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Multidrug Resistant Bacteria Isolated From Some Basrah Hospitals

Bakteri Resistan Multiobat Diisolasi Dari Beberapa Rumah Sakit Di Basrah

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Abstract

General Background: Antibiotic resistance is a significant and growing public health concern, especially in hospital settings, where intensive care units (ICUs) often harbor multidrug-resistant organisms. **Specific Background:** Antimicrobial resistance in ICUs is a significant issue, necessitating a thorough assessment of bacterial susceptibility patterns to develop effective treatment protocols. **Knowledge Gap:** Despite the increasing concern, comprehensive studies focusing on bacterial resistance patterns in ICUs, particularly in diverse hospital settings, remain limited. **Aims:** The study aimed to assess the resistance patterns of bacterial isolates from blood, urine, and ICU surfaces to various antibiotics and identify the most resistant species. **Results:** Thirty blood, twenty urine, and fifty-six environmental samples were collected and cultured. Staphylococcus spp. exhibited 75% resistance to erythromycin, while Klebsiella spp., Pantoea spp., and E. coli showed 100% resistance to multiple antibiotics, including Ticarcillin, Piperacillin, and Cefixime. Confirmatory bacterial identification was performed using the Vitek 2 compact system, and resistance was measured across 25 antibiotics from various classes. **Novelty:** The study highlights the alarming 100% antibiotic resistance in various ICU-associated bacterial species, emphasizing the urgent need for revised antibiotic stewardship programs. **Implications:** The study underscores the importance of monitoring AMR patterns in hospitals and adjusting antibiotic therapies to combat rising resistance, particularly in ICUs, highlighting the need for robust surveillance.

Highlights:

100% resistance: Klebsiella, Pantoea, E. coli resist multiple antibiotics in ICU.

ICU risk: Multidrug-resistant bacteria prevalent in intensive care units.

Urgent need: Update antibiotic protocols, enhance AMR surveillance in hospitals.

Keywords: Antibiotic resistance, ICU, bacterial susceptibility, multidrug-resistant organisms, hospital infections

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Introduction

ICUs, or intensive care units, seem to have an effect on patient outcomes. One of the main causes of morbidity and death is still infections with Gram-negative germs [1]. The underlying sickness of the patient, the intensity of their condition, the kind of intensive care unit (ICU) they are in, how long they stay there, and the quantity, kind, and duration of intrusive equipment and treatments are all intricately interacting to cause this. In [2,22] Antibiotic resistance in hospitals, particularly is a major worldwide concern in the critical care unit (ICU). It is well known that the emergence of drug-resistant organisms in the critical care unit is correlated with the widespread use of antibiotics. Compared to a typical hospital context, the ICU has a multifold greater risk of antibiotic resistance. Numerous monitoring initiatives have brought this phenomena to light [3, 4]. The most frequent isolates found in clinical specimens in Canadian intensive care units (ICUs) are *P. aeruginosa*, *Staphylococcus aureus*, *Haemophilus influenzae*, *Enterococcus* spp., *Staphylococcus pneumoniae*, and *K. pneumoniae*, according to research conducted in Canada by Zanel et al. in 2006 [5]. In addition, *P. aeruginosa* is the most common phenotype that is resistant to several drugs, meaning that it can withstand the effects of a minimum of three antibiotics, including ciprofloxacin, amikacin or gentamicin, meropenem, cefepime, and piperacillin-tazobactam. In Thailand, resistance to imipenem *P. aeruginosa*, resistant to ceftazidime Third-generation cephalosporin-resistant *K. pneumoniae*, *Acinetobacter baumannii*, and quinolone-resistant The most frequent cause of infection in intensive care units was *E. Coli*. [6]. Many resistant Gram-positive bacteria (GPB) have either decreased or stayed relatively steady in prevalence. In addition, methicillin-resistant *Staphylococcus aureus* (MRSA) has started to become less common in a few nations recently [7]. Gram-negative bacteria (GNB) are more dangerous than GPB because AMR levels have risen in China in a number of significant pathogens, such as *Escherichia coli*, *Pseudomonas aeruginosa*, *Acinetobacter baumannii*, and *Klebsiella pneumoniae* [8]. According to Akhtar 2010 [9], the respiratory and urinary systems are the most likely organs to become infected. *Pseudomonas aeruginosa*, *Klebsiella pneumoniae*, *Escherichia coli*, and *Candida* spp. are the most common pathogens associated with these diseases

