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ORIGINAL ARTICLE

Antimicrobial Profile of Pathogens Causing Community Acquired Urinary Tract Infection in Ain Shams University Hospitals

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ABSTRACT

Background*: Community-acquired urinary tract infection (CA-UTI) is considered from the most common bacterial infections that is caused by wide range of Gram positive and Gram-negative bacteria. The increasing antimicrobial resistance and high recurrence rates of this infection threaten to increase the economic burden due to prolonged consumption of antibacterial agents.* ***OBJECTIVE****: Is to determine the susceptibility pattern of common pathogens causing CA-UTI in patients attending Ain Shams University Hospitals.* ***Methodology****: A total number of 385 midstream urine samples were collected from patients attending Ain Shams University Hospitals and subjected to conventional microbiological work up to isolate pathogens causing UTI. Antimicrobial susceptibility testing was done for isolates and the results were interpreted according to Clinical and Laboratory Standards Institute guidelines 2022.* ***Results****: From collected samples, 232 (60.3%) yielded significant growth, while 153 (39.7%) samples yielded insignificant or no growth after 48 hours incubation period. Most of isolated pathogens were retrieved from female patients (70.25%). The most common isolated pathogens were E. coli 105 (45.25%), followed by Klebsiella pneumoniae 45 (19.4%). Most isolates were susceptible to carbapenems and aminoglycosides. Least susceptibility was recorded to penicillin group.* ***Conclusion****: CA-UTI is more common in females and is mainly caused by E. coli and Klebsiella pneumoniae. Reporting pattern of Antimicrobial susceptibility of pathogens causing CA- UTI is crucial for better prescription of empirical treatment.*

INTRODUCTION

Urinary tract infection (UTI) is one of the most common causes of both community and hospital acquired infections and one of most common infections worldwide[1]. This leads to consumption of large proportion of antibacterial agents, and causes different socio-economic burden[2]. Since most of cases are treated empirically, the microbial profile and epidemiological characteristics of most common organisms causing this infection is crucial to be known. These data will help to optimize the treatment and decrease the emergence of antimicrobial resistance.

UTI may be asymptomatic or symptomatic, the symptoms ranged from mild irritation, frequency, urgency up to bacteremia and sepsis[3].

UTI is caused by both Gram-negative and Gram-positive bacteria, as well as by certain fungi like candida spp. The most common bacterial cause of uncomplicated community-acquired UTI is uropathogenic *Escherichia coli* (UPEC), representing >80% of infections [4].

Antimicrobial resistance are frequently observed even for community acquired UTI (CA-UTI). Extended spectrum β lactamase (ESBL) producing Enterobacteriaceae shows co-resistance to fluoroquinolones. Resistance data shows high rates of resistance to ampicillin, amoxicillin/clavulanic acid, oral cephalosporins, co-trimoxazole and ciprofloxacin in many countries. Resistance patterns of *E. coli* strains, the dominant uropathogen, vary considerably among regions and countries[5].

Also, World Health Organization's (WHO) reported that *Klebsiella pneumoniae* is the second most frequent etiological agent involved in community-acquired (CA) UTIs, and it is one of the top three pathogens of international concern documented in the 2017 WHO Global Priority List of Antibiotic-Resistant Bacteria to Guide Research, Discovery, and Development of New Antibiotics[6].

Other pathogens commonly associated with uncomplicated CA-UTI include *Staphylococcus saprophyticus, Proteus mirabilis, Enterococcus faecalis, Staphylococcus aureus* and *Pseudomonas aeruginosa*[7].

The awareness of regional susceptibility data regarding the common uropathogens is mandatory for selecting appropriate empirical antibiotics, so in this study we aimed to determine susceptibility pattern of common pathogens causing CA-UTI in patients attending Ain Shams University Hospitals.

METHODOLOGY

The study was approved by The Research Ethics Committee, Ain Shams University, Faculty of Medicine (FWA 000017585), and from MASRI (FMASU R185/2022).

Sampling

A total number of the three hundred eighty-five (385) midstream urine samples were collected from the Main Microbiology laboratory, Faculty of Medicine, Ain Shams University and from patients attending different outpatient clinics of Ain Shams University Hospitals complaining from symptoms of UTI from the October to December 2022. Freshly voided samples were collected into sterile screw capped plastic universal containers. Full history was taken from the patients and a verbal informed consent was taken after the explanation of the rational of this study. All samples were properly labeled with the patients' data and date and processed immediately in the Microbiology laboratory, of Faculty of Medicine, Ain Shams University.

Processing of Samples

Samples were tested for significant bacteriuria by use of a modified semi quantitative technique described by Cheesbrough[8]. Bacteriological loop of each urine sample (0.01ml) was spread over the Cystine Lactose Electrolyte Deficient (CLED) and blood agar plates (Oxoid, UK), the plates were incubated at 37^{o} C for 24 hrs. The number of bacterial colonies were counted and any count equal to or more than 10^5 per millilitre was considered significant bacteriuria. And also the samples were cultured on MacConkey's agar and Sabouraud Dextrose agar (Oxoid, UK) plates for isolation and identification of the uropathogens.

Conventional identification of the isolated uropathogens

Pure isolates were then identified conventionally by gram stain, catalase, coagulase tests and Mannitol salt agar for *Staphylococcus*, biochemical reactions for lactose and non-lactose fermenting Gram negative bacteria, bile esculin test for *Enterococci* as shown in fig1, 2 and 3.

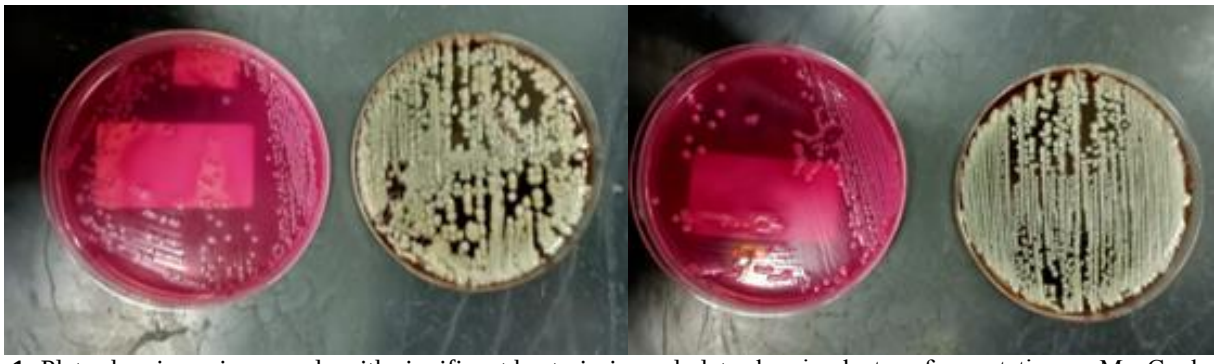

Fig 1: Plate showing urine sample with significant bacteriuria. and plate showing lactose fermentation on MacConkey's agar

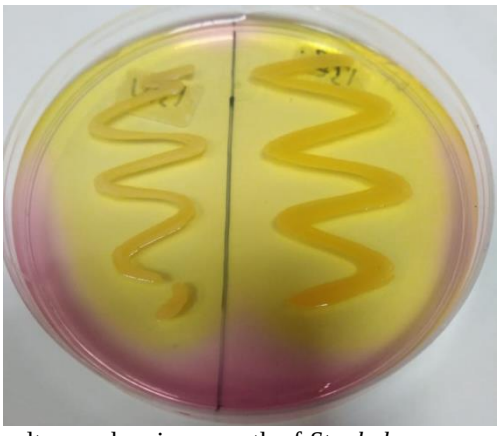

Fig. 2: Mannitol salt agar showing growth of *Staphylococcus aureus* (*S. aureus)*

Fig. 3: Biochemical reaction of *Klebsiella pneumoniae and proteus spp.*

Identification and antifungal susceptibility of *Candida spp*.

Colonies on Sabouraud Dextrose agar were confirmed by gram stain, then identified and tested for antifungal susceptibility by the VITEK 2 AST-YSO8 (bioMérieux, Inc., Hazelwood, MO) which is a fully automated system that allows species identification and antifungal susceptibility testing.

Antimicrobial susceptibility testing of uropathogens

All isolates were tested for antimicrobial susceptibility using Kirby–Bauer Disk diffusion method and interpreted according to CLSI guidelines [10]as shown in fig 4.

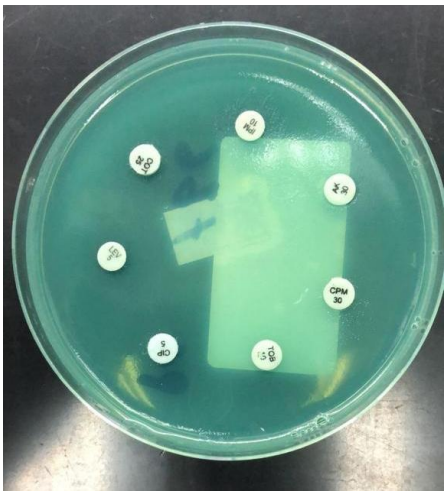

Fig .4: Muller Hinton plate showing multi drug resistant *Pseudomonas aeruginosa*

Antimicrobial susceptibility pattern of Gram-negative bacteria:

Gram-negative isolates were tested for their susceptibility to the following antibiotics (Oxoid, UK): aztreonam 30µg (ATM), cefepime 30µg (FEP), cefazolin 30µg (CZ), cefaclor 30µg (CEC), cefoxitin 30µg (FOX), ceftazidime 30µg (CAZ), amoxicillin+clavulanic 20/10µg (AMC), ceftriaxone 30µg (CRO), ceftotaxime 30µg (CTX), ciprofloxacin 5µg (CIP), ofloxacin 5µg (OFX), norfloxacin 5µg (NOR), gentamicin10µg (GN), tobramycin10µg (TOB), amikacin 30µg (AK), nitrofurantoin 10µg (F), sulbactam+ampicillin 10/10µg (SAM), ampicillin10µg (AM), meropenem 10µg (MEM), imipenem 10µg (IPM), piperacillin \ Tazobactam 100/10µg (TPZ) and levofloxacin 5µg (LEV).

ESBL detection was performed by double disc synergy testing by placing amoxicillin-clavulinic acid at a distance of 20-30 ml from third generation cephalosporin. A positive result is indicated when the inhibition zones around any of the cephalosporin disks are augmented or there is a 'keyhole' or "champagne cork" in the direction of the disk containing clavulanic acid as shown in figure 5.

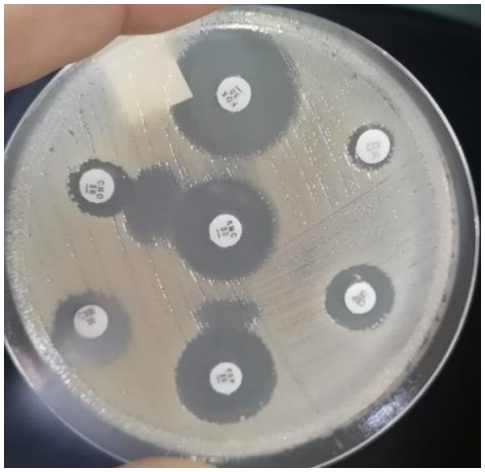

Fig. 5 : Muller Hinton agar Showing *E. coli* with ESBL production

Antimicrobial susceptibility pattern of Gram-positive bacteria:

S. aureus isolates were tested for their susceptibility to the following antibiotics (Oxoid, UK): cefoxitin 30µg (FOX), ciprofloxacin 5µg (CIP), ofloxacin 5µg (OFX), norfloxacin 5µg (NOR), tobramycin 10µg (TOB), amikacin 30µg (AK), nitrofurantoin 10µg (F), sulbactam+ampicillin 10/10µg (SAM), ampicillin 10µg (AM), ceftazidime 30µg (CAZ), amoxicillin+clavulanic 20/10µg (AMC), levofloxacin 5µg (LEV) and cephalexin 30µg (CN), linezolid 30µg (LZD), rifampin 5µg (RA), teicoplanin 30µg (TEC), doxycline 30µg (DO) and penicillinG 10 units(P).

Enterococci spp. were tested for their susceptibility to the following antibiotics (Oxoid, UK): ciprofloxacin 5µg (CIP), ofloxacin 5µg (OFX), norfloxacin 5µg (NOR), nitrofurantoin 10µg (F), sulbactam+ampicillin 10/10µg (SAM), ampicillin10µg (AM), Cephalexin 30µg (CN), levofloxacin 5µg (LEV), Linezolid 30µg (LZD), Rifampin 5µg (RA), Teicoplanin 30µg (TEC), Doxycline 30µg (DO) and PenicillinG 10 units(P).

RESULTS

A total of 385 midstream urine samples were processed. 153 (39.7%) samples yielded insignificant or no growth after 48 hours incubation period and 232 (60.3%) samples yielded significant growth.

Regarding sex distribution of the patients included in our study. Out of 232 sample showing significant growth, 163 were female patients (70.25%) and 69 (29.75%) were male patients. The prevalence of the community acquired UTI in female was more than twice the male patients as shown in table (1).

Table 1: The prevalence of community acquired UTI in male vs. female.

