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Prevalence and antimicrobial susceptibility of bacterial pathogens isolated from urine specimens received in rizgary hospital — Erbil

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ABSTRACT

Background: Urinary tract infection (UTI) is a common health-associated problem worldwide. Like other medical conditions, UTI patients may suffer from poor treatment outcomes due to the emergence of antimicrobial resistance. Determining patterns of antimicrobial susceptibility in uropathogens will guide physicians to choose the best antibiotics for treating affected patients. In this project we aimed to evaluate the frequencies of pathogens associated with UTI and their antimicrobial susceptibility patterns.
Methods: This study was conducted on 2692 urine samples of patients visited Rizgary Teaching Hospital in Erbil city. Aerobic bacterial growth identification and antimicrobial susceptibility tests were performed using VITEK® 2 compact system.
Results: Our data show that more than 20% of all studied samples were negative for bacterial growth; only 16.72% of them were pathogenic bacteria in which 82.44% of them were Gram negative bacteria (GNB) and the rest were Gram positive bacteria (GPB). *Escherichia coli* was the most frequent, and *Acinetobacter baumannii* was the most resistant GNB. *Staphylococcus haemolyticus* was the most frequent, and *Enterococcus faecalis* was the most resistant GPB. In general GNB were highly resistant to Ticarcillin and Cefepime, and GPB were also resistant to Ticarcillin, and Tigecycline antibiotics.
Conclusions: The amount of negative culture growth indicates that symptoms only based diagnosis for UTI detection is unreliable. *E. coli* is the most UTI related pathogen, *E. faecalis* and *A. baumannii* were among highly antibiotic resistant bacteria. Finally, since many of GNG and GPB isolates were resistant to several antibiotics, there might be a high possibility for multi drug resistant among local population in Erbil.

Introduction

Health conditions that associate between clinical symptoms and detection of pathogenic microorganisms in the urine, urethra, bladder, kidneys, and even in prostate, is described as urinary tract infection (UTI) [1]. UTI considered as the most common and costly health-related problem worldwide [2,19]. UTI's severity differs by age and gender, as women and elderly are more vulnerable than men and younger individuals [4,5]. Gram negative bacteria (GNB), Gram positive bacteria (GPB), and some fungi found to be involved in the development of UTI [6,7,8]. There are different types of antibiotics routinely prescribed for UTI treatment [9], but they share similar mechanisms of action like: inhibition of cell wall synthesis, inhibition of protein synthesis, interference with nucleic acid synthesis, interference with signalling pathways involved in biosynthetic processes, and disruption of cell membrane integrity [10,11].

Diagnosis and treatment of UTI based on clinical symptoms only rather than depending on laboratory examinations is inaccurate [12], as the error rate in diagnosis may reach more than 30% [13]. When laboratory procedures are applied, urine samples are the most dependant specimen type used to confirm the occurrence of UTI [14,15]. Like other medical conditions, UTI patients may suffer from poor outcomes of their treatments due to the emergence of antimicrobial resistance (AMR) [16,17,18]. AMR takes place when microorganisms show resistance to antimicrobial drugs that were previously effective. AMR for long term may cause economic burden for governments as it will raise health care costs through longer hospital stays, and increase morbidity and mortality among populations [19,20]. Resistance toward antibiotics could be natural (intrinsic) or due to genetic alterations. GNB

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may holdback antibiotics (e.g. penicillin G) from entering the cell due to the natural composition of the cell wall. Other bacteria may efflux antibiotics before they reach their targets, through enzymes known as translocases. Others microorganisms may naturally lack the target for certain antibiotics, e.g. mycoplasma doesn't produce peptidoglycan which is the main target for penicillin. Other bacteria may cancel the cytotoxic effects of drugs by activating alternative pathways, e.g. aminoglycoside antibiotics are acetylated or phosphorylated by the action of family of enzymes knows as transferases [10,21,22,23,24]. AMR is described as molecular evolution, as different types of mutations may trigger certain mechanisms allowing microorganisms to thrive within unfavourable conditions. For understanding AMR, scientists proposed a concept known as resistome, which mainly studies the total genetic elements that functions to reverse the toxic effects of antibiotics [25,26]. AMR may be caused by random mutations in chromosomal DNA, or via transferring and acquiring new genetic materials between bacteria (by plasmids or transposons) from the same or different genera [27,28,29].

