British Microbiology Research Journal
10(6): 1-10, 2015, Article no.BMRJ.20821
ISSN: 2231-0886, NLM ID: 101608140

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Antibiotic Resistance Patterns of Bacterial Isolates in Adult Intensive Care Unit at Nizwa Hospital, Oman

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Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

Article Information

DOI: 10.9734/BMRJ/2015/20821
Editor(s):
(1) Giuseppe Blaiotta, Department of Food Science, Via Università, Italy.
(2) Hung-Jen Liu, Distinguished professor, Director, Institute of Molecular Biology, National Chung Hsing University, Taiwan.
Reviewers:
(1) H. Mythri Sree, Siddhartha Dental College, Karnataka, India.
(2) S. Thenmozhi, Periyar University, India.
Complete Peer review History: http://sciencedomain.org/review-history/11599

Original Research Article

Received 11th August 2015
Accepted 5th September 2015
Published 28th September 2015

ABSTRACT

Background and Objectives: Infection is a commonly encountered problem for patients in intensive care units (ICUs) and Multidrug-resistant (MDR) bacterial infection is predominant. The aim of this study was to detect the frequency of different bacterial isolates and their antibiotic susceptibility pattern from patients admitted to adult ICU in a 5 year period from January 2008 to December 2012 at Nizwa hospital, Oman.
Materials and Methods: Different microbiological samples were collected and analyzed by routine conventional methods at microbiology section, laboratory department; Nizwa hospital. Antibiotic susceptibility (ABS) test was done using modified Kirby-Bauer disk diffusion method as per Clinical and Laboratory Standards Institute (CLSI) guidelines.
Results: Total (3930) clinical samples were processed, out of which 12.8% (504/3930) showed evidence of infection, 73.6% (371/504) were Gram-negative bacteria, 22.8% (115/504) were Gram-positive and 3.6% (18/504) were Candida species. Respiratory tract infection was the most common site of infection. Among the isolates, the most commonly found microorganism was *Pseudomonas aeruginosa* in respiratory samples, pus and wound infection, However *Klebsiella*

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spp. and *Escherichia coli* were predominant in urinary tract infection. Coagulase negative *Staphylococcus* was the predominant in blood. Extended-spectrum β-lactamase (ESBL)-producing *Escherichia coli, Klebsiella* spp. and *Proteus* occurred in 43.2% (29/67), 28.6% (18/63) and 45.5% (5/11) of total *Escherichia coli, Klebsiella* spp. and *Proteus* isolates. While 16.6% of *Staphylococcus aureus* isolates were Methicillin Resistant *Staphylococcus aureus* (MRSA).
Conclusion: Adult ICUs are faced with the increasingly rapid emergence and spread of antibiotic-resistant bacteria. Excellent antibiotic policy and infection control implementation are important priorities for these critically ill patients.

Keywords: Antibiotic susceptibility; multidrug resistant organisms; intensive care unit.

1. INTRODUCTION

Patients in intensive care units (ICUs) have a higher risk of acquiring hospital acquired infections (HAIs) than those in non-critical care areas [1]. ICU-acquired infection rate is five to ten times higher than hospital-acquired infection rates in general ward patients [2].

This is related to the use of large numbers of invasive monitoring devices, tracheostomy and endotracheal tubes; patient factors including extremes of age, immunocompromised state, malnutrition and severe underlying disease; and to a high incidence of cross infection [3].

The consequence and complications of infection might have variable clinical (sepsis, organ failure, death), health economic (prolonged hospital stay, cost of care and antibiotic utilisation) and infection control impact (spread of infection to patient/ staff/ visitor) [4].

Antimicrobial resistance in ICU infections is increasing worldwide. Both morbidity and mortality is greater when infection is caused by drug resistant organisms [5].

Among Gram-positive organisms, the most important resistant microorganisms in the ICU are currently methicillin resistant *Staphylococcus aureus*, and vancomycin-resistant enterococci. In Gram-negative bacteria, the resistance is mainly due to the rapid increase of extended-spectrum Beta-lactamases (ESBLs) in *Klebsiella pneumonia*, *Escherichia coli* and *Proteus mirabilis.* MDR in *Pseudomonas aeruginosa, Acinetobacter* spp. and *Stenotrophomonas maltophilia* has also increased [6].

It is important to take steps to prevent ICU infections, but when they occur, effective and early institution of appropriate antibiotic therapy is crucial. This will improve patient outcome and decrease the incidence of multiple drug resistant organisms [5].

The purpose of this study was to detect the frequency of different bacterial isolates and their antibiotic resistance pattern from patients admitted to adult ICU in a 5 year period from January 2008 to December 2012 at Nizwa hospital, Oman.

2. MATERIALS AND METHODS

2.1 Setting

This study is a retrospective, 5-year study (1st January2008 to 31st December 2012)

This study was conducted at adult ICU in Nizwa hospital, Oman. Adult ICU has 8 beds and manage approximately 240 critically ill patients annually

The study was approved by Al-Dakhilyia regional research and research ethics committee to conduct the present study at Nizwa hospital

2.2 Collection of Data

All patients' demographic and microbiological data were collected retrospectively from the electronic database in Nizwa hospital called (Al-SHIFA system) and were transferred to SPSS software for analysis.

The main inclusion criterion was a positive culture for producing bacteria in any clinical isolate from hospitalized patients. Successive cultures from the same patient were excluded to avoid duplicating data. If multiple sites of isolation occurred in the same patient, all were registered.

2.3 Sample Collection and Processing

Different Microbiological samples including blood, urine, sputum, endotracheal aspirate (respiratory samples), pus and other body fluids;

were collected and processed following conventional microbiological procedures for correct management of clinical samples [7].

Sputum and endotracheal aspirate were inoculated onto 5% sheep blood agar, MacConkey agar, and Chocolate agar. Wound swabs were inoculated onto blood agar and MacConkey agar. Urine specimens were inoculated onto Cystiene Lactose Electrolyte Deficient (CLED) media with a calibrated loop. For blood culture 5-10 ml of blood for adult and 1-5 ml for children and was collected. Blood cultures were processed using the BacT/ALERT® 3D blood culture system (Biomerieux, USA).

2.4 Identification of the Isolated Bacteria

Microbial isolates were identified on the basis of morphological and biochemical characters and confirmed using the API 20E and API 20 NE identification systems *(Biomeriux SA, Montalien Vercica and France*).

2.5 Antimicrobial Susceptibility

Antimicrobial susceptibility test was performed on each of the isolates by Kibry-Bauer's disc diffusion method on Muller-Hinton agar as recommended by Clinical Laboratory Standards Institute, CLSI [8].

The following antibiotics were used (Oxoid, UK): β-Lactams: Ampicillin, amoxicillin / clavulanate (20/10 µg), cefuroxime, ceftriaxone (30 µg), ceftazidime (30 µg), piperacillin / tazobactam (100/10 µg), cefoperazone / sulbactam (75/30 µg), cefoperazone (30 µg), cefpodoxime (30 µg), cefuroxime (30 µg), aztreonam (30 µg), imipenem (10 µg), meropenem (10 µg). Aminoglycosides: amikacin (30 µg), gentamicin (30 µg). Quinolones: ciprofloxacin (5 µg). Others: nitrofurantoin (300 µg), trime-thoprim / sulfamethoxazole (1.25/23.75 µg), nalidixic acid (30 µg) colistin (10 µg) and tetracycline (10 µg).

For Gram positive bacteria: pencillin, cloxacillin, methicillin, fusidic acid and vancomycin were added *Pseudomonas aeuroginosa* ATCC 27853, *Escherichia coli* ATCC 25922 and *Staphylococcus aureus* 25923 were used as a control strain.

2.6 Detection of MRSA

Plate containing 6 µg/ml of oxacillin in Mueller-Hinton agar supplemented with 4% NaCl and cefoxitin disk screen test methods were used for detection of MRSA according to the guidelines of the (CLSI) [8].

