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Original Article

Emergence of High Drug Resistant Bacterial Isolates in Al-Kharj

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ABSTRACT

Background: Continuous utilization of antimicrobial drugs in treating infections has led to the development of resistance among various strains of bugs. The aim of this study was to determine the prevalence of antibiotic-resistant bacteria in a military hospital in Al-Kharj. **Methods:** This study is a retrospective study that include collecting the results of bacterial cultures. After collecting the data, an antibiogram was prepared and after that the resistance rates for each bacterium were calculated by subtraction of 100% from the susceptibility rate for each result (Resistance rate= 100% - Susceptibility rate). **Results:** *Acinetobacter baumannii* was resistant to most tested antibiotics and *Klebsiella pneumonia* was resistant to several antibiotics in 2018 and 2019. In the present study, there were a high resistance rate of *Klebsiella pneumonia* and *Acinetobacter baumannii* and there were 2 main threats which include Carbapenem-resistant *Acinetobacter* and Ciprofloxacin-resistant *Salmonella*. **Conclusion:** It is recommended to increase the awareness of the health care professionals regarding the appropriate prescribing of antibiotics based on antimicrobial resistance rate and to increase the awareness of the public about the wise use of antibiotics.

Key words: Antibiotics, Bacteria, Bacterial Isolates, Multidrug Resistant, Resistance.

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INTRODUCTION

Antibiotics are medications used to treat several infections. The era from 1930s to 1960s was considered the golden era of antibiotics which gave rise to numerous antibiotics.[1] This era ended because the researchers were unable to keep up with the pace of antibiotic discovery in the face of emerging resistant bugs. The predisposing factors that are associated with the emergence of antibiotic resistance include the failure to discover or develop novel antibiotics and the inappropriate use of antibiotics.[2] The development of antimicrobial resistance was observed shortly after the introduction of novel antimicrobial agents.[3] Therefore, continuous utilization of antimicrobial drugs in treating infections has led to the development of resistance among numerous strains of bugs. Multidrug resistance is defined as the resistance or insensitivity of a microbe to antimicrobial medicine despite the sensitivity to it previously.[4,5]

Multidrug resistant bacteria are one of the main threats to public health.[6-8] Typically, Multidrug resistant microbes are associated with nosocomial infections. However, some of these bacteria have become moderately prevalent causes of community-acquired infections.[6] Multidrug resistant bacteria result in numerous negative consequences, the outcomes in patients infected with multidrug resistant bacteria tend to be worse than the outcomes in patients infected with more susceptible bacteria.[9,10] Studies from World Health Organization report have shown very high rates of resistance in several bacteria such as *Klebsiella pneumoniae* against carbapenems and cephalosporin, *Escherichia coli* against antibiotics as fluoroquinolones and cephalosporin, *Streptococcus pneumoniae* against penicillin, *Staphylococcus aureus* against methicillin, *Shigella* species against fluoroquinolones, Nontyphoidal *Salmonella* against fluoroquinolones, *Neisseria gonorrhoeae* against cephalosporin and *Mycobacterium tuberculosis* against fluoroquinolone, rifampicin and isoniazid.[11,12] An international panel of experts stated that the bacterial resistance is classified as **multidrug-resistant** if the bacteria acquired non-susceptibility to at least one antibiotic in three or more antibiotic classes.[13]

It is important to know the antibiotic resistance rate in clinical isolates to give the appropriate antibiotic treatment. Additionally, knowing the resistance rate could help health planners to develop strategies to prevent the spread of antibiotic resistance. There is a lack of studies about antibiotic-resistant bacteria in Al-Kharj. Therefore, the aim of this study was to determine the prevalence of antibiotic-resistant bacteria in a military hospital in Al-Kharj.

MATERIALS AND METHODS

Setting

The study was conducted at the Military Industrial Corporation Hospital in Al-Kharj. This hospital is initiated in 1979 in Alkharj that is located near Riyadh city, the capital of Saudi Arabia. The hospital includes only 60 beds, so it is considered a small hospital (with less than 100 beds).

Inclusion/exclusion criteria

The results of all bacterial cultures in 2018 and 2019 were included. Bacterial cultures before 2018 or after 2019 were excluded and the results of fungal cultures were also excluded.

Data collection and analysis

The data were collected from the bacterial cultures' results that were prepared by the help of Microbiology department in the hospital. The data was represented in 4 tables: the gram-negative bacterial resistance rates in 2018, the gram-positive bacterial resistance rates in 2018, the gram-negative bacterial resistance rates in 2019 and the gram positive bacterial resistance rates in 2019. After collecting the data, an antibiogram was prepared and after that the resistance rates for each bacterium were calculated by subtraction of 100% from the susceptibility rate for each result (Resistance rate= 100% - Susceptibility rate). If the bacteria are resistant to at least one antibiotic in three or more antibiotic classes, these bacteria are classified as **multidrug-resistant** bacteria.

Ethical approval

The study was approved by the IRB Ethical Committee of the hospital No: 4101728. The study excluded any patient' identifiers to protect the patients' privacy.

RESULTS

Total number of bacterial isolates in 2018 and 2019

In 2018 and 2019, there were a total of 1735 bacterial isolates, the most prevalent bacteria were *Escherichia coli* bacteria (28.41%), *Staphylococcus aureus* (22.54%), *Pseudomonas aeruginosa* (11.64 %), *Klebsiella pneumonia* (11.47%) and *group B Streptococcus* (5.82%). These 5 bacteria form 79.88 % of the total bacteria isolates in the 2 years.

Number of bacterial isolates in 2018

In 2018, there were 743 bacterial isolates. The most common organism was *Escherichia coli* (32.84%) followed by *Pseudomonas aeruginosa* (14.14%), *Staphylococcus aureus* (12.52%) and *Klebsiella pneumonia* (10.50%). Table 1 shows the total number of bacterial isolates in 2018.

Table 1: Total number of bacterial isolates in 2018.

Bacteria	Number	Percentage
Escherichia coli	244	32.84
Pseudomonas aeruginosa	105	14.14
Staphylococcus aureus	93	12.52
Klebsiella pneumonia	78	10.50
Acinetobacter baumannii	51	6.87
Coagulase –ve Staphylococcus	33	4.44
Group B Streptococcus	30	4.04
Enterobacter cloacae	20	2.69
Proteus mirabillis	17	2.29
Enterococcus faecalis	17	2.29
Salmonella	11	1.48
Serratia marcescens	10	1.35
Group A Streptococcus	7	0.94
Enterobacter aerogenes	5	0.67
Brucella	5	0.67
Haemophillus Spp	4	0.54
Providencia stuartii	4	0.54
Morganella morganii	3	0.40
Citrobacter Koseri	3	0.40
Citrobacter youngea	1	0.13
Pseudomonas fluorescens	1	0.13
Citrobacter freundii	1	0.13
Total	**743**	**100.00**

Number of bacterial isolates in 2019

In 2019, there were 992 bacterial isolates. The most common organism was *Staphylococcus aureus* (30.04%) followed by *Escherichia coli* (25.10%), *Klebsiella pneumonia* (12.20%) and *Pseudomonas aeruginosa* (9.78%). Table 2 shows the total number of bacterial isolates in 2019.

The resistance rate of gram negative and gram-positive bacteria in 2018

The resistance rate for most of gram-negative bacteria in 2018 was generally low. Only there was a high resistance rate for *Acinetobacter baumannii* that was resistant to most tested antibiotics. Table 3 shows the gram-negative bacterial resistance rates in 2018. Regarding gram positive bacteria, the resistance rate generally was low and there were no multidrug resistant bacteria. The gram-positive bacterial resistance rates in 2018 are shown in Table 4.

The resistance rate of gram negative and gram-positive bacteria in 2019

The resistance rate for most of gram-negative bacteria in 2019 was generally low. Only there were high resistance rate for *Acinetobacter baumannii* and *Klebsiella pneumonia*. *Acinetobacter baumannii* was resistant to most tested antibiotics and *Klebsiella pneumonia* was resistant to several antibiotics. Table 5 shows the gram-negative bacterial resistance rates in 2019. Regarding gram positive bacteria, the resistance rate generally was low. Only *Coagulase –ve Staphylococcus* bacteria were resistant to 3 antibiotics, erythromycin, oxacillin, and clindamycin. The gram-positive bacterial resistance rates in 2019 are shown in Table 6.

DISCUSSION

In 2018 and 2019, the most prevalent bacteria were *Escherichia coli* (28.41%), *Staphylococcus aureus* (22.54%), *Pseudomonas aeruginosa* (11.64 %), *Klebsiella pneumonia* (11.47%) and *Group B Streptococcus* (5.82%). These 5 bacteria form approximately 80 % of the total bacteria isolates. Likewise, Bono *et al*. reported that in patients with renal diseases the most frequently isolated bacterial pathogens were *Escherichia coli* and *Staphylococcus aureus* followed by *Enterococcus faecalis*, *Pseudomonas*

Table 2: Total number of bacterial isolates in 2019.

