University of Thi-Qar Journal of Science (UTJsci)
E-ISSN: 2709-0256, P-ISSN: 1991-8690, Vol. 11, No. 1, Jun. 2024

Microbial Detection and Antibiotic Susceptibility patterns of Clinical Isolates from Women With Urinary Tract Infection in AL-Nasiriyah City/Iraq

Muna Faisal Jihad[1a*] and Manal Badi Salih[2b]
[1]Department of Biology, College of Science , University of Thi-Qar.Thi-Qar/64001,Iraq.

[a*] [b]Email: manalbadi_p@sci.utq.edu.iq
[a*]Corresponding author: Email: muna.jihad@ sci.utq.edu.iq

Received: 2024-02-15, Revised: 2024-02-29, Accepted: 2024-03-06, Published: 2024-06-01

Abstract*— Urinary tract infections (UTIs) in women are one of the most common diseases affecting at different ages of the life. This study was aimed to investigate the uropathogenes in women with UTI and to test their antibiotic susceptibility pattern. A total of 150 urine samples were collected from patients women and healthy in Thi-Qar Province, southern Iraq, between December 2022 and March 2023.Urine samples were collected from each participant women and cultured on media, then identified by different laboratory methods such as characteristic of colony on culture media, Gram stain, biochemical tests and morphologic chromatic properties on Hi UTI chromogenic agar and confirmed by API 20E system. The majority of females (44%) were the age groups 25 to 34 years followed by the (34%) patients were age group from 15 to 24 years. Antibiotic susceptibility testing for bacteria species was performed using the Kirby Bauer disc diffusion technique. Out of 136 different isolates with noticeable growth were found in the urine sample after microbiological cultures were performed, bacteria species was represented (63.24%) more than *Candida* species which was (36.76%). The most frequent bacterium was *Staphylococcus species* (40.69%) followed by *Escherichia coli* (18.60%). These bacterial exhibited extremely resistance to antibiotics. Gram positive isolates showed the highest resistant against Amoxicillin-clavulanate (100%), Ampicillin (100%), Oxacillin (100%), and Trimethoprim (91.66%), on the other hand Gram negative bacteria also showed the highest resistance against Amoxicillin-clavulanate (100%), Piperacillin (100 %), and both Ceftazidime and Nitrofurantoin (86.36 %). Other antibiotics showed different results by different bacterial species.

***Keywords*— Microbial infection, Antibiotic Resistance, UTI in women, MDR**

I. INTRODUCTION

Urinary tract infections (UTI) are among the most common clinical infections in health care and society, causing significant morbidity and mortality [1]. Urinary tract infections (UTIs) are inflammatory disorders caused by the presence and proliferated abnormally of microorganisms in the urinary system, which represents the most common infection in all age groups [2]. UTI are severe economic burden on the community and healthcare systems all over the world, and it is the most prevalent diseases that caused bacterial infection [3].Community acquired UTI are frequent problem affecting both genders but women more susceptive due to the distinctions in urogenital, reproductive anatomy, proximity of the urethra to gut opening , physiology and lifestyle [4],[5],[6]. There are different clinical manifestations of UTI such as cystitis, pyelonephritis, asymptomatic bacteriuria, chronic and recurrent UTIs, which may be classified as uncomplicated or complicated [7],[8]. The clinical appearance of a urinary tract infection depends on the type of causative agent, the severity of the disease, and the immune response of the infected person[9]. Clinically, UTI symptoms include dysuria, hematuria, fever, chills, flank pain, and bacteremia, which can lead to serious morbidity such hypertension, sepsis, and death [10],[11].

Urinary tract infections (UTIs) are caused by a variety of different bacteria, which differs depending on the patient's resistance, and the type of infection with these microorganisms [12]. The most common etiologic agents isolated from the urinary system are enteric Gram-negative rods, Gram-positive bacteria, and some fungi [13]. The most prevalent bacteria causing UTI is *Escherichia coli*, followed by *Klebsiella pneumoniae, Pseudomonas aeruginosa*, *Staphylococcus aureus Proteus mirabilis.*, *Enterococcus sp., and Enterobacter sp*. with variations in their sequence of prevalence [14]. Uropathogenic *Escherichia coli* (UPEC) is the most common causative agent for both uncomplicated urinary tract infection (uUTIs) and complicated urinary tract infection (cUTIs) caused approximately 80% of UTIs [15], in addition ,its virulence factors implicated in several pathways of UTI, including adhesion, immune evasion, toxin, and iron acquisition [16]. The susceptibility- patterns of uropathogens and species distribution varied substantially throughout time, geographic areas, and populations investigated [17].

In the past decade, bacteria with new virulence mechanisms and new modes of resistance to antimicrobial agents have emerged, due to the indiscriminate and excessive use of antibiotics, which has led to the rapid spread of bacterial strains resistant to all antibiotics [18]. Also various studies indicate that antibiotic resistance genes can spread among bacterial populations. This is due to their ability to repeatedly develop new resistance mechanisms [19]. The increasing incidence of therapy resistance among uropathogens poses major threat to

https://doi.org/10.32792/utq/utjsci/v11i1.1168

public health [20]. Therefore, to initiate appropriate empiric antibiotic therapy, prior knowledge of the causative organism and its antibiotic susceptibility pattern is necessary to prevent the increase of antibiotic resistance in urinary pathogens [2]. Thus, the study aimed to increase knowledge about diversity and abundance of uropathogens responsible for urinary tract infection in women and their antibiotic susceptibility patterns may help the clinicians to choose the right empirical treatment in AL-Nasiriyah city, southern Iraq.

II. MATERIALS AND METHODS

A. *Collection sample and cultivation*

150 urine samples collected from women with different ages attending to the Al Nasiriyaih Teaching Hospital, Bint Al Huda Hospital and private clinics for women in Thi-Qar Province, southern Iraq ,between December 2022 and March 2023 . These samples were collected using sterile urine container and cultured within 3hrs.of collection. All collected samples inoculated onto different culture media (such as Blood Agar, MacConkey’s Agar, Mannitol salt Agar, Nutrient Agar, SDA, Malt Extract Agar, and Brain heart- infusion broth and Agar) for the detection of aerobic bacteria and fungi species in the clinical medically microbiology laboratory of Public Health Laboratory

B. *Identification of Bacteria Strains*

Identification of bacterial species isolates using traditional microbiological techniques, including biochemical testing and culture microscopy. All bacteria collected from the urine samples were identified by cultural characteristics on Blood agar, MacConkey agar, Mannitol salt agar, Eosin methylene blue agar, and Hi chrom-UTI Agar. Furthermore, Furthermore, diagnosed with results biochemical tests including Oxidase- test, Catalase test, Coagulase- test, novobiocin tests, Gram stain properties and urease -test, IMVIC- test and Kligler iron Agar for Gram negative bacteria. Diagnosis confirmed with Api-20E System (Bio-Merieux, France) [21].

C. *Culture of Fungi*

Urine samples inoculated on to Sabouraud dextrose Agar and Malt Extract- Base Agar, supplemented with chloramphenicol then incubated (at 30 °C) under aerobic conditions for 72 hours. All isolates identified by laboratory methods such as characteristic of colony on culture media, Gram stain, germ tube, macroscopic appearance of colonies on Chromogenic agar compared to manufacturer-supplied standard color photos [22].

Table 1: Distribution of patients according to age groups

Age Groups in years	**Patients**		**Control**		**Total**	
	No.	**%**	**No.**	**%**	**No.**	**%**
15 – 24	37	34.26	14	33.33	51	34.00
25 – 34	50	46.30	16	38.10	66	44.00
35 – 44	12	11.11	5	11.90	17	11.33
> 44	9	8.33	7	16.67	16	10.67
Total	108	72.0	42	28.0	150	100
CalX2= 4.055 TabX2= 7.81 DF= 3 p. value 0.256						

D. *Antibiotic Susceptibility Testing*

For investigation the antimicrobial susceptibility pattern of aerobic bacteria isolated from women with UTI, performed onto Mueller–Hinton Agar (HiMedia Laboratories, India) using Kirby–Bauer disk diffusion method, then interpreted according to Clinical Laboratory Standard Institute guideline (CLSI- 22) [21], [23]. The following Gram negative bacteria were tested against 10 antibiotics for each type of bacteria, which included Amikacin AK, Ciprofloxacin CIP, Piperacillin PIP, Azithromycin AZM, Amoxicillin–clavulanate AMC, Gentamicin GEN, Ceftriaxone CRO , Nitrofurantoin NIT, Ceftazidime CAZ , Levofloxacin LEV ,while Gram positive bacteria was tested against 13 antibiotics for each type of bacteria, which included Amikacin AK, Ciprofloxacin CIP, Amoxicillin-clavulanate AM, Oxacillin OX, Azithromycin AZM, Ceftriaxone CTR, Norfloxacin NOR, Nitrofurantoin NIT ,Vancomycin VAN, Ampicillin AMP ,Doxycycline DXT, Levofloxacin LEV, Clindamycin CD, Trimethoprim TMP

E. *Statistical Analysis*

The current data were statistically analysis by using Statistical software program SPSS (Statistical Package of Social Science version 26),based in using both descriptive and, non-parametric, Descriptive Chi-Square , and independent sample t test at p. value < 0.05.

III. RESULTS

A. *Sampling and Patient Demographics*

One-hundred and fifty samples included of patients women and control group have been divided into four age groups in this study. The age group of females were (15-24), (25-34), (35-44), and (above 44 years). The study recorded the majority of both patients and control group were in the age (25-34) second group 46.3% and 38.10% respectively. The results recorded a non-significant difference at p. value < 0.05. as in Table 1

B. *Frequency of uropathogenes in current study*

The current study recorded among samples culture was positive for 86 (63.23%) for bacterial isolates and 50 *Candida spp.* (36.76%) for patients suffer with urinary tract infection and healthy group. Bacteria isolation showed that 82 urine samples of 108 patients were positive for culture with rate of 75.92%. As for control group three samples was positive for bacteria culture of 42 samples with rate of 7.14%.

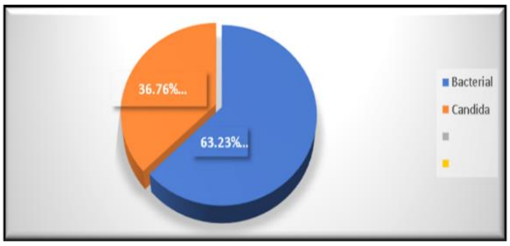
Table 3 : percentage of antimicrobial susceptibility test for Gram positive bacteria according to CLSI 2022 . The results recorded significant difference with p. value < 0.05.

Types of antibiotics	*S. aureus*			*Enterococcus*			*Streptococcus*		
	S	R	I	S	R	I	S	R	I
AMC	0	17 100%	0	0	6 100%	0	0	1 100%	0
CIP	11 64.7%	5 29.4%	1 5.9%	6 100%	0	0	1 100%	0	0
AK	14 82.4%	3 17.6%	0	6 100%	0	0	0	1 100%	0
NIT	5 29.4%	7 41.17%	5 29.4%	3 50%	2 33.3%	1 16.7%	0	1 100%	0
CRO	3 17.6%	14 82.4%	0	0	5 83.3%	1 16.7%	0	1 100%	0
GEN	14 82.4%	2 11.8%	1 5.9%	6 100%	0	0	1 100%	0	0
LEV	10 58.8%	6 35.3%	1 5.9%	5	1 16.66%	0	1 100%	0	0
VAN	4 23.5%	13 76.5%	0	3 50%	2 33.3%	1 16.7%	1 100%	0	0
OXA	0	17 100%	0	0	6 100%	0	0	1 100%	0
AZM	4 23.5%	12 70.6%	1 5.9%	2 33.3%	3 (50%)	1 16.7%	0	1 10%	0
NOR	13 76.4%	3 17.6%	1 5.9%	6 100%	0	0	1 10%	0	0
TMP	2 11.7%	15 88.2%	0	0	6 100%	0	0	1 10%	0
AMP	0	17 100%	0	0	6 100%	0	0	1 10%	0
S. aureus		$CalX^2 = 128.4$		$Tabx^2 = 36.42$		DF=24		P. value < 0.001	
Enterococcus		$CalX^2 = 76.81$		$Tabx^2 = 36.42$		DF=24		P. value < 0.001	
Streptococcus		$CalX^2 = 130.2$		$Tabx^2 = 21.03$		DF=12		P. value < 0.001	