Methods

Thirty blood sample were collected from hospitalized patient, A sterile disposable syringe was used to draw five millilitres of blood. Twenty urine specimens were collected in a sterile plastic container made of polyethylene. Twenty millilitres of urine were collected from inpatients and outpatients suffering from UTIs who presented at six different hospitals. Fifty-six sterile swabs, saturated with sterile normal saline, were taken from tables, beds, walls, and various equipment and instruments in the ICU. all samples cultured on nutrient agar ,manitol agar and macConke agar and incubated at 37° C for 24 h. and then subcultured on nutrient agar to have a pure colonies . then all the isolates stained by Gram stain. All bacterial isolates were stained by Gram-stain, then examined under light microscope. catalse and oxidase teat were done and Confirmatory Identification of bactria spp. by Vitek 2 compact. Antibiotics discussed in the present study listed

NO.	Antibiotic class	Symbol
1	Cefoxitin Screen	FOX
2	Benzylpenicillin	BEZ
3	Oxacillin	OXA
4	Gentamicin	GEN
5	Tobramycin	TOB
6	Levofloxacin	LVX
7	Moxifloxacin	MXF
8	Clindamycin	CIN
9	+Azithromycin	AZM
10	Erythromycin	ERY
11	Clindamycin	CLI
12	Linezolid	LZD
13	Teicoplanin	TIC
14	Vancomycin	VAN
15	Tetracycline	TET
16	Tigecycline	TGC
17	Nitrofurantoin	NIT
18	Rifampicin	RIF
19	rimethoprim/Sulfamethoxazole	TMP
20	Cefepime	CPM
21	Cefixime	CFM

22	Imipenem	IPM
23	Meropenem	MEM
24	Piperacillin	PEP
25	Ticarcillin	TIC

Table 1.

Result and Discussion

According to the results of antimicrobial susceptibility test figure 8 showed that (75%) Staphylococcus SPP. was resistant to Erythromycin followed by Clindamycin with percentage (50%) ,Trimethoprim/Sulfamethoxazole (35.50%) , Gentamicin (25%),Tobramycin (25%) ,Tetracycline (25%), Rifampicin(25%), Levofloxacin(18.75%), Moxifloxacin(18.75%), Teicoplanin(12.50%), Vancomycin (12.50%), Nitrofurantoin(6.25%).On the other hand most Enterobacter spp showed (13.33%) percentage of resistance to antibiotics followed by Ticarcillin , Ticarcillin/Clavulanic Acid, Piperacillin and Piperacillin/Tazobactam (6.66%) as showed in figure (9), Pseudomonas spp showed low percentage of resistance to Ticarcillin (14.28%) and Piperacillin(14.28%) and show no resistance to the other antibiotics used as showed in figure (10), Klebsiella spp showed high resistance to Ticarcillin,Piperacillin,Cefixime,Ceftazidime,Cefepime,Minocyclin,Trimethoprim/Sulfamethoxazole and Aztreonam with percentage of (100%) while, Imipenem, Meropenem, Amikacin, Gentamicin Tobramycin, Ciprofloxacin and Levofloxacin(50%) as showed in figure (11), pantoea spp exhibited (100%) resistant to antibiotics Ampicillin, Amox, Cefoxitin, Cefixime, Cefpodoxime (100%) and 50% for Ticarcillin, Piperacillin/Tazobactam and Ceftriaxone Aztreonam, ,Piperacillin, Tobramycin, Ciprofloxacin, Gatifloxacin, Levofloxacin, Moxifloxacin, Ofloxacin, Minocycline, Trimethoprim. Trimethoprim/ Sulfamethoxazole as showed in figure (12), Escherichia coli showed highly resistant(100%) to Ticarcilli , Piperacillin, Piperacillin/ Tazobactam, Cefixime, Ceftazidime, Ceftriaxone Cefepime, Aztreonam and Trimethoprim/ Sulfamethoxazole as showed in tables (2,3,4).