	Males	Females
Insignificant growth n= 153	54 (35.29%)	99 (64.7%)
Significant growth n= 232	69 (29.75%)	163 (70.25%)

The total number of isolated uropathogens was 79.32% and 20.68% for both Gram-negative and Gram-positive organisms respectively. The most common isolated uropathogen was *E.coli* 105 (45.25%) followed by *Klebsiella pneumonia* 45 (19.4%), *Enterococci spp.* 26 (11.20%), *Pseudomonas aeruginosa* 21 (9.1%), *Proteus spp*. 12 (5.17%), *S. aureus* 12 (5.17%), *Candida albicans* 10 (4.31%) and only one *Acinetobacter spp.*(0.4%) as shown in fig. (6).

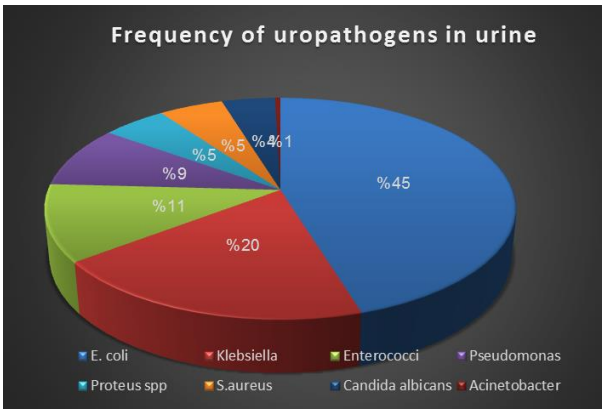

Fig. 6: Distribution of isolated uropathogens among obtained isolates

Table 2: Distribution of isolated uropathogens according to sex

	Total (%)	SEX	
		Male (N= 69)	Female (N= 163)
	N(%)	N(%)	N(%)
E.coli	105 (45.25%)	23 (33.3%)	82 (50.3%)
Klebsiella pneumoniae	45 (19.4%)	12 (17.4%)	33 (20.2%)
Enterococci spp.	26 (11.20%)	6 (8.7%) 4.9	20 (12.3%)
Pseudomonas aeruginosa	21 (9.1%)	13 (18.8%)	8 (4.9%)
Proteus spp.	12 (5.17%)	7 (10.1%)	5 (3.1%)
S. aureus	12(5.17%)	3 (4.3%) 2.4	9 (5.5%)
Candida albicans	10 (4.31%)	4 (5.8%) 3.3	6 (3.7%)
Acinetobacter spp.	1 (0.4%)	1 (1.4%)	0 (0%)

As shown in table (2), half of the isolated organisms among female patients were *E. coli* (50.3%) followed by *Klebsiella pneumoniae* (20.2%), *Enterococci* (12.3%) and *S.aureus* (5.5%). In male patients, the most common isolated organisms were *E. coli* (33.3%) followed by *Pseudomonas aeruginosa* (18.8%), *Klebsiella pneumoniae* (17.4%) and *Proteus spp*. (10.1%).

Table 3: Antimicrobial susceptibility pattern of Gram-negative bacteria

Antibiotic	*E.coli* (N = 105)	*Klebsiella pneumoniae* (N = 45)	*Pseudomonas aeruginosa* (N = 21)	*Proteus spp.* (N = 12)	*Acinetobacter spp.* (N = 1)
CAZ	23 (21.9%)	8 (17.87%)	8 (38.1%)	3 (25%)	0 (0%)
AMC	12 (11.42%)	9 (20%)	8 (38.1%)	2 (16.7%)	0 (0%)
CRO	47 (44.79%)	21 (46.67%)	9 (42.86%)	8 (66.67%)	0 (0%)
CTX	47 (44.79%)	22 (48.98%)	8 (38.1%)	7 (58.3%)	0 (0%)
CEC	30 (23.8%)	17 (37.78%)	9 (42.86%)	7 (58.3%)	0 (0%)
FEP	60 (57.14%)	27 (60%)	11 (52.38%)	8 (66.67%)	0 (0%)
CZ	29 (27.61%)	20 (44.44%)	9 (42.86%)	7 (58.3%)	0 (0%)
FOX	87 (82.9%)	35 (77.77%)	9 (42.86%)	8 (66.67%)	1 (100%)
CIP	70 (66.7%)	26 (57.78%)	10 (47.62%)	10 (83.3%)	0 (0%)
OFX	82 (78.1%)	28 (62.22%)	13 (61.9%)	8 (66.67%)	0 (0%)
NOR	85 (80.95%)	31 (68.89%)	13 (61.9%)	8 (66.67%)	0 (0%)
TOB	100(95.23%)	43 (95.56%)	18 (85.71%)	10 (83.3%)	1 (100%)
AK	90(85.71%)	45 (100%)	20 (95.24%)	12 (100%)	1 (100%)
F	72 (68.57%)	12 (26.67%)	9 (42.86%)	4 (33.33%)	0 (0%)
SAM	20 (19.04%)	5 (1.11%)	8 (38.1%)	2 (16.7%)	0 (0%)
AM	5 (4.76%)	1 (2.22%)	1 (4.76%)	2 (16.7%)	0 (0%)
IPM	102 (97.14%)	40 (88.8%)	18 (85.7%)	12 (100%)	1 (100%)
MEM	105 (100%)	42 (93.3%)	19 (90.47%)	12 (100%)	1 (100%)
ATM	47 (44.76%)	23 (51.11%)	13 (61.9%)	8 (66.67%)	0 (0%)
TPZ	80 (66.67%)	27 (60%)	11 (52.38%)	8 (66.67%)	1 (100%)
LEV	80 (66.67%)	32 (71.11%)	13 (61.9%)	8 (66.67%)	0 (0%)

The Result of antimicrobial susceptibility testing was shown in table (3). All *E. coli* isolates were sensitive to meropenem (100%), Imipenem (97.14%), tobramycin (95.23%) and amikacin (85.71%). Least sensitivity was found to ampicillin (4.7%), amoxicillin+clavulanic (11.4%) sulbactam+ampicillin (19%), and ceftazidime (21.9%). Among these isolates, 22 (20.95%) were ESBL producer.

For *Klebsiella* isolates, most sensitivity was found to amikacin (100%) followed by tobramycin (95.6%), meropenem (93.3%) and Imipenem (88.8%). Isolates were least sensitive was to amoxicillin+clavulanic (1.1%), ampicillin (2.2%), and ceftazidime (17.87%). Among these isolates, 2 (4.4%) were ESBL producer.

Regarding *Pseudomonas aeruginosa*., the isolates were most sensitive to amikacin (95.24%) followed by meropenem was (90.47%), sensitivity to tobramycin (85.7%), however they were least sensitive to ampicillin (4.7%).

Proteus spp. isolates were highly sensitive for amikacin, meropenem and imipenem (100%), followed by ciprofloxacin and tobramycin (83.3%). Least sensitivity was found for amoxicillin+clavulanic ampicillin and sulbactam+ampicillin (16.7%).

Lastly, one *Acinetobacter* isolate was sensitive for amikacin, meropenem, imipenem ,cefoxitin, tobramycin and piperacillin \ Tazobactam.

S. aureus susceptibility revealed for 12 isolates, 8 (66.7%) of them were sensitive for cefoxitin (Methicillin sensitive *staphylococcus aureus*, MSSA), while 4 isolates (33.3%) were Methicillin resistant *staphylococcus aureus*, (MRSA). table (4) shows susceptibility of *S. aureus* to different antibiotics.

Table 4: Antimicrobial susceptibility pattern of *S. aureus*

Antibiotic	N. of sensitive isolates	Antibiotic	N. of sensitive isolates
FOX	8 (66.66%)	AM	0 (0%)
CIP	5 (41.66 %)	CN	2 (16.66%)
OFX	7 (58.33%)	LEV	5 (41.66 %)
NOR	5 (41.66%)	LZD	9 (75%)
TOB	4 33.33%	P	0 (0%)
AK	6 (50%)	DA	4 (33.3%)
F	8 (66.66%)	DO	4 (33.33%)
SAM	5 (41.66%)		

Regarding *Enterococci* (26 isolates), 100% susceptibility was found for vancomycin and teicoplanin. Susceptibility for linezolid was 96%, sulbactam+ampicillin was 92.3% and for penicillin was 80.6%.

Table 5: Antimicrobial susceptibility pattern of *Enterococci*

Antibiotic	N. of sensitive isolates	Antibiotic	N. of sensitive isolates
CIP	23 (88.46%)	LEV	23 (88.46%)
OFX	22 (84.61)%	LZD	24 (96%)
NOR	23 (88.46%)	VA	26 (100%)
F	23 (88.46%)	TEC	26 (100%)
SAM	24 (92.3%)	DO	12(46.15%)
AM	15 (57.69%)	P	21 (80.6%)

All ten isolates of *Candida albicans* were 100% susceptible for fluconazole, Vorioconazole , flucytosine and micafungin. Only one isolate was resistant for amphotericin B, with 90% susceptibility.