Gram-negative bacteria were predominant; constituting 44 (51.16%) of the total 86 isolates, among seven different Gram-negatives bacterial species *Escherichia coli*. were the most frequently isolated species with (18.60%) followed by *Enterobacter cloacae* (12.79%), while *Pseudomonas. aeruginosa* isolates (8.14%), (5.81%) isolates diagnosed as *Klebsiella pneumonia*, isolates (3.49 %) diagnosed as *Proteus mirabilis* and one isolate (1.16%) diagnosed as both *Acinetobacter baumannii* and *Serratia Spp.*

Gram positive organisms constituted (48.83%) of total isolates, that include isolates (40.69%) were *Staphylococcus Spp.*, isolates (6.98%) diagnosed as *Enterococcus Spp*. and one isolate (1.16%) diagnosed as *Streptococcus* .*Staphylococcus Spp*. divided in two group that include isolates (19.77%) diagnosed as *S. aureus* and isolates (20.93%) diagnosed as *Staphylococcus epidermidis* .

The *Candida* identification was done on 50 isolates, which were included four *Candida* species (*C. albicans* (19.85%), *C. krusei* (8.82%), *C. glabrata* (5.88%), *and C. tropicalis* (2.21%). The results recorded a significant difference within bacteria isolated, and within *Candida* isolated, and between yeast and bacteria isolates at p. value < 0.05, Table 2, Figure 1



Figure(1): Overall incidence of bacteria and Candida spp. isolated in currents study.

Table 2: Percentages and kind of Isolates bacterial and *Candida spp*. in present study

Genus	No.	% Within same organism	% Of total isolate
Candida albicans	27	54.00	19.85
Candida krusei	12	24.00	8.82
Candida glabrata	8	16.00	5.88
Candida tropicalis	3	6.00	2.21
Total	50	100	36.76
Escherichia coli	16	18.60	11.76
Enterobacter cloacae	11	12.79	8.09
Klebsiella pneumoniae	5	5.81	3.68
Pseudomonas aeruginosa	7	8.14	5.15
Proteus mirabilis	3	3.49	2.21
Serratia marcescens	1	1.16	0.74
Acinetobacter baumannii	1	1.16	0.74
Staphylococcus aureus	17	19.77	12.50
Staphylococcus epidermidis	18	20.93	13.24
Enterococcus spp.	6	6.98	4.41
Streptococcus spp.	1	1.16	0.74
Total	86	100	63.24
For *Candida spp*.	CalX^2= 51.3	TabX^2= 7.81	DF= 3 p. value < 0.001
For Bacteria	CalX^2= 38.4	TabX^2= 15.51	DF= 8 p. value < 0.001
Both	CalX^2= 98.8	TabX^2= 21.03	DF= 12 p. value < 0.001

C. *Antibiotic Susceptibility Test*

Antibiotic susceptibility test was applied to 68 pathogenic bacterial isolates performed on Muller Hinton agar by modified Kirby Bauer disc diffusion method. *S. epidermidis* was excluded from antibiotic susceptibility because it considers a part of normal human flora. The results demonstrated that bacterial isolates varied in their resistance and sensitivity to antibiotic. Gram positive uropathogenic bacterial isolates showed high resistant against Amoxicillin-clavulanate (100%), Ampicillin (100%), Oxacillin (100%), Trimethoprim (91.66%). On the other hand, Gram negative bacteria isolates exhibited the highest resistance to Amoxicillin-clavulanate (100%), Piperacillin (100 %), Ceftazidime (86.36%), Nitrofurantoin (86.36 %). All isolates were high sensitive to Amikacin ,Gentamicin , and Ciprofloxacin ,while other antibiotics showed different results by different bacterial species (Table 3, 4). The results recorded significant difference with p. value < 0.05 sample petri dishes of Muller Hinton medium demonstrated isolates varied in their resistance and sensitivity to antibiotics used in our study as shown in the figure (2)

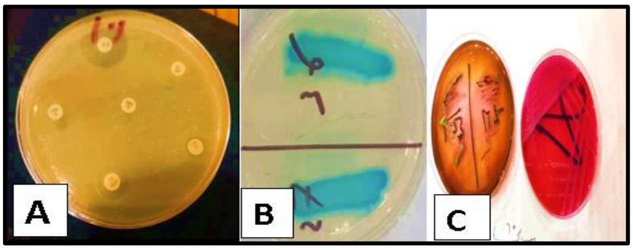


Figure 2:Antimicrobial susceptibility Test for bacterial isolate **A**, *Enterococcus* on HI UTI chromo agar **B**, *E. coli* on EMB agar and Mac .agar **C**

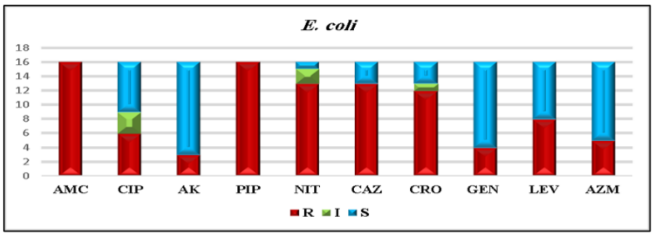


Figure 3: Antibiotic susceptibility pattern of *E.coli* to various antibiotics

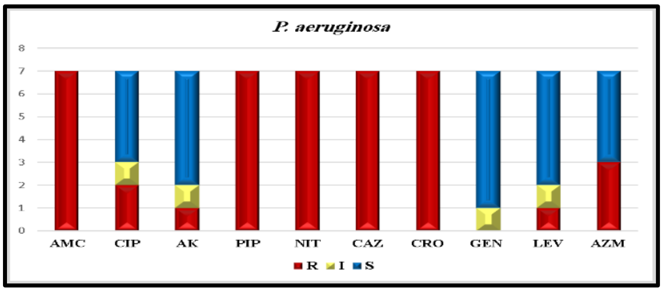


Figure 4: Antibiotic susceptibility pattern of *Pseudomonas aeruginosa*

Table 4 : Antibiotic susceptibility pattern of Gram-negative bacteria and the results also, recorded significant difference at p. value < 0.05

