



Bacterial Profile and Antimicrobial Resistance Patterns of Pleural Empyema in Pekanbaru Hospitals

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Abstract

Background: Empyema is a problem worldwide due to its high incidence, mortality, and morbidity rates. So, administering antibiotics is mandatory to treat the disease. It should be sensitive to the causal microorganisms and avoid resistant ones for treatment efficacy. This research aimed to determine bacterial profile and antimicrobial resistance, which can be fundamental foundations for clinical practices in the treatment of patients, especially in Pekanbaru.

Methods: This was a cross-sectional study from medical records at Arifin Achmad and Eka Hospitals from January 1, 2015, to December 31, 2022, including culture and antibiotic resistance test results with samples from pleural fluid and antibiotic susceptibility test using VITEK 2.0.

Results: A total of 197 pleural fluid specimens were obtained. Gram-negative bacteria were found to be the most prevalent at 79.7%, namely *Klebsiella pneumoniae* (18.5%), *Escherichia coli* (12.0%), and *Pseudomonas aeruginosa* (11.0%). Gram-positive bacteria were found at 12.2%, the most common being *Staphylococcus aureus* (6.1%) and *Enterococcus faecalis* (2.0%). Antibiotic sensitivity tests for Gram-negative bacteria showed that amikacin and tigecycline were the most sensitive, and Gram-positive bacteria showed the most sensitivity to linezolid, tigecycline, and vancomycin. The resistance of *Klebsiella pneumoniae* and *Escherichia coli* to cephalosporins was 18.5% and 75.0%, respectively. The resistance of *Klebsiella pneumoniae*, *Escherichia coli*, and *Pseudomonas aeruginosa* to carbapenems was 8.0%, 13.0%, and 53.0%, respectively.

Conclusion: Gram-negative is the most common microorganism found in pleural empyema. The resistance of multiresistant bacteria to antibiotics is high and requires supervision to apply appropriate antibiotic administration based on local antimicrobial patterns and the need to strengthen antimicrobial stewardship programs.

Keywords: *Klebsiella pneumoniae*, *Staphylococcus aureus*, amikacin, tigecycline

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INTRODUCTION

Empyema is a condition characterized by the presence of pus in the pleural cavity. This ailment remains a global concern due to a significant rise in reported cases. According to a study by Arnold et al conducted in UK hospitals, the morbidity rate of empyema doubled over a ten-year period. In 2008, there were only around 4,447 cases, but in 2017, the number had surged to 7,268. Similarly, the incidence of thoracic empyema in Riau Province has witnessed

annual increases over the past three years, ranging from 5.0% to 10.0% each year from 2016 to 2019.^{1,2}

Year by year, there has been a growing incidence rate, mortality rate, and morbidity rate. According to Garvia et al, the mortality rate associated with empyema varies from 20.0% to 30.0%.³ In a study conducted in Kansas, the mortality rate reached 24.5 per 100,000 people annually, with the majority of cases occurring in male patients aged 65 years or older.⁴ In contrast, data on empyema

mortality in Indonesia is still limited.

Research by Lehtomäki et al, at the Finnish University Hospital, revealed that the most common bacteria responsible for empyema were gram-positive, with *Streptococcus* sp. accounting for 21.0% and *Staphylococcus* sp. also at 21.0%. These findings exceeded the presence of gram-negative bacteria causing empyema, particularly *Pseudomonas aeruginosa*, which was only present in approximately 1.9% of cases.⁵ These results are in line with those of Hassan et al, who reported that pleural fluid cultures mostly yielded gram-positive bacteria, totaling 37.5%.⁶

On the other hand, a study by Atif et al in Pakistan yielded different results, with gram-negative bacteria dominating pleural fluid cultures at 43.4%, primarily *Pseudomonas aeruginosa*, *Escherichia coli*, and *Klebsiella pneumoniae*.⁷ Similar findings were reported by Sharma et al in India, where 80.9% of empyema cases were attributed to gram-negative bacteria, with *Acinetobacter baumannii* at 33.3%, *Escherichia coli* at 14.3%, *Klebsiella pneumoniae* at 9.5%, *Enterobacter aerogenes* at 9.5%, *Citrobacter koseri* at 9.5%, and *Pseudomonas aeruginosa* at 4.86%. Most of these gram-negative bacteria displayed good sensitivity to amikacin and piperacillin-tazobactam.⁸

Data from Dr. Zainal Abidin Hospital in Banda Aceh, as studied by Habibie and Hamdani, also showed similar trends. In this research, gram-negative bacteria were the predominant findings in pleural fluid cultures, with *Klebsiella pneumoniae* being the most common isolate. Additionally, some gram-positive bacteria, such as *Staphylococcus* sp., *Pseudomonas aeruginosa*, and *Streptococcus* B group, were also identified.⁹

The situation in Pekanbaru is that there is no research that describes the bacterial profile and antimicrobial resistance patterns of pleural empyema, which can be the basis for clinical practice in treating patients, especially thoracic empyema, in Pekanbaru Hospital. Meanwhile, understanding the bacteria responsible is crucial for expanding knowledge and identifying the sensitivity of these bacteria to antibiotics. This knowledge allows for

more precise antibiotic therapy, reducing unnecessary antibiotic use. Pleural fluid culture is the gold standard for diagnosing pulmonary empyema, which takes 3–5 days for results. During this period, patients usually receive antibiotic empirical therapy, which should be based on antibiotic sensitivity patterns in the region to minimize the development of resistance. The study aims to describe bacterial profile and antimicrobial resistance patterns that can be fundamental foundations for clinical practices in the treatment of patients, especially in Pekanbaru Hospital.

METHODS

This study had a cross-sectional design. The data were taken from medical records and included pleural fluid culture results and antibiotic sensitivity tests from Arifin Achmad and Eka Hospitals from January 1, 2015, to December 31, 2022. This study incorporated all empyema samples that underwent both culture and antibiotic susceptibility testing. Incomplete data and missing information on the type of bacteria and antibiotic resistance test results were excluded, and the bacteria that are susceptible to contamination, such as *Coagulase-negative Staphylococci* (CoNS), were deliberately excluded from the analysis.

Pleural fluid samples were cultured in BacTAlert PN pediatric blood culture bottles (bioMérieux, Marcy l'Etoile, France). A positive culture was determined by bacterial growth on blood agar and MacConkey agar media, which were used for identifying an antibiotic sensitivity test. The experiments were conducted in the Clinical Pathology Laboratory Microbiology Section at Arifin Achmad General Hospital and Eka Hospital.

Various antibiotics were tested for sensitivity, including amikacin, ampicillin, ampicillin-sulbactam, azithromycin, aztreonam, cefazolin, cefepime, cefoxitin, ceftazidime, ceftriaxone, ciprofloxacin, clarithromycin, clindamycin, doxycycline, ertapenem, erythromycin, gentamycin, imipenem, levofloxacin, linezolid, meropenem, moxifloxacin, oxacillin, piperacillin-tazobactam, quinupristin/dalfopristin,

tetracycline, tigecycline, cotrimoxazole, and vancