ORIGINAL ARTICLE

Prevalence of Multidrug and Extensive drug resistance of bacterial isolates from different clinical sources in Tikrit Teaching Hospital-Iraq

[1]Abdalmohaimen M. Suood*, [2]Kadhim K. Kadhim, [3]Falah S. Dawood, [4]Saade A. Jasim

[1]Department of Biology, University of Tikrit, Collage of Education for Pure Sciences, Tikrit, Iraq.
[2]Directorate of Babylon Education, Ministry of Education, Babylon, Iraq
[3]Department of Home Economics, College of Education for Girls, Tikrit University, Tikrit, Iraq
[4]Medical Laboratory Techniques Department, College of Health and Medical Technology, Al-maarif University, Anbar, Iraq, 31001

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Corresponding Author:
Abdalmohaimen Mohammed Suood
Department of Biology, University of Tikrit, Collage of Education for Pure Sciences, Tikrit, Iraq.
a.m.suood@tu.edu.iq

ABSTRACT

Background*: The most prevalent hospital issues globally are multidrug resistant (MDR) and extensive drug resistant (XDR) pathogens.* ***Objective****: The study aimed to identify and profile various antibiotic-resistant isolates in Tikrit Teaching Hospital.* ***Methodology****: The study at Tikrit Teaching Hospital in Iraq involved collecting 197 samples from various clinical sources and incubating them in various culture media for growth and identification.* ***Results****: Of 197 samples obtained from different clinical sources, 177 were pathogen-infected isolates. Urine was the most common sample source (71.5%), with females collecting more samples than males (90.3%). Staphylococcus aureus had a higher frequency (52%), while other bacteria had lower frequencies such as Escherichia coli, Klebsiella spp, Streptococcus spp, Pseudomonas aeroginosa and Proteus spp (26.6%, 7.3%, 12.5%, 1.1%, and 0.5%). The study assessed the susceptibility and resistance of common antimicrobial isolates, revealing a high resistance rate for all antibiotics, including Staphylococcus aureus (70.9%), Escherichia coli (77%), Klebsiella spp (79.8%), and Streptococcus spp (64.8%).The prevalence of MDR isolates was also high for Staphylococcus aureus, Escherichia coli, Klebsiella spp and Streptococcus spp (61.9%, 68%, 77% and 54.5%) and lower for XDR (6.5%,17%, 23% and 9%). The study showed no pan-drug resistance (PDR) isolates, but a higher MDR bacteria rate (65.3%) in the studied isolates, compared with lower rates in XDR (13.9%) and non-MDR isolates (20.8%).* ***Conclusions****: The finding indicate that pathogenic bacteria have developed resistance to 22 antimicrobial agents and spread of more MDR isolates than XDR and non-MDR isolates among isolated bacteria from Tikrit Teaching Hospital.*

INTRODUCTION

The use of antibiotic therapy for invasion pathogens in human host has been known for many years. Antibacterial therapy is a significant medical achievement in the 20th century, preventing millions of premature deaths due to bacterial infections. Before this, the only medical solution for wound infections was often amputation, especially during disasters[1]. Antibiotics have profoundly changed the old protocol that was used to treat and cure bacterial diseases. Unsettlingly, the increased resistance rate in the hospital environment put in danger the tremendous benefits obtained by antibiotic therapy [2].

Antibiotic resistance is a serious health issue. The resistance of antibiotics is the development of resistance in bacteria for antibiotics and possibly other kinds of microorganisms, making the antibiotic therapy less useful. This issue is responsible for the increased death rate worldwide each year [3]. Antibiotic resistance has increased dramatically during the last few decades. This flashing is intricately linked to diseases of infectious and pathogenicity [4]. Antibiotics are widely accessible in Iraq, which has caused the growth of germs that are dangerously resistant [5]. The current situation poses a significant threat to public health and regional stability. The outpatients frequently use antibiotics as a self-medication without fully comprehending its risks and implications. Furthermore, physicians who administer antibiotics without performing procedures that are necessary for diagnosis and susceptibility testing, which contributes to the rapid development of fierce bacteria. For example, Al-Naqshbandi [6] studied urinary tract infections and discovered the existence of MDR bacteria. Moreover, the inappropriate use and occasional outright abuse of antibiotics accelerates the growth and

spread of antibiotic-resistant microorganisms. For instance, bacteria can employ penicillin as a signal with regulatory functions if they are exposed to non-lethal doses of the antibiotic. One way bacteria get around antibiotics is by releasing β-lactamase enzymes, which break down the amide bond of the four-membered β-lactam ring and render the β-lactam antibiotic inactive. The mentioned case is just one of several ways bacteria can defend themselves against antibiotics. Many antibiotics have been developed and manufactured by researchers in the last few decades. However, the number of antibiotic-resistant agents has alarmingly increased during the 1990s, while the discovery of novel antimicrobial agents has been declining. In 2016, the WHO reported a list of the world's leading fiercer bacteria that required new antibiotics [7].

Antibiotics are classified into common classes and subclasses based on chemical or molecular structures and each class has a specific target in its structure or contains bacteria [8]. These classes and subclasses of antibiotics are subject to many bacteria originating from different sources. Most sources that produce most multidrug-producing bacteria are urinary tract infections. In the abstract of the study by AL-Khikani et al,[9] most specimens with bacterial growth were taken from urine and fewer from cervical swabs, with all specimens resistant to antibiotics. Vaginal swabs also are considered another source of MDR bacterial isolates[10]. Another source, such as pus wounds and mucus, is a smaller number of sources of MDR bacteria [11]. The terminology of the degree of antimicrobial resistance in any bacteria such as MDR, XRD and pan drug-resistant (PDR) were organized in a scientific article in 2012[16].

The diversity of species in different sources is distributed between *Escherichia coli*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Klebsiella oxytoca*, *Proteus mirabilis*, *Enterococcus faecalis*, and *Proteus vulgaris* [12]. The most dangerous pathogens in health centers are those from the genera of acinetobacter, *Pseudomonas* spp and Enterobacteriaceae, which can cause fatal infections. These infections have easy dealing with carbapenems, which are incredibly potent antibiotics that are frequently employed as life-saving medications inpatients. The rise of carbapenem-resistant enterobacteriaceae infections is concerning, because these bacteria create carbapenemase that can deactivate carbapenems and β-lactams. Additionally, It should be highlighted that those who have not been directly exposed to some antibiotics suffer from poor health outcomes due to the potential spread of resistant organisms. Faced with this scenario, which is no longer science fiction but a reality, there is an urgent need for novel active antibacterial components to ensure successful treatment of illnesses resistant to existing antibiotics.

The aim of the study is to count the spreading of MDR and XDR pathogens isolated from different sources over 12 months, and detecting the levels of MDR and XDR bacteria in Tikrit Teaching Hospital.

METHODOLOGY

The protocol of the study was approved by the Ethics Committee of Tikrit University on March, 2024, no. 2024.2. Prior to sample collection, the verbal and written approval of each patient was also obtained. The forms for the samples with the names of the sources were completed and ready at request.

Isolation and identification of clinical isolates

The study was carried out in Tikrit Teaching Hospital - Iraq, from January 14 to December 13, 2022. Health safety precautions and free germ conditions were taken for swab sampling (wounds, vaginal, uterus and mucus), and urine samples. All 197 swabs and liquid samples were collected from different clinical samples of admitted patients of different genders (Table. 1), swab sample immediately dropped in sterilized normal saline tube (0.85%) to help maintain cell integrity and viability until cultivated [13]. The samples were transported to microbiology laboratory and inoculated in suitable broth medium (brain heart infusion, HIMEDIA company-India) for 24 h at 37 °C, then sub cultured on differential and selective media (blood agar, chocolate agar and MacConkey agar (HIMEDIA company-India)). Then incubated at 37°C for 24-48±2 h. All isolates were identified by the conventional bacteriological methods [13].

Table 1: Sources and number of samples

Sources	No.
Urine	141
Pus wound	10
Vagina - high vaginal swab (HVS) - Uterus-cervix (Cx)	19
Endo (Uterus)	20
Seminal – Seminal Fluid Analysis (SFA)	4
Sputum sample (mucus)	1
Swab	2
Total	197
Pregnant sample	15

Antimicrobial susceptibility testing

Antibacterial susceptibility testing was performed using the disc diffusion method as described by Kirby-Baur method [14]. Twenty two different antibacterial antibiotics belonging to varying classes were used (Bioanalyse, Turkey). Minimum Inhibitory Concentration (MIC) of the antibiotics were calculated and the findings were interpreted by recommendations of the Clinical and Laboratory Standards Institute (CLSI) guideline [13]. Any bacterial isolate was resistant

to at least three different antibacterial classes considered MDR bacteria, if any bacterial isolate was indicated to all antimicrobial classes except one or two antimicrobial classes considered XDR bacteria and when any bacterial isolate was resistant to all used antimicrobial classes considered PDR bacteria [16]. All antibiotics were used under the description of physicians (table 2).

Table 2: Antibiotics details and targets [13].

Antibiotics	Symbol	Disc content (µg)	Drug classes or subclasses	Primary Target
Cefotaxime	CTX	30	Cephem-Cephalosporins III	Penicillin binding proteins
Norfloxacin	Nor	30	Quinolone -Fluoroquinolone	Topoisomerase II and IV
Gentamicin	Gen	10	Aminoglycosides	30S ribosomal subunit
Amoxicillin-clavulanic	AMC	30	β-lactam combination agent	Cell wall structure
Amikacin	AK	10	Aminoglycosides	30S ribosomal subunit
Pipracillin	PRI-PI	100	Penicillin-Ureidopenicillins	Penicillin binding proteins
Clindamycin	DA	10	Lincosamides	50S ribosomal subunits
Amoxicillin	AX	25	Penicillin-Aminopenicillins	Penicillin binding proteins
Levofloxacin	Lev	5	Quinolone-Fluoroquinolone	Topoisomerase II and IV
Nitrofurantoin	NIT	300	Nitroheterocyclics-Nitrofuran	DNA inhibition
Vancomycin	VA	30	Glycopeptides	Peptidoglycan units
Ciprofloxacin	Cip	10	Quinolone-Fluoroquinolone	Topoisomerase II and IV
meropenem	mem	10	Penems-Carbapenems	Penicillin binding proteins
Ceftriaxone	CRO	10	Cephem- Cephalosporins III	Penicillin binding proteins
Azithromycin	AZM	15	Macrolides	30S ribosomal subunit
Ofloxacin	OFX	5	Quinolone-Fluoroquinolone	Topoisomerase II and IV
Erythromycin	E	10	Macrolides	30S ribosomal subunit
Doxycycline	DO	10	Tetracyclines	30S ribosomal subunit
Imipenem	IPM	10	Penems-Carbapenems	Penicillin binding proteins
Trimethoprim	TMP	10	Folate pathway antagonist	Dihydrofolate reductase inhibitors
Ampicillin	AMP	10	Penicillin-Aminopenicillins	Penicillin binding proteins
Ceftazidime	CAZ	30	Cephem- Cephalosporins III	Penicillin binding proteins

MDR, XDR and PDR bacterial detection

Detection of MDR bacteria was done according to Kallau et al,[15]. While, Magiorakos et al [16]. give details about categorizing the bacteria into three types: MDR, XDR and PDR bacterial infections. 12 antibiotic classes were used, resistant isolate to one or two antimicrobial classes or subclasses were considered non-MDR bacteria, when any bacterial isolates acquired non-susceptibility to at least one agent in three or more antimicrobial categories were considered as MDR. The bacteria was detected as XDR if resistant to all antimicrobial studied classes except at least one or two classes, and finally, PDR were resistant to all antimicrobial agents in all antimicrobial categories.

Statistical analysis

The antimicrobial susceptibility data were analyzed in this study to reveal the spread of the prevalence of MDR, XDR and PDR isolates using Excel 2010 Office software 32 bit, Microsoft Company, USA.

RESULTS

Collection and distribution of bacterial isolates

Of the 197 different clinical samples, the most common source was urine 141 (71.5%) samples (Fig 1), and 21 (11%) from vaginal source 20 (10%) endo (Uterus) source, pus wound 10 (5 %), seminal 4 (2%) and sputum source 1 (0.5%). Out of 197 samples, 15 (7.6%) were pregnant and required special antibiotics. As well, the majority of the current study clinical samples belonged to females, approximately 90.3% (178 females and 19 males), most of whom had UTIs, for that reason the urine source was the majority of clinically different sources.