Bacterial spp.	**%**	**AMC**	**CIP**	**AK**	**PIP**	**NIT**	**CAZ**	**CRO**	**GEN**	**LEV**	**AZM**
E.coli	R	100	37.5	18.75	100	81.25	81.25	75	25	50	31.25
	I	0	18.75	0	O	12.5	0	6.25	0	0	0
	S	0	43.75	81.25	0	6.25	18.75	18.75	75	50	68.75
Enterobacter	R	100	72.72	0	100	81.81	90.90	72.72	27.27	72.72	18.18
	I	0	9.09	0	O	9.09	0	9.09	0	0	0
	S	0	18.18	100	0	9.09	9.09	18.18	72.72	27.27	81.81
Klebsiella	R	100	20	0	100	100	60	40	0	20	20
	I	0	0	0	O	0	20	20	0	0	0
	S	0	80	100	0	0	20	40	100	80	80
Proteus	R	100	66..66	33.33	100	100	100	100	66.66	100	66.66
	I	0	33.33	0	0	0	0	0	0	0	0
	S	0	O	66.66	0	0	0	0	33.33	0	33.33
Pseudomonas	R	100	28.57	14.28	100	100	100	100	0	14.28	42.85
	I	0	14.28	14.28	0	0	0	0	14.28	14.28	0
	S	0	57.14	71.42	O	0	0	0	85.71	71.42	57.14
Serratia	R	100	100	0	100	0	100	100	0	0	100
	I	0	0	0	0	100	0	0	0	0	0
	S	0	0	100	O	0	0	0	100	100	0
Acinetobacter	R	100	0	0	100	100	100	100	0	0	0
	I	0	0	0	0	0	0	0	0	0	0
	S	0	100	100	0	0	0	0	100	100	100
Total Susceptibility%	R	100	43.18	11.36	100	86.36	86.36	77.27	20.25	47.72	31.81
	I	O	13.63	2.27	0	9.09	2.27	6.81	2.27	2.27	0
	S	O	43.18	86.36	0	4.54	11.36	15.90	77.27	50	68.18
$CalX^2$= 219.5 $TabX^2$= 28.87 DF= 18 p .value < 0.001											

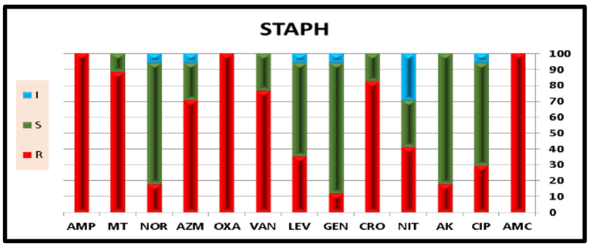


FIGURE 5: ANTIBIOTIC SUSCEPTIBILITY PATTERN OF *S.*

IV. DISCUSSION

Urinary tract infections (UTIs) are most prevalent infectious diseases in developing countries with high economic cost [24]. The prevalence difference of women with UTI has been observed among different age groups. This variation in age suggests crucial risk factor associated with UTI. It can be seen from this study that the age groups 15 to 24 and 25to 34 had the highest number of positive cases. The elevated prevalence recorded among young group would be due to this is evident from the fact that women in these age groups are more sexually active and are thus expected to have higher incidence [2]. Those at the older age above 35 had the lowest number and hence the lowest incidence. The results in this study correspond with the results in Kurdistan Region, Iraq [1]. Dissimilarity results indicated UTI the most common infection among elderly populations [25].

In current study, the frequency of positive cultures for microorganisms isolated from urine samples (90%). The results in present study in accordance with previous studies in Ethiopia [26], and convergence with other studies [27] and [28].The finding is higher than reported conducted in Baghdad city, Iraq [29] and Italy [30]. The differences could be attributed to geographical variations where the studies conducted as well as sample size, sanitation status, educational level, awareness, community customs and sexual traditions [29].

UTIs caused by Gram-positive and Gram-negative bacteria and fungi, but bacterial species more predominant uropathogens compared to other groups of microorganisms [31]. In current study, bacterial species were predominantly cultured (57.33%) compared with fungal species (33.33%). This result come to an agreement with those previous study [54] [26] and [29]. Among the isolates, Gram-negative bacteria and Gram-positive bacteria constituted 51.16% and 48.83%, respectively. Highest prevalence of gram-negative bacteria during this study is agreement with that reported by [32] and [33]. On the other hand , the our finding differed with other studies that showed a different observation [34] and [9]. The difference in the incidences of Gram positive and Gram negative bacterial UTIs etiologies may be attributed to differences in methodologies employed, socioeconomic conditions, the personal hygiene standard and the education level [24]. According to the current study's bacterial identification, *Staphylococcus spp*. account for 40% of all isolated strains among Gram-positive bacteria, with *Staphylococcus aureus* accounting for 19.76% and *Staphylococcus epidermidis* for 20%. The high frequency of *Staphylococcus spp*. in our data is concurred with the study reported by [35] and [36], while our finding's contradicts with those of [37]. Moreover, this study showed that *Staphylococcus aureus* are the most common etiological agents causing UTIs in current study. The results of the present study corresponds with those of [38] and [39].The results of the current study differed with other studies in Saudi Arabia [30]. The high frequency of *S. aureus* in present study was attributable to its virulence, low growth requirements, and capacity to survive long periods in unfavorable environments [25]. However, *Staphylococcus epidermidis* was considers a part of normal human flora [22]. This organism can be spread by the hands, expelled from the respiratory tract or transmitted by animate or inanimate objects [40].The occurrence of *S. epidermidis* 20% in our study is comparable with study reported by [41]. In the present study, among seven different Gram-negative bacteria were the most prominent uropathogens *Escherichia coli* .These results are in agreement with those of [42]. In this study, *E. coli* was the second as a uropathogen isolated from all isolated cases, this results in line with the data reported in Iraq [43]. Whereas these results disagree with [44]. The reason for the most prominent uro-pathogenic *Escherichia coli* due to their unique structures and number of virulence factors such as flagella, pili, which help attach to uroepithelium. Furthermore, microorganisms spreading from per urethral areas contaminated with fecal flora due to proximity to anus and warm, moist environment to the urethra and bladder lead to increase the risk infection [45]and [28].

