the indiscriminate and prolonged use of antibiotics in healthcare settings (Imarenezor *et al*., 2021). This concerning trend highlights the importance of understanding the antibiogram patterns of uropathogens to guide the appropriate selection of antibiotics for UTI management and to prevent further misuse of antimicrobial drugs (Shinggu *et al.,* 2023). Identifying the causative organisms of urinary tract infections and determining their antimicrobial susceptibility patterns is essential, particularly in light of the increasing prevalence of antibiotic-resistant uropathogens (Nuhu *et al.,* 2020). The failure of first-line antibiotics often requires the use of more expensive or broad-spectrum drugs, leading to prolonged hospital stays and extended treatment courses. This not only escalates healthcare costs but also places a heavier economic burden on households and the wider community. As a result, antibiotic resistance poses a significant challenge to the effective practice and progress of modern medicine (Imarenezor *et al.,* 2020).

Antimicrobial resistance patterns exhibit significant historical and geographical variation (Belete *et al.,* 2019). To date, few studies have investigated the antibiotic resistance profiles of urinary tract infections (UTIs) in our region, particularly among female patients in Southern Taraba aged 15 to 55 years. Therefore, this study aimed to assess the antibiotic

resistance patterns of selected gram-negative uropathogens within this defined age group of female patients.

MATERIALS AND METHODS

Study Area

This study was conducted in parts of Southern Taraba. Southern Taraba is made up of five Local Government Areas (LGAs), namely; Wukari, Donga, Ibi, Takum and Ussa LGA. But this research was conducted in three LGAs, namely; Wukari, Donga and Ibi LGA. Wukari Local Government Area (LGA) is situated between latitude 7°55'42"N and longitude 9°47'59"E, covering an area of 4,308 km² with a population of 241,546 (Imarenezor *et al.,* 2023). Donga Local Government Area (LGA) is headquartered in the town of Donga, situated along the Donga River at coordinates 7°43'00"N 10°03'00"E. The LGA has an estimated population of approximately 177,900 (Citypopulation.de, 2022). Ibi Local Government Area (LGA), located in southern Taraba State, is one of the state's 16 LGAs. It borders Plateau State to the north, Nasarawa State to the west, Gassol LGA to the east, and Wukari LGA to the south, covering a total area of 2,672 km² (Benjamin and Williams, 2022).

Study Population

This study population comprises all female patients aged 15 to 55 attending the study center who present with a presumptive clinical diagnosis of urinary tract infection, characterized by symptoms such as dysuria, urinary frequency, fever, and lower abdominal pain. Additionally, pregnant women attending the antenatal clinic (ANC) during the study period are included. Patients currently taking antibiotics are required to discontinue use at least 48 hours prior to participation. A freshly voided mid-stream urine (MSU) specimen yielding bacterial growth of $\geqslant 10^5$ colony-forming units per milliliter (CFU/mL) is considered indicative of a positive culture.

Study Design

This study employed a cross-sectional design. Urine samples were collected from female patients receiving medical care at hospitals in Wukari, Donga, and Ibi Local Government Areas (LGAs). Participants' demographic information, along with factors

associated with urinary tract infections (UTIs) and contributors to antibiotic resistance, were obtained using a structured questionnaire.

Determination of Sample Size

The required sample size for this study was determined using the single population proportion formula: $N = \frac{Z^2P(1-P)}{d^2}$, where P represents a prevalence of 18.8%, N is the calculated sample size, Z is the standard score for a 95% confidence interval (1.96), d is the margin of error (5%), and q = 1 – P = 0.812. Based on this formula, the initial calculated sample size was 234, which was increased to 300 to account for potential non-responses, as recommended by Amrutha *et al.* (2023).

Ethical Consideration

Prior to data collection, an introductory letter from the Department of Microbiology, Federal University Wukari, was presented to the respective hospitals to obtain ethical approval. The aim and objectives of the study were clearly explained to all participants before the interviews. Verbal informed consent was obtained from the participants and/or their caregivers. Confidentiality was assured by informing respondents that no identifiable information would be disclosed without their explicit consent.

Collection of Samples

A total of 300 clean-voided midstream urine (MSU) samples (10–20 mL) were collected from suspected female patients presenting with clinical features suggestive of urinary tract infection, including dysuria, urinary frequency, urgency, suprapubic pain, or cloudy urine. Pregnant women who met these criteria were also included. Samples were collected in wide-mouthed sterile containers, properly labeled, and stored at 2-8°C before being transported to the microbiology laboratory within four hours of collection for bacteriological analysis. Laboratory processing was carried out in accordance with the method described by Imarenezor *et al.* (2017), with slight modifications. To minimize contamination, participants received clear instructions on proper midstream urine collection prior to sampling.

Isolation and Identification of The Bacterial Uropathogens

Isolation

Following standard microbiological procedures, 0.5 mL of each urine sample was aseptically inoculated onto Blood Agar, Cysteine Lactose Electrolyte Deficient (CLED) agar, and MacConkey agar. The inoculated plates were incubated aerobically at 37 °C for 24 hours and examined for bacterial growth. Significant bacteriuria, indicative of urinary tract infection, was defined as a bacterial colony count of $\geqslant 10^5$ colony-forming units per milliliter (CFU/mL), in accordance with the criteria described by Gessese *et al.* (2017) and Majumder *et al.* (2022).

Characterization and Identification of Bacterial Isolates

Bacterial isolates were phenotypically characterized using standard microbiological identification methods. Initial classification was based on Gram staining to differentiate Gram-negative from Gram-positive organisms. Further identification was achieved through the assessment of biochemical reaction patterns using citrate utilization, catalase, oxidase, indole production, and Triple Sugar Iron (TSI) agar tests. The collective results of these biochemical tests were used to characterize and identify the uropathogenic bacterial isolates. Final identification was confirmed by comparing the observed phenotypic characteristics with standard descriptions in Bergey's Manual of Determinative Bacteriology (Williams and Hakam, 2016).

Molecular Characterization of Bacteria Isolates

Molecular analysis of the bacterial isolates involved genomic DNA extraction using a standard spin-column purification method, after which the DNA was either used immediately or stored at −20 °C. The 16S rRNA gene was amplified by polymerase chain reaction (PCR) using universal bacterial primers under optimized cycling conditions. PCR products were confirmed by agarose gel electrophoresis and visualized under ultraviolet light, with fragment sizes estimated using a molecular weight marker. The amplified products were subsequently sequenced using the Sanger sequencing method on an automated ABI 3730XL DNA analyzer. Sequence quality assessment and assembly were performed using appropriate bioinformatics software, and taxonomic identification of the isolates was achieved by comparing the obtained sequences with those in the NCBI

database using the Basic Local Alignment Search Tool (BLAST), with identification based on the highest sequence similarity scores (Bhutia *et al*., 2021).

Antibiotic Susceptibility Test (AST)

Antibiotic susceptibility testing of the selected uropathogenic bacterial isolates was performed using the Kirby-Bauer disc diffusion method on Mueller–Hinton agar in accordance with the Clinical and Laboratory Standards Institute (CLSI) guidelines (CLSI, 2024). The antibiotics tested included ampicillin (30 μg), augmentin (30 μg), gentamicin (10 μg), ciprofloxacin (5 μg), nitrofurantoin (300 μg), norfloxacin (10 μg), ceftriaxone (10 μg), cefuroxime (10 μg), cotrimoxazole (1.25 μg), and ceftazidime (10 μg). Zones of inhibition were measured in millimeters, and the susceptibility profiles of the isolates were interpreted as susceptible, intermediate, or resistant according to CLSI 2024 interpretive criteria.

Assessment of Risk Factors

Risk factors for urinary tract infections, as well as factors contributing to antibiotic resistance, were assessed using a structured questionnaire written in English to collect participants' demographic and related information. For individuals who were unable to read or write, the questions were read aloud, and any items that were unclear were explained to ensure accurate understanding and responses.

Statistical Analysis

Data collected from the questionnaire and laboratory analyses were entered and managed using Microsoft Excel and analyzed with R statistical software. Descriptive statistics were used to summarize the variables, and the Chi-square test was applied to compare proportions between positive and negative cases. A p-value of < 0.05 was considered statistically significant.

RESULTS AND DISCUSION

The biochemical identification of selected bacterial uropathogens among female patients is presented in table 4.1. Out of the samples examined, most of the isolates were negative to indole test except *Escherichia coli,* which was positive to indole test. *Alcaligenes faecalis, Brucella intermedia* were oxidase positive unlike other selected isolates in this study. Gram staining revealed that the isolates consisted of Gram-negative bacilli (rods) and

Gram-positive cocci. The probable organisms in the isolates were *Escherichia coli, Proteus app., Klebsiella pneumoniae, Alcaligenes faecalis, Brucella intermedia* and *Staphylococcus aureus.*

Table 1. Biochemical identification of uropathogenic bacteria from female patients cross the study centers

S/No.	Gram Rxn	Biochemical tests					Probable organism
		CAT	IND	CIT	TSI RXN	OXIDASE	
1.	Gram- negetive bacilli	+	+	-	Acid Slant/acid butt with gas production	-	*Escherichia coli*
2.	Gram- negative bacilli	+	-	+	alkaline slant/ acid butt with gas production	-	*Proteus* species
3.	Gram- negative bacilli	+	-	+	Acid slant/acid butt with gas production	-	*Klebsiella* species
4.	Gram- negative Rods	+	-	+	Alkaline slant/acid butt without gas and H_2S production	+	*Alcaligenes* species
5.	Gram negative Short rods	+	-	+	Alkaline slant/alkaline butt without gas production	+	*Brucella* species
6.	Gram positive cocci	+	-	+	Not applicable	-	*Staphylococcus* species

Table 1 presents the profile of culture-positive uropathogenic bacteria among the study participants. A total of 300 female patients were screened, and urine culture tests revealed that 41 (13.6%) samples were positive for bacterial growth, while 259 (86.3%) showed no growth. Among the Gram-negative uropathogens, *Escherichia coli* was the most prevalent, detected in 19 (6.3%) samples, followed by *Klebsiella pneumoniae* in 10 (3%), *Proteus* spp. in 7 (2.3%), and both *Brucella intermedia* and *Alcaligenes faecalis* in 1 (0.3%) each. *Staphylococcus aureus* (1%) was the only Gram-positive bacterium identified.

The higher prevalence of *E. coli* in this study may be attributed to factors such as poor personal hygiene, use of contaminated toilet facilities, and the anatomical proximity of the female urethra to the anus, where *E. coli* commonly colonizes. Similar findings have been reported by Nuhu *et al.* (2020) in Sokoto, Nigeria, and Majumder *et al.* (2020) in Bangladesh, who also identified *E. coli* as the predominant uropathogen. Additionally, Shinggu *et al.* (2023) in Taraba, Nigeria, and Khan *et al.* (2020) reported *E. coli* prevalence of 69.7% among UTI patients. While these findings differ from those of Mistry *et al.* (2022) and Basset *et al.* (2025), who reported *Klebsiella pneumoniae* as the predominant uropathogen in urinary tract infections.

The detection of *Brucella intermedia* (0.3%) and *Alcaligenes faecalis* (0.3%) in the urine samples represents a notable observation in this study. These organisms are uncommon causative agents of urinary tract infections. However, the findings are consistent with reports by Furuya *et al.* (2025) and Momtaz *et al.* (2018), which identified *B. intermedia* and *A. faecalis* as emerging opportunistic pathogens capable of causing UTIs in

immunocompetent individuals. Their opportunistic nature and rarity in the human urinary tract likely account for the low prevalence observed in this study.

Table 2. Profile of the selected uropathogenic bacteria isolates across the study centres

S/N	Bacterial Isolates	Total Positive (n = 300)	Percentage (%)
1.	Escherichia coli	19	6.3
2.	Proteus mirabilis	7	2.3
3.	Klebsiella pneumonia	10	3.0
4.	Alcaligenes faecalis	1	0.3
5	Brucella intermedia	1	0.3
6.	Staphylococcus aureus	3	1.0
	Total	41	13.6

The molecular characterization of selected uropathogenic isolates using 16S rRNA gene sequencing confirmed their identity and showed high similarity to reference sequences in GenBank. Specifically, the isolates matched *Brucella intermedia* strain ZJ499 (80.15%), *Alcaligenes faecalis* strain T17 (87.5%), and *Staphylococcus aureus* strain 19KS01SA08 (93.33%), as summarized in Table 3. These findings corroborate the phenotypic identification from biochemical testing, which suggested that the predominant uropathogens in the study included *Escherichia coli, Proteus* spp., *Klebsiella pneumoniae, Alcaligenes faecalis, Brucella intermedia*, and *Staphylococcus* aureus.

It is important to note that molecular analysis was conducted on selected isolates rather than all recovered uropathogens, serving as a confirmatory approach to validate phenotypic identification. The molecular data generated in this study provide a foundation for future research on the genetic diversity, evolutionary relationships, and functional potential of microbial communities within the urinary tract. This integrated approach, combining phenotypic and molecular analyses, strengthens the reliability of uropathogen identification and enhances understanding of their epidemiology in the study population.

Table 3. Molecular identification of bacteria isolates from urine sample using basic local alignment search tool

S/N	Description	Scientific Name	Max Score	Total Score	Query Cover (%)	E value	Per. ident	Acc. Len	Accession number
	Brucella intermedia strain ZJ499 chromosome 1, complete sequence	Brucella intermedia	363	363	71	1e-95	80.15	2682891	NZ_CP061039.1
2	Alcaligenes faecalis strain T17 chromosome, complete genome	Alcaligenes faecalis	732	2197	91	0	87.5	4277602	NZ_CP092182.1

S/N	Description	Scientific Name	Max Score	Total Score	Query Cover (%)	E value	Per. ident	Acc. Len	Accession number
3	Staphylococcus aureus strain 19KS01SA08 chromosome, complete genome	Staphylococcus aureus	65.8	394	23	3e-06	93.33	2754846	CP127638.1

Table 4 presents the antibiotic resistance profiles of the selected uropathogenic bacterial isolates. Among the isolates, *Escherichia coli*, the most frequently encountered uropathogen, exhibited the highest resistance to ampicillin (12; 63.15%). The predominant Gram-positive isolate, *Staphylococcus aureus*, showed the highest resistance rates to ampicillin, augmentin, and ceftriaxone (2; 66.66% each). Among all Gram-negative uropathogens, the highest and most concerning resistance rates were observed for ampicillin, gentamicin, ceftriaxone, and ciprofloxacin.

Notably, 12.6% of Gram-negative isolates exhibited multidrug resistance (MDR) to ampicillin, gentamicin, ceftriaxone, and ciprofloxacin. This observation aligns with the findings of Gessese *et al.* (2017) in Ambo Town, Central Ethiopia, and may be linked to the production of extended-spectrum beta-lactamases (ESBLs) by many Gram-negative bacteria, which likely contributed to the observed MDR (Belete, 2020). Conversely, this finding differs from reports from Addis Ababa, where most Gram-negative isolates were highly susceptible to gentamicin.

Table 4. Antibiotic resistance profile of the selected uropathogenic bacterial isolates

Antibiotic Agent	Number of Resistant Isolates (%)					
	Escherichia coli (n = 19)	Proteus Spp. (n = 7)	Klebsiella pneumonia (n = 10)	Alcaligenes faecalis (n= 1)	Brucella intermedia (n=1)	Staphylococcus aureus (n = 3)
Augmentin (30 µg)	1(5.26)	0(0.0)	1(10.0)	0(0.0)	0(0.0)	2(66.66)
Gentamycin (10 µg)	11(57.89)	2(28.57)	5(50.0)	1(100)	0(0.0)	1(33.33)
Cefurozine (10 µg)	5(26.31)	1(14.28)	3(30.0)	0(0.0)	1(100)	0(0.0)
Ceftriaxone (10 µg)	8(42.10)	3(42.85)	3(30.0)	0(0.0)	0(0.0)	2(66.66)
Ceftazidime (10 µg)	0(0.0)	2(28.57)	0(0.0)	1(100)	1(100)	0(0.0)
Nitrofurantoin (300 µg)	3(15.78)	0(0.0)	1(10.0)	0(0.0)	0(0.0)	0(0.0)
Ciprofloxacin (5 µg)	1(5.26)	3(42.85)	2(20.0)	1(100)	0(0.0)	1(33.33)
Ampicillin (30	12(63.15)	4(57.14)	7(70.0)	1(100)	1(100)	2(66.66)

µg)						
Cotrimoxazole (1.25 µg)	1(5.26)	1(14.28)	0(0.0)	0(0.0)	0(0.0)	1(33.33)
Norfloxacin (10 µg)	1(5.26)	0 (0.0)	1(10.0)	0(0.0)	0(0.0)	1(33.33)

Table 5 presents the demographic characteristics of the study participants. The socio-demographic variables assessed included age, educational level, marital status, occupation, residence, and religion. Among these, age, educational level, occupation, and residence showed a statistically significant association with urinary tract infections ($p < 0.05$). This may be attributed to limited knowledge and awareness about UTIs among affected female patients, including understanding of transmission, prevention, and treatment. Additionally, poor sanitation and challenges with water quality could compromise personal hygiene, further increasing the risk of infection.