DISCUSSION

UTI is frequent infection caused by different organisms. Successful diagnosis of causative pathogens and antimicrobial susceptibility are mandatory for treatment. Management with inappropriate antibiotics leads to increase course of disease, prone patients for complications and promote bacterial resistance. In our study a total of 385 midstream urine samples were processed. 153 (39.7%) samples yielded insignificant or no growth after 48 hours incubation period and 232 (60.3%) samples yielded significant growth. Similar results were reported by *O*tajevwo and Amedu[3], who analysed 390 midstream urine samples and found that 40.8% samples yielded insignificant or no growth, while 59.2% samples yielded significant growth. Different results were obtained by Ahmed et al.[1], who found that only 32.6% urine yielded significant growth and by Tesfa et al.,[11], who found 28.38% of the participants had a culture-positive result. Mohapatra et al.[12], stated that only 10.1% of urine samples showed significant growth. The disparity between studies could result from the difference in sample size, different population, methodology and inclusion and exclusion criteria provided by the researchers.

In this study, 70.25% (163) of positive cultures were obtained from female patients while 29.75% (69) were collected from male patients. Many studies agreed that female patients have the main portion of positive culture with different percentages. Tesfa et al[11], Stefaniuk et al.[13], Ahmed et al.[1], Chervet et al.[14], reported 56.62%, 77.2%, 73%, 81.4% of samples were from females respectively. This is attributed to short urethra, moist environment of female's perineum and bacteria being passed from the urethra into the bladder during pregnancy.

In our study, Gram-negative bacteria had a higher prevalence, accounting for 79.3%, while Gram-positive bacteria was 20.7%. Similar results were obtained by Ahmed et al.[1] in Saudi Arabia, who found that Gram-negative and Gram-positive uropathogens accounts for 86.5% and 13.5% respectively. Tesfa et al.[11] in Ethiopia, reported that prevalence of Gram-negative bacteria was 62%, while Gram-positive bacteria was 38%. However, Stefaniuk et al.[13], reported that 93.3% of isolates were for Gram-negative organisms, while Gram-positive cocci accounts only for 6.6%. Otajevwo and Amedu[15], stated that, total Gram-negative and Gram-positive organisms isolated represented 43.4% and 48.7%.

Our results showed that the most common isolated uropathogen among the studied groups were *E.coli* 105 (45.25%) followed by *Klebsiella pneumoniae* 26 (11.20%), *Pseudomonas aeruginosa* 21 (9.1%), *Proteus spp*. 12 (5.17%), *S. aureus* 12 (5.17%), *Candida albicans* 10 (4.31%) and only one *Acinetobacter spp.* (0.4%).

Similar results were observed by Mohapatra et al.[12], who declared that *E. coli* was the commonest uropathogen (68.3%), followed by *Klebsiella pneumoniae* (17.6%), *Proteus spp.* (3.2%), *Acinetobacter spp*. (1.2%), *Enterococcus spp*. (5.6 %). Chervet et al.[14] announced that the most frequently isolated species were *E. coli*, *Klebsiella* spp., *Enterococcus* spp., *Proteus* spp., and *Citrobacter* spp. in 69%, 8%, 6%, 6%, and 4% of patients, respectively. In Jordan, Faris[16], declared that the most common isolated uropathogen was *E.coli* (70%) followed by β-hemolytic streptococcus group B (8%), *Klebsiella spp* (7.6%) and Enterococci (3.6%). Stefaniuk et al.[13] reported that (71.4%) of isolates were for *E. coli*, followed by *Klebsiella spp*. (10.8%) and *Proteus spp.* (7.6%).

Ahmed et al.[1] reported that the most common Gram-negative urinary pathogens isolated were *E. coli* (27%), *Klebsiella pneumoniae* (12.4%), *Enterobacter cloacae* (5.6%) *Proteus mirabilis* (4.5%) and *Pseudomonas aeruginosa* (4.5%). Tesfa et al.[11] recorded that *E. coli* was the leading pathogen (25.34%), followed by *S. saprophyticus, S. warneri, coagulase-negative Staphylococci* (CONS), and *Pseudomonas spp.*

All the previous researches agreed that the most common isolated uropathogen was *E. coli* followed by *Klebsiella spp.* On the contrary, one study done by Otajevwo and Amedu[15] showed that the frequently occurring UTIs are caused mainly by *S. aureus* (33.1%) followed by *E. coli* (20.8%), CoNS (15.6%), *klebsiella aerogenes* (7.9%), *Candida albicans* (7.9%) and *Proteus spp* (6.8%).