2.7 Detection of Extended-spectrum β Lactamases

2.7.1 Method

For the detection of ESBL, CLSI screening method and CLSI phenotypic confirmatory method were used

2.7.1.1 CLSI screening method

Ceftazidime, ceftriaxone and cefotaxime disks were placed on a MHA plate at appropriate distance. The plates were incubated aerobically overnight (18-24 hours/35℃). The strains showing ≤ 22 mm zone of inhibition around ceftazidime, ≤ 25 mm around ceftriaxone and ≤ 27 mm around cefotaxime disks were suspected to be ESBL producers

2.7.1.2 CLSI phenotypic confirmatory method

2.7.1.2.1 Double Disk Synergy Test (DDST).

A suspension of the test organism was inoculated on Mueller- Hinton agar. A disk containing 30 µg Amoxicillin plus Clavulanic acid was placed centrally on the plate. Disks containing Ceftazidime, Cefotaxime and Ceftriaxone were placed round the Amoxicillin + Clavulanic acid disk at a distance of 20mm (center to center) from the latter. The plates were incubated over night at 35℃. The patterns of zones of inhibition were noted. Isolates that exhibited a distinct shape/size with potentiation towards Amoxicillin + Clavulanate disk were considered ESBL producers [9].

2.7.1.2.2 Combination disk method

In this test, an overnight culture suspension of the test isolate which was adjusted to 0.5 McFarland's standard was inoculated by using sterile cotton swab on the surface of a Mueller Hinton Agar plate. The Cefotaxime (30 µg) and cefotaxime-clavulanic acid (30 µg / 10 µg) discs were placed 20 mm apart on the agar. Similarly, the ceftazidime (30 µg) and ceftazidime clavulanic acid (30 µg/ 10 µg) discs were placed 20 mm apart. After incubating overnight at 37℃, ≥5 mm increase in the zone diameter for either antimicrobial agent which were tested in combination with clavulanic acid versus its zone

when tested alone, was interpreted as positive for ESBLs production [9].

2.7.1.3 Definition of resistance

MDR for Gram-negative organisms was defined as resistance to three or more classes of antimicrobial agents, while pan-drug resistant strains are those which showed resistance to all classes [10].

2.8 Statistical Analysis

The recorded results was statistically analyzed by using Statistical Package for Social Sciences (SPSS) version (18) Frequency Distributions and Crosstabs Data were expressed as number (n) and percentage (%). As there were no groups to compare, only descriptive statistics were performed

3. RESULTS

During January 2008 to December 2012, Total (3930) clinical samples were processed out of which 12.8% (504/3930) showed evidence of infection.

3.1 Most Common Organisms Isolated from Adult ICU

Pseudomonas aeruginosa was the most frequently isolated bacteria (23%) followed by *Acinetobacter* spp. (18.7%), Coagulase negative *Staphylococcus* (11.3%), *Klebsiella* spp. (8.9%) and *Escherichia coli* (7.5%) (8.9%), respectively as shown in table (1)

3.2 Most Common Organisms Isolated by Specimen Site

Table (3) shows the 10 most common isolates recovered from microbiological specimens. Within the respiratory tract, *Pseudomonas aeruginosa* (28.5%) was the most common isolate followed by *Acinetobacter* spp. (MDR) (20.8%), *Klebsiella* spp. (10.2%), *Staphylococcus aureus* (8.4%) and *Escherichia coli* (6.6), respectively.

Among blood culture isolates, *coagulase-negative staphylococci* (63.2), *Pseudomonas aeruginosa* (8.8%) and *Escherichia coli* (ESBL) (5.3%) made up 77.3% of the isolates

For wound/pus specimens, *Pseudomonas aeruginosa* (27.2%) *Acinetobacter* spp. (MDR) (14.8%), *Escherichia coli* (12.3%) and *Klebsiella* spp. (9.9%), respectively were the most common isolates.