Table 5. Socio-demographic characteristics

	Bacterial	**Culture (%)**			
Variables	**Positive= 41(14)**	**Negative=259(86)**	**Total**	**X^2**	**P-value**
Age in years					
15-25	9(14)	55(86)	64	13.198	0.004
26-35	14(15)	82(85)	96		
36-45	12(14)	73(86)	85		
46-55	6(11)	49(89)	55		
Educational Level					
Primary	10(15)	56(85)	66	75.181	3.314e-16
Secondary	13(10)	111(90)	124		
Tertiary	15(16)	80(84)	95		
None	3(20)	12(80)	15		
Marital status					
Married	25(14)	156(86)	181	2.4344	0.48
Single	12(11)	92(89)	104		
Divorced	3(30)	7(70)	10		
Widowed	1(20)	4(80)	5		
Occupation					
Farmer	13(13)	86(87)	99	46.557	4.317e-10
Trader	15(13)	105(87)	120		
Civil servant	12(17)	60(83)	72		
Applicant	1(11)	8(89)	9		

	Bacterial	Culture (%)			
Variables	**Positive= 41(14)**	**Negative=259(86)**	**Total**	**X^2**	**P-value**
Residence					
Urban	18(15)	100(85)	118	158.1	2.2e-16
Sub-urban	10(13)	67(87)	77		
Rural	13(12)	92(88)	105		
Religion					
Christian	29(14)	172(86)	201	6.71	0.08
Islamic	12(13)	77(87)	89		
Traditional	0(0)	10(100)	10		
Others	0(0)	0(0)	0		

Key;

e-10 = 0.00000000004 while, e-16 = 0.00000000000000002. Same to others but last figure might vary

Table 6 assessed risk factors associated with urinary tract infections. Most variables, including awareness of UTIs, number of sexual partners, presence of diabetes or a weakened immune system, and use of contraceptives, showed $p > 0.05$, indicating no statistically significant association with UTIs in this study population. This suggests that these factors were not major contributors to infection risk in the study area, which differs slightly from previous findings by Ahmad *et al.* (2021) and Hussein *et al.* (2023). While sexual activity showed a statistically significant association ($p<0.05$) with UTIs, highlighting its role as an important risk factor. This is consistent with previous research by Mishra *et al.* (2018), which reported that 75-90% of bladder infections in young sexually active women are linked to sexual activity, with the risk of infection increasing with frequency of intercourse.

Table 6. Assessment of the risk factors associated with urinary tract infection (UTI)

	Bacterial	Culture (%)			
Variables	**Positive=41(14)**	**Negative=259(86)**	**Total**	**X^2**	**P-value**
Heard of UTI					
Yes	26(13)	175(87)	201	0.12022	0.72
No	15(14)	84(86)	109		
Sexually Active					
Yes	41(14)	259(86)	300	NaN	NA
No	0(0)	0(0)	0		

Sex partners					
Single	36(14)	223(86)	259	0.0025567	0.95
Multiple	5(12)	36(88)	41		
Pregnancy					
Yes	18(14)	114(86)	132	6.7696e-30	1.0
No	23(14)	145(86)	168		
Hospitalized/medical procedure					
Yes	31(15)	182(85)	213	0.2651	0.60
No	10(11)	77(89)	87		
Diabetic/weak immune system					
Yes	27(17)	128(83)	155	3.1979	0.07
No	14(10)	131(90)	145		
Practice good hygiene					
Yes	22(13)	152(87)	174	0.1900	0.06
No	19(15)	107(85)	126		
Use of contraceptive					
Yes	23(14)	136(86)	159	0.067243	0.79
No	18(13)	123(87)	141		

Key: NAN = None-available number, NA = None-available

Table 7 presents the assessment of risk factors contributing to antibiotic resistance. The analysis identified type of medication used, antibiotic misuse, and international travel as factors significantly associated with antibiotic resistance ($p < 0.05$). These associations may be attributed to inappropriate dosing or use of antibiotics and herbal remedies, frequent use of clinically unsuitable antibiotics, poor adherence to prescribed treatments, and exposure to resistant pathogens during travel to regions with high prevalence of antibiotic resistance. These findings are consistent with previous studies by Chen *et al.* (2021) and Belete *et al.* (2019).

Table 7. Assessment of the risk factors contributing to antibiotic resistant

	Bacterial	**Culture (%)**			
Variables	**Positive=41(14)**	**Negative=259(86)**	**Total**	**X**	**P value**
Recently treated with antibiotic					
Yes	33(15)	181(85)	214	1.4623	0.22
No	8(9)	178(91)	86		
Currently on medication					
Yes	4(11)	34(89)	38	0.117	0.73
No	37(14)	226(86)	262		

Types of medication					
Antibiotic	28(15)	163(85)	191	179.7	2.2e-16
Herbs	1(3)	35(97)	36		
Both	12(16)	61(84)	73		
Recent antibiotic prescription					
Yes	33(26)	196(74)	129	0.2264	0.63
No	8(11)	63(89)	71		
Antibiotic misuse					
Yes	23(16)	118(84)	141	1.1832	0.02
No	18(11)	141(89)	159		
Hospitalized in the past year					
Yes	37(14)	224(86)	261	0.17208	0.67
No	4(10)	35(90)	39		
Travel internationally					
Yes	5(26)	14(74)	19	127.35	2.2e-16
No	36(13)	245(87)	281		
Consume antibiotic treated food					
Yes	17(12)	120(88)	137	0.1704	0.67
No	24(15)	139(85)	163		

The assessment of clinical features (symptoms) is shown in Table 8. Blood in urine ($p = 0.0030$) and urinary pain/sensation ($p = 0.0031$) were identified as the most statistically significant symptoms of urinary tract infection.

A study by Rajanbir and Rajinder (2021) reported that symptoms of UTIs include frequent urination, burning sensation during urination, lower abdominal pain even with small urine volumes, hematuria, and unusually strong-smelling urine. These findings align with the present study, particularly regarding blood in the urine and urinary pain/burning sensation ($p = 0.003$), which showed a statistically significant association with UTI symptoms.

Table 8. Assessment of clinical features (symptoms)

	Bacterial	**Culture (%)**			
Variables	**Positive = 41(14)**	**Negative=259(86)**	**Total**	**X^2**	**P-value**
Urinary frequency					
Yes	19(18)	89(82)	108	1.7151	0.19
No	22(11)	170(89)	192		
Urinary Pain					
Yes	31(19)	128(81)	159	8.7229	0.0031

	Bacterial	Culture (%)			
Variables	**Positive = 41(14)**	**Negative=259(86)**	**Total**	**X^2**	**P-value**
No	10(7)	131(93)	141		
Blood in urine					
Yes	17(25)	50(75)	67	8.7829	0.0030
No	24(10)	209(90)	233		
Abdominal pain					
Yes	35(27)	196(73)	131	1.3695	0.24
No	6(9)	63(91)	69		
Fever					
Yes	33(14)	203(86)	236	0.010243	0.91
No	8(13)	56(87)	64		
Urinary Incontinence					
Yes	12(19)	52(81)	64	1.2762	0.25
No	29(21)	207(79)	136		

CONCLUSION

This study highlights that urinary tract infections among women in Southern Taraba are influenced by both biological and behavioral factors, and the growing prevalence of antibiotic-resistant uropathogens poses a significant public health challenge. Effective management of UTIs requires targeted interventions, including improved hygiene practices, rational use of antibiotics, and continuous monitoring of resistance patterns. Addressing these factors is essential to reduce infection rates, limit the spread of multidrug-resistant pathogens, and improve overall reproductive and urinary health in the population.

Recommendations

1. Further research should be carried out on the identification of genes that confer antibiotic resistance in bacterial uropathogens.
2. The periodic evaluation of the frequency of uropathogens with their antibiotic resistance pattern is recommended in different geographical locations for therapeutic advice and antimicrobial prevention.

3. The implementation of molecular tests as a means of confirming diagnosis in the study area is recommended to avoid misidentification/wrong identification of bacterial uropathogens.

4. Effective infection control measures to prevent the spread of resistant bacteria should be implemented.

5. Educate the public about the risks of antibiotic resistance and the importance of responsible antibiotic use.

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