

MDRO

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2

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14

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Multidrug-resistant organisms (MDRO) patterns of GICU patients in Dr Mohammad Hoesin Hospital Palembang

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Abstract. *Multidrug-Resistant Organisms* (MDRO) are organisms (bacteria) that are resistant to at least one antimicrobial of ≥ 3 antimicrobial classes. MDRO transmission most recorded in General intensive care unit (GICU), which is also the high risk units of nosocomial infection. A total of 549 from 611 samples (89.8%) was identified as MDRO in 2015 and as many as 490 of the 552 samples (88.7%) in 2016. The most gram-negative bacteria in 2015 and 2016 were *Acinetobacter baumannii* (33% vs 30.4%), followed by *Pseudomonas aeruginosa* (24% vs 29.3%) and *Klebsiella pneumoniae* (11% vs 13.2%). In 2015, gram-positive bacteria had the highest level of resistance to antibiotics norfloxacin and ceftazidime, while in 2016 gram-positive bacteria had the high levels of resistance to antibiotics cotrimoxazole and ceftazidime. Gram-negative bacteria in 2015 had resistance to the antibiotic ampicillin, cefazolin, and tigecycline, whereas, in 2016, Gram-negative bacteria had resistance to the antibiotic imipenem, cefazolin, and tigecycline. The incidence of MDRO in 2016 decreased compared to 2015. In 2015 and 2016, a bacterial infection of GICU patient more often caused by gram-negative bacteria.

1. Introduction

Antibiotics are an antibacterial substance produced by various species of microorganisms (bacteria, fungi, and actinomycetes) that suppress the growth of other microorganisms [1]. Antibiotic and the similar drugs, called antimicrobial agent, has been used for the past 70 years to treat patients with infectious diseases. Since the 1940s, the drug is much-reduced illness and death from infectious diseases. These drugs have been used widely and for long time so that the microorganism is able to adapt to an antibiotic (antibiotic resistance), making these drugs less effective [2].

Antibiotic resistance is a major problem that is growing worldwide. Resistant germs arising from excessive use of antibiotics will cause difficult the problems [3]. Multidrug-Resistant or MDR is a condition where bacteria are resistant to at least one class of antimicrobials of ≥ 3 antimicrobial [4]. Multidrug-Resistant Organisms (MDRO) is the organism largely bacteria experience MDR [2]. Germs resistant to the antibiotic that is widely known and cause many problems in the world which are Methicillin-resistant *Staphylococcus aureus* (MRSA), Vancomycin-resistant *Enterococci* (VRE),

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penicillin-resistant pneumococci, Extended-spectrum beta-lactamase *Klebsiella pneumoniae* producing (ESBL), carbapenem-resistant *Acinetobacter baumannii* (CRAB), and multi-resistant *Mycobacterium tuberculosis* [3]. Estimated, 2 million people are infected by bacteria that are resistant to antibiotics and 23,000 people die every year as a direct result of that infection [5].

Many factors influence the emergence of bacteria resistant to antibiotics, the most important factor is the use of antibiotics and infection control. Therefore the rational use of antibiotics is very important, in addition to the implementation of good infection control to prevent the development of germs resistant [3].

Transmission MDRO most recorded in acute care facilities, and now all the health care facilities are also facing the transmission and severity/MDRO problems due to this. The severity of the infection MDRO determined by the infected population and the type of care facilities such as Intensive Care Unit (ICU), Burn Unit, and patients with long term treatment, so that prevention and control of these pathogens need to be tailored to the specific needs of each population and individuals [2].

ICU is a nosocomial infection wards. The international study on nosocomial infections in the ICU were conducted in 2007 at 265 ICUs from 75 countries, shows that patients whose length of stay in the ICU have a higher risk of infection, especially infection due to resistance against *Staphylococcus*, *Acinetobacter*, *Pseudomonas* species, and *Candida* species. In addition, the mortality rate in the ICU for patients infected two times more than patients who did not infection [6].