From the urinary tract, the most commonly isolated organisms were *Klebsiella* spp. *(ESBL) (16.7%), Acinetobacter* spp. (*MDR) (16.7), Pseudomonas aeruginosa* (14.8%) and *Escherichia coli* (ESBL) (11.1%) were the most common isolate (Table 2).

Table 1. Frequency of microorganisms isolated from patients admitted at AICU of Nizwa hospital

No	Organism	No. of isolates	% of total
1	*Pseudomonas aeruginosa*	116	23.0
2	*Acinetobacter* spp.	94	18.7
3	*Coagulase-negative Staphylococcus*	57	11.3
4	*Klebsiella* spp.	45	8.9
5	*Escherichia coli*	38	7.5
6	*Staphylococcus aureus* (MSSA)	30	5.9
7	*Escherichia coli (ESBL)*	29	5.8
8	*Klebsiella* spp. *(ESBL)*	18	3.6
7	*Candida*	18	3.6
8	*Streptoccus* spp.	13	2.6
10	*Enterococcus* spp.	9	1.8
11	*Haemophilus*	7	1.4
12	*Staphylococcus aureus* (MRSA)	6	1.2
13	*Proteus* spp.	6	1.2
14	*Proteus* spp. *(ESBL)*	5	1.0
15	*Morganella*	2	.4
16	*Serratia marcescens*	4	.8
17	*Enterobacter* spp.	4	.8
18	*Salmonella*	1	.2
19	*Moraxella catarrhalis*	1	.2
20	*Stenotrophomonas maltophilia*	1	.2
	Total	504	100.0

MSSA, methicillin-sensitive Staphylococcus aureus; MRSA, methicillin-resistant Staphylococcus aureus

3.3 Characteristics of MRSA

MRSA was detected in (16.6%) of all *S. aureus* isolated from adult ICUs,

3.4 ESBL

(ESBL)-producing *Escherichia coli, Klebsiella* spp, and *Proteus* occurred in 43.2% (29/67), 28.6% (18/63) and 45.5% (5/11) of total *E. coli,*

Klebsiella spp. and *Proteus* isolates, respectively, as shown in Table (2).

Table 2. Percentage of ESBL isolated from patients at AICU of Nizwa hospital

Organism	Total no	No. of ESBL	% of ESBL
Escherichia coli	67	29	43.2
Klebsiella spp.	63	18	28.6
Proteus	11	5	45.5

3.5 Antimicrobial Susceptibility

The antimicrobials tested and percentages of isolates determined to be resistant are listed in Table 4 (Gram negative bacilli) and table 5 (Gram-positive cocci). Resistance rates for *Pseudomonas aeruginosa* were as follows: amikacin, 11.2%; ceftazidime, 18.1%; gentamicin, 15.5%; ciprofloxacin, 12.9; meropenem, 8.6%; and piperacillin- tazobactam, 7.7% (Table 4). With *Acinteobacter* 2.1% resistance was observed to tigecycline and colistin. Resistance rates for *E. coli* were as follows: ampicillin, 76.3%; Amoxicillin plus Clavulanic acid, 36.8%; ciprofloxacin, 7.9%; cefuroxime, 15.8%; gentamicin, 2.6%, respectively.

Resistance rate for (ESBL)-producing *Escherichia coli, Klebsiella* spp., and *Proteus* were as follow for ciprofloxacin 44.8%, 44.4% and 40%; gentamicin 41.4%, 55.6%, 60%; piperacillin- tazobactam 13.8%, 5.6%, 0%, respectively and for imipenem and meropenem, no resistance were reported.

For Gram positive bacteria, Resistance rate for *Staphyloccus aureus* were as follow: pencillin 93.3%; ciprofloxacin 13.3%, trimethoprim +sulphamethoxazole 30% and gentamcin 3.3%. MRSA showed 100% resistance to oxacillin, 50% resistance to Ciprofloxacin, Fusidic acid and 33.3% for Trimethoprim +Sulphamethoxazole and gentamicin.