Bacteria	Number	Percentage
Staphylococcus aureus	298	30.04
Escherichia coli	249	25.10
Klebsiella pneumonia	121	12.20
Pseudomonas aeruginosa	97	9.78
Group B Streptococcus	71	7.16
Coagulase –ve Staphylococcus	32	3.23
Proteus mirabillis	28	2.82
Enterococcus faecalis	21	2.12
Acinetobacter baumannii	19	1.91
Enterobacter cloacae	15	1.51
Salmonella	12	1.21
Serratia marcescens	10	1.01
Group A Streptococcus	9	0.91
Enterobacter aerogenes	5	0.50
Providencia stuartii	5	0.50
Total	**992**	**100.00**

Table 3: **The gram-negative bacterial resistance rates in 2018.**

Bacteria \ Antibiotics	#	Amikacin	Ampicillin	Augmentin	Aztreonam	Cefepime	Cefoxitin	Ceftazidime	Ceftriaxone	Cefuroxime	Cephalothin	Ciprofloxacin	Colistin	Ertapenem	Gentamicin	Imipenem	Levofloxacin	Meropenem	Nitrofurantoin	Piperacillin / Tazobactam	Trimethoprim / Sulfamethoxazole
Escherichia coli	244	0	60	37	30	28	7	28	27	29	82	25	NA	12	18	7	25	5	3	4	53
Enterobacter aerogenes	5	0	NA	NA	20	20	NA	0	20	NA	NA	0	NA	0	20	0	0	0	NA	0	0
Enterobacter cloacae	20	0	NA	NA	20	2	NA	0	20	NA	NA	0	NA	2	2	0	0	0	NA	20	0
Haemophillus Spp	4	NA	0	0	NA	NA	NA	NA	25	25	NA	0	NA	NA	NA	NA	NA	NA	NA	NA	75
Klebsiella pneumonia	78	5	NA	30	32	35	20	30	35	28	40	20	NA	25	15	18	16	18	55	25	30
Citrobacter freundii	1	0	NA	NA	0	0	NA	NA	NA	NA	NA	NA	NA	0	0	0	NA	0	0	0	0
Citrobacter Koseri	3	0	NA	0	0	0	NA	0	0	0	0	0	NA	NA	0	0	0	0	NA	0	0
Serratia marcescens	10	15	NA	NA	15	15	NA	15	35	NA	NA	15	NA	35	15	35	15	35	NA	0	0
Proteus mirabillis	17	10	48	27	14	14	0	14	14	29	43	100	NA	0	29	NA	29	0	NA	0	71
Providencia stuartii	4	0	NA	NA	50	50	0	50	50	50	NA	NA	NA	50	NA	50	NA	50	NA	0	50
Morganella morganii	3	0	NA	NA	0	0	0	0	0	NA	NA	34	NA	0	0	0	0	0	NA	0	0
Citrobacter youngea	1	0	NA	NA	0	0	NA	0	0	0	NA	0	NA	0	0	0	0	0	NA	0	0
Pseudomonas fluorescens	1	0	NA	NA	0	0	NA	0	NA	0	NA	0	0	NA	0	0	0	0	NA	100	NA
Salmonella	11	NA	28	NA	NA	NA	NA	NA	0	NA	NA	70	NA	NA	NA	NA	NA	NA	NA	NA	34
Pseudomonas eruginosa	105	0	NA	NA	15	17	NA	15	NA	NA	NA	21	10	NA	10	20	20	18	NA	10	NA
Acinetobacter baumannii	51	45	NA	NA	NA	60	NA	60	70	NA	NA	60	1	NA	67	67	70	67	NA	67	20
Brucella	5	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	NA	NA	0	NA	NA	NA	NA	NA	25