No	Antibiotics	<i>Stentis</i> N=5		<i>Shenolyticis</i> N=2		<i>Saureis</i> N=1		<i>S.xglosis</i> N=2		<i>S.saprophyticis</i> N=4		<i>S.vitulinis</i> N=1		<i>S.epidemidis</i> N=1																
		S	R	S	R	S	R	S	R	S	R	S	R	S	R															
		No	%	No	%	No	%	No	%	No	%	No	%	No	%	No	%													
1	GEN	3	60	2	100	0	0	0	0	1	100	2	100	0	0	3	75	1	25	1	100	0	0	1	100	0	0			
2	TOP	5	100	0	0	0	0	2	100	0	0	1	100	1	50	1	50	4	100	0	0	0	0	1	100	1	100	0	0	
3	CIP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4	LVX	5	100	0	0	0	0	2	100	0	0	1	100	2	100	0	0	4	100	0	0	1	100	0	0	1	0	0	0	0
5	ERY	5	100	0	0	2	100	0	0	0	0	1	100	0	0	2	100	4	100	0	0	0	0	1	100	0	0	0	0	
6	CIN	3	60	2	100	0	0	0	0	1	100	2	100	0	0	4	100	0	0	1	100	0	0	1	100	0	1	100	0	0
7	TEC	5	100	0	0	2	100	0	0	0	0	1	100	2	100	0	0	4	100	0	0	1	100	0	0	0	0	1	100	
8	VAN	5	100	0	0	2	100	0	0	0	0	1	100	0	0	2	100	4	100	0	0	1	100	0	0	0	0	1	100	
9	TET	5	100	0	0	0	0	2	100	0	0	1	100	0	0	2	100	4	100	0	0	1	100	0	0	1	100	0	0	
10	TS	5	100	0	0	2	100	0	0	0	0	1	100	0	0	2	100	0	0	4	100	1	100	0	0	1	100	0	0	

Figure 1. Antimicrobial susceptibility of staphylococcus spp

No	Antibiotics	<i>E.aerogenes</i> N=1				<i>E.cloacae</i> N=19				<i>P.stutzeri</i> N=5				<i>P.luteola</i> N=1				<i>P.alcaligenes</i> N=1			
		S		R		S		R		S		R		S		R		S		R	
		No	%	No	%	No	%	No	%	No	%	No	%	No	%	No	%	No	%	No	%
1	TIC	1	100	0	0	18	94.7	1	5.3	4	80	1	20	1	100	0	0	1	100	0	0
2	PIP	1	100	0	0	18	94.7	1	5.3	4	80	1	20	1	100	0	0	1	100	0	0
3	CFM	1	100	0	0	18	94.7	1	5.3	5	100	0	0	1	100	0	0	1	100	0	0
4	CAZ	1	100	0	0	18	94.7	1	5.3	5	100	0	0	1	100	0	0	1	100	0	0
5	CRO	1	100	0	0	18	94.7	1	5.3	5	100	0	0	1	100	0	0	1	100	0	0
6	CEF	1	100	0	0	18	94.7	1	5.3	5	100	0	0	1	100	0	0	1	100	0	0
7	AZI	1	100	0	0	16	84.2	3	15.8	5	100	0	0	1	100	0	0	1	100	0	0
8	IPM	1	100	0	0	18	94.7	1	5.3	5	100	0	0	1	100	0	0	1	100	0	0
9	MEM	1	100	0	0	16	84.2	3	15.8	5	100	0	0	1	100	0	0	1	100	0	0
10	AMK	1	100	0	0	19	100	0	0	5	100	0	0	1	100	0	0	1	100	0	0
11	GEN	1	100	0	0	18	94.7	1	5.3	5	100	0	0	1	100	0	0	1	100	0	0
12	TOP	1	100	0	0	17	89.5	2	10.5	5	100	0	0	1	100	0	0	1	100	0	0
13	CIP	1	100	0	0	17	89.5	2	10.5	5	100	0	0	1	100	0	0	1	100	0	0
14	TS	1	100	0	0	18	94.7	1	5.3	5	100	0	0	1	100	0	0	1	100	0	0