In our research, half of the isolated organisms among female patients were *E. coli* (50.3%) followed by *Klebsiella pneumoniae* (20.2%), *Enterococci* (12.3%) and *S. aureus* (5.5%). In male patients, the most common isolated organisms were *E. coli* (33.3%) followed by *Pseudomonas spp.* (18.8%), *Klebsiella pneumoniae* (17.4%) and *Proteus spp*. (10.1%).

In agreement with our results, Stefaniuk et al.[13], observed that *E.coli* was mainly responsible for UTIs in females (77.9%), followed by *Klebsiella spp*. (8.8%) and *Proteus spp.* (4.4 %). Also half of the isolates from UTI in men were *E. coli* (49.4%), followed by *Klebsiella spp*. (17.2 %). Moreover, they observed that a higher proportion of *Proteus spp.* was observed in men compared to women, with 16.1% and 4.4%, respectively. Chervet et al.[14] stated that the most common isolated organisms in females and males were *E. coli* and *Enterococci spp* respectively.

On the other hand, Otajevwo and Amedu[15] stated that the highest occurring uropathogen in females was *S. aureus* (30.3%) followed by *E. coli* (18.2%) then *CONS* (12.1%) and *Candida albicans* (12.1%). In males the dominant organisms were *S. aureus* (34.1%), *E. coli* (22.7%) and *CONS* (18.2%).

In our work, antimicrobial susceptibility pattern of *E. coli* isolates showed high susceptibility to meropenem (100%), Imipenem (97.14%), tobramycin (95.23%), amikacin (85.71%) and nitrofurantoin (68.5%). Least sensitivity was found to ampicillin (4.7%), amoxicillin+clavulanic (11.4%) sulbactam + ampicillin (19%), and ceftazidime (21.9%). Among these isolates, 22 (20.95%) were ESBL producer.

These results are in accordance with Chervet et al.[14] who reported that *E. coli* isolates were sensitive to ertapenem (100%), nitrofurantoin (98.9%), amikacin (98.5%). They also stated that the least sensitivity was found to ampicillin (49.5%), and amoxicillin+clavulanic (61.8%). The prevalence of ESBL was (5.1%) among *E. coli.*which is lower than our results, the higher prevalence of ESBL among isolates in our study may be due to unrestricted use of antibiotics in Egypt.

On the other hand, *Tesfa and* his colleagues[11] reported that *E. coli* had high resistance to ciprofloxacin (64.3%), commonly prescribed to UTI while their results came similar to our results as isolates were susceptible to meropenem (92.8%) and gentamicin (75%). Another study done in Saudi Arabia by Al-Mijalli[17] who reported that isolates of *E. coli* and *K. pneumoniae* were highly susceptible to Meropenem, Imipenem, Colistin, Ertapenem and Amikacin.

Stefaniuk et al.[13], noted that sensitivity of *E. coli* causing uncomplicated UTI for nitrofurantoin, ciprofloxacin, trimethoprim/sulfamethoxazole, and fosfomycin 67.2%, 73.7%, 68.1% and 77.6% respectively.

Faris[16] reported that *E. coli* showed high susceptibility to nitrofurantoin then gentamicin, to ceftaxime, while low susceptibility was reported to ampicillin, imipenem and amikacin

For *Klebsiella* isolates in our study, most sensitivity was to amikacin (100%) followed by tobramycin (95.6%), meropenem (93.3%) and Imipenem (88.8%). Isolates were least sensitive was to amoxicillin + clavulanic (1.1%), ampicillin (2.2%), and ceftazidime (17.87%). Among these isolates, 2 (4.4%) were ESBL producer.

Faris[16], recorded that *Klebsiella spp* showed high susceptiblity to amikacin (84%) followed by cefotaxime (43%) and cephalothin (44%) and lowest susceptibility was reported to nitrofurantoin (23%), norfloxacin (28%), ciprofloxacin (11%), cotrimoxazole (18%) and ampicillin (21%).

CONCLUSION

In conclusion, CA-UTI is considered one of most common infections among female patients and is commonly caused by Gram-negative bacteria like *E. coli* and *klebsiella spp*. Inspite of the unrestricted use of antimicrobials, common uropathogens isolated in this study showed about 70% susceptibility to commonly used antibiotics in treatment of uncomplicated CA-UTI. This highlights the importance of reporting the pattern of antimicrobial susceptibility of pathogens causing CA-UTI which guides clinicians in prescribing empirical treatment correctly.