Table 4: **The gram-positive bacterial resistance rates in 2018.**

Bacteria \ Antibiotics	#	Ciprofloxacin	Clindamycin	Daptomycin	Erythromycin	Gentamicin	Linezolid	Moxifloxacin	Nitrofurantoin	Oxacillin	Rifampin	Teicoplanin	Tetracycline	Trimethoprim / Sulfamethoxazole	Vancomycin	Mupirocin HL	Cefuroxime	Penicillin	Chloramphenicol	Ceftriaxone	Meropenem	Ampicillin
Staphylococcus aureus	93	13	17	2	29	7	0	0	0	37	0	3	15	19	0	2	NA	NA	NA	NA	NA	NA
Coagulase –ve Staphylococcus	33	70	30	20	40	30	2	0	0	60	10	10	15	40	2	2	NA	NA	NA	NA	NA	NA
Group A Streptococcus	7	NA	NA	NA	0	NA	NA	NA	NA	NA	NA	NA	NA	0	0	NA	0	0	0	NA	NA	NA
Group B Streptococcus	30	NA	NA	NA	40	NA	NA	NA	NA	NA	NA	NA	70	30	5	NA	0	5	15	5	10	NA
Enterococcus faecalis	17	45	NA	NA	NA	45	0	NA	NA	NA	NA	NA	NA	NA	0	NA	NA	NA	NA	NA	NA	15

aeruginosa, *Staphylococcus epidermidis* and *Klebsiella pneumonia.*[14] Ahmed *et al*. reported that ESKAPE pathogens (*Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa* and Enterobacter spp.) cause nearly half of the infections that were caused by bacteria and the most common ESKAPE pathogens were *Klebsiella pneumonia* and Pseudomonas aeruginosa.[15]

The resistance rate for most of gram-negative bacteria in the present study in 2018 was generally low. *Escherichia coli* was highly resistant to cephalothin (82%), ampicillin (60 %) and to trimethoprim / sulfamethoxazole (53 %). *Klebsiella pneumonia* was highly resistant to nitrofurantoin (55%) but the number of *Klebsiella pneumonia* bacteria were low (17 isolates). *Proteus mirabillis* bacteria was highly resistant to ciprofloxacin (100%) and to trimethoprim / sulfamethoxazole (71%). *Salmonella* was highly resistant to ciprofloxacin (70%) but the number of *Salmonella* bacteria were low (11 isolates). In 2018, there was a high resistance rate for *Acinetobacter baumannii* which was resistant to most of the tested antibiotics. For example, the resistance rate of *Acinetobacter baumannii* was 70 % to ceftriaxone and levofloxacin. The resistance rate was 67 % to gentamicin, imipenem, meropenem and piperacillin / tazobactam. The resistance rate was 60 % to cefepime, ceftazidime and ciprofloxacin.

The resistance rate for most of gram-negative bacteria in the present study in 2019 was generally low. *Escherichia coli* was highly resistant to

Table 5: The gram-negative bacterial resistance rates in 2019.

Antibiotics / Bacteria	#	Amikacin	Ampicillin	Ampicillin/sulbactam	Augmentin	Aztreonam	Cefepime	Cefoxitin	Ceftazidime	Ceftriaxone	Cefuroxime	Cephalothin	Ciprofloxacin	Colistin	Ertapenem	Gentamicin	Imipenem	Levofloxacin	Meropenem	Nitrofurantoin	Piperacillin / Tazobactam	Trimethoprim / Sulfamethoxazole	Norfloxacin	Gentamicin synergy	Quinupristin / Dalfopristin	Streptomycin synergy
Escherichia coli	249	2	47	NA	39	47	41	10	45	27	47	82	35	NA	6	8	6	36	4	NA	NA	NA	NA	NA	NA	NA
Enterobacter Aerogenes	5	0	NA	NA	NA	33	33	NA	0	33	NA	NA	0	NA	0	33	0	0	0	NA	NA	NA	NA	NA	NA	NA
Enterobacter cloacae	15	0	NA	NA	NA	33	27	NA	0	10	NA	NA	13	NA	13	20	7	0	13	NA	NA	NA	NA	NA	NA	NA
Klebsiella pneumonia	121	42	NA	NA	55	58	57	49	55	35	58	74	45	NA	51	43	42	43	43	74	68	32	NA	NA	NA	NA
Serratia marcescens	10	0	NA	NA	NA	10	0	NA	10	NA	NA	NA	0	NA	20	10	10	0	0	NA	0	0	NA	NA	NA	NA
Proteus mirabillis	28	7	64	NA	46	21	18	25	18	14	37	43	47	NA	0	36	NA	21	0	NA	11	71	NA	NA	NA	NA
Providencia stuartii	5	0	NA	60	NA	80	NA	NA	NA	NA	20	NA	NA	NA	0	NA	20	NA	20	NA	0	NA	80	NA	NA	NA
Salmonella	12	NA	33	NA	NA	NA	NA	NA	NA	0	NA	NA	33	NA	NA	NA	NA	NA	NA	NA	NA	12	NA	NA	NA	NA
Pseudomonas eruginosa	97	0	NA	NA	NA	24	20	NA	22	NA	NA	NA	19	11	NA	8	22	21	21	NA	19	NA	NA	NA	NA	NA
Acinetobacter baumannii	19	70	NA	NA	NA	NA	70	NA	70	70	NA	NA	50	0	NA	60	60	70	60	NA	70	60	NA	60	80	50