The details of antibiotic resistance pattern among isolated bacteria are shown in Tables (4,5)

4. DISCUSSION

ICU acquired infections, which are often caused by antibiotic resistant bacteria, pose a threat to patients admitted to ICUs. Invasive procedures, high antibiotic usage and transmission of bacteria between patients due to inadequate infection control procedures may explain why ICUs are “hot zones” for the emergence and spread of microbial resistance [11].

In the present study, the most common bacterial pathogen in adult ICU infections was *Pseudomonas aeruginosa* which is in accordance with the results of several similar studies conducted worldwide [12,13].

The other common Gram negative bacteria involved in ICU infection were *Acinetobacter* spp. (MDR)*, Klebsiella* spp.*, E. coli* these result are consistent with the finding of a previous study conducted by Ravan et al. [14].

Another study performed at ICU of a tertiary care center in Saudi Arabia showed that *Acinetobacter baumannii, Pseudomonas aeruginosa, Escherichia coli, K. pnemoniae* were the most common isolates [15].

In this study, respiratory tract infection was the most frequent site of infection. This is in agreement with other studies [15,16].

Pseudomonas isolates in our study show low resistance rate against the entire list of antibiotic used, This finding goes in line with study conducted by Radj et al. [13].

In our study, Overall 16.6% of all *Staphylococcus aureus* associated infections in ICU were caused by Methicillin-Resistant strains. This is in accordance with study conducted by Al-Yaqoubi and Elhag, [17] who reported that MRSA represented 12.2% of the isolate. Higher results were reported in Canada 22.3% [12] and India 59.4% [14].

Widespread use of antibiotics without properly identifying the organism or its antibiotic sensitivity pattern has led to the emergence of multi-drug resistant organisms.

ESBL are becoming a great challenge and an increasing problem for hospitals worldwide. ESBLs are plasmid mediated, and their potentials for transfer makes effective control and treatment difficult, which has resulted in endemic and epidemic outbreaks [18].

In the present study Extended-spectrum β-lactamase (ESBL)-producing *E. coli, Klebsiella* spp. *and Proteus* occurred in 43.2% (29/67), 28.6% (18/63) and 45.5% (5/11) of isolates, respectively.

In a similar study by Singhal et al. [19] 62% of the *E. coli* and 73% of the *K. pneumoniae* isolates were reported to be ESBL producers, also Mohammadi and Feizabadi, [20] reported (ESBLs) was found in 46.6% of isolates of both organisms. Higher results, were also observed that 81% and 74% of the *E. coli* and *K. pneumoniae* isolates were ESBL producers in a study conducted by Umadevi et al. [9].

This percentage is considered to be very high compared to the prevalence of ESBL production worldwide among this species when compared with the 20% prevalence of the Italian study [21], 11.3% in the Saudi Arabian study [22] and 13.3% in the Kuwaiti study [23].

The difference with our study may be assumed to the difference in the study number population, time of collection, types of organisms tested, tests done for ESBLs confirmation. More patients being referred from local hospitals; and the spread of resistant strains from adult wards.

ESBL producing isolates should be reported as resistant to all penicillins, cephalosporins, and aztreonam. Carbapenems are the treatment of choice for serious infections due to ESBL-producing organisms [24].

Carbapenems have been the most effective antibiotics against ESBL-producing bacteria because of their beta-lactamase stability, and continue to be the treatment of choice. Nevertheless, the emergence of new resistance mechanisms such as carbapenemases, and the abuse or under dosing of these antibiotics represents a constant threat to their efficacy [25].

Fortunately, no carbapenem-resistant strains were identified in our study. This is in accordance with previous studies [26].