The incidence numbers of antibiotic resistance from this research can be considered as a reference for policy of antibiotic use control in GICU wards. This study will be compared the incidence of MDRO in GICU patients of Dr. Mohammad Hoesin Hospital Palembang in 2015 and 2016 based on specimens type. This research can showed the patterns of bacterial sensitivity to antibiotics for gram-positive and gram-negative bacteria that can later be used as a reference therapy for GICU patients at Dr. Mohammad Hoesin Hospital Palembang.

2. Methods

This research was descriptive study with a cross-sectional approach based on secondary data from medical records of the General Intensive Care Unit (GICU) patients in Dr. Mohammad Hoesin Hospital Palembang.

The population in this study were all GICU patients of Dr. Mohammad Hoesin Hospital Palembang who done the culture and antibiotic resistance testing in 2015 and 2016. This study was held from October to December 2017. The inclusion criteria of this research were GICU patients with complete medical records and the results of positive bacterial cultures.

The data obtained in this study were processed and analyzed descriptively by using Microsoft Excel program. The results of the study are presented in tables and graphs are further described in narrative form.

3. Result

3.1. Research subject

The population from this research was GICU patients in 2015 and 2016 with total population is 1092 and 1265. In this study, the sample with the results of bacterial culture positive specimens in 2015 was 611 (55, 9%) and in 2016 a number of 552 samples (43,6%). The types of clinical specimens obtained are sputum, blood, pus, urine, swabs (pharynx, tissue, abscess, throat, and secretions), and others (fluid, bronchial washings, and feces).

12

3.2. Distribution of bacterial isolates in clinical specimen

13 table 1 and table 2 are presented the distribution of bacteria in clinical specimens from GICU patients at Dr. Mohammad Hoesin Hospital Palembang in 2015 and 2016. From 611 samples in 2015 with positive bacterial culture results, obtained the highest distribution of gram-negative bacteria (n = 535/611) were *Acinetobacter baumannii* (33%) followed by *Pseudomonas aeruginosa* (24%) and *Klebsiella pneumoniae* (11%). Bacterial isolates based on clinical specimens most commonly found in

sputum (n = 542), followed by blood (n = 25), pus (n = 22), swabs (n = 11), urine (n = 6), and others (n = 5).

In 2016, from 552 samples with positive bacterial culture results, obtained the highest distribution of gram-negative bacteria (n = 494/552) were *Acinetobacter baumannii* (30.4%) followed by *Pseudomonas aeruginosa* (29.3%) and *Klebsiella pneumoniae* (13.2%). Bacterial isolates based on clinical specimens most commonly found in sputum (n = 506), followed by blood (n = 20), pus (n = 11), swabs (n = 7), urine (n = 4), and others (n = 4).

Table 1. Distribution of bacterial isolates in clinical specimens (2015).

No.	Isolates	Gram	Clinical specimen					Number (n)	(%)	
			Sputum	Blood	Pussy	Swab	Urine			Others
1	<i>Acinetobacter baumannii</i>	-	187	0	8	3	2	0	200	33
2	<i>Pseudomonas aeruginosa</i>	-	139	1	6	1	2	0	149	24
3	<i>Klebsiella pneumoniae</i>	-	61	3	1	1	0	1	67	11
4	<i>Proteus mirabilis</i>	-	26	0	4	3	0	0	33	5.4
5	<i>Staphylococcus aureus</i>	+	22	6	2	0	0	0	30	4.9
6	<i>Enterobacter agglomerans</i>	-	27	0	0	0	0	0	27	4.4
7	<i>Streptococcus epidermidis</i>	+	11	9	0	0	0	1	21	3.4
8	<i>Escherichia coli</i>	-	14	0	1	2	1	2	20	3.3
9	<i>Enterobacter aerogenes</i>	-	12	1	0	0	0	0	13	2.1
10	<i>Streptococcus viridans</i>	+	12	1	0	0	0	0	13	2.1
11	<i>Enterobacter cloacae</i>	-	12	1	0	0	0	0	13	2.1
12	<i>Streptococcus bovis</i>	+	6	0	0	0	1	1	8	1.3
13	<i>Enterococcus faecalis</i>	+	2	2	0	0	0	0	4	0.7
14	<i>Enterobacter hafniae</i>	-	4	0	0	0	0	0	4	0.7
15	<i>Burkholderia cepacia</i>	-	3	0	0	0	0	0	3	0.5
16	<i>Morganella morganii</i>	-	2	0	0	0	0	0	2	0.3
17	<i>Klebsiella ozaenae</i>	-	0	0	0	1	0	0	1	0.2
18	<i>Citrobacter diversus</i>	-	1	0	0	0	0	0	1	0.2
19	<i>Cronobacter sakazakii</i>	-	0	1	0	0	0	0	1	0.2
20	<i>Proteus vulgaris</i>	-	1	0	0	0	0	0	1	0.2
	Total		542	25	22	11	6	5	611	100

Table 2. Distribution of bacterial isolates in clinical specimens (2016).

No.	Isolates	Gram	Clinical specimens					Number (n)	(%)	
			Sputum	Blood	Pussy	Swab	Urine			Others
1	<i>Acinetobacter baumannii</i>	-	155	5	3	5	0	0	168	30.4
2	<i>Pseudomonas aeruginosa</i>	-	155	3	3	1	0	0	162	29.3
3	<i>Klebsiella pneumoniae</i>	-	65	5	1	1	0	1	73	13.2
4	<i>Enterobacter agglomerans</i>	-	32	1	0	0	0	0	33	6
5	<i>Staphylococcus aureus</i>	+	26	1	1	0	0	0	28	5.1
6	<i>Streptococcus epidermidis</i>	+	17	2	0	0	0	1	20	3.6
7	<i>Escherichia coli</i>	-	12	0	1	0	2	1	16	2.9
8	<i>Enterobacter cloacae</i>	-	8	0	0	0	0	1	9	1.6
9	<i>Enterobacter aerogenes</i>	-	6	1	1	0	0	0	8	1.4
10	<i>Proteus mirabilis</i>	-	4	0	1	0	0	0	5	0.9
11	<i>Providencia rettgeri</i>	-	5	0	0	0	0	0	5	0.9
12	<i>Streptococcus bovis</i>	+	3	0	0	0	1	0	4	0.7
13	<i>Streptococcus viridans</i>	+	3	0	0	0	0	0	3	0.5
14	<i>Enterococcus faecalis</i>	+	1	1	0	0	1	0	3	0.5
15	<i>Achromobacter xylosoxidans</i>	-	3	0	0	0	0	0	3	0.5
16	<i>Enterobacter hafniae</i>	-	2	0	0	0	0	0	2	0.4
17	<i>Morganella morganii</i>	-	1	1	0	0	0	0	2	0.4
18	<i>Klebsiella oxytoca</i>	-	2	0	0	0	0	0	2	0.4
19	<i>Providencia alcalifaciens</i>	-	2	0	0	0	0	0	2	0.4
20	<i>Burkholderia cepacia</i>	-	1	0	0	0	0	0	1	0.2
21	<i>Citrobacter freundii</i>	-	1	0	0	0	0	0	1	0.2
22	<i>Elizabethkingia meningoseptica</i>	-	1	0	0	0	0	0	1	0.2
23	<i>Stenotrophomonas maltophilia</i>	-	1	0	0	0	0	0	1	0.2
	Total		506	20	11	7	4	4	552	100

3.3. Distribution of sensitivity test results against bacteria antibiotics

Figure 1 and figure 2 showed the pattern of gram-positive bacteria sensitivity to antibiotics in 2015 and 2016. It appears that the majority of gram-positive bacteria isolated in 2015 had the highest sensitivity to vancomycin (86.44%) and the highest level of resistance against antibiotics norfloxacin (100%) and ceftazidime (70.18%). In 2016, the data showed the highest sensitivity to vancomycin

(99%) and the highest levels of resistance to the antibiotic cotrimoxazole (100%) and ceftazidime (66.36%).

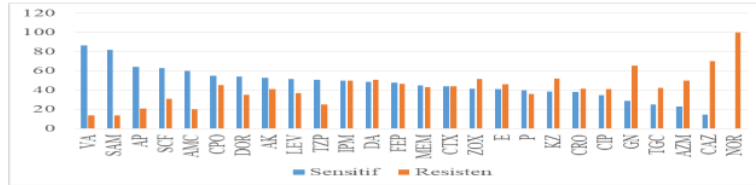


Figure 1. The sensitivity patterns of gram-positive bacteria to antibiotics in 2015.

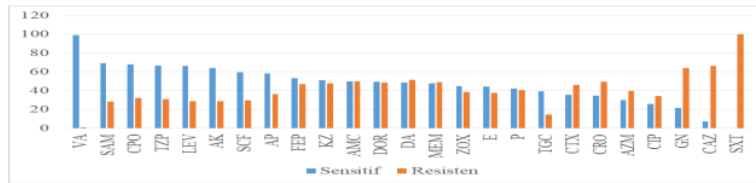


Figure 2. The sensitivity pattern of gram-positive bacteria to antibiotics in 2016.

Overall, gram-negative bacteria isolated of GICU patients in 2015 had the highest sensitivity to antibiotics cefoperazone sulbactam (88.4%), piperacillin tazobactam (73.31%), and doripenem (72.3%). While most demonstrated resistance to antibiotics ampicillin (100%). In 2016, GICU patients had the highest sensitivity to antibiotics sulbactam cefoperazone (67.36%), meropenem (61.62%), and doripenem (61.49%). While most indicated resistance to the antibiotic imipenem (100%). Details of the data can be seen in figure 3 and figure 4.

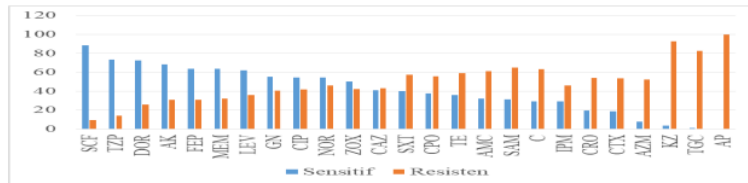


Figure 3. The sensitivity pattern of gram-negative bacteria to antibiotics in 2015.

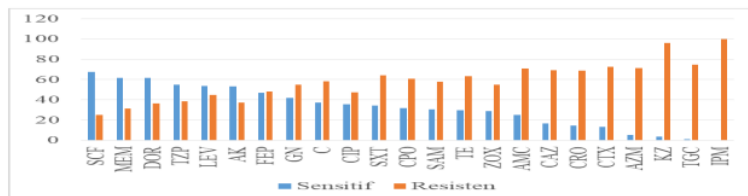


Figure 4. The Sensitivity pattern of Gram-Negative Bacteria to Antibiotics in 2016.

As many as 549 from 611 samples (89.8%) was identified as MDRO in 2015 dan as many as 490 from 552 samples (88.7%) in 2016. Table 3 showed MDRO incidence of gram-positive bacteria which 4 out of 5 bacteria identified as MDRO except for *S. viridans*. In gram-negative bacteria, all the bacteria have been identified as MDRO except *C. diversus* in 2015. The data are presented in table 5 and table 6.

This data showed MDRO bacteria are resistant to at least three classes of antibiotics. Antibiotics that are tested are the class of cephalosporin, carbapenem, aminoglycoside, macrolides, fluoroquinolones, combination, and other groups. *A. calcoaceticus*, *M. morgani*, and *S. maltophilia* were bacteria that resistant to all types of antibiotics.

Table 3. The MDRO incidence of gram-positive bacteria in 2015.

No	Bacteria	Antibiotics																Resistance												
		I		II		III		IV				V		VI		VII			VIII											
		P	AP	AMC	MEM	DOR	IPM	AK	GN	FEP	CTX	CRO	ZOX	CAZ	CPO	KZ	E	AZM	CIP	LEV	NOR	TGC	DA	VA	SCF	SAM	TZP			
1	<i>S. aureus</i>	R	R	R	R	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	MDRO
2	<i>S. epidermidis</i>	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	MDRO
3	<i>S. viridans</i>	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	NON MDRO
4	<i>S. bovis</i>	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	MDRO
5	<i>E. faecalis</i>	R	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	MDRO

Description: I = penicillin; II = carbapenem; III = aminoglycosides; IV = cephalosporins; V = macrolides; VI = fluoroquinolone; VII = other groups; VIII = combination

Table 4. The MDRO incidence of Gram-positive bacteria in 2016.

No	Bacteria	Antibiotics																Resistance												
		I		II		III		IV				V		VI		VII			VIII											
		P	AP	AMC	MEM	DOR	AK	GN	FEP	CTX	CRO	ZOX	CAZ	CPO	KZ	E	AZM	CIP	LEV	TGC	DA	VA	SXT	SCF	SAM	TZP				
1	<i>S. aureus</i>	R	R	-	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	MDRO
2	<i>S. epidermidis</i>	R	R	R	R	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	MDRO
3	<i>S. bovis</i>	R	R	R	R	R	-	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	MDRO
4	<i>S. viridans</i>	S	S	S	S	S	R	I	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	NON MDRO
5	<i>E. faecalis</i>	R	S	R	R	S	S	S	S	S	S	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	MDRO

Description: I = penicillin; II = carbapenem; III = aminoglycosides; IV = cephalosporins; V = macrolides; VI = fluoroquinolone; VII = other groups; VIII = combination

Table 5. The MDRO incidence of gram-negative bacteria in 2015.

No	Bacteria	Antibiotics																Resistance													
		I		II		III		IV				V		VI		VII			VIII												
		AMC	AP	MEM	DOR	IPM	AK	GN	FEP	CTX	CRO	ZOX	CAZ	CPO	KZ	AZM	CIP	LEV	NOR	TE	TGC	C	SXT	SCF	SAM	TZP					
1	<i>A. baumannii</i>	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	MDRO	
2	<i>P. aeruginosa</i>	R	-	R	S	S	S	R	S	R	R	R	R	R	R	R	R	R	R	S	R	R	R	R	R	S	R	S	S	MDRO	
3	<i>K. pneumoniae</i>	R	-	S	S	R	S	R	R	R	R	S	R	R	R	R	R	R	R	S	R	R	S	R	S	R	S	R	S	MDRO	
4	<i>P. mirabilis</i>	S	-	S	S	I	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	MDRO	
5	<i>E. agglomerans</i>	R	-	S	S	-	S	S	S	R	R	R	R	S	R	I	S	S	-	S	R	S	R	S	R	S	R	S	S	MDRO	
6	<i>E. coli</i>	S	-	S	S	-	S	R	S	R	R	S	R	R	R	I	R	R	-	R	R	R	R	S	R	S	R	S	S	MDRO	
7	<i>E. aerogenes</i>	R	-	S	S	-	S	S	S	R	R	S	I	R	R	I	S	S	-	R	R	S	R	S	R	S	R	S	S	MDRO	
8	<i>E. cloacae</i>	R	-	S	S	-	S	S	R	R	S	R	R	R	R	S	S	-	R	R	R	R	R	R	R	R	R	R	MDRO		
9	<i>E. hafniae</i>	R	-	S	S	-	S	S	S	R	R	S	S	R	R	R	S	S	-	R	R	S	S	S	R	S	R	S	S	MDRO	
10	<i>B. cepacia</i>	R	-	R	R	-	S	S	S	S	R	R	I	S	R	I	S	S	-	S	I	S	S	S	R	S	S	R	S	MDRO	
11	<i>M. morgani</i>	R	-	S	S	-	S	S	S	I	S	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	MDRO	
12	<i>K. ozaenae</i>	S	-	S	S	-	S	S	S	I	I	S	S	S	R	I	S	S	-	S	R	R	S	S	S	S	S	S	MDRO		
13	<i>C. diversus</i>	S	-	S	-	-	S	S	S	I	I	S	S	S	R	I	S	S	-	S	R	R	S	S	S	S	S	S	S	NON MDRO	
14	<i>C. sakazaki</i>	R	-	S	-	-	S	S	S	S	S	S	S	S	R	R	S	S	-	R	-	S	S	S	R	I	S	R	S	MDRO	
15	<i>P. vulgaris</i>	R	-	R	-	-	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S	MDRO

Description: I = penicillin; II = carbapenem; III = aminoglycosides; IV = cephalosporins; V = macrolides; VI = fluoroquinolone; VII = other groups; VIII = combination

4. Discussions

13

Bacterial isolates based on clinical specimens from GICU patients at Dr. Mohammad Hoesin Hospital Palembang in 2015 most commonly found in sputum (n = 542/611), followed by blood (n = 25), pus (n = 22), swabs (n = 11), urine (n = 6), and the others (n = 5). In 2016, isolates based on clinical specimens most commonly found in sputum (n = 506/552), followed by blood (n = 20), pus (n = 11), swabs (n = 7), urine (n = 4), and the others (n = 4). Sputum was the most specimens compared to other isolates, this signified a bacterium commonly found in the airways which are an indicator of respiratory tract infections.

The types of bacteria found in the positive bacterial culture results of GICU patients Dr. Mohammad Hoesin Hospital Palembang in 2015 and 2016 were divided into gram-negative and gram-positive bacteria. Gram-negative bacteria with the three most isolated bacteria were *A. baumannii*, *P.aeruginosa* and *K. pneumoniae*, while gram-positive bacteria are found in small quantities. This is due to gram-positive bacteria is the cause of the most nosocomial infections in the era before the use of antibiotics in 1940, but after antibiotics are used the infection-causing gram experiencing positive changes so infrequently this founding [7]. Hal according to some research conducted on the pattern of gram-negative bacteria in GICU among others, research by Saharman [8] in Indonesia, Lestari [9] in Indonesia, and the surveillance research at GICU MDRO Dr. Mohammad Hoesin Hospital Palembangperiod of 2014 by Herprananda [10].

Table 6. The MDRO incidence of gram-negative bacteria in 2016.

N O	Bacteria	Antibiotics																Resistance								
		I	II	III	IV	V	VI	VII	VIII																	
		AMC	MEM	DOR	IPM	AK	GN	FEP	CTX	CRO	ZOX	CAZ	CFO	KZ	AZM	CIP	LEV	TE	TGC	C	SXT	SCF	SAM	TZP		
1	<i>A. baumannii</i>	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	MDRO	
2	<i>P. aeruginosa</i>	R	R	R	R	S	R	S	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	MDRO	
3	<i>K. pneumoniae</i>	R	S	S	-	S	R	R	R	R	S	R	R	R	R	R	S	R	R	R	R	R	S	R	MDRO	
4	<i>E. agglomerans</i>	R	R	R	-	S	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S	R	MDRO	
5	<i>E. coli</i>	R	S	S	-	S	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S	R	S	R	MDRO	
6	<i>E. cloacae</i>	R	R	R	-	S	R	S	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	MDRO	
7	<i>E. aerogenes</i>	R	S	S	-	S	S	R	R	R	S	R	R	R	R	S	S	R	R	S	S	S	R	S	MDRO	
8	<i>P. mirabilis</i>	S	S	S	-	S	R	R	R	I	R	R	R	R	R	R	R	R	R	R	R	R	S	S	MDRO	
9	<i>P. rettgeri</i>	R	S	S	-	S	R	S	R	R	S	R	S	R	R	S	S	R	R	R	R	R	S	R	MDRO	
10	<i>A. xylosoxidans</i>	R	S	S	-	S	S	R	R	R	R	R	R	R	R	S	S	R	R	S	S	R	R	R	MDRO	
11	<i>E. hafniae</i>	R	S	S	-	S	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S	S	S	MDRO	
12	<i>M. morgani</i>	R	R	R	-	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	MDRO	
13	<i>K. coytoca</i>	R	S	S	-	S	S	R	R	R	R	R	R	R	R	S	S	R	R	R	R	R	R	R	MDRO	
14	<i>P. alcalifaciens</i>	R	S	S	-	R	R	S	I	I	S	R	R	R	R	R	R	R	R	R	R	R	S	S	MDRO	
15	<i>B. cepacia</i>	R	R	R	-	I	S	R	R	R	I	R	R	R	I	S	I	I	S	S	S	S	R	R	MDRO	
16	<i>C. freundt</i>	R	S	S	-	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	MDRO	
17	<i>E. meningoseptica</i>	S	I	R	-	R	R	S	R	R	R	R	S	R	I	I	S	S	R	S	R	R	I	S	MDRO	
18	<i>S. maltophilia</i>	R	R	R	-	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	MDRO

Description: I = penicillin; II = carbapenem; III = aminoglycosides; IV = cephalosporins; V = macrolides; VI = fluoroquinolone; VII = other groups; VIII = combination

Gram-negative bacteria was the most bacteria that cause infections in GICU. The predominant ones are *Acinetobacter baumannii*. This bacteria is a normal flora but can be opportunistic pathogens that cause nosocomial infections through the water in a humidifier or vaporizer rooms and intravenous catheter [11].

As a whole, gram-positive bacteria had a high resistance to norfloxacin and ceftazidime in 2015, while in 2016, this bacteria had the highest levels of resistance to cotrimoxazole and ceftazidime. This research showed the highest sensitivity to vancomycin either in 2015 or 2016.

On the other hands, in 2015 gram-negative bacteria have the highest sensitivity to sulbactam-cefoperazone, piperacillin-tazobactam, and doripenem. High resistance was shown by gram-negative bacteria to ampicillin, tigecycline, cefazolin, ampicillin-sulbactam, and chloramphenicol. Whereas in 2016, Gram-negative bacteria had the highest sensitivity to sulbactam-cefoperazone, meropenem, and doripenem. High resistance was shown by gram-negative bacteria to imipenem, cefazolin, tigecycline, azithromycin, and amoxicillin. The resistance is caused by an enzyme that was produced by bacteria. The enzymes can convert the active substance becomes inactive, causing resistance to penicillins and cephalosporins. The bacteria produce the penicillinase enzymes capable of breaking down the beta-lactam ring penicillin, penicilloic acid is converted into inactive likewise degraded by beta-lactamase cephalosporin. Many bacteria are capable of producing beta-lactamase include Gram-positive and negative bacteria. This enzyme has a major role in causing gram-positive bacterial resistance to penicillin and cephalosporin [7].

The antimicrobial sensitivity showed any Multidrug-Resistant Organisms (MDRO). MDRO classified as bacteria are resistant to least one class of antimicrobials of ≥ 3 antimicrobial [4]. MDR can be caused by the use of less appropriate as antibiotics that are too short, in doses that are too low, the lack of proper prescribing, or mistaken early diagnosis [12]. WHO in 2017 published for the first time, a list of the priority pathogens resistant to antibiotics in an effort to guide and promote research and

development (research and development) a new antibiotic as part of efforts to overcome global resistance the WHO against antimicrobial drugs because the high incidence of multidrug resistant. WHO divided into three categories (priorities are critical, high, and medium) in accordance with the urgency for new antibiotics and critical priority category, *Acinetobacter baumannii* was the first ranked, the second ranked *Pseudomonas aeruginosa* and the third *Enterobacteriaceae*. These bacteria are commonly found in hospitals, nursing homes, and in patients who need treatment tools such as ventilators and catheters blood. These bacteria can also cause severe infections and deadly bloodstream infections and pneumonia.

5. Conclusions

All gram-positive bacteria (except *S. viridans*) and gram-negative (except *C. Diversus*) has been identified as being multidrug-resistant organisms (MDRO) in 2015. Whereas in 2016, all gram-positive bacteria (except *S. viridans*) and gram-negative bacteria have been identified as being MDRO. There was a slight decrease in MDRO incidence at 2016. Bacteriologic isolates based on clinical specimens in 2015 and 2016 most commonly found in sputum. The gram-positive bacteria had the highest sensitivity to vancomycin and the highest resistance to norfloxacin and ceftazidime in 2015. In 2016, the gram-positive bacteria had the highest sensitivity to vancomycin and the highest resistance to cotrimoxazole and ceftazidime. In 2015 a gram-negative bacterium had the highest sensitivity to cefoperazone sulbactam, piperacillin-tazobactam, and doripenem with the highest resistance to ampicillin. In 2016, a gram-negative bacterium had the highest sensitivity to sulbactam cefoperazone, meropenem, and doripenem with the highest resistance to imipenem.

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