During the year 2014 in the United States of America alone more than 266 million antimicrobial prescriptions were provided, about 30% of them were described later as unnecessary [30]. In the United Kingdom, 69% of all prescriptions included antimicrobial drugs and more than 20% of them were described as inappropriate [31]. Similarly in Iraq about 70% of all medical prescriptions contain antibiotics [20], but there is no sufficient data about the necessity of their use and their health outcomes. The development of multi drug resistance (MDR) in UTI patients was reported earlier in many countries [18,32,33]. There are several studies suggesting the existence of MDR among pathogens isolated from UTI patients in Erbil city, however they do not reflect the proportion of the problem as they covered limited numbers of specimens and the tested antimicrobial drugs [34,35]. Therefore, a comprehensive investigation is required to uncover the scope of MDR problem among local population. The present study aims to evaluate types of bacterial pathogens associated with UTI patients, and to determine their antimicrobial susceptibility patterns.

Materials and methods

Specimen collection and transport

The urine samples were collected from patients attended Rizgary Teaching Hospital in Erbil city of Kurdistan Region — IRAQ for the period between: January, 2014 to December, 2016. Midstream specimens of urine (MSU) were collected in labeled and sterile wide mouth plastic container [36]. After collection the specimens were transported to be analysed in the laboratory of Microbiology Department.

Bacterial culture and identification

Without centrifugation urine samples were mixed thoroughly. After transferring urine samples into a sterile cup, using a sterile calibrated loop (0.01 mL), a loop-full of each sample inoculated

Table 1
Detection and distribution of pathogenic bacterial growth isolated from urine samples.

Growth type	No. & percentile of growth	
No growth of bacteria	541 (20.09%)	
No uro-pathogenic bacteria isolates	1701 (63.19%)	
	450 (16.72%)	
Pathogenic bacteria isolates:	Gram + Ve	Gram – Ve
	79 (17.56%)	371 (82.44%)

Table 2
Classification of detected Gram positive and Gram negative bacteria.

	Bacteria isolated from urine samples														
	Gram positive				Gram negative										
Genus and sp.	*Enterococcus faecalis*	*Staphylococcus aureus*	*Staphylococcus haemolyticus*	*Streptococcus agalactiae*	*Acinetobacter baumannii*	*Enterobacter aerogenes*	*Enterobacter cloacae*	*Escherichia coli*	*Klebsiella oxytoca*	*Klebsiella pneumonia*	*Morganella morganii*	*Proteus mirabilis*	*Pseudomonas aeruginosa*	*Serratia marcescens*	*Serratia rubidaea*
No. & percentile of growth	10 (12.66%)	15 (18.99%)	39 (49.36%)	15 (18.99%)	10 (12.66%)	4 (1.08%)	4 (1.08%)	255 (68.73%)	4 (1.08%)	76 (20.48%)	1 (0.27%)	17 (4.58%)	2 (0.54%)	2 (0.54%)	1 (0.27%)

on blood agar and MacConkey media separately. Inoculation was accomplished by striking the inoculum from the centre of the plate and downward. Without flaming the loop, the plate was then streaked side to side across the initial inoculum for evenly distribution of bacteria on the plate. The plates were incubated overnight at 37 °C. Number of colonies was counted to calculate the bacterial numbers per mL of urine sample [36]. The aerobically incubated bacterial growths were identified based on colony characteristics and Gram's staining, according to Bhatia and Lchhpujani (2008) protocol [37]. Identification of GPB, GNB, and antimicrobial sensitivity tests were performed following VITEK® 2 compact system protocols by using these kits: VITEK®2 GN Reference 21341, VITEK®2 GP Reference 21342, VITEK®2 AST-GN 69 Reference 413400, VITEK®2 AST-P580 Reference 22233, and VITEK®2 AST-ST01 Reference 410028.

Antibiotics

The following antibiotics were investigated in this study via VITEK® 2 kits: Ampicillin, Ciprofloxacin, Clindamycin, Ceftriaxone, Cefotaxime, Erythromycin, Fusidic acid, Fosfomycin, Nitrofurantoin, Gentamicin, Levofloxacin, Linezolid, Mupirocin, Moxifloxacin, Oxacillin, Benzylpenicillin, Quinupristin/Dalfopristin, Rifampicin, Trimethoprim/Sulfamethoxazole, Tetracycline, Teicoplanin, Tigecycline, Ticarcillin, Tobramycin, and Vancomycin.

Direct microscopy examination

A part of urine specimens were centrifuged at 3000 rpm for three minutes at room temperature. The sediments were examined under light microscopy (40× objective lens) for detection of pus cells, red blood cells, and bacteria. Presence of more than three pus cells per microscopic field was considered as an indication for UTI infection [36].

Data analysis

The dominant and abundant bacterial isolates were presented in percentage (%). Bacterial isolates were considered resistant toward specific antibiotic when the resistant rate was equal or greater than 70%. In regard to the collective antibiotic resistance in Gram positive and Gram negative bacteria, only the highly resisted drugs were presented (when the value was equal or greater than 90%).

Results

Our results show that, out of 2692 urine samples, 79.9% of them were positive for bacterial growth, and 16.72% of which were pathogenic bacteria (Table 1). Data retrieved from VITEK® 2 compact system revealed that out of 450 pathogenic isolates only 17.56% were Gram positive bacteria, while the majority (82.44%) were Gram negative bacteria (Table 1).

In regard to Gram positive bacteria our data show that *Staphylococcus haemolyticus* was the most frequent bacteria and *Enterococcus faecalis* was the least detected one (Table 2). For Gram negative bacteria, our data uncovered that *Escherichia coli* is the most abundant, and *Morganella morganii* and *Serratia rubidaea* were among less detected bacteria (Table 2).

VITEK® 2 compact system was used to check for antibiotic sensitivity among all of the identified isolates. The extracted data show that out of 25 drugs tested, *Enterococcus faecalis* was resistant to 18 drugs, and *Staphylococcus aureus* was sensitive toward 17 drugs (Tables 3 and 6). VITEK® 2 compact system also revealed that in Gram negative bacteria *A. baumannii* was resistant to 23 drugs, and *Escherichia coli* was sensitive to 16 drugs (Tables 4–6).

Last but not the least, our data also show that the Gram positive bacteria were collectively 100% resistant to TIC- Ticarcillin, and more than 78% of them were sensitive to TGC-Tigecycline. Gram negative bacteria on the other hand were also collectively resistant to TIC-Ticarcillin, by 95.06%, and about 88% of them were sensitive to FEP-Cefepime (Table 7).

Discussion

Treating patients, including UTI ones, suffering from infections caused by MDR bacteria is a challenging task, due to that focusing efforts to deal with this issue is crucial to provide a better

Table 3
Responses of Gram positive bacteria to different antimicrobial agents.

Agency	*Enterococcus faecalis* (10)		*Staphylococcus aureus* (15)		*Staphylococcus haemolyticus* (39)		*Streptococcus agalactiae* (15)	
AM-Ampicillin	S1 (10%)	R9 (90%)	R15 (100%)		R39 (100%)		S13 (86.67%)	R2 (13.33%)
CIP-Ciprofloxacin	R10 (100%)		S2 (13.33%)	R13 (86.67%)	S1 (2.56%)	R38 (97.44%)	S1 (6.67%)	R14 (93.33%)
CM-Clindamycin	R10 (100%)		S9 (60%)	R6 (40%)	S17 (43.59%)	R22 (56.41%)	S10 (66.67%)	R5 (33.33%)
CRO-Ceftriaxone	R10 (100%)		R15 (100%)		R39 (100%)		S15 (100%)	
CTX-Cefotaxime	R10 (100%)		R15 (100%)		R39 (100%)		S15 (100%)	
E-Erythromycin	S1 (10%)	R9 (90%)	S9 (60%)	R6 (40%)	S9 (23.08%)	R30 (76.92%)	S5 (33.33%)	R10 (66.67%)
FA-Fusidic acid	R10 (100%)		S9 (60%)	R6 (40%)	S28 (71.79%)	R11 (28.21%)	R10 (100%)	
FOS-Fosfomycin	R10 (100%)		S9 (60%)	R6 (40%)	S12 (30.77%)	R27 (69.23%)	R10 (100%)	
FT-Nitrofurantoin	S10 (100%)		S12 (80%)	R3 (20%)	S39		R10 (100%)	
GM-Gentamicin	R10 (100%)		S14 (93.33%)	R1 (6.67%)	S31 (79.49%)	R8 (20.51%)	R10 (100%)	
LEV-Levofloxacin	S6 (60%)	R4 (40%)	S13 (86.67%)	R2 (13.33%)	S29 (74.36%)	R10 (25.64%)	S12 (80%)	R3 (20%)
LNZ-Linezolid	S7 (70%)	R3 (30%)	S14 (93.33%)	R1 (6.67%)	S39		S15 (100%)	
MUP-Mupirocin	R10 (100%)		S11 (73.33%)	R4 (26.67%)	S29 (74.36%)	R10 (25.64%)	R10 (100%)	
MXF-Moxifloxacin	S6 (60%)	R4 (40%)	S15 (100%)		S39		S2 (13.33%)	R13 (86.67%)
OX1-Oxacillin	R10 (100%)		S10 (66.67%)	R5 (33.33%)	S7 (17.95%)	R32 (82.05%)	R10 (100%)	
P-Benzylpenicillin	S1 (10%)	R9 (90%)	R15 (100%)		S2 (5.13%)	R37 (94.87%)	S12 (80%)	R3 (20%)
QDA-Quinupristin/Dalfopristin	S1 (10%)	R9 (90%)	S2 (13.33%)	R13 (86.67%)	S3 (7.69%)	R36 (92.31%)	R10 (100%)	
RA-Rifampicin	R10 (100%)		S10 (66.67%)	R5 (33.33%)	S30 (76.92%)	R9 (23.08%)	R10 (100%)	
SXT-Trimethoprim/Sulfamethoxazole	S3 (30%)	R7 (70%)	S13 (86.67%)	R2 (13.33%)	S31 (79.49%)	R8 (20.51%)	S15 (100%)	
TE-Tetracycline	S2 (20%)	R8 (80%)	S4 (26.67%)	R11 (73.33%)	S20 (51.28%)	R19 (48.72%)	R15 (100%)	
TEC-Teicoplanin	S6 (60%)	R4 (40%)	S8 (53.33%)	R7 (46.67%)	S23 (58.97%)	R16 (41.03%)	S2 (13.33%)	R13 (86.67%)
TGC-Tigecycline	S10 (100%)		S15 (100%)		S39		S2 (13.33%)	R13 (86.67%)
TIC- Ticarcillin	R10 (100%)		R15 (100%)		R39 (100%)		R10 (100%)	
TM-Tobramycin	R10 (100%)		S11 (73.33%)	R4 (26.67%)	S31 (79.49%)	R8 (20.51%)	R10 (100%)	
VA-Vancomycin	S6 (60%)	R4 (40$)	S10 (66.67%)	R5 (33.33%)	S24 (61.54%)	R15 (38.46%)	S15 (100%)	

S: Sensitive, R: Resistant.

Table 4
Responses of Gram negative bacteria to different antimicrobial agents.

Agency	*Acinetobacter baumannii* (5)		*Enterobacter aerogenes* (4)		*Enterobacter cloacae* (4)		*Escherichia coli* (255)		*Klebsiella oxytoca* (4)	
AM-Ampicillin	R (100%)		R (100%)		R (100%)		S73 (28.63%)	R182 (71.37%)	R4 (100%)	
AMC-Amoxicillin/Clavulanic Acid	R (100%)		R (100%)		R (100%)		S138 (54.12%)	R117 (45.88%)	S3 (75%)	R1 (25%)
AN-Amikacin	R (100%)		S3 (75%)	R1 (25%)	S1 (25%)	R3 (75%)	S81 (31.76%)	R184 (68.24%)	R4 (100%)	
ATM-Aztreona	R (100%)		S3 (75%)	R1 (25%)	S1 (25%)	R3 (75%)	S57 (22.35%)	R198 (77.65%)	R4 (100%)	
CAZ-Ceftazidime	S1 (20%)	R4 (80%)	S (100%)		S3 (75%)	R1 (25%)	S206 (80.78%)	R49 (19.22%)	S4 (100%)	
CIP-Ciprofloxacin	S1 (20%)	R4 (80%)	S (100%)		S3 (75%)	R1 (25%)	S171 (67.06%)	R84 (32.94%)	S4 (100%)	
CRO-Ceftriaxone	S1 (20%)	R4 (80%)	S3 (75%)	R1 (25%)	S2 (50%)	R2 (50%)	S189 (74.12%)	R66 (25.88%)	S4 (100%)	
CS-Colistin	R (100%)		S1 (25%)	R3 (75%)	S1 (25%)	R3 (75%)	S26 (10.2%)	R229 (89.8%)	R4 (100%)	
CZ-Cefazolin	R (100%)		R (100%)		R (100%)		S171 (67.06%)	R84 (32.94%)	S4 (100%)	
ETP-Ertapenem	R (100%)		S3 (75%)	R1 (25%)	S2 (50%)	R2 (50%)	S228 (89.41%)	R27 (10.59%)	S4 (100%)	
FEP-Cefepime	S1 (20%)	R4 (80%)	S4 (100%)		S3 (75%)	R1 (25%)	S215 (84.31%)	R40 (15.69%)	S4 (100%)	
FT-Nitrofurantoin	R (100%)		S1 (25%)	R3 (75%)	S3 (75%)	R1 (25%)	S185 (72.55%)	R70 (27.45%)	S4 (100%)	
GM-Gentamicin	S1 (20%)	R4 (80%)	S4 (100%)		S3 (75%)	R1 (25%)	S205 (80.39%)	R50 (19.61%)	S4 (100%)	
IPM-Imipenem	S1 (20%)	R4 (80%)	S4 (100%)		S3 (75%)	R1 (25%)	S251 (98.43%)	R4 (1.57%)	S4 (100%)	
LEV-Levofloxacin	S1 (20%)	R4 (80%)	S3 (75%)	R1 (25%)	S2 (50%)	R2 (50%)	S161 (63.14%)	R94 (36.86%)	S4 (100%)	
MEM-Meropenem	R (100%)		S3 (75%)	R1 (25%)	S1 (25%)	R3 (75%)	S71 (27.84%)	R184 (72.16%)	R4 (100%)	
MNO-Minocycline	R (100%)		S1 (25%)	R3 (75%)	S1 (25%)	R3 (75%)	S22 (8.63%)	R233 (91.37%)	R4 (100%)	
PEF-Pefloxacin	R (100%)		S1 (25%)	R3 (75%)	S1 (25%)	R3 (75%)	S13 (5.1%)	R242 (94.9%)	R4 (100%)	
PIP-Piperacillin	R (100%)		S1 (25%)	R3 (75%)	S1 (25%)	R3 (75%)	S11 (4.31%)	R244 (95.69%)	R4 (100%)	
SAM-Ampicillin/Sulbactam	S2 (40%)	R3 (60%)	R (100%)		R (100%)		S129 (50.59%)	R126 (49.41%)	S3 (75%)	R1 (25%)
SXT-Trimethoprim/Sulfamethoxazole	S2 (40%)	R3 (60%)	S4 (100%)		S2 (50%)	R2 (50%)	S133 (52.16%)	R122 (47.84%)	S4 (100%)	
TGC-Tigecycline	S1 (20%)	R4 (80%)	S2 (50%)	R2 (50%)	R (100%)		S42 (16.47%)	R213 (83.53%)	R4 (100%)	
TIC-Ticarcillin	R (100%)		S1 (25%)	R3 (75%)	S1 (25%)	R3 (75%)	S11 (4.31%)	R244 (95.69%)	R4 (100%)	
TM-Tobramycin	S1 (20%)	R4 (80%)	S4 (100%)		S3 (75%)	R1 (25)	S215 (84.31%)	R40 (15.69%)	S4 (100%)	
TZP-Piperacillin/Tazobactam	S1 (20%)	R4 (80%)	S4 (100%)		S3 (75%)	R1 (25%)	S220 (86.27%)	R35 (13.73%)	S3 (75%)	R1 (25%)

S: Sensitive, R: Resistant.

Table 5
Responses of Gram negative bacteria to different antimicrobial agents.

Agency	*Klebsiellapneumonia* (76)		*Morganella morganii* (1)	*Proteus mirabilis* (17)		*Pseudomonas aeruginosa* (2)		*Serratia marcescens* (2)		*Serratia rubidaea* (1)
AM-Ampicillin	R76 (100%)		R (100%)	S7	R10	R4 (100%)	R2 (100%)	R2 (100%)		R (100%)
AMC-Amoxicillin/ Clavulanic Acid	S41 (53.95%)	R35 (46.05%)	R (100%)	S15 (88.24%)	R2 (11.76%)	R4 (100%)	R2 (100%)	R2 (100%)		S (100%)
AN-Amikacin	S20 (26.32%)	R56 (73.68%)	R (100%)	R17 (100%)		R4 (100%)	R2 (100%)	R2 (100%)		R (100%)
ATM-Aztreona	S16 (21.05%)	R60 (78.95%)	R (100%)	R17 (100%)		R4 (100%)	R2 (100%)	R2 (100%)		R (100%)
CAZ-Ceftazidime	S64 (84.21%)	R12 (15.79%)	S (100%)	S17 (100%)		S4 (100%)	S2 (100%)	S2 (100%)		S (100%)
CIP-Ciprofloxacin	S58 (76.32%)	R18 (23.68%)	S (100%)	S17 (100%)		R4 (100%)	S2 (100%)	S2 (100%)		S (100%)
CRO-Ceftriaxone	S59 (77.63%)	R17 (22.39%)	S (100%)	S17 (100%)		R4 (100%)	S2 (100%)	S2 (100%)		S (100%)
CS-Colistin	S5 (6.58%)	R71 (93.42%)	R (100%)	R17 (100%)		R4 (100%)	R2 (100%)	R2 (100%)		R (100%)
CZ-Cefazolin	S51 (67.11%)	R25 (32.89%)	R (100%)	S15 (88.24%)	R2 (11.76%)	R4 (100%)	R2 (100%)	R2 (100%)		R (100%)
ETP-Ertapenem	S67 (88.16%)	R9 (11.84%)	S (100%)	S17 (100%)		R4 (100%)	S2 (100%)	S2 (100%)		S (100%)
FEP-Cefepime	S65 (85.53%)	R11 (14.47%)	S (100%)	S17 (100%)		S4 (100%)	S2 (100%)	S2 (100%)		S (100%)
FT-Nitrofurantoin	S51 (67.11%)	R25 (32.89%)	S (100%)	S15 (88.24%)	R2 (11.76%)	S4 (100%)	S2 (100%)	S2 (100%)		S (100%)
GM-Gentamicin	S60 (78.95%)	R16 (21.05%)	R (100%)	S13 (76.47%)	R4 (23.53%)	R4 (100%)	S2 (100%)	S2 (100%)		S (100%)
IPM-Imipenem	S62 (81.58%)	R14 (18.42%)	R (100%)	R17 (100%)		R4 (100%)	S2 (100%)	S2 (100%)		S (100%)
LEV-Levofloxacin	S59 (77.63%)	R17 (22.39%)	S (100%)	S15 (88.24%)	R2 (11.76%)	R4 (100%)	S1 (50%)	S1 (50%)	R1 (50%)	S (100%)
MEM-Meropenem	S20 (26.32%)	R56 (73.68%)	R (100%)	R17 (100%)		R4 (100%)	R2 (100%)	R2 (100%)		R (100%)
MNO-Minocycline	S2 (2.63%)	R74 (97.37%)	R (100%)	R17 (100%)		R4 (100%)	R2 (100%)	R2 (100%)		R (100%)
PEF-Pefloxacin	S3 (3.95%)	R73 (96.05%)	R (100%)	R17 (100%)		R4 (100%)	R2 (100%)	R2 (100%)		R (100%)
PIP-Piperacillin	S1 (1.32%)	R75 (98.68%)	R (100%)	R17 (100%)		R4 (100%)	R2 (100%)	R2 (100%)		R (100%)
SAM-Ampicillin/Sulbactam	S42 (55.26%)	R34 (44.74%)	R (100%)	S12 (70.59%)	R5 (29.41%)	R4 (100%)	R2 (100%)	R2 (100%)		R (100%)
SXT-Trimethoprim/ Sulfamethoxazole	S48 (63.16%)	R28 (36.84%)	R (100%)	S5 (29.41%)	R12 (70.59%)	R4 (100%)	S2 (100%)	S2 (100%)		S (100%)
TGC-Tigecycline	S15 (19.74%)	R61 (80.26%)	R (100%)	R17 (100%)		R4 (100%)	R2 (100%)	R2 (100%)		R (100%)
TIC-Ticarcillin	R76 (100%)		R (100%)	R17 (100%)		R4 (100%)	R2 (100%)	R2 (100%)		R (100%)
TM-Tobramycin	S65 (85.53%)	R11 (14.47%)	S (100%)	S16 (94.12%)	R1 (5.88%)	R4 (100%)	S2 (100%)	S2 (100%)		S (100%)
TZP-Piperacillin/Tazobactam	S57 (75%)	R19 (25%)	S (100%)	S17 (100%)		R4 (100%)	S2 (100%)	S2 (100%)		S (100%)

S: Sensitive, R: Resistant.

health care service [38,39,40]. This study was conducted to focus some light on MDR in UTI isolates collected from patients who visited Rizgary Hospital in Erbil, Kurdistan Region—Iraq. Out of 2692 urine samples collected during this study, culture growth showed the following results: 20.1% no bacterial growth, 63.19% non-pathogenic bacterial growth, and 16.71% pathogenic bacterial growth. Our data also show that, out of all pathogenic bacterial isolates only 17.56% of them were Gram positive and the rest, 82.44%, were Gram negative bacteria (Table 1). Amraei et al. (2016) reported similar results to ours in regard to the percentile of

Table 6
Pattern of antimicrobial resistance among detected bacteria.