Table 3. The most common organisms isolated by specimen site from patients admitted at AICU of Nizwa hospital

	Organism	**No**	**%**
Respiratory specimen	*Pseudomonas aeruginosa*	78	28.5
(274)	*Acinetobacter* spp.*(MDR)*	57	20.8
	Klebsiella spp.	28	10.2
	Staphylococcus aureus	23	8.4
	Escherichia coli	18	6.6
	Others	70	25.5
Urine	*Klebsiella* spp. *(ESBL)*	9	16.7
(54)	*Acinetobacter* spp.*(MDR)*	9	16.7
	Pseudomonas aeruginosa	8	14.8
	Escherichia coli (ESBL)	6	11.1
	Escherichia coli	6	11.1
	others	16	29.6
Blood	*Coagulase-negative staphylococcus*	36	63.2
(57)	*Pseudomonas aeruginosa*	5	8.8
	Escherichia coli (ESBL)	3	5.3
	Streptoccus spp.	2	3.5
	Klebsiella spp.	2	3.5
	others	9	15.8
Pus	*Pseudomonas aeruginosa*	22	27.2
(81)	*Acinetobacter* spp.*(MDR)*	12	14.8
	Escherichia coli	10	12.3
	Klebsiella spp.	8	9.9
	Coagulase-negative staphylococcus	7	8.6
	others	22	27.2
Others*	*Acinetobacter* spp.*(MDR)*	14	36.84
38	*Staphylococcus aureus*	6	15.8
	Klebsiella spp.	4	10.5
	Methicillin resistance *S. aureus* (MRSA)	3	7.9
	Others	11	28.9

**Others (fluid, aspirates, stool,…)*

Table 4. Antibiotic resistance pattern of predominant gram negative bacteria isolated from patients admitted at adult ICU

Antibiotic	*Pseudomonas aeruginosa* (n=116)		*Acinetobacter* spp. (n=94)		*Escherichia coli* (n=38)		*Klebsiella* spp. (n=45)		*Proteus* spp. (n=6)		*Escherichia coli* (ESBL) (n=29)		*Klebsiella* spp. (ESBL) (n=18)		*Proteus* spp. (ESBL) (n=5)	
	no	**%**	**no**	**%**	**no**	**%**	**no**	**%**	**no**	**%**	**no**	**%**	**no**	**%**	**no**	**%**
AMP	**-**		**94**	100	**29**	76.3	**45**	100	**4**	66.7	**29**	100	**18**	100	**5**	100
AMC	**-**		**94**	100	**14**	36.8	**4**	8.9	**1**	16.6	**29**	100	**18**	100	**5**	100
CXM	**-**		**94**	100	**6**	15.8	**3**	6.7	**0**	0	**29**	100	**18**	100	**5**	100
CRO			**94**	100	**0**	0	**0**	0	**0**	0	**29**	100	**18**	100	**5**	100
CAZ	**21**	18.1	**94**	100	**0**	0	**0**	0	**0**	0	**29**	100	**18**	100	**5**	100
CN	**18**	15.5	**93**	98.9	**1**	2.6	**3**	6.6	**3**	50	**12**	41.4	**10**	55.6	**3**	60
CIP	**15**	12.9	**68**	72.3	**3**	7.9	**2**	4.4	**0**	0	**13**	44.8	**8**	44.4	**2**	40
AK	**13**	11.2	**87**	92.6		-		-		-	**3**	10.3	**3**	16.6	**0**	0
IPM	**15**	12.9	**87**	92.5		-		-		-	**0**	0	**0**	0	**0**	0
MEM	**10**	8.6	**88**	93.6		-		-		-	**0**	0	**0**	0	**0**	0
TZP	**9**	7.7	**68**	72.3		-		-		-	**4**	13.8	**1**	5.6	**0**	
CT			**2**	2.1		-		-		-						
TGC			**2**	2.1				-								

Antimicrobial abbreviations: AMC, Amoxicillin plus Clavulanic acid; AMK, amikacin; AMP, ampicillin; CAZ, cetazidime; CFR, ceftriaxone; CIP, ciprofloxacin; CXM, cefuroxime; GEN, gentamicin; MER, meropenem; TZP, piperacillin-tazobactam; TGC, tigecycline; SXT, trimethoprim-sulfamethoxazole; CT, colistin

Table 5. Antibiotic resistance pattern of predominant Gram positive microorganisms isolated from patients admitted at adult ICU of Nizwa Hospital %

Antibiotic	*S. aureus* (n=30)		*MRSA* (n=6)		*CONS* (n=57)		*Streptoccus* spp. (n=13)		*Enterococcus* spp. (n=9)	
	no	%	no	%	no	%	no	%	no	%
P	**28**	93.3	**6**	100	**38**	66.7	**6**	46.2	**5**	55.6
AMP		-	**-**		**-**		**-**		**3**	33.3
AMC	**2**	6.7	**6**	100	**-**		**-**			
MET	**0**	0	**6**	100	**30**	52.6	**-**		**2**	22.2
FOX	**0**	0%	**6**	100	**30**	52.6	**-**		**-**	
CXM	**10**	33.3	**6**	100	**40**	70.2	**2**	15.4		
VA	**0**	0	**0**	0	**0**	0	**-**		**0**	0
E	**14**	46.7	**1**	16.6	**29**	50.8	**6**	46.2	**0**	0
DA	**14**	46.7	**1**	16.6	**29**	50.8	**6**	46.2		
CN	**1**	3.3	**6**	0	**17**	30	**-**			
FD	**18**	60	**3**	50	**40**	70.2	**-**		**0**	0
SXT	**9**	30	**2**	33.3	**9**	15.7	**-**		**0**	0
CIP	**4**	13.3	**3**	50	**8**	14	**1**	7.6	**3**	33.3
TE	**13**	43.3	**2**	33.3	**8**	14	**-**			

P, pencillin; AMP, ampicillin; AMC, Amoxicillin plus Clavulanic acid, MET, methicillin, Fox, cefoxitin; CXM, cefuroxime VA, vancomycin, FD, fusidic acid, E , erythromycin, DA, Clindamycin,TE, Tetracycline; SXT, trimethoprim-sulfamethoxazole CIP, ciprofloxacin;

Multi drug resistant strain of *A. baumannii* (MRAB) is resistant to all beta-lactams, fluoroquinolones and aminoglycoside. In our study MDR *Acinetobacter* spp accounted 18.7% of all isolates and out of these 2.1% were found to be pandrug- resistant. These findings are consistent with the study performed by Saeed et al. [16].

Because of the emergence of multidrug-resistance and pandrug-resistance associated with *Acinetobacter spp*, the role of preventing spread of this pathogen to other patients is vital. [15].

5. CONCLUSION

In conclusion, *Pseudomonas aeruginosa* was the most frequently isolated bacteria (23%) followed by *Acinetobacter spp.* (18.7%), Coagulase negative *Staphylococcus* (11.3%), *Klebsiella* spp. (8.9%) and *Escherichia coli* (7.5%) (8.9%), respectively. Extended-spectrum β-lactamase (ESBL)-producing *Escherichia coli, Klebsiella* spp. and *Proteus* occurred in 43.2% (29/67), 28.6% (18/63) and 45.5% (5/11) of total *Escherichia coli, Klebsiella* spp. and *Proteus* isolates, respectively.

Piperacillin- tazobactam and Imipenem, Meropenem and amikacin were the antibiotic with high susceptibility rates for the treatment of infections which are caused by ESBL producing organisms.

Ciprofloxacin showed moderate resistance pattern to both ESBL producing *E. coli and K. pneumonia,* but high resistance pattern to ESBL *Proteus*

The high prevalence of MDR organisms in the ICUs emphasizes the need for an early detection of the β-lactamase producing organisms by simple screening methods, which can help in providing an appropriate antimicrobial therapy and avoiding the development and the dissemination of these multidrug resistant strains.

Excellent antibiotic policy, periodical antibacterial sensitivity assessment in ICUs and infection control implementation are important priorities for the critical patient areas.

We hope that this data will be useful for healthcare professionals in deciding antibiotic cycling policies and helping clinicians to make the most rational choices of empiric antibiotic regimes based on common organisms and their antimicrobial susceptibility.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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