Table 6: The gram-positive bacterial resistance rates in 2019.

Antibiotics / Bacteria	#	Ciprofloxacin	Clindamycin	Daptomycin	Erythromycin	Gentamicin	Linezolid	Moxifloxacin	Nitrofurantoin	Oxacillin	Rifampin	Teicoplanin	Tetracycline	Trimethoprim / Sulfamethoxazole	Vancomycin	Mupirocin HL	Cefuroxime	Penicillin	Chloramphenicol	Ceftriaxone	Ampicillin	Nitrofloxacin
Staphylococcus aureus	298	24	17	4	23	16	2	15	50	53	0	1	11	20	0	3	NA	NA	NA	NA	NA	NA
Coagulase –ve Staphylococcus	32	25	53	0	84	28	3	9	NA	81	9	6	16	3	3	9	NA	NA	NA	NA	NA	NA
Group A Streptococcus	9	NA	NA	NA	33	NA	NA	NA	NA	NA	NA	NA	NA	22	0	NA	0	0	44	0	NA	NA
Group B Streptococcus	71	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	17	0	NA	0	0	10	0	NA	NA
Enterococcus faecalis	21	48	NA	0	NA	NA	0	NA	NA	NA	30	20	90	NA	0	NA	NA	0	NA	NA	19	29

cephalothin (82%). *Klebsiella pneumonia* was highly resistant to nitrofurantoin (74%), cephalothin (74%), piperacillin / tazobactam (68%), aztreonam (58%), cefuroxime (58%), augmentin (55%), ceftazidime (55%) and ertapenem (51%). *Acinetobacter baumannii* was highly resistant to quinupristin / dalfopristin (80%). The resistance rate of *Acinetobacter baumannii* to amikacin, cefepime, ceftazidime, ceftriaxone, levofloxacin, piperacillin / tazobactam was 70%. Moreover, the resistance rate of *Acinetobacter baumannii* was 60 % to gentamicin, imipenem, meropenem, trimethoprim / sulfamethoxazole and gentamicin synergy. The resistance rate was 50 % to ciprofloxacin and streptomycin synergy. Nevertheless, the resistance rate of *Acinetobacter baumannii* was 0 % to colistin.

The bacterial resistance is classified by the number of antibiotics that the bacteria resist. If the bacteria are not susceptible to at least one agent in three or more antibiotic classes it is classified as a multidrug-resistant, if the bacteria are not susceptible to at least one agent in all but two or fewer antibiotic classes it is classified as extensively drug-resistant and if the bacteria are not susceptible to all agents it is classified as pandrug-resistant.[16] In 2018, regarding gram negative only *Acinetobacter baumannii* was multidrug resistant. In 2019, *Klebsiella pneumonia* was multidrug resistant organism in 2019 and *Acinetobacter baumannii* was extensively drug-resistant organism. Ahmed *et al*. reported that in a public hospital in Alkharj, *Klebsiella pneumonia* was a multidrug resistant organism and *Acinetobacter baumannii* bacteria were extensively drug resistance organism.[15] Ruiz *et al*. stated that in critically ill patients, 17.9% of the patients were positive for multidrug resistant *Klebsiella pneumonia*.[17]