Antibiotics are necessary to treatment bacterial infections. However, their effectiveness relies on susceptibility of pathogenic bacteria. Therefore, understanding bacterial susceptibility patterns to antibiotics is critical for management of all types of bacterial infections [28]. In our study, both gram positive and gram-negative bacteria isolated were resistant to different classes of antibiotics. Among the gram-positive isolates, the high resistance 100% observed in *S. aureus* for Amoxicillin –clavulanate, Ampicillin and Oxacillin. This finding in agreement with previous studies in Iraq [46] and Libya [25]. The high resistance of *S. aureus* may produce penicillinase enzymes and other penicillin-binding proteins that help organism convert resistant to Beta -lactam antibiotic, in addition other resistance mechanisms and uncontrolled use of antibiotics [47].Higher sensitivity of Gram-positive isolates for Gentamicin, Amikacin , Norfloxacin , and Ciprofloxacin in current study is agreement with those of [34] and [47]. The present study showed that *Staph. aureus* isolates were highly susceptible with rate 82.4% for both Gentamycin and Amikacin. These results were consistent to that reported by [48], where they recorded a sensitive rate 80% for gentamicin , On the other hand, these results were compatible with similar studies performed by [47]. Who recorded a resistance rate 20% for amikacin [47]. This may be because injectable forms of gentamicin and amikacin are accessible, but tablets are not, and limiting usage in community care settings lessens the potential for abuse [26], [47]. In addition, these variation in the susceptibility pattern of *Staphylococcus aureus* can be related to environmental difference like overuse and misuse of antibiotics, which led to the developing resistant strains [49].

In current study, all Gram-negative bacterial isolates exhibited significant resistance towards most antibiotics, such as Amoxicillin-clavulanate and piperacillin. These resistances of Gram-negative bacterial isolates were agreement with previous study from Iraq [50]. The development of resistance has several risk factors associated with severity of infection and resistance linked with increase mortality [51] . The most efficient antibiotics on Gram-negative bacteria were amikacin, gentamicin, Azithromycin, and levofloxacin. The findings were congruent with those of [38]. *Escherichia coli*, major Gram-negative isolate in present study, demonstrated 100% resistance towards Amoxicillin-clavulanate and piperacillin. These results are in agreement with those of [1]. Other gram-negative bacteria *Pseudomonas aeruginosa* were also increasing antimicrobial resistance against five antibiotics: amoxicillin/clavulanate, nitrofurantoin, piperacillin, ceftazidime, and ceftriaxone. A similar result was reported [31] and [43]. All bacterial isolates of current study demonstrated resistance to at least three antimicrobials (MDR) and no isolate susceptible to all antimicrobials tested. This correlates with study conducted by [52]. The increase incidence of MDR reported in our study due to frequent use or prolonged exposure uro-pathogens to antibiotics [1].Frequently use of antibiotics can damage the microflora surrounding the urethra, which allowing urinary pathogens to colonize and damage the urinary tract [53]. Furthermore, Because of this condition, bacteria can exchange genetic material with one another through horizontal gene transfer, producing resistance genes that give resistance to specific antibiotics [54]. In almost all cases of urinary tract infection, treatment with empiric antibiotics is initiated before urine culture results are available. Therefore, misuse antibiotic therapy increases resistance to antibiotics among urinary pathogens. Numerous studies emphasize the need of appropriately using antibiotics, in order to overcome this issue resistance of antibiotic [55]. However, continuous monitoring with reporting of antimicrobial resistance patterns is important for assist physicians in treating as well as managing infections caused by uropathogens that exhibit multidrug resistance patterns.

V. CONCLUSION

Bacterial Infection In The Urinary Tract Represent Significant Health Concern Among Women. The Current Study Shows *S. Aureus* And *E. Coli* Were The Predominant Uropathogens. Selection Of Antimicrobials For Uti Should Be Guided By Culture And Sensitivity And Empirical Adjunctive Therapy

Must Be Considered On The Recent Antibiogram. Gentamicin And Amikacin Are Suitable For Empirical Therapy

ACKNOWLEDGMENT

We would like to thank all of the investigators and supervisors who participated in the reflection's writing our manuscript.

ETHICAL CONSIDERATION

To conduct ethical research, permission was obtained from the hospital and all those involved in this work, and the selection of the patient was accomplished with the assistance of gynecologists at the hospital and private clinics in Thi Qar Governorate.

CONFLICT OF INTEREST

Authors declare that they have no conflict of interest.

REFERENCES

[1] M. Mirzarazi, S. E. Rezatofighi, M. Pourmahdi, and M. R. Mohajeri, "Antibiotic resistance of isolated gram negative bacteria from urinary tract infections (UTIs) in Isfahan," *Jundishapur J. Microbiol.*, vol. 6, no. 8, pp. 6–10, 2013, doi: 10.5812/jjm.6883.

[2] G. Liu, L. E. Thomsen, and J. E. Olsen, "Antimicrobial-induced horizontal transfer of antimicrobial resistance genes in bacteria: A mini-review," *J. Antimicrob. Chemother.*, vol. 77, no. 3, pp. 556–567, 2022, doi: 10.1093/jac/dkab450.

[3] M. A. K. Al-saadi, N. M. S. Al-hilli, and N. A. Sheriff, "Association of TLR4 Polymorphisms with Susceptibility to Urinary Tract Infection Caused by Gram Positive Bacteria in Pregnant Women," *Indian J. Public Heal. Res. Dev.*, vol. 11, no. 6, 2020, doi: 10.37506/ijphrd.v11i4.9201.