Figure 2. Antimicrobial susceptibility of *Enterobacter*

No	Antibiotics	<i>K.pneumoniae</i> N=2				<i>Pantoea</i> N=1				<i>E.coli</i> N=1			
		S		R		S		R		S		R	
		No	%	No	%	No	%	No	%	No	%	No	%
1	TIC	0	0	2	100	0	0	1	100	0	0	1	100
2	PIP	0	0	2	100	0	0	1	100	0	0	1	100
3	CFM	0	0	2	100	0	0	1	100	0	0	1	100
4	CAZ	2	100	0	0	0	0	1	100	1	100	0	0
5	CRO	0	0	2	100	1	100	0	0	1	100	0	0
6	CEF	0	0	2	100	0	0	1	100	0	0	1	100
7	AZI	0	0	2	100	0	0	1	100	0	0	1	100
8	IPM	1	50	1	50	0	0	1	100	0	0	1	100
9	MEM	1	50	1	50	0	0	1	100	1	100	0	0
10	AMK	2	100	0	0	0	0	1	100	0	0	1	100
11	GEN	1	50	1	50	0	0	1	100	0	0	1	100
12	TOP	1	50	1	50	0	0	1	100	0	0	1	100
13	CIP	1	50	1	50	0	0	1	100	0	0	1	100
14	TS	0	0	2	100	0	0	1	100	0	0	1	100

Figure 3. Antimicrobial susceptibility of *Klebsiella* spp, *Escherichia coli* spp and *Pantoea* spp

Although there were only 9 isolates of *Staphylococcus aureus* overall, the percentage of methicillin-resistant *Staphylococcus aureus* (MRSA) among all *Staphylococcus aureus* was 44.4%, making it difficult to make firm conclusions. *Pseudomonas aeruginosa*, as opposed to MRSA, was the main pathogen recovered from sick patients in Greece, Morocco, and Saudi Arabia [10, 11, 12, 20]. Maksum et al. discovered that *K. pneumoniae* was similarly multidrug resistant to quinolone and third-generation cephalosporin medicines. Cephalexin (86.5%), ceftriaxone (75.7%), ceftazidime (73.0%), ceftipime (73.0%), and cefotaxime (67.9%) were all highly resistant to *K. pneumoniae*. Similar findings to our investigation showed that ceftazidime-resistant *K. pneumoniae* and *P. aeruginosa* were isolated from ICU patients in 96%–100% of cases [13, 21]. *P. aeruginosa*, resistance to amikacin, gentamicin, ciprofloxacin, and levofloxacin decreased over time, while resistance to ticarcillin/clavulanic acid, cefoperazone/sulbactam, cefepime, imipenem, and meropenem increased over time in both the ICUs and the entire hospital. Regarding *A. baumannii*, resistance to amikacin, gentamicin, tobramycin, piperacillin/tazobactam,

ciprofloxacin, imipenem, and tigecycline decreased with time in the ICUs, whereas resistance to cefoperazone/sulbactam increased in the ICUs as well as across the hospital. Accordingly, [15,18] made the point that insufficient data regarding the prevalence of bacteria and their pattern of resistance to antibiotics may allow for the prescription of multiple antibiotics in a row. This type of antibiotic prescription not only has no therapeutic benefit but may also cause side effects in patients, such as diarrhoea brought on by *Clostridium difficile* that arises from the indiscriminate use of antibiotics [15, 16,23]. The new antibiotic management strategy, which was introduced by the MOH in May 2011 with the goal of standardising antibiotic consumption and reducing antibiotic abuse, may be the cause of the current reduced proportion of antimicrobial usage. [17,19, 24].

Conclusion

Most bacteria isolated from intensive care units in hospitals showed varying resistance to the antibiotics that were used to test their susceptibility.

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