No.	Bacterial isolates	No. of R.A.	Resisted antibiotics
Gram positive bacteria			
1	*Enterococcus faecalis*	18	Ciprofloxacin, Clindamycin, Ceftriaxone, Cefotaxime, Fusidic acid, Fosfomycin, Gentamicin, Mupirocin, Oxacillin, Rifampicin, Ticarcillin, Tobramycin, Ampicillin, Erythromycin, Benzylpenicillin, Quinupristin/Dalfopristin, Tetracycline, and Trimethoprim/Sulfamethoxazole.
2	*Streptococcus agalactiae*	15	Fusidic acid, Fosfomycin, Nitrofurantoin, Gentamicin, Mupirocin, Oxacillin, Quinupristin/Dalfopristin, Rifampicin, Tetracycline, Ticarcillin, Tobramycin, Ciprofloxacin, Moxifloxacin, Teicoplanin, and Tigecycline.
3	*Staphylococcus haemolyticus*	9	Ampicillin, Ceftriaxone, Cefotaxime, Ticarcillin, Ciprofloxacinm, Benzylpenicillin, Quinupristin/Dalfopristin, Oxacillin, and Erythromycin
4	*Staphylococcus aureus*	8	Ampicillin, Ceftriaxone, Cefotaxime, Benzylpenicillin, Ticarcillin, Ciprofloxacin, Quinupristin/Dalfopristin, and Tetracycline.
Gram negative bacteria			
1	*Acinetobacter baumannii*	23	Ampicillin, Amoxicillin/Clavulanic Acid, Amikacin, Aztreona, Colistin, Cefazolin, Ertapenem, Nitrofurantoin, Meropenem, Minocycline, Pefloxacin, Piperacillin, Ticarcillin, Ceftazidime, Ciprofloxacin, Ceftriaxone, Cefepime, Gentamicin, Imipenem, Levofloxacin, Tigecycline, Tobramycin, and Piperacillin/Tazobactam.
2	*Pseudomonas aeruginosa*	22	Ampicillin, Amoxicillin/Clavulanic Acid, Amikacin, Aztreona, Cefazolin, Ertapenem, Nitrofurantoin, Meropenem, Minocycline, Ticarcillin, Ceftazidime, Ciprofloxacin, Ceftriaxone, Cefepime, Gentamicin, Imipenem, Levofloxacin, Tigecycline, Tobramycin, Piperacillin/Tazobactam, Ampicillin/Sulbactam, and Trimethoprim/Sulfamethoxazole
3	*Morganella morganii*	16	Ampicillin, Amoxicillin/Clavulanic Acid, Amikacin, Aztreona, Nitrofurantoin, Meropenem, Ticarcillin, Ceftazidime, Ceftriaxone, Cefepime, Gentamicin, Imipenem, Levofloxacin, Tigecycline, Tobramycin, Piperacillin/Tazobactam.
4	*Enterobacter cloacae*	13	Ampicillin, Amoxicillin/Clavulanic Acid, Cefazolin, Ampicillin/Sulbactam, Tigecycline, Amikacin, Aztreona, Colistin, Meropenem, Minocycline, Pefloxacin, Piperacillin, and Ticarcillin.
5	*Serratia marcescens*	13	Ampicillin, Amoxicillin/Clavulanic Acid, Amikacin, Aztreona, Nitrofurantoin, Meropenem, Ceftriaxone, Cefepime, Gentamicin, Imipenem, Levofloxacin, Tobramycin, and Piperacillin/Tazobactam.
6	*Serratia rubidaea*	12	Ampicillin, Amikacin, Aztreona, Nitrofurantoin, Meropenem, Ceftriaxone, Cefepime, Gentamicin, Imipenem, Levofloxacin, Tobramycin, and Piperacillin/Tazobactam.
7	*Proteus mirabilis*	11	Amikacin, Aztreona, Nitrofurantoin, Ceftazidime, Ceftriaxone, Cefepime, Gentamicin, Imipenem, Tobramycin, Piperacillin/Tazobactam, and Tigecycline
8	*Enterobacter aerogenes*	10	Ampicillin, Amoxicillin/Clavulanic Acid, Cefazolin, Ampicillin/Sulbactam, Colistin, Nitrofurantoin, Minocycline, Pefloxacin, Piperacillin, and Ticarcillin.
9	*Klebsiella oxytoca*	10	Ampicillin, Amikacin, Aztreona, Colistin, Meropenem, Minocycline, Pefloxacin, Piperacillin, Tigecycline, and Ticarcillin.
10	*Klebsiella pneumonia*	10	Ampicillin, Piperacillin/Tazobactam, Imipenem, Cefepime, Gentamicin, Nitrofurantoin, Tobramycin, Aztreona, Amikacin, and Ceftriaxone.
11	*Escherichia coli*	9	Piperacillin, Ticarcillin, Pefloxacin, Minocycline, Colistin, Tigecycline, Aztreona, Meropenem, and Ampicillin.

R.A.: Resisted antibiotics.

Table 7
Collective resistance of Gram positive and negative bacteria to antibiotics.

No.	Gram Positive Bacteria		Gram Negative Bacteria	
	Antibiotics	% Resistance	Antibiotics	% Resistance
1	Ticarcillin	100.00	Ticarcillin	95.06
2	Ciprofloxacin	94.36	Piperacillin	94.94
3	Quinupristin/Dalfopristin	92.25	Pefloxacin	94.63
4	Oxacillin	78.85	Minocycline	94.43
5	Fosfomycin	77.31	Colistin	93.93
6	Benzylpenicillin	76.22	Ampicillin	93.65
7	Ampicillin	75.83	Tigecycline	90.34
8	Tetracycline	75.51	Aztreona	86.96
9	Ceftriaxone	75.00	Meropenem	85.99
10	Cefotaxime	75.00	Amikacin	85.63
11	Gentamicin	71.80	Ampicillin/Sulbactam	73.51
12	Erythromycin	68.40	Cefazolin	70.68
13	Fusidic acid	67.05	Amoxicillin/Clavulanic Acid	66.24
14	Rifampicin	64.10	Trimethoprim/Sulfamethoxazole	42.30
15	Mupirocin	63.08	Imipenem	38.64
16	Tobramycin	61.80	Levofloxacin	34.18
17	Clindamycin	57.44	Gentamicin	33.56
18	Teicoplanin	53.59	Ceftriaxone	27.57
19	Moxifloxacin	31.67	Ertapenem	27.04
20	Nitrofurantoin	30.00	Nitrofurantoin	24.74
21	Vancomycin	27.95	Piperacillin/Tazobactam	24.40
22	Trimethoprim/Sulfamethoxazole	25.96	Ciprofloxacin	23.78
23	Levofloxacin	24.74	Tobramycin	21.91
24	Linezolid	24.18	Ceftazidime	12.73
25	Tigecycline	21.67	Cefepime	12.29

non-pathogenic, uro-pathogenic, Gram positive and Gram negative bacteria [40]. As more than 20% of all tested urine samples were negative for any kind of bacterial growth, this indicates that diagnosis of UTI based on clinical symptoms only may give false results. This came in agreement with previous studies suggested significant correlation between misdiagnosed and symptom only based methodology for UTI detection [12,13].

Following the classification of the detected pathogenic bacteria, our data revealed that among the isolated Gram positive pathogens *S. haemolyticus* was the most abundant (49.36%), and *E. faecalis* was the least detected one (12.66%) (Table 2). Later on, antibiotic susceptibility test identified *E. faecalis* as the most resistant Gram positive bacteria (especially to: Ciprofloxacin, Clindamycin, Ceftriaxone, Cefotaxime, Fusidic acid, Fosfomycin, Gentamicin, Mupirocin, Oxacillin, Rifampicin, Ticarcillin, and Tobramycin), and *S. aureus* as the most sensitive one (especially to: Moxifloxacin and Tigecycline) (Tables 3 and 6). Comparison between the most and the least effective antibiotics showed that Gram positive bacterial isolates, in general, were highly resistant to following drugs: Ticarcillin, Ciprofloxacin, and Quinupristin/Dalfopristin (Table 7).

In regard to Gram negative bacterial isolates, *E. coli* was the most abundant (68.73%), and *M. morganii* and *S. rubidaea* were the rarest (0.27%) (Table 2). For antibiotic sensitivity test, *A. baumannii* was the most resistant bacteria (especially to: Ampicillin, Amoxicillin/Clavulanic Acid, Amikacin, Aztreona, Colistin, Cefazolin, Ertapenem, Nitrofurantoin, Meropenem, Minocycline, Pefloxacin, Piperacillin, Ticarcillin, Ceftazidime, Ciprofloxacin, Ceftriaxone, Cefepime, Gentamicin, Imipenem, Levofloxacin, Tigecycline, Tobramycin, and Piperacillin/Tazobactam.), and *E. coli* was the most sensitive one (especially to: Imipenem, Ertapenem, and Piperacillin/Tazobactam) (Tables 4–6). Finally, our data also show that Gram negative bacterial isolates, in general, were highly resistant to: Ticarcillin, Piperacillin, Pefloxacin, Minocycline, Colistin, Ampicillin, and Tigecycline, as shown in Tables 6 and 7. Interestingly, despite the structural differences between Gram positive and Gram negative bacteria they were both resistant to Ticarcillin and Ampicillin antibiotics (Table 7).

Since a GPB like *E. faecalis* resisting 72%, and a GNB like *A. baumannii* resisting 92% of all screened antibiotics, this indicates that MDR dilemma dose exist strongly in this region and it needs to be dealt with urgently for wellbeing of local population. In this regard, it's important to make advantage of previous studies that were carried out to deal with this issue [39], but at the same time its crucial to enrich and integrate these studies with local ones. The best strategy to achieve that is through conducting periodic investigations by collecting larger scale sample size from local patinas to establish a standard guiding protocol that clearly describes the most appropriate antibiotics for detected isolates.

Conclusion

It is concluded from this study that to avoid misdiagnosis of UTI it is important to run urine samples through standard culture growth to identify pathogen causing symptoms. Gram negative bacteria (especially *E. coli*) were the most UTI related pathogen, *E. faecalis* (GPB) and *A. baumannii* (GNB) bacteria were among the most resilient bacterial isolates. Generally speaking GPB were highly resistant to Ticarcillin, Ciprofloxacin, and Quinupristin/Dalfopristin antibiotics, and GNB were highly resistant to Ticarcillin, Piperacillin, Pefloxacin, Minocycline, Colistin, Ampicillin, and Tigecycline. Finally, based on our data MDR may exist strongly among local population especially those who visited Rizgary hospital for UTI treatment.

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