The present study showed that *Acinetobacter baumannii* was extensively drug-resistant organism. *Acinetobacter baumannii* is one of the 6 ESCAPE organisms that also include *Enterococcus faecium*, *Staphylococcus aureus*, Clostridioides (formerly Clostridium) difficile, *Pseudomonas aeruginosa* and *Enterobacteriaceae*. This group include clinically important and predominantly health care-associated bacteria that have the potential for significant antimicrobial resistance.[18,19] Moreover, Carbapenem-resistant *Acinetobacter baumannii* is nowadays one of the critical-priority microbes on the World Health Organization priority list of antibiotic-resistant bacteria for effective drug development.[20] The prevalence of Carbapenem resistant *Acinetobacter baumannii in* Saudi Arabia have also increased intensely over the years. A recent study from Riyadh reported that the susceptibilities of *Acinetobacter baumannii* to meropenem and imipenem were changed from a range of 64-81.2% in 2006 to the susceptibility ranged between 8.3-11% in 2012.[21] The result of the present study showed that colistin is an appropriate treatment for *Acinetobacter baumannii* infections because the resistance rate of *Acinetobacter baumannii* to colistin was only 1 % in 2018 and 0% in 2019. Polymyxin B and colistin (polymyxin E) are the most commonly used agents for *Acinetobacter* isolates that are resistant to the first-line agents. Polymyxins, such as colistin, generally have *in vitro* activity against *Acinetobacter*.[22,23] Nowadays, resistance to polymyxins has been observed.[24,25] In one surveillance report, the resistance rate of Acinetobacter baumannii to colistin was 2.7 percent of clinical isolates in Europe and 1.7 percent in North and Latin America.[24] Zilberberg *et al*. reported that colistin resistance in Acinetobacter baumannii isolates during 2009 to 2012 in the United States was 6.9 percent.[26]

Regarding gram positive bacteria in 2018, the resistance rate generally was low. *Coagulase –ve Staphylococcus* was highly resistant to ciprofloxacin (70%) and to oxacillin (60%). *Group B Streptococcus* was highly resistant to tetracycline (70%). Regarding gram positive bacteria in 2019, *Staphylococcus aureus* was resistant only to oxacillin (53%) and nitrofurantoin (50%). *Coagulase –ve Staphylococcus* was resistant to erythromycin (84%), oxacillin (81%) and clindamycin (53%). So, there were no multidrug resistant gram-positive bacteria in 2018 and in 2019, *Coagulase –ve Staphylococcus* was a multidrug resistant organism in 2019. May *et al*. study demonstrated that the antibiotic resistance in *Coagulase –ve Staphylococcus* pathogens has increased significantly over the previous years.[27] Marincola *et al*. stated that the infections that are associated with *Coagulase –ve Staphylococcus* from healthcare environments are typically characterized by pronounced antimicrobial resistance including both methicillin- and multidrug-resistant isolates.[28]

Centers for Disease Control and Prevention listed some bacterial resistant threats into three categories which are urgent threats, serious threats and concerning threats. Each category includes several resistant bacteria.[29] In the present study, there was one urgent threat that was Carbapenem-resistant *Acinetobacter*. There was one serious threat that was Ciprofloxacin-resistant *Salmonella*. There was no concerning threats in the present study because concerning threats include 2 subcategories, Erythromycin-Resistant *Group A Streptococcus* that was not present in this study and Clindamycin-resistant *Group B Streptococcus* that was not tested in the present study.

In general, the resistance rate was low for most bacteria except for *Klebsiella pneumonia, Coagulase –ve Staphylococcus* and *Acinetobacter baumannii*. If we compare the resistance rate in 2018 and 2019, we could find that the resistance rate was increased in 2019. The main change in the resistance rate was for *Klebsiella pneumonia*. In 2018, the resistant rate of *Klebsiella pneumonia* to all antibiotics except nitrofurantoin was less than 50 % but in 2019, the resistance rate of *Klebsiella pneumonia* to 9 antibiotics was more than 50 %.

CONCLUSION

In the present study, there were a high resistance rate of *Klebsiella pneumonia*, *Coagulase –ve Staphylococcus* and *Acinetobacter baumannii* mainly and there were 2 main threats which include Carbapenem-resistant *Acinetobacter* and Ciprofloxacin-resistant *Salmonella*. The causes of increasing resistance rate should be determined to decrease the occurrence of infections that are caused by multidrug resistant organisms. Moreover, it is recommended to increase the awareness of the health care professionals regarding the appropriate prescribing of antibiotics based on antimicrobial resistance rate and to increase the awareness of the public about the wise use of antibiotics.

Limitations

The main limitations in the study were that resistance of some bacteria to numerous antibiotics was not tested. For example, the resistance rate of *Group B Streptococcus* to clindamycin was not tested in the present study and Clindamycin-resistant *Group B Streptococcus* are considered as a concerning threat. Furthermore, there was a lack of information about the previous use of antibiotics so if this information will be available in the future, the researchers could find the relation between the bacterial resistance and antibiotics use.

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CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

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