[4] F. R. DeLeo, B. A. Diep, and M. Otto, "Host Defense and Pathogenesis in Staphylococcus aureus Infections," *Infect. Dis. Clin. North Am.*, vol. 23, no. 1, pp. 17–34, 2009, doi: 10.1016/j.idc.2008.10.003.

[5] C. Elias, L. Moja, D. Mertz, M. Loeb, G. Forte, and N. Magrini, "Guideline recommendations and antimicrobial resistance: The need for a change," *BMJ Open*, vol. 7, no. 7, pp. 1–8, 2017, doi: 10.1136/bmjopen-2017-016264.

[6] S. Selim *et al.*, "Incidence of Vancomycin-Resistant Staphylococcus aureus Strains among Patients with Urinary Tract Infections," *Antibiotics*, vol. 11, no. 3, pp. 1–8, 2022, doi: 10.3390/antibiotics11030408.

[7] F. S. Pasillas Fabian, R. Cremades, E. Sandoval Pinto, C. Beas Ruiz Velasco, C. J. Hernandez Rios, and E. Sierra-Diaz, "Microbiological profile of urinary tract infections in a tertiary medical facility in Western Mexico: An update," *Sci. Prog.*, vol. 104, no. 1, pp. 1–13, 2021, doi: 10.1177/00368504211000886.

[8] H. Mousa and T. Abd Al-Amir, "Infections in Urinary Tract among Pregnant Women in Nasiriya City, Iraq," *Univ. Thi-Qar J. Sci.*, vol. 10, no. 1, pp. 117–121, 2023, doi: 10.32792/utq/utjsci/v10i1.1039.

[9] P. Ramart and A. L. Ackerman, "Recurrent Urinary Tract Infection in Women from a Urologist's Perspective," *Siriraj Med. J.*, vol. 75, no. 1, pp. 55–61, 2023, doi: 10.33192/smj.v75i1.260531.

[10] A. Ullah, "Prevalence of symptomatic urinary tract infections and antimicrobial susceptibility patterns of isolated uropathogens in kohat region of Pakistan," *MOJ Biol. Med.*, vol. 3, no. 2, 2018, doi: 10.15406/mojbm.2018.03.00082.

[11] A. A. Al-Naqshbandi, M. A. Chawsheen, and H. H. Abdulqader, "Prevalence and antimicrobial susceptibility of bacterial pathogens isolated from urine specimens received in rizgary hospital — Erbil," *J. Infect. Public Health*, vol. 12, no. 3, pp. 330–336, 2019, doi: 10.1016/j.jiph.2018.11.005.

[12] B. Kot, "Antibiotic Resistance among Uropathogenic Escherichia coli," *Polish J. Microbiol.*, vol. 68, no. 4, pp. 403–415, 2019, doi: 10.33073/PJM-2019-048.

[13] S. ISA, K. MUSTAPHA Y, J. HAMZA A, and S. RASHIDA, "Evaluation of the Incidence of Uropathogenic Bacteria Among Pregnant Women Attending Antenatal Clinic Doma Hospital Gombe," *Bima J. Sci. Technol.*, vol. 6, no. 03, pp. 129–135, 2022, doi: 10.56892/bima.v6i03.60.

[14] Muna F. Jahad and Mohammed Hashim AL-Yasiri, "Microbial Infections Associated with Diabetic Foot Ulcer in Nasiriyah City," *Indian J. Forensic Med. Toxicol.*, vol. 15, no. 2, pp. 2887–2892, 2021, doi: 10.37506/ijfmt.v15i2.14808.

[15] I. Khatoon, S. Khanam, A. Azam, S. Qadeer, S. Naz, and N. U. Hassan, "Incidence Pattern, Antibiotic Susceptibility Pattern and Associated

Risk Factors of Bacterial Uropathogens Among General Population of Pakistan,” *Infect. Drug Resist.*, vol. 16, no. 6, pp. 4995–5005, 2023, doi: 10.2147/IDR.S418045.

[16] B. S. Fazly Bazzaz, S. Darvishi Fork, R. Ahmadi, and B. Khameneh, “Deep insights into urinary tract infections and effective natural remedies,” *African J. Urol.*, vol. 27, no. 1, pp. 1–13, 2021, doi: 10.1186/s12301-020-00111-z.

[17] B. John *et al.*, “Occurrence of Staphylococcus associated with Urinary Tract Infections among women attending Ibrahim Badamasi Babangida (IBB) specialist hospital, Minna, Nigeria.,” *Tanzan. J. Health Res.*, vol. 24, no. 2, pp. 17–30, 2023, doi: 10.4314/thrb.v24i2.2.

[18] E. N. AKYOL ONDER and P. ERTAN, “Antibiotic Resistance Patterns in Pediatric Urinary Tract Infections: A Comparison Between 2013-2015 and 2019-2021,” *Celal Bayar Üniversitesi Sağlık Bilim. Enstitüsü Derg.*, vol. 9, no. 3, pp. 381–385, 2022, doi: 10.34087/cbusbed.1076551.

[19] G. Shaheen *et al.*, “Therapeutic potential of medicinal plants for the management of urinary tract infection: A systematic review,” *Clin. Exp. Pharmacol. Physiol.*, vol. 46, no. 7, pp. 613–624, 2019, doi: 10.1111/1440-1681.13092.

[20] R. D. Klein and S. J. Hultgren, “Urinary tract infections: microbial pathogenesis, host–pathogen interactions and new treatment strategies,” *Nat. Rev. Microbiol.*, vol. 18, no. 4, pp. 211–226, 2020, doi: 10.1038/s41579-020-0324-0.

[21] S. Sahel and I. Abid, “Phenotypic detection of extended spectrum beta-lactamases (ESBLs) in Gram-negative bacilli isolated from deferent clinical source,” *Univ. Thi-Qar J. Sci.*, vol. 9, no. 2, pp. 46–49, 2022, doi: 10.32792/utq/utjsci/v9i2.902.

