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Research

Antibiotic susceptibility of uropathogens: a 3-year retrospective study at Ho Teaching Hospital of Ghana

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Abstract

Background Urinary tract infection (UTI) remains one of the most treated infections in primary healthcare over the last two decades. The infection is treated with antibiotics. However, there have been reported cases of increasing antibiotic resistance globally, limiting the available antibiotics for the treatment of the infection. The study aimed to determine the frequency of bacterial urinary tract infections and their antibiotic resistance pattern in Ho Teaching Hospital of Ghana from 2019–2021.

Methodology Data on urine culture and susceptibility testing and patient demographics from 2019–2021 were collected from the microbiology unit archives with a designed Microsoft Excel 2019 form and later exported to IBM SPSS (v26) for statistical analysis on the uropathogens and their antibiotic resistance pattern. P-value < 0.05 was considered statistically significant.

Results Out of 4806 records, 1005 bacterial isolates were found, with a total prevalence of 20.91%. The most prevalent group of organisms was the Enterobacteriaceae, with *E. coli* 409 (40.70%) being the most frequent isolate. Of the 772 isolates subjected to amikacin, 48(6.22%) and 6(0.78%) of the Gram-negative and Gram-positive bacterial organisms showed resistance to the antibiotic respectively. 58.96% (148/251) and 3.59% (9/251) of Gram-negatives and Gram-positives were resistant to cotrimoxazole. Out of the 1005 bacterial isolates, 165(16.42%), 161(16.02%) and 2(0.20%) showed multidrug resistance (MDR), extensively-drug resistance (XDR), and pandrug resistance (PDR) respectively.

Conclusion There was a high antibiotic-resistant pattern among the uropathogens reported in this current study, hence, the Standard Treatment Guidelines may need to be updated to reflect the high rates of antibiotic resistance exhibited by most prevalent isolates.

Keywords Urinary tract infections · Antibiotics · Resistance · Ho Teaching Hospital

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1 Introduction

Urinary tract infections (UTIs) are a group of infections that affect any component of the urinary tract, including the kidneys, ureters, bladder, and urethra. The urinary tract is separated into two parts: the upper (kidneys and ureters) and lower (bladder and urethra) tracts [1]. UTIs are caused by both Gram-negative and Gram-positive bacteria, as well as by certain fungi [2]. However, Gram-negative bacteria are the most commonly seen, with *E. coli* representing the majority of bacterial uropathogens worldwide [3]. Other causative bacteria species are *K. pneumoniae, P. mirabilis, E. faecalis,* and *S. saprophyticus* [2].

High recurrence rates and rising antibiotic resistance among uropathogens threaten the financial burden of these illnesses [2]. A study by Medina and Castillo-Pino [4] found asymptomatic bacteriuria (ABU) as the most common diagnosis, followed by cystitis, pyelonephritis, and urosepsis. The dominant pathogen isolated in all conditions was *E. coli.* Antibiotic resistance is one of the most serious problems in clinical practice due to the widespread and injudicious use of antibacterial agents in the general population [5].

According to Shailaja, Kumar [5], bacterial agents of UTIs display high rates of antibiotic resistance, similar to other clinical diseases. Various studies have found that antibiotic resistance patterns among uropathogens are increasing at an alarming rate in developing countries when compared to developed countries. Antibiotic resistance patterns vary from one geographical area to the other, and most laboratories in the Volta Region of Ghana are not equipped to perform antibiotic susceptibility testing; hence, there is a need to establish local resistance patterns to help in the empiric treatment of bacterial infections.

For effective care of patients with UTIs, accurate identification of bacterial uropathogens and determination of their antibiotic resistance pattern are essential. This calls for continuous surveillance of uropathogens and their antibiotic resistance. This study was designed to identify the bacterial causes of UTIs and their antibiotic resistance patterns among patients visiting the Ho Teaching Hospital (HTH).

2 Methodology

2.1 Study design

The study was a hospital-based retrospective study on the analysis of secondary data collected from the hospital microbiology laboratory unit. Secondary data on urine culture and susceptibility testing from 2019–2021 were used in the study. Interpretation of antibiotic susceptibility was done based on the Clinical and Laboratory Standards Institute protocol [6].

2.2 Study site

The study was conducted at the microbiology laboratory unit of the HTH which is located in the Ho Municipality of the Volta Region of Ghana. The city lies between Mount Adaklu and Mount Galenukui. The population of Ho municipality is approximately 177,281, representing 8.4 percent of the region's total population according to the 2010 Population and Housing Census. Females constituted 52.7%, and males represented 43%. Approximately 62% of the population resides in urban localities [7]. The Municipality shares boundaries with Adaklu and Agotime—Ziope districts to the south, Ho west district to the north and west and the Republic of Togo to the east. Its total land area is 2361 square kilometres, thus representing 11.5% of the region's total land area. HTH has coordinates 6.60126°N 0.48404°E. The HTH is the main referral facility in the Volta region, with a bed capacity of 340.

2.3 Study participants

The study participants included records of urine culture and susceptibility performed and archived between 2019 and 2021 at the HTH.

2.4 Inclusion and exclusion criteria

Archived records of urine culture and antibiotic susceptibility test results from 2019–2021 were included in the study. Records with incomplete data (age, sex, bacterial isolate, and antibiotic susceptibility test result) were excluded.

2.5 Data collection, handling and analysis

Archived data on urine culture and susceptibility test results from the hospital microbiology unit were retrieved and entered into Microsoft Excel 2019. Data in Microsoft Excel 2019 was exported into IBM Statistical Package for the Social Sciences version 22.0 (SPSS v26) and GraphPad Prism version 6.0 for statistical analysis. Categorical data were analysed using the chi-square (X) or Fisher's exact t-test. A $P\ value < 0.05$ was considered to indicate statistical significance.

2.6 Ethical consideration

Ethical approval with reference number UHAS-REC A.6 [108] 22–23 was obtained from the University of Health and Allied Sciences Research Ethics Committee. In addition, written permission was sought from the management of the HTH for the use of data generated at the microbiology unit of the facility for the study. The study was carried out according to the ethical standards and regulations laid down by the University of Health and Allied Sciences Research Ethics Committee. Informed consent was not sought from the participants because the study was a retrospective one. All archived data for the study was kept undisclosed and used for the study only.

3 Results

Urine samples from a total of 4806 participants were subjected to laboratory analysis and examination for bacterial isolates. Of this number, 65.50% were samples from female subjects. A greater proportion of the subjects were in their thirties (27.00%) and twenties (24.55%) at the time of sample collection. The lowest proportions were subjects in their fifties or older and teenagers or younger. For the period of the study, there was an observation of an upwards trajectory in the frequency of participants from 923 (19.20%) in 2019 to 2495 (51.90%) in 2021, as shown in Table 1.

The overall prevalence of UTI among patients visiting the HTH from 2019–2021 stood at 20.91% (1005/4806). 10.97% of the samples showed no significant growth, whereas 68.13% showed no bacterial growth at all. *E. coli* was the most abundant bacterial agent identified, with a prevalence rate of 40.70% of the total samples under study. The next most prevalent pathogens isolated were *K. oxytoca* (13.93%) and *Citrobacter spp*. (13.53%), with *S. marcescens* being the least prevalent (0.20%) (Figure 1).

Generally, a larger proportion (62.09%) of the total isolates were from samples of female participants. In terms of specific pathogen or species distribution, the majority (64.55%) of the *E. coli* isolates were recovered from female samples. A similar female preponderance was observed for the various species of bacteria isolated, except for *P. vulgaris*

Table 1 Demographic characteristics of the study participants

Parameter	Frequency	Percentage
Gender		
Male	1656	34.50
Female	3150	65.50
Age group		
≤ 10	320	6.70
11–19	316	6.60
20–29	1179	24.50
30–39	1299	27.00
40–49	421	8.80
50–59	310	6.50
60–69	409	8.50
≥ 70	552	11.50
Period		
2019	923	19.20
2020	1388	28.90
2021	2495	51.90
Total	4806	100.00

and *Citrobacter spp.,* where higher percentages of the isolates were from male samples. The distribution of *K. oxytoca, K. pneumoniae*, *P. aeruginosa, P. vulgaris, Enterobacter spp* and *Acinetobacter spp* were all found to be statistically significant at $P < 0.05$. For the distribution of the isolates by the study period, 55.32% of the total isolates were isolated from samples taken in 2021, followed by 29.75% in 2020 and 14.93% in 2019.

For the specific bacterial pathogens, similar patterns were observed for most of the isolates. The majority of *Acinetobacter spp., Citrobacter spp., E. coli, Enterococcus spp., K. oxytoca, K. pneumoniae, P. aeruginosa, S. aureus, S. saprophyticus, and S. saprophyticus* were retrieved from samples collected in 2021. However, a greater proportion of *P. vulgaris*, *P. mirabilis*, was retrieved in 2020. Similarly, the highest proportions of *Enterobacter spp.* were retrieved in 2019. This observed variation in pathogen distribution across the study period was statistically significant ($P < 0.05$) for *K. oxytoca, Citrobacter spp, K. pneumoniae*, *S. aureus, S. saprophyticus,* and *Enterobacter spp*. (Table 2).

The highest prevalence of the isolates was recorded among samples of participants aged from 30 to 39 (22.59%) years at the time of sample collection. This was closely followed by participants aged 70 years or more (19.60%) and those within the age brackets of 20–29 years (19.40%). The least was among those below or equal to 10 years of age, with an infection rate of 3.98%. These variations in pathogen distributions among the age groups of study participants were statistically significant for *Citrobacter spp, E. coli, K. oxytoca, K. pneumoniae, and P. mirabilis*. Also, *S. saprophyticus* and *P. aeruginosa* were significant at $P = 0.0024$ and $P = 0.0080$ respectively (Table 3).

Table 4 presents a comprehensive overview of antibiotic resistance for various antibiotics against both Gram-negative and Gram-positive bacterial isolates. The results show that Gram-negative isolates were generally more prevalent than Gram-positive ones across most antibiotics tested. Gram-negative and Gram-positive bacterial isolates showed 6.22% and 0.78% resistance against amikacin respectively. 64 and 1 Gram-negative and Gram-positive isolates, representing 12.65% and 0.20% respectively were resistant to Levofloxacin. Gram-negative bacterial isolates were highly resistant to cotrimoxazole 148 (58.96%) and chloramphenicol 141 (67.14%). For some antibiotics like ampicillin and penicillin, there's a significant presence of isolates with intermediate susceptibility, as seen in Table 4.

As shown in Tables 5 and 6, analysis of the resistance pattern by the pathogen revealed that each species of bacteria is resistant to at least two different antibiotics. Various pathogens showed varying resistance patterns against different antibiotics. The highest resistant rates for *Acinetobacter spp.* were found to be 100% against piperacillin, cefuroxime, and cefotaxime. *Acinetobacter spp.,* however, were found to be 100% susceptible to amoxicillin, levofloxacin and novobiocin. For *E. coli*, the highest resistance pattern was observed against piperacillin (83.19%), cefuroxime (70.00%), chloramphenicol (62.11%) and tetracycline (60.45%), with the lowest against amikacin (5.49%). *P. aeruginosa* exhibited 88.89%, 84.62% and 80% resistance against cotrimoxazole, nitrofurantoin, and chloramphenicol, respectively, as the highest resistance against any agent used in the current study. On the other hand, *P. aeruginosa* had the lowest resistance

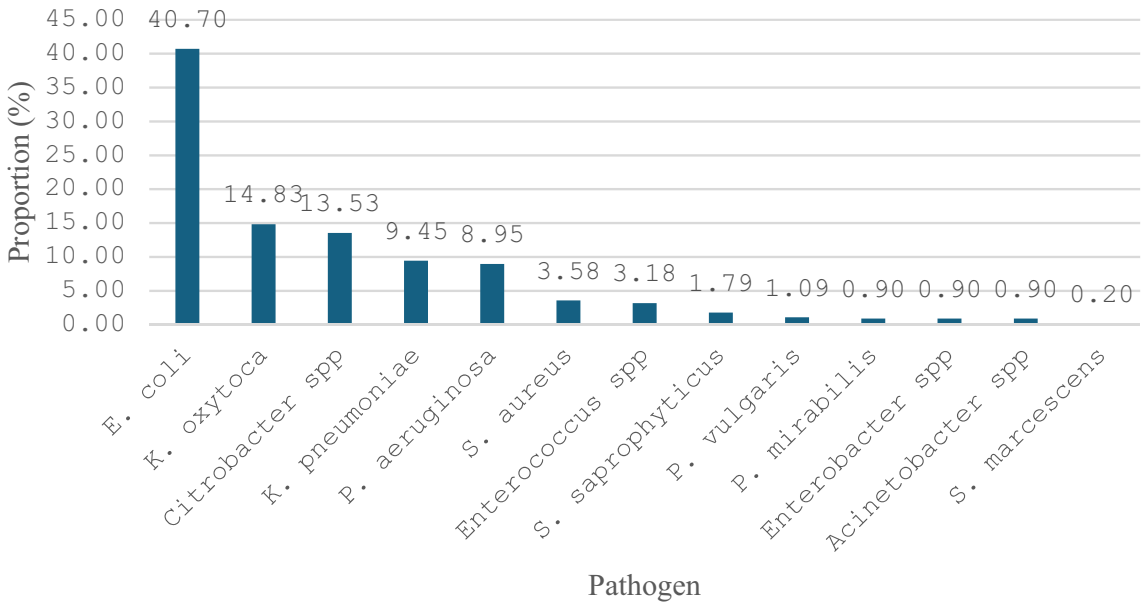

Fig. 1 Proportions of various UTI pathogens isolated from urine samples of patients visiting HTH from 2019–2021

Table 2 Proportion of bacterial isolates stratified by sex of participants and study period

Pathogen	Total	Gender		P value	Period			P value
		Male	Female		2019	2020	2021	
E. coli	409 (8.51)	145 (35.45)	264 (64.55)	0.5054	59 (14.43)	118 (28.85)	232 (56.72)	0.7862
K. oxytoca	149 (3.10)	57 (38.25)	92 (61.74)	**0.0001**	14 (9.40)	47 (31.54)	88 (59.06)	**0.0023**
Citrobacter spp	136 (2.83)	69 (50.74)	67 (49.26)	0.7046	13 (9.56)	36 (26.47)	87 (63.97)	**0.0119**
K. pneumoniae	95 (1.98)	39 (41.05)	56 (58.95)	**0.0324**	16 (16.84)	32 (33.68)	47 (49.47)	**0.0019**
P. aeruginosa	90 (1.87)	44 (48.89)	46 (51.11)	**0.0081**	14 (15.56)	30 (33.33)	46 (51.11)	0.2162
S. aureus	36 (0.75)	3 (8.33)	33 (91.67)	0.2421	8 (22.22)	10 (27.78)	18 (50.00)	**0.0041**
Enterococcus spp	32 (0.67)	4 (12.50)	28 (87.50)	0.1917	10 (31.25)	10 (31.25)	12 (37.50)	0.4921
S. saprophyticus	18 (0.37)	4 (22.22)	14 (77.78)	0.7273	7 (38.89)	2 (11.11)	9 (50.00)	**< 0.0001**
P. vulgaris	11 (0.23)	8 (72.73)	3 (27.27)	**0.0052**	0 (0.00)	7 (63.64)	4 (36.36)	0.4351
P. mirabilis	9 (0.19)	4 (44.44)	5 (55.56)	0.5054	2 (22.22)	4 (44.44)	3 (33.33)	0.5099
Enterobacter spp	9 (0.19)	0 (0.00)	9 (100.00)	**0.0111**	6 (66.67)	0 (0.00)	3 (33.33)	**0.0251**
Acinetobacter spp	9 (0.19)	4 (44.44)	5 (55.56)	**0.0006**	1 (11.11)	3 (33.33)	5 (55.56)	0.9613
S. marcescens	2 (0.04)	0 (0.00)	2 (100.00)	0.3294	0 (0.00)	0 (0.00)	2 (100.00)	0.0841
Total	1005 (20.91)	381 (37.91)	624 (62.09)	0.5483	150 (14.93)	299 (29.75)	556 (55.32)	0.3830

Data are presented as frequencies with corresponding percentages in parentheses. The P value is significant at $P < 0.05$

Table 3 Proportion of bacterial isolates stratified by age groups of participants

Age	Total	≤ 10	11–19	20–29	30–39	40–49	50–59	60–69	≥ 70	P Value
Pathogen										
Gram-negatives										
E. coli	409 (8.51)	16 (3.91)	22 (5.38)	77 (18.83)	81 (19.80)	30 (7.33)	37 (9.05)	59 (14.43)	87 (21.27)	**< 0.0001**
K. oxytoca	149 (3.10)	10 (6.71)	5 (3.36)	26 (17.45)	31 (20.81)	14 (9.40)	14 (9.40)	17 (11.41)	30 (20.13)	**< 0.0001**
Citrobacter spp	136 (2.83)	4 (2.94)	5 (3.68)	20 (14.71)	30 (22.06)	12 (8.82)	14 (10.29)	22 (16.18)	29 (21.32)	**< 0.0001**
K. pneumoniae	95 (1.98)	5 (5.26)	1 (1.05)	19 (20.00)	20 (21.05)	8 (8.42)	10 (10.53)	10 (10.53)	22 (23.16)	**< 0.0001**
P. aeruginosa	90 (1.87)	1 (1.11)	6 (6.67)	19 (21.11)	16 (17.78)	4 (4.44)	9 (10.00)	15 (16.67)	20 (22.22)	**0.0080**
P. vulgaris	11 (0.23)	0 (0.00)	0 (0.00)	2 (18.18)	2 (18.18)	1 (9.09)	1 (9.09)	2 (18.18)	3 (27.27)	0.0632
P. mirabilis	9 (0.19)	0 (0.00)	0 (0.00)	2 (22.22)	1 (11.11)	0 (0.00)	1 (11.11)	3 (33.33)	2 (22.22)	**< 0.0001**
Enterobacter spp	9 (0.19)	1 (11.11)	1 (11.11)	3 (33.33)	3 (33.33)	1 (11.11)	0 (0.00)	0 (0.00)	0 (0.00)	0.7461
Acinetobacter spp	9 (0.19)	1 (11.11)	1 (11.11)	0 (0.00)	3 (33.33)	0 (0.00)	2 (22.22)	2 (22.22)	0 (0.00)	0.1216
S. marcescens	2 (0.04)	0 (0.00)	1 (50.00)	0 (0.00)	1 (50.00)	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)	0.5357
Gram-positives										
S. aureus	36 (0.75)	0 (0.00)	1 (2.78)	8 (22.22)	22 (61.11)	2 (5.56)	2 (5.56)	0 (0.00)	1 (2.78)	0.3347
Enterococcus spp	32 (0.67)	1 (3.13)	0 (0.00)	11 (34.38)	14 (43.75)	4 (12.50)	0 (0.00)	0 (0.00)	2 (6.25)	0.1161
S. saprophyticus	18 (0.37)	1 (5.56)	2 (11.11)	6 (33.33)	3 (16.67)	1 (5.56)	3 (16.67)	1 (5.56)	1 (5.56)	**0.0024**
Total	1005 (20.91)	40 (3.98)	45 (4.48)	195 (19.40)	227 (22.59)	77 (7.66)	93 (9.25)	131 (13.03)	197 (19.60)	0.4536

Data are presented as frequencies with corresponding percentages in parentheses. The P value is significant at $P < 0.05$

against amikacin, with a resistant rate of 7.25%. *S. aureus* also recorded the highest resistance against cefuroxime and penicillin at a 100.00% resistant rates, followed by ampicillin (76.92%), novobiocin (75%), and chloramphenicol (66.67%).

Table 7 below shows the categorisation of various antibiotic resistance by the bacterial isolates according to multidrug resistance (MDR), extensively-drug resistance (XDR), and pandrug resistance (PDR). For Gram-negative isolates, the highest extensively drug resistance was observed for *Enterobacter spp* 4 (44.44%), followed by *P. vulgaris* 4 (36.36%). *Enterobacter spp* showed the highest level of multidrug resistance 2 (22.22%). Most of the multidrug resistance 2 (11.11%) and extensively drug resistance 4 (22.22%) were recorded for *S. saprophyticus* among the Gram-positive isolates. *K. oxytoca* was the only bacterial isolate with pandrug resistance 2 (1.43%).

Table 4 Prevalence of antimicrobial resistance of Gram-negative and Gram-Positive isolates

Antimicrobial agent	Nitrofurantoin		Novobiocin		Amikacin		Cefotaxime	
	Gram-Negative Isolates	Gram-Positive Isolates	Gram-Negative Isolates	Gram-Positive Isolates	Gram-Negative Isolates	Gram-Positive Isolates	Gram-Negative Isolates	Gram-Positive Isolates
Susceptible	196 (47.92)	19 (4.65)	53 (42.74)	8 (6.45)	683 (88.47)	21 (2.72)	91 (20.36)	2 (0.45)
Intermediate	24 (5.87)	6 (1.47)	3 (2.42)	2 (1.61)	14 (1.81)	0 (0.00)	15 (3.36)	0 (0.00)
Resistant	156 (38.14)	8 (1.96)	50 (40.32)	8 (6.45)	48 (6.22)	6 (0.78)	331 (74.05)	8 (1.79)
Total	376 (91.93)	33 (8.07)	106 (85.48)	18 (14.52)	745 (96.50)	27 (3.50)	437 (97.76)	10 (2.24)
Antimicrobial agent	Nalidixic Acid		Cotrimoxazole		Tetracycline		Ceftriaxone	
	Gram-Negative Isolates	Gram-Positive Isolates	Gram-Negative Isolates	Gram-Positive Isolates	Gram-Negative Isolates	Gram-Positive Isolates	Gram-Negative Isolates	Gram-Positive Isolates
Susceptible	151 (44.41)	4 (1.18)	76 (30.28)	14 (5.58)	188 (33.04)	22 (3.87)	48 (41.74)	3 (2.61)
Intermediate	9 (2.65)	3 (0.88)	3 (1.20)	1 (0.40)	18 (3.16)	2 (0.35)	3 (2.61)	2 (1.74)
Resistant	168 (49.41)	5 (1.47)	148 (58.96)	9 (3.59)	305 (53.60)	34 (5.98)	53 (46.09)	6 (5.22)
Total	328 (96.47)	12 (3.53)	227 (90.44)	24 (9.56)	511 (89.81)	58 (10.19)	104 (90.43)	11 (9.57)
Antimicrobial agent	Ciprofloxacin		Cefuroxime		Levofloxacin		Piperacillin	
	Gram-Negative Isolates	Gram-Positive Isolates	Gram-Negative Isolates	Gram-Positive Isolates	Gram-Negative Isolates	Gram-Positive Isolates	Gram-Negative Isolates	Gram-Positive Isolates
Susceptible	343 (45.43)	46 (6.09)	51 (22.97)	5 (2.25)	366 (72.33)	36 (7.11)	29 (11.20)	4 (1.54)
Intermediate	38 (5.03)	9 (1.19)	12 (5.41)	0 (0.00)	36 (7.11)	3 (0.59)	24 (9.27)	1 (0.39)
Resistant	311 (41.19)	8 (1.06)	148 (66.67)	6 (2.70)	64 (12.65)	1 (0.20)	197 (76.06)	4 (1.54)
Total	692 (91.66)	63 (8.34)	211 (95.05)	11 (4.95)	466 (92.09)	40 (7.91)	250 (96.53)	9 (3.47)
Antimicrobial agent	Ampicillin		Vancomycin		Penicillin		Amoxicillin	
	Gram-Negative Isolates	Gram-Positive Isolates	Gram-Negative Isolates	Gram-Positive Isolates	Gram-Negative Isolates	Gram-Positive Isolates	Gram-Negative Isolates	Gram-Positive Isolates
Susceptible	12 (16.00)	11 (14.67)	8 (53.33)	3 (20.00)	9 (37.50)	1 (4.17)	7 (87.50)	0 (0.00)
Intermediate	35 (46.67)	17 (22.67)	3 (20.00)	1 (6.67)	5 (20.83)	9 (37.50)	1 (12.50)	0 (0.00)
Total	47 (62.67)	28 (37.33)	11 (73.33)	4 (26.67)	14 (58.33)	10 (41.67)	8 (100.00)	0 (0.00)
Antimicrobial agent	Gentamicin		Chloramphenicol					
	Gram-Negative Isolates	Gram-Positive Isolates	Gram-Negative Isolates	Gram-Positive Isolates	Gram-Negative Isolates	Gram-Positive Isolates	Gram-Negative Isolates	Gram-Positive Isolates
Susceptible	387 (49.94)	35 (4.52)	51 (24.29)	6 (2.86)				
Intermediate	27 (3.48)	5 (0.65)	5 (2.38)	0 (0.00)				
Resistant	303 (39.10)	18 (2.32)	141 (67.14)	7 (3.33)				
Total	717 (92.52)	58 (7.48)	197 (93.81)	13 (6.19)				

Data are presented as frequencies with corresponding percentages in parentheses

Table 5 Antibiotic resistance prevalence of bacteria isolate

Agent	NIT	NAL	CIP	GEN	AMI	TET	LEV	PIP	NOV
Gram negatives									
E. coli	57 (30.48)	86 (55.13)	146 (48.03)	111 (34.58)	18 (5.49)	133 (60.45)	30 (13.95)	99 (83.19)	25 (56.82)
K. oxytoca	31 (54.39)	32 (50.82)	52 (44.64)	58 (49.57)	11 (9.57)	57 (59.09)	11 (15.07)	30 (76.92)	6 (40.00)
Citrobacter spp	25 (43.10)	28 (65.12)	50 (49.02)	55 (52.38)	7 (5.93)	66 (70.97)	5 (7.04)	31 (83.78)	8 (42.11)
K. pneumoniae	24 (54.55)	12 (30.00)	25 (35.21)	39 (48.75)	7 (8.33)	33 (54.10)	5 (10.00)	19 (76.00)	3 (27.27)
P. aeruginosa	11 (84.62)	6 (40.00)	30 (43.48)	29 (42.65)	5 (7.25)	7 (33.33)	13 (33.33)	8 (47.06)	5 (50.00)
P. vulgaris	2 (100.00)	1 (100.00)	5 (50.00)	6 (66.67)	0 (0.00)	5 (62.50)	0 (0.00)	2 (100.00)	
P. mirabilis	0 (0.00)	1 (25.00)	2 (33.33)	1 (25.00)	0 (0.00)	2 (40.00)	0 (0.00)	1 (50.00)	0 (0.00)
Enterobacter spp	4 (57.14)	2 (33.33)	2 (22.22)	3 (42.86)	0 (0.00)	6 (66.67)	0 (0.00)	4 (66.67)	3 (60.00)
Acinetobacter spp	2 (66.67)	1 (50.00)	1 (14.29)	2 (28.57)	0 (0.00)	1 (20.00)	0 (0.00)	2 (100.00)	0 (0.00)
S. marcescens	0 (0.00)		0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)	1 (100.00)	
Gram positives									
S. aureus	3 (21.43)	0 (0.00)	3 (10.00)	8 (27.59)	2 (18.18)	14 (50.00)	0 (0.00)	1 (33.33)	6 (75.00)
Enterococcus spp	3 (23.08)	3 (60.00)	4 (19.05)	7 (53.85)	2 (25.00)	12 (63.16)	1 (5.88)	1 (25.00)	0 (0.00)
S. saprophyticus	2 (33.33)	2 (100.00)	1 (8.33)	3 (18.75)	2 (25.00)	8 (72.73)	0 (0.00)	2 (100.00)	2 (50.00)
Total	164 (40.00)	174 (51.03)	322 (42.09)	324 (41.27)	55 (7.02)	348 (60.21)	65 (12.82)	201 (77.61)	58 (46.77)

Data are presented as frequencies with corresponding percentages in parentheses. *NIT* Nitrofurantoin, *CIP* Ciprofloxacin, *AMI* Amikacin, *NAL* Nalidixic Acid, *GEN* Gentamicin, *TET* Tetracycline, *LEV* Levofloxacin, *PIP* Piperacillin, *NOV* Novobiocin

Table 6 Antibiotic resistance prevalence of bacteria isolate

Agent	COT	CEFU	CHL	CEFO	AMP	CEFT	PEN	VAN	AMO
Gram negatives									
E. coli	54 (52.43)	63 (70.00)	59 (62.11)	152 (74.51)	14 (58.33)	19 (37.25)	2 (22.22)	1 (14.29)	
K. oxytoca	34 (81.58)	31 (83.33)	27 (89.66)	64 (77.50)	13 (100.00)	8 (58.33)	2 (100.00)	1 (100.00)	
Citrobacter spp	25 (73.53)	23 (79.31)	24 (80.00)	54 (84.38)	7 (100.00)	7 (63.64)	1 (100.00)	1 (50.00)	1 (100.00)
K. pneumoniae	20 (62.50)	17 (60.71)	16 (69.57)	34 (73.91)	1 (50.00)	13 (76.47)	0 (0.00)		
P. aeruginosa	8 (88.89)	8 (47.06)	8 (80.00)	19 (70.37)	1 (50.00)	4 (66.67)			
P. vulgaris	6 (100.00)	4 (57.14)	5 (83.33)	3 (42.86)	1 (100.00)	1 (33.33)			
P. mirabilis	2 (100.00)	1 (50.00)	1 (50.00)	3 (75.00)		0 (0.00)			
Enterobacter spp	1 (100.00)	1 (100.00)	1 (100.00)		1 (100.00)	1 (100.00)			
Acinetobacter spp	1 (50.00)	1 (100.00)	1 (100.00)	3 (75.00)		1 (100.00)			
S. marcescens				1 (100.00)					
Gram positives									
Enterococcus spp	1 (12.50)	1 (50.00)	3 (50.00)	3 (75.00)	3 (37.50)		1 (50.00)		
S. aureus	5 (41.67)	2 (50.00)	4 (66.67)	2 (100.00)	10 (76.92)	5 (50.00)	3 (100.00)		
S. saprophyticus	3 (75.00)	3 (60.00)	0 (0.00)	3 (75.00)	4 (57.14)	1 (100.00)	5 (100.00)	1 (33.33)	
Total	163 (62.69)	159 (70.04)	152 (71.03)	345 (76.16)	56 (70.00)	61 (51.69)	14 (56.00)	4 (25.00)	1 (11.11)