This manuscript has not been previously published and is not under consideration in the same or substantially similar form in any other reviewed media. I have contributed sufficiently to the project to be included as author. To the best of my knowledge, no conflict of interest, financial or others exist. All authors have participated in the concept and design, analysis, and interpretation of data, drafting and revising of the manuscript, and that they have approved the manuscript as submitted.

REFERENCES

1. Ahmed SS, Shariq A, Alsalloom AA, Babikir IH, Alhomoud, BN. Uropathogens and their antimicrobial resistance patterns: Relationship with urinary tract infections. International journal of health sciences,2019; 13(2), 48–55.
2. WHO Target product profiles for oral therapy of urinary tract infections. Geneva: World Health Organization; 2020. Licence: http://apps.who.int/iris
3. Otajevwo, F.D and Eriagbor, C. Asymptomatic urinary tract infection occurrence among students of a private university in western Delta, Nigeria. World Journal of Medicine and Medical Science.2014; 2: 455-463
4. Foxman B. Urinary tract infection syndromes: occurrence, recurrence, bacteriology, risk factors, and disease burden. Infect Dis Clin North Am. 2014; 28:1–13.
5. Chin TL, McNulty C, Beck C, MacGowan A. Antimicrobial resistance surveillance in urinary

tract infections in primary care. J Antimicrob Chemother. 2016;71(10):2723–8.

6. WHO. Global Priority List of Antibiotic-Resistant Bacteria to Guide Research, Discovery, and Development of New Antibiotics. Available online: https://www.who.int/medicines/publications/global-priority-list-antibiotic-resistant-bacteria/en/
7. Spring, S, Uncomplicated urinary tract infections: developing drugs for treatment: guidance for industry. US Department of Health and Human Services, Food and Drug Administration; 2019 (https://www.fda. gov/media/129531/download, accessed 4 February 2020).
8. Cheesbrough M. Medical laboratory Manual for tropical countries. 2007. In: Micobiology. 2nd edition, Cambridge Univ Press
9. Pfaller MA, Diekema DJ, Procop GW, Rinaldi MG. Multicenter comparison of the VITEK 2 yeast susceptibility test with the CLSI broth microdilution reference method for testing fluconazole against Candida spp. J Clin Microbiol. 2007; 45:796-802.
10. Clinical and Laboratory Standards Institute: Performance Standards for Antimicrobial Susceptibility Testing. 31th ed. CLSI supplement M100S. Wayne, PA: CLSI, 2022.
11. Tesfa T, Baye Y, Sisay M, Amare F and Gashaw T. Bacterial uropathogens and susceptibility testing among patients diagnosed with urinary tract infections at Hiwot Fana Specialized University Hospital, Eastern Ethiopia. 2021: Vol. 9. Pp 1-10 ps://doi.org/10.1177/20503121211001162
12. Mohapatra S, Panigrahy R, Tak V, Shwetha JV, Sneha KC, Chaudhuri S et al. Prevalence and resistance pattern of uropathogens from community settings of different regions: An experience from India. Access. Microbiol.2022; 4:000321.
13. Stefaniuk E, Suchocka U, Bosacka K, Hryniewicz W. Etiology and antibiotic susceptibility of bacterial pathogens responsible for community-acquired urinary tract infections in Poland. Eur J Clin Microbiol Infect Dis 2016; 35:1363–1369 DOI 10.1007/s10096-016-2673-1
14. Chervet D, Lortholary O, Zahar JR., Dufougeray A, Pilmis B, Partouche H: Antimicrobial resistance in community-acquired urinary tract infections in Paris in 2015. Médecine et maladies infectieuses.2017; 48 (2018) 188–192
15. Otajevwo FD, Amedu SS. Community Acquired Urinary Tract Infection Prevalence in a Tertiary Institution Based in Evbuobanosa, Edo State, Nigeria. Global Journal of Medical Research, 2015; vol.15, ver.3, pp. 53-64
16. Faris NS. Community-Acquired Urinary Tract Infection (Etiology and Bacterial Susceptibility). Journal of Biology, Agriculture and Healthcare. 2013; Vol.3, No.3, pp 36-41
17. Al-Mijalli SHS. Bacterial uropathogens in urinary tract infection and antibiotic susceptibility pattern in Riyadh Hospital, Saudi Arabia. Cell Mol Med 2017; 3: 1–6.