[22] G. D. Christensen *et al.*, “crossm CLSI Methods Development and Standardization Working,” *J. Clin. Microbiol.*, vol. 56, no. 4, pp. 1–10, 2018.

[23] Ö. Kandemir, A. Akdağ, and A. Öne Kurt, “Antibiotic susceptibility of bacterial strains isolated from patients with community acquired urinary tract infections in mersin,” *TAF Prev. Med. Bull.*, vol. 11, no. 5, pp. 589–598, 2012, doi: 10.5455/pmb.1-1321538566.

[24] M. Shirvani, A. Keramati, and M. Esmaeli, “Evaluating the pattern of antibiotic resistance of urinary tract infection (UTI)-causing bacteria in the urine culture samples of patients in the infectious ward of Imam Khomeini Hospital, Kermanshah, in Iran from 2016–2018,” *African J. Urol.*, vol. 29, no. 1, pp. 1–11, 2023, doi: 10.1186/s12301-023-00364-4.

[25] M. A. Mohammed, T. M. S. Alnour, O. M. Shakurfo, and M. M. Aburass, “Prevalence and antimicrobial resistance pattern of bacterial strains isolated from patients with urinary tract infection in Messalata Central Hospital, Libya,” *Asian Pac. J. Trop. Med.*, vol. 9, no. 8, pp. 771–776, 2016, doi: 10.1016/j.apjtm.2016.06.011.

[26] H. A. Salih and A. T. Abbas, “Microorganism Prevalence and Antibiotic Sensitivity for Imipenem and Meropenem in Patients with Diabetic Foot Ulcers in Thi Qar, Iraq,” *J. Pharm. Negat. Results*, vol. 13, no. S01, pp. 1047–1051, 2022, doi: 10.47750/pnr.2022.13.s01.125.

[27] G. E. A. Dogonchi AA Ardebili A Yazdansetad S and P. A, “Metallo-β-lactamase-mediated resistance among clinical carbapenem-resistant,” *Tzu Chi Med. j*, vol. 30, no. 2, pp. 90–96, 2018, doi: 10.4103/tcmj.tcmj.

[28] H. Jassim, “The Prevalence of blaCTX-M, blaTEM Genes in Bacteria Isolated From Bladder Cancer Patients with Urinary Tract Infections,” *Univ. Thi-Qar J. Sci.*, vol. 10, no. 1, pp. 16–26, 2023, doi: 10.32792/utq/utjsci/v10i1.919.

[29] F. M. Al-Asady, D. A. Al-Saray, and A. E. Al-Araji, “Screening of urinary tract bacterial infections and their antibiogram among non-pregnant women admitted to Al-Sadiq hospital, Iraq,” *AIP Conf. Proc.*, vol. 2386, no. 1, pp. 1–9, 2022, doi: 10.1063/5.0066884.

[30] A. L. Flores-Mireles, J. N. Walker, M. Caparon, and S. J. Hultgren, “Urinary tract infections: Epidemiology, mechanisms of infection and treatment options,” *Nat. Rev. Microbiol.*, vol. 13, no. 5, pp. 269–284, 2015, doi: 10.1038/nrmicro3432.

[31] P. Behzadi, E. Urbán, M. Matuz, R. Benkő, and M. Gajdács, “The Role of Gram-Negative Bacteria in Urinary Tract Infections: Current Concepts and Therapeutic Options,” *Adv. Exp. Med. Biol.*, vol. 1323, no. 6, pp. 35–69, 2021, doi: 10.1007/5584_2020_566.

[32] G. Mancuso, A. Midiri, E. Gerace, M. Marra, S. Zummo, and C. Biondo, “Urinary Tract Infections: The Current Scenario and Future Prospects,” *Pathogens*, vol. 12, no. 4, pp. 1–17,

2023, doi: 10.3390/pathogens12040623.

[33] M. Negri, R. dos S. B. R. W. Bárbara Martins Lima, R. A. S. Molina, L. C. de S. Carla Maria, Germano, Débora Gusmão Melo, Avó, and L. R. da S. De, “Prevalence and antimicrobial resistance profile of pathogens isolated from patients with urine tract infections admitted to a university hospital in a medium-sized Brazilian city,” *Rev. Inst. Med. Trop. Sao Paulo*, vol. 4, no. 1, pp. 1–7, 2010, [Online]. Available: http://kiss.kstudy.com/journal/thesis_name.asp?tname=kiss2002&key=3183676

[34] Y. Alhamadani and A. Oudah, “Study of the Bacterial Sensitivity to different Antibiotics which are isolated from patients with UTI using Kirby-Bauer Method,” *J. Biomed. Biochem.*, vol. 1, no. 2, pp. 1–5, 2022, doi: 10.57238/jbb.2022.19387.

[35] A. Halinski *et al.*, “Spectrum of Bacterial Pathogens from Urinary Infections Associated with Struvite and Metabolic Stones,” *Diagnostics*, vol. 13, no. 1, pp. 1–10, 2023, doi: 10.3390/diagnostics13010080.

[36] M. Drahansky *et al.*, “Estimation of Some Plant Extract Activity against Bacterial Cystitis Isolated from Urinary Tract Infection,” in *Intech*, no. 2, 2016, p. 13. doi: http://dx.doi.org/10.5772/57353.

[37] A. Bitew, T. Molalign, and M. Chanie, “Species distribution and antibiotic susceptibility profile of bacterial uropathogens among patients complaining urinary tract infections,” *BMC Infect. Dis.*, vol. 17, no. 1, pp. 1–8, 2017, doi: 10.1186/s12879-017-2743-8.

[38] S. A. Ali, S. Mandal, A. Georgalas, and S. A. D. Gilani, “A Pattern of Antibiotic Resistance in Gram-Negative Rods Causing Urinary Tract Infection in Adults,” *Cureus*, vol. 13, no. 1, pp. 1–6, 2021, doi: 10.7759/cureus.12977.

[39] W. D. Seifu and A. D. Gebissa, “Prevalence and antibiotic susceptibility of Uropathogens from cases of urinary tract infections (UTI) in Shashemene referral hospital, Ethiopia,” *BMC Infect. Dis.*, vol. 18, no. 1, pp. 1–9, 2018, doi: 10.1186/s12879-017-2911-x.

[40] S. Choubey and M. Verma, “Common cause of UTI and its regimen a review paper,” *J. Adv. Microbiol. Res. 2022;*, vol. 3, no. 2, pp. 83–86, 2022.

[41] Q. hassan Aubais aljelehawy, L. H. Hadi Alshaibah, and Z. K. Abbas Al- Khafaji, “Evaluation of virulence factors among Staphylococcus aureus strains isolated from patients with urinary tract infection in Al-Najaf Al-Ashraf teaching hospital,” *Cell. Mol. Biomed. Reports*, vol. 1, no. 2, pp. 78–87, 2021, doi: 10.55705/cmbr.2021.144995.1017.

[42] T. E., T. M., M. Y., K. B., and S. T., “Asymptomatic urinary tract infection among pregnant women attending the antenatal clinic of Hawassa Referral Hospital, Southern Ethiopia.,” *BMC Res. Notes*, vol. 7, p. 155, 2014, [Online]. Available: http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L373978494%5Cnhttp://dx.doi.org/10.1186/1756-0500-7-155%5Cnhttp://sfx.hul.harvard.edu/sfx_local?sid=EMBASE&issn=17560500&id=doi:10.1186%2F1756-0500-7-155&atitle=Asymptomatic+urinary+

[43] A. H. Mohamed, N. M. S. Omar, M. M. Osman, H. A. Mohamud, A. Eraslan, and M. Gur, “Antimicrobial Resistance and Predisposing Factors Associated with Catheter-Associated UTI Caused by Uropathogens Exhibiting Multidrug-Resistant Patterns: A 3-Year Retrospective Study at a Tertiary Hospital in Mogadishu, Somalia,” *Trop. Med. Infect. Dis.*, vol. 7, no. 3, pp. 1–9, 2022, doi: 10.3390/tropicalmed7030042.

[44] Y. A. Gessese *et al.*, “Urinary pathogenic bacterial profile, antibiogram of isolates and associated risk factors among pregnant women in Ambo town, Central Ethiopia: A cross-sectional study,” *Antimicrob. Resist. Infect. Control*, vol. 6, no. 1, pp. 1–10, 2017, doi: 10.1186/s13756-017-0289-6.

[45] A. Girma and A. Aemiro, “The Bacterial Profile and Antimicrobial Susceptibility Patterns of Urinary Tract Infection Patients at Pawe General Hospital, Northwest Ethiopia,” *Scientifica (Cairo).*, vol. 2022, no. 3, pp. 1–8, 2022, doi: 10.1155/2022/3085950.

[46] B. S. Alsaywid *et al.*, “Urinary tract infection in children: A narrative review of clinical practice guidelines,” *Urol. Ann.*, vol. 15, no. 2, pp. 113–132, 2023, doi: 10.4103/ua.ua_147_22.

[47] V. Folliero *et al.*, “Prevalence and antimicrobial susceptibility patterns of bacterial pathogens in urinary tract infections in university hospital of campania ‘luigi vanvitelli’ between 2017 and 2018,” *Antibiotics*, vol. 9, no. 5, pp. 1–9, 2020,

doi: 10.3390/antibiotics9050215.

[48] C. Smoglica *et al.*, “Antimicrobial Resistance Profile of Bacterial Isolates from Urinary Tract Infections in Companion Animals in Central Italy,” *Antibiotics*, vol. 11, no. 10, pp. 1–14, 2022, doi: 10.3390/antibiotics11101363.

[49] S. Kumar, P. L. Kashyap, R. Singh, and A. K. Srivastava, “Preservation and Maintenance of Microbial Cultures,” in *Analyzing Microbes*, 2013, pp. 135–152. doi: 10.1007/978-3-642-34410-7_11.

[50] M. N. A. Al-Muaala, S. Y. A. Al-Ethari, A. A. I. Al-Kraety, and G. S. Al-Muhanna, “Molecular Detection of Clumping factor A gene and Antibiotic Susceptibility Evaluation of Staphylococcus Aureus Isolated from Urinary Tract Infections,” *Arch. Razi Inst.*, vol. 77, no. 2, pp. 573–578, 2022, doi: 10.22092/ARI.2022.357153.1985.

[51] L. Deltourbe, L. Lacerda Mariano, T. N. Hreha, D. A. Hunstad, and M. A. Ingersoll, “The impact of biological sex on diseases of the urinary tract,” *Mucosal Immunol.*, vol. 15, no. 5, pp. 857–866, 2022, doi: 10.1038/s41385-022-00549-0.

[52] G. Gebremariam, H. Legese, Y. Woldu, T. Araya, K. Hagos, and A. Gebreyesuswasihun, “Bacteriological profile, risk factors and antimicrobial susceptibility patterns of symptomatic urinary tract infection among students of Mekelle University, northern Ethiopia,” *BMC Infect. Dis.*, vol. 19, no. 1, pp. 1–11, 2019, doi: 10.1186/s12879-019-4610-2.

[53] S. Malik, J. S. Rana, and K. Nehra, “Prevalence and Antibiotic Susceptibility Pattern of Uropathogenic Escherichia Coli Strains in Sonipat Region of Haryana in India,” *Biomed. Biotechnol. Res. J.*, vol. 13, no. 3, pp. 80–87, 2021.

[54] A. La Vecchia *et al.*, “Epidemiology and antimicrobial susceptibility of Staphylococcus aureus in children in a tertiary care pediatric hospital in Milan, Italy, 2017—2021,” *Ital. J. Pediatr.*, vol. 48, no. 1, pp. 1–8, 2022, doi: 10.1186/s13052-022-01262-1.

[55] N. Ehiaghe, J. I, Amengialue, O.O, Ehiaghe, F.A, Maduka, “Plasmid Profile of Bacterial Isolates from Asymptomatic Bacteriuria among Undergraduate Students of a Tertiary Institution in Benin city, Nigeria,” *Niger. J. Microbiol.*, vol. 34, no. 1, pp. 5007–5017, 2020.