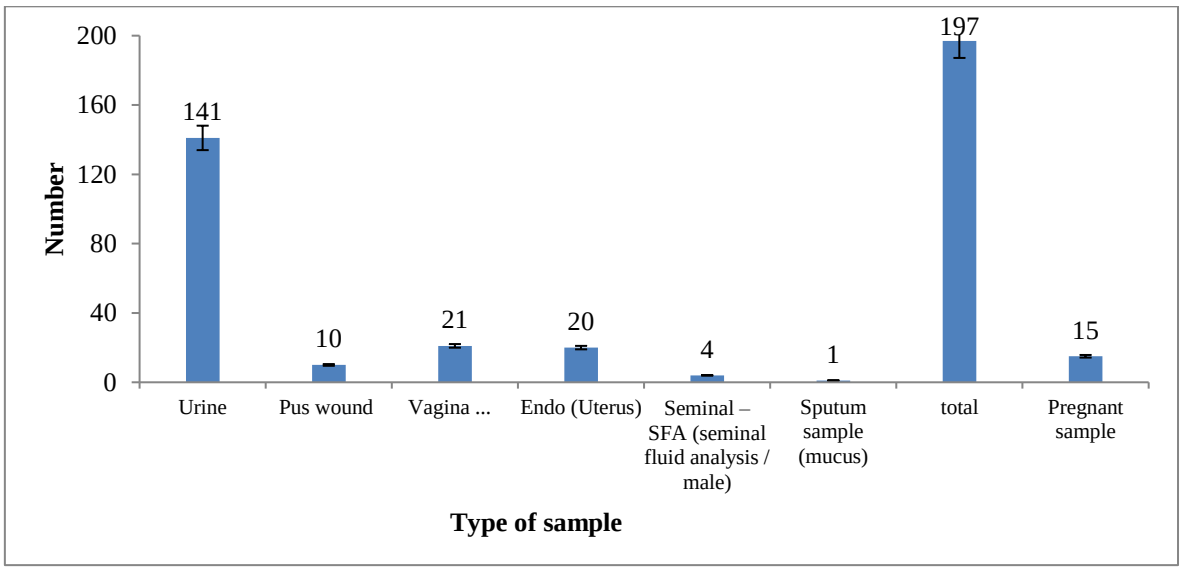

Fig. 1 The clinically different sources of the samples

177 isolates were isolated are shown in figure 2. The distribution of the isolates according to the sources was as follows: 127 isolates from urine, 10 isolates from pus wounds, 17 isolates from vagina (HVS), 20 isolates from Endo-uterus, 2 isolates from SFA and the last 1 isolate from sputum. *Staphylococcus aureus* was found to be the most common pathogen isolated (92), followed by *Escherichia coli* (47), *Streptococcus sp* (22), *Klebsiella sp* (13), *Pseudomonas aeroginosa* (2) and *Proteus sp* (1).

Antimicrobial susceptibility of pathogens

Staphylococcus aureus

The results of the antimicrobial susceptibility test and resistance of 92 *Staphylococcus aureus* to 11 antimicrobials are presented in table 3 (seven classes of antibiotics). The results showed that a high level of resistance was found in AX, AZM, E, Cip, Lev, Nor, OFX and DA antibiotics (87.5%, 86.3%, 100%, 69%, 72.6%, 70.4%, 60% and 86.7%). The Gen and TMP antibiotics were (50%) susceptible to *Staphylococcus aureus*. Another important finding was also to have found the potential to be resistant to some antibiotics with intermediate levels, such as TMP (16.7%). Ultimately, 70.9% of used antibiotics showed resistance to *Staphylococcus aureus*, 8.3% had intermediate activity and 20.8% were susceptible to *Staphylococcus aureus*.

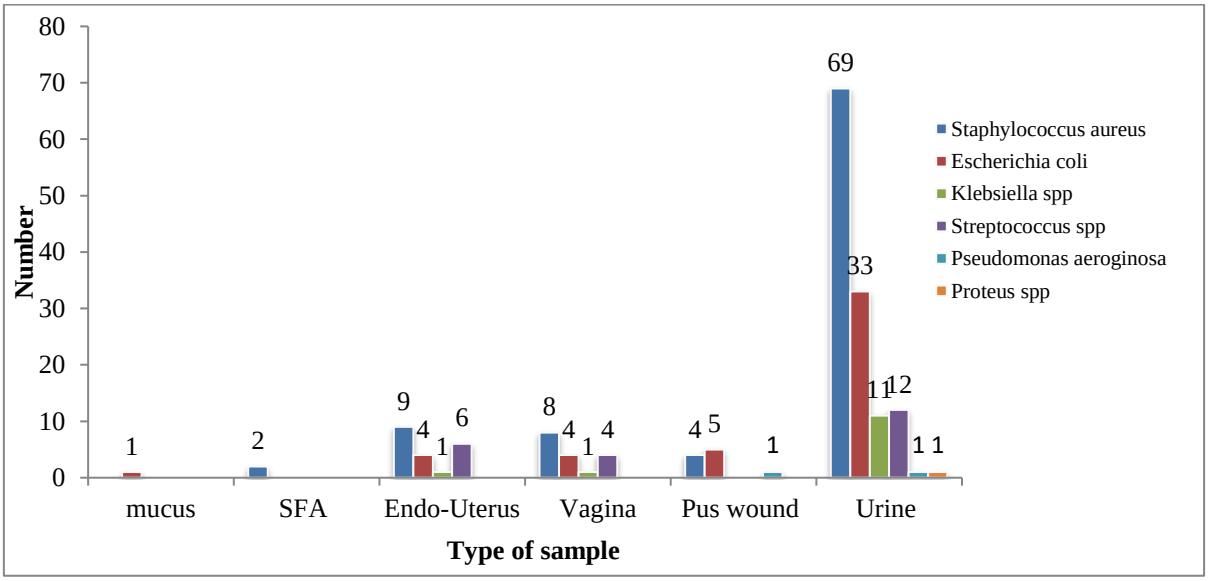

Fig. 2 Distribution of bacterial isolates from different clinical sources.

Escherichia coli

The results of the antimicrobial susceptibility test and resistance of 47 *Escherichia coli* to 19 antimicrobial agents are shown in table 4 (11 classes of antibiotics). The antimicrobial sensitivity pattern of different sources showed that *Escherichia coli* isolates were highly resistant to AMP, PRI, AMC, CTX, CRO, CAZ, TMP, NIT, AK, AZM, DO, Cip and Lev (100%, 100%, 97.7%, 92.3%, 100%, 100%, 75%, 90%, 6.9%, 75%, 90.5%, 85.3% and 73.4%), whereas were moderately susceptible to Gen, Nor, OFX and IPM (46.7%, 40%, 41.2% and 36.4%).

The antibiotic sensitivity profile showed that *Escherichia coli* isolates were moderately susceptible to Gen (46.7%). Another antibiotics that were also shown to be acceptable were Nor, OFX and IPM. *Escherichia coli* exhibited 77% resistance to tested antibiotics and 13.6% susceptibility.

Table 3: Breakpoints, numbers, and percentages of *Staphylococcus aureus* that are resistant, intermediate and susceptible to 11 antimicrobials.

***Staphylococcus aureus* / seven antibiotic classes**								
Types of antibiotics	**breakpoints**	**Σ**	**Number and percentage of resistant**		**Number and percentage of Intermediates**		**Number and percentage of Susceptible**	
	R/I/S (mm)		Σ	%	Σ	%	Σ	%
AX	≤28/ - /≥ 29	8	7	87.5	0	0	1	12.5
VA	≤ / - /≥-	42	-	-	-	-	-	-
Gen	≤12/13-14 /≥15	58	25	43.1	4	6.9	29	50
AZM	≤ 13/14-17/ ≥18	51	44	86.3	3	5.9	4	7.8
E	≤13 /14-22 /≥23	30	30	100	0	0	0	0
Cip	≤ 15/16-20 /≥21	55	38	69	10	18.2	7	12.8
Lev	≤15 /16-18/ ≥19	62	45	72.6	2	3.2	15	24.2
Nor	≤ 12/13-16/ ≥17	44	31	70.4	6	13.7	7	15.9
OFX	≤ 14/15-17/ ≥18	20	12	60	1	5	7	35
DA	≤14 /15-20/ ≥21	30	26	86.7	4	13.3	0	0
TMP	≤ 10/11-15/≥16	6	2	33.3	1	16.7	3	50
Total %				70.9		8.3		20.8

Data are presented as numbers (Σ) and percentages (%). AX: amoxicillin, VA: vancomycin, Gen: Gentamicin, AZM: azithromycin, E: Erythromycin, Cip: Ciprofloxacin, Lev: levofloxacin, Nor: norfloxacin, OFX: ofloxacin, DA: clindamycin, TMP: trimethoprim.

Table 4: Breakpoints, numbers, and percentages of *Escherichia coli* isolates that are resistant, intermediate and susceptible to 19 antimicrobials.

***Escherichia coli* / Eleven antibiotic classes**								
Types of antibiotics	**Breakpoints**	**Σ**	**Number and percentage of resistant**		**Number and percentage of Intermediates**		**Number and percentage of Susceptible**	
	R/I/S (mm)		Σ	%	Σ	%	Σ	%
AMP	≤ 13/ 14 - 16 /≥ 17	5	5	100	0	0	0	0
AX	≤ / - /≥-	3	-	-	-	-	-	-
PRI	≤17/18-20 /≥21	8	8	100	0	0	0	0
AMC	≤ 13/14-17/ ≥18	44	43	97.7	1	2.3	0	0
CTX	≤22/23-25/≥26	13	12	92.3	1	7.7	0	0
CRO	≤ 19/20-22 /≥23	22	22	100	0	0	0	0
CAZ	≤17 /18-20/ ≥21	7	7	100	0	0	0	0
mem	≤ / - / ≥-	35	-	-	-	-	-	-
TMP	≤ 10/11 - 15/≥16	8	6	75	0	0	2	25
NIT	≤14/15-16/ ≥17	20	18	90	2	10	0	0
Gen	≤ 12/13-14/≥15	30	14	46.7	2	6.6	14	46.7
AK	≤ 14/15-16/≥17	26	20	76.9	5	19.3	1	3.8
AZM	≤ 12/ - /≥13	32	24	75	0	0	8	25
DO	≤ 10/ 11 - 13 /≥14	21	19	90.5	2	9.5	0	0
Cip	≤ 21/22-25/≥26	34	29	85.3	5	14.7	0	0
Lev	≤ 16/17-20/≥21	30	22	73.4	4	13.3	4	13.3
Nor	≤ 12/13-16/≥17	20	9	45	3	15	8	40
OFX	≤ 12/13-15/≥16	17	6	35.3	4	23.5	7	41.2
IPM	≤ 19/20-22/≥23	11	3	27.2	4	36.4	4	36.4
Total %				77		9.4		13.6

Data are presented as numbers (Σ) and percentages (%). AMP: ampicillin, AX: amoxicillin, PRI: pipracillin, AMC: amoxicillin-clavulanic, CTX: cefotaxime, CRO: ceftriaxone, CAZ: ceftazidime, mem: meropenem, TMP: trimethoprim, NIT: nitrofurantoin, Gen: Gentamicin, AK: amikacin, AZM: azithromycin, DO: doxycycline, Cip: Ciprofloxacin, Lev: levofloxacin, Nor: norfloxacin, OFX: ofloxacin, IPM: imipenem.

***Klebsiella* spp**

Table 5. shows the resistance rates of the isolated *Klebsiella* spp to common antibiotics in various clinical samples. *Klebsiella* spp were observed to be highly resistant to almost all tested antibiotics. According to our findings, 57.1% were resistant to Gen. While only OFX showed activity against *Klebsiella* spp (66.7%). The intermediate activity was found in Nor (50%). Lastly, *Klebsiella* spp recorded the highest resistance in the entire current study (79.8%), and almost all antibiotics aren't working with these isolates with the exception of OFX.

***Streptococcus* spp**

The resistance of *Streptococcus* spp showed a high resistance rate (Table 6). The resistant patterns of *Streptococcus* spp revealed that all isolates were resistant to E, AZM, Lev, OFX and DA (100%, 90%, 53%, 62.5% and 83.3%). In contrast, only VA showed sensitivity of 75%.

Table 5: Breakpoints, numbers, and percentages of *Kledsiella* spp that are resistant, intermediate and susceptible to 18 antimicrobials.

***Klebsiella* spp / Ten antibiotic classes**								
Types of antibiotics	**breakpoints**	**Σ**	**Number and percentage of resistant**		**Number and percentage of Intermediates**		**Number and percentage of Susceptible**	
	R/I/S (mm)		Σ	%	Σ	%	Σ	%
AMP	≤ 13/ 14 - 16 /≥ 17	4	4	100	0	0	0	0
PRI	≤17/18-20 /≥21	2	2	100	0	0	0	0
AMC	≤ 13/14-17/ ≥18	9	9	100	0	0	0	0
CTX	≤22/23-25/≥26	2	2	100	0	0	0	0
CRO	≤ 19/20-22 /≥23	2	2	100	0	0	0	0
CAZ	≤17 /18-20/ ≥21	3	3	100	0	0	0	0
mem	≤ -/ - /≥	8	-	-	-	-	-	-
TMP	≤10 /11-15/ ≥16	2	2	100	0	0	0	0
NIT	≤14/15-16/ ≥17	10	7	70	2	20	1	10
Gen	≤ 12/13-14/≥15	7	4	57.1	0	0	3	42.9
AK	≤ 14/15-16/≥17	7	5	71.4	1	14.3	1	14.3
AZM	≤ 12/ - /≥13	11	7	63.6	0	0	4	36.4
DO	≤ 10/ 11 - 13/≥14	4	3	75	0	0	1	25
Cip	≤ 21/22-25/≥26	9	6	66.7	3	33.3	0	0
Lev	≤ 16/17-20/≥21	10	7	70	2	20	1	10
Nor	≤ 12/13-16/≥17	4	2	50	2	50	0	0
OFX	≤ 12/13-15/≥16	3	1	33.3	0	0	2	66.7
IPM	≤ 19/20-22/≥23	2	2	100	0	0	0	0
Total %				79.8		8.1		12.1

Data are presented as numbers (Σ) and percentages (%). AMP: ampicillin, PRI: pipracillin, AMC: amoxicillin-clavulanic, CTX: cefotaxime, CRO: ceftriaxone, CAZ: ceftazidime, mem: meropenem, TMP: trimethoprim, NIT: nitrofurantoin, Gen: Gentamicin, AK: amikacin, AZM: azithromycin, DO: doxycycline, Cip: Ciprofloxacin, Lev: levofloxacin, Nor: norfloxacin, OFX: ofloxacin, IPM: imipenem.

Table 6: Breakpoints, numbers, and percentages of *Streptococcus* spp that are resistant, intermediates and susceptible to 6 antimicrobials.

***Streptococcus* spp / Four antibiotic classes**								
Types of antibiotics	**breakpoints**	**Σ**	**Number and percentage of resistant**		**Number and percentage of Intermediates**		**Number and percentage of Susceptible**	
	R/I/S (mm)		Σ	%	Σ	%	Σ	%
VA	≤ -/ - /≥ 17	4	0	0	1	25	3	75
E	≤15/16-20/≥21	9	9	100	0	0	0	0
AZM	≤ 13/14-17/ ≥18	20	18	90	2	10	0	0
Lev	≤13/14-16/≥17	17	9	53	4	23.5	4	23.5
OFX	≤ 12/13-15 /≥16	8	5	62.5	1	12.5	2	25
DA	≤15 /16-18/ ≥19	6	5	83.3	0	0	1	16.7
Total %				64.8		11.9		23.3

Data are presented as numbers (Σ) and percentages (%). VA: vancomycin, E: erythromycin, AZM: azithromycin, Lev: levofloxacin, OFX: ofloxacin, DA: clindamycin.

Profiles of non-MDR, MDR, XDR and PDR in studied isolates.

Recorded data revealed that non-MDR occurred in 31.6% of all *Staphylococcus aureus* cases, with a significant prevalence of MDR (61.9%) (Table 7).Whereas less with XDR (6.5). *Escherichia coli* exhibited the highest incidence of MDR (68%), followed by a lower incidence of non-MDR and XDR (15%, 17%). MDR was more common in *Klebsiella* spp (77%) with a lower frequency in XDR (23%). *Streptococcus* spp also showed a significant frequency of MDR (54.5%) among non-MDR and XDR (36.5%, 9%). In contrast, PDR has not yet been recorded for all isolates. Shortly, the significant increase in all isolates exhibiting MDR (65.3%), whereas no significant difference was observed between the prevalence of non-MDR and XDR (20.8%, 13.9%). All study pathogenic bacteria showed no PDR for any antimicrobial categories.

Table 7: Numbers and percentages of MDR, XDR and PDR profiles among pathogenic bacteria.

Species	Number and % of non-multi-drugs resistant		Multi-drugs resistant MDR		extensive-drug resistant XDR		pan-drug resistant PDR		Total
	No	%	No	%	No	%	No	%	
Staphylococcus aureus	29	31.6	57	61.9	6	6.5	0	0	92
Escherichia coli	7	15	32	68	8	17	0	0	47
Klebsiella spp	0	0	10	77	3	23	0	0	13
Streptococcus spp	8	36.5	12	54.5	2	9	0	0	22
Total percentage		20.8		65.3		13.9		0	
Total No.									174

DISCUSSION

The majority of pathogenic bacteria were isolated from urine sources. This finding correlate with the study of Deku et al,[17] where most isolates were recovered from urine (72.6%), the others that remained isolates from other clinical sources were 7.4% from HVS, 10.4% from wound swabs, and 1.5% from sputum. More isolates belonged to females than males. The current reporting was similar to Al-Jebouri and Mdish,[18] who revealed most isolates were obtained from females than males with UTIs. Females were more prone to UTIs than males because the urethra is much shorter and closer to the anus in females than in males, and they lack prostatic secretions that have bacteriostatic properties [19].

The most isolates obtained from urine samples were *Staphylococcus aureus*. A Similar study reported that *Staphylococcus aureus* was the predominant isolated uropathogen from patients with symptoms of UTIs and the least frequently isolates were *Escherichia coli* and other bacteria [20]. The high proportion of *Staphylococcus aureus* was previously linked to an increased cause of UTIs associated with the increased use of instrumentation such as bladder catheterization [21].

Periodic examination by a gynecologist using medical tools with less attention to continuous sterilization may be a secondary reason for the increase in staphylococcal morbidity among patients, especially females with UTIs. However, the observed high proportion of *Staphylococcus* varied according to some previously published studies [6,22] in which *Escherichia coli* was found to be the predominant urinary tract pathogen. This variation further supports the fact that the distribution of UTI-causing pathogens, including their antimicrobial susceptibility patterns, varies from place to place and changes from time to time [23, 24]. The second prevalent microorganism was *Escherichia coli*, which was confirmed by Naqid et al,[25] who found that the overwhelming majority of *Escherichia coli* isolates were isolated from urine sources. The findings of pus wound isolates were approved by Mohammed et al,[26] who showed that *Escherichia coli* and *Staphylococcus aureus* were the most common isolates from infected wounds. Ditto vaginal isolate results were similar to the study of Al-Dahmoshi [27] who also showed that *Staphylococcus aureus* was the most common isolate from vaginitis. The findings of Al-Jebouri and Mdish,[28] concluded that the most common isolate was *Staphylococcus aureus* isolated from bacteriospermia.

Resistance to *Staphylococcus aureus* has become the first threat to be noticed in our study. Cip antibiotics are susceptible to *Staphylococcus* spp,[29] but our study revealed resistance to Cip. The intermission to use Gen antibiotics by patients has been one of the causes of resistance to Gen antibiotics in the future. The TMP antibiotics include those that inhibit dihydrofolate reductase, which catalyzes the reduction of dihydrofolate to tetrahydrofolate in microbial and eucaryotic cells. The investigation by Wood et al,[30] through 10 years of increased Methicillin-resistant *Staphylococcus aureus* (MRSA) incidence in the United

States, helped increase the use of TMP and trimethoprim-sulfamethoxazole antibiotics. This increase will ring the alarm in the near future from the abovementioned synopsis and the overuse of drugs against *Staphylococcus aureus*.

Escherichia coli is a common causative agent of infections [31]. The resistance profile of *Escherichia coli* continues to pose a great threat to public health, especially in our studied area and can lead to serious health problems, such as prolonged hospitalization and treatment failure. The findings of Gen were conducted by a previous study in the northern Iraq [25], who found that 51.9% of *Escherichia coli* isolates from urine were sensitive to Gen antibiotics. The study of Ibrahim et al,[32] and Nwokafor et al,[33] reported moderate susceptibility of *Escherichia coli* to Nor (56%) and high sensitivity to OFX (83.3%). Another finding by Polse et al,[34] showed that *Escherichia coli* is 100% susceptible to IPM, but in the current study, the isolates appeared moderately susceptible to Nor, OFX and IPM due to the different durations and extensive uncontrolled use of antibiotics, which reduced the activity of IPM to half. This scenario gives a clear picture of what will happen in the next decades with continuous overuse of antibiotics.

Currently, resistance to antibiotics against human pathogenic bacteria such as *Klebsiella* spp is frequently reported worldwide [35]. This scenario is considered an alarming issue worldwide due to the misuse of the antibiotics, especially those used in medical practice.

A similar observation regarding *Streptococcus* spp results was previously reported in Egypt [36]. VA belongs to the glycopeptide classes of antibiotics, which work on peptidoglycan units in the cell walls of pathogenic bacteria. Thus, *Streptococcus* spp are susceptible to VA. These findings gives specialists in the medical field an additional threat to quickly resolve the problem of misuse of antibiotics in the next decades.

The findings of *Staphylococcus aureus* were similar to those of Sadat and Ahani,[37] who found that *Staphylococcus aureus* recorded a high rate of MDR (96.8%) and a lower rate of XDR (12.5%). Whereas Al-Hasani et al,[38] reported that most *Escherichia coli* isolates were classified as MDR (98.2%, while only 2 (1.7%) isolates were susceptible to almost all tested antimicrobial agents, moreover, their study showed only 24 (21.2%) isolates were classified as XDR. Regarding *Klebsiella* spp findings, it was also proved by Aljanaby and Alhasnawi,[39] who found a high rate of MDR (74.4%) for *Klebsiella pneumonia* compared with other classes. Another dangerous scenario was noted for *Streptococcus* spp which showed a high rate of MDR compared with non-MDR classes. There are almost no published papers about MDR in clinical isolates of *Streptococcus* spp in Iraq or other countries. All isolates did not present with PDR for any of the antimicrobial category. The final percentage appeared to be a high prevalence of MDR for all antimicrobial agents studied by isolates. The increased number of MDR classes in pathogen bacteria for most used antibiotics can be caused by mutation either in chromosomally encoded genes or by horizontal gene transfer of antimicrobial resistance determinants [40].

CONCLUSION

The most common source of pathogens was urine, followed by a lower rate of vaginal sources. The most common pathogenic isolates were *Staphylococcus aureus*, followed by *Escherichia coli*. The susceptibility and resistance profiles of pathogenic bacteria in the current study illustrate that there was a general increase in the resistance patterns of isolates to most antibiotics used. Such as *Staphylococcus aureus* possesses high resistance to almost all antimicrobial agents. Finally, the misuse of antibiotics resulted in an increased rate of MDR for isolates, among other definitions of XDR and PDR. Imminent threats of pathogenic bacteria in medical facilities or hospitals will be the exclusive concern of physicians for pathogen treatments in the future, unless the existing situation is controlled.

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Limitations of the study

The *Pseudomonas aeroginosa* and *Proteus* spp were excluded because of the small number of isolates (2,1). This limited number of bacteria does not have any significant effect on the results of our work.

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