Data are presented as frequencies with corresponding percentages in parentheses. *COT* Cotrimoxazole, *CHL* Chloramphenicol, *CEFU* Cefuroxime, *CEFO* Cefotaxime, *CEFT* Ceftriaxone, *AMP* Ampicillin, *PEN* Penicillin, *VAN* Vancomycin, *AMO* Amoxicilllin

4 Discussion

There are emerging reports globally on the changing pattern of urinary tract pathogens to antibiotics. To ensure appropriate treatment, adequate information on the trend of antibiotic resistance patterns of pathogens through regular surveillance is highly recommended. To this effect, the current study aimed to determine the prevalence and antibiotic resistance pattern of microorganisms isolated from urine samples of UTI patients at the Ho Teaching

Table 7 Classification of bacterial isolates according to antibiotic resistance

Bacterial isolates	Category of antibiotic resistance		
	MDR n (%)	XDR n (%)	PDR n (%)
Gram-negatives			
E. coli (n = 409)	69 (16.87)	70 (17.11)	0 (0.00)
K. oxytoca (n = 149)	30 (20.13)	32 (21.48)	2 (1.34)
Citrobacter spp (n = 136)	22 (16.18)	29 (21.32)	0 (0.00)
K. pneumoniae (n = 95)	20 (21.05)	10 (10.53)	0 (0.00)
P aeruginosa (n = 90)	13 (14.44)	4 (4.44)	0 (0.00)
P. vulgaris (n = 11)	1 (9.09)	4 (36.36)	0 (0.00)
P. mirabilis (n = 9)	0 (0.00)	1 (11.11)	0 (0.00)
Enterobacter spp (n = 9)	2 (22.22)	4 (44.44)	0 (0.00)
Acinetobacter spp (n = 9)	0 (0.00)	0 (0.00)	0 (0.00)
S. marcescens (n = 2)	0 (0.00)	0 (0.00)	0 (0.00)
Gram-positives			
S. aureus (n = 36)	3 (8.33)	3 (8.33)	0 (0.00)
Enterococcus spp (n = 32)	3 (9.38)	0 (0.00)	0 (0.00)
S. saprophyticus (n = 18)	2 (11.11)	4 (22.22)	0 (0.00)
Total (n = 1005)	165 (16.42)	161 (16.02)	2 (0.20)

MDR non-susceptible to ≥ 1 agent in ≥ 3 antimicrobial categories, *XDR* non-susceptible to ≥ 1 agent in all but ≤ 2 categories, *PDR* non-susceptible to all antimicrobial agents listed

Hospital's Laboratory. The prevalence of UTIs at Ho Teaching Hospital within the study period was 20.19%. Despite the study's rate being noticeably high, it was lower than the results of other investigations [8–10].

The current study revealed that enterobacterial pathogens were the most frequently isolated group of pathogens, with *E. coli* and *Klebsiella spp* being the most frequent isolates and *Staphylococcus spp* being the most frequent Gram-positive organisms, similar to several studies conducted in some major hospitals in Ghana [9, 11–14]. These findings are similar to the results in other studies where *E. coli* at 68.3% and *K. pneumoniae* at 31.7% were the most predominant isolates from UTIs [9, 11, 12]. In another study from India, *E. coli* was the predominant isolate at 77.9%, followed by *Klebsiella spp*. at 22.1% [15]. The human intestinal microbiota is dominated by enterobacteria, which are recognized to be a common cause of autoinfection for UTIs [16].

Apart from *Citrobacter spp.* and *P. vulgaris*, more of every bacterium isolate in the current investigation was found in samples taken from female study participants. The considerable microbial presence in urine samples from females compared to males (62.09% and 37.91%, respectively) confirms findings from earlier studies indicating that prevalence is typically higher in females than males [9–12, 14]. The fairly high incidence of UTIs seen among females in this study may be caused by variables such as the different anatomies of the male and female urethras, the female urethra's proximity to the anal orifice, and poor personal hygiene, as extrapolated by Gyansa-Lutterodt, Afriyie [10]. There was also an increasing trend in the proportions of pathogens recovered per year across the study period from 2019 to 2021.

In terms of age distribution, participants between 20 and 40 years were the most infected (41.99%) compared to those in other age categories. These findings slightly disagreed with reports by other studies that concluded that growing older is linked to increased antibiotic usage and misuse, which increases the chance of developing multidrug-resistant infections [11]. Similarly, our findings do not corroborate the reports by Pujades-Rodriguez, West [17], who also suggested that old age is linked to an increased risk of developing multidrug resistance UTI.

High levels of resistance to the standard treatment guidelines (STGs) recommended antibiotics for treating urinary tract infections were observed in this study. All bacterial isolates (100.00%) were resistant to at least two antibiotics. This corroborated a previous finding in 2021 [18]. Antibiotic-resistant prevalence across various antibiotics used in this study in both Gram-negative and Gram-positive bacterial isolates and the findings have significant implications for clinical practice and public health. The use of antibiotics from five different classes; penicillin, tetracyclines, sulfamethoxazole/trimethoprim, chloramphenicol, and cephalosporins indicates that the bacterial isolates can withstand a wide spectrum of antibiotics. *E. coli*, *Klebsiella spp*., *Pseudomonas spp*., and *Proteus spp*. in particular demonstrated (> 50%) resistance to the generally affordable antibiotics such as tetracycline, cotrimoxazole, cefuroxime, and chloramphenicol, and this

observation is consistent with results from previous studies in Ghana [13, 19]. Amikacin emerges as the most effective antibiotic against Gram-negative isolates, with a high susceptibility rate, underscoring its potential as a frontline treatment. Conversely, cefotaxime presents a troubling scenario with a high resistance rate among Gram-negative bacteria, signaling the urgent need for alternative therapeutic options and stricter antibiotic stewardship to curb resistance development.

Vancomycin, a key treatment for Gram-positive infections, shows moderate susceptibility, hinting at potential resistance issues that warrant further investigation and prudent use. The presence of significant intermediate susceptibility for antibiotics like ampicillin and penicillin indicates that a considerable proportion of isolates may not be fully resistant or susceptible, complicating treatment decisions. These findings collectively emphasize the importance of continuous surveillance and tailored antibiotic therapy to combat antibiotic resistance effectively.

Collectively, amikacin was discovered to be the most efficacious antibiotic agent against all bacterial species, including both Gram-positive and Gram-negative isolates [18]. This discovery supports research that indicated that amikacin was the most effective antibiotic treatment for clinical isolates in Ghana [13, 20]. Compared to pharmaceuticals such as ampicillin and chloramphenicol, this medication has only recently entered the Ghanaian market. Additionally, the extremely pricey medications; ciprofloxacin, amikacin, and ceftriaxone are typically prescribed for serious infections [21]. Hence, these might also be reasons for their relatively lower levels of resistance.

The study also reports on antibiotic resistance profiles of various bacterial isolates according to MDR, XDR, and PDR categories, highlighting critical insights into the growing challenge of antibiotic resistance. Among Gram-negative isolates, *Enterobacter spp* exhibited the highest extensively drug resistance 4/9(44.44%), followed by *P. vulgaris* 4/11 (36.36%). This suggests that these species are developing resistance mechanisms against a broad-spectrum antibiotics, making infections increasingly difficult to treat. In addition, *Enterobacter spp* also demonstrated the highest level of multidrug resistance 2/9 (22.22%), indicating its ability to resist multiple antibiotic classes simultaneously, which complicates therapeutic options and underscores the need for vigilant antibiotic stewardship.

In Gram-positive isolates, *S. saprophyticus* exhibited significant levels of resistance, with 2 out of 18 and 4 out of 18 isolates showing multidrug and extensively drug resistance, representing 11.11% and 22.22% respectively. These findings are particularly concerning given the clinical relevance of *S. saprophyticus* in urinary tract infections, emphasizing the necessity for effective antimicrobial strategies to manage such infections. Additionally, the presence of pandrug resistance in *K. oxytoca* [2/149 (1.34%)] is alarming. PDR indicates resistance to all listed antibiotics, posing a severe threat to public health as it leaves limited or no treatment options, highlighting an urgent need for the development of new antibiotics or alternative treatment approaches. These findings collectively illustrate the pervasive and escalating issue of antibiotic resistance across both Gram-negative and Gram-positive bacteria.

Consistent with the result of this current study, *S. aureus*, *Enterococcus* spp., Enterobacteriaceae, *P. aeruginosa* and *Acinetobacter* spp., were responsible for MDR in healthcare setting [22]. The incidence of severe infection caused by MDR and even XDR *A. baumannii* has been increasing worldwide as a result of its ability to survive in environmental and human reservoirs [23]. Contrarily, *Acinetobacter spp in* this current study showed no MDR, XDR, and PDR.

The high levels of MDR, XDR, and PDR observed in this study necessitate immediate attention to antibiotic usage policies, enhanced surveillance, and innovative research to combat antibiotic-resistant infections. This evidence underscores the importance of ongoing efforts to monitor resistance patterns and develop novel therapeutic strategies to mitigate the impact of antibiotic resistance on global health.

5 Limitations

A significant drawback of this study is the inability to separate the data into outpatient and inpatient groups. The division of community- and hospital-acquired infections would have been made possible with the aid of such information. The study did not report on antibiotic-resistant genes of the pathogens.

6 Conclusions

Gram-negative organisms, particularly *E. coli* and *Klebsiella spp.* were the most frequent cause of UTIs during the three-year study period. The prevalence of MDR was 16.42% hence, the STG recommendations may need to be updated to reflect the high rates of antibiotic resistance exhibited by most prevalent isolates.

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Declarations

Competing interests The authors declare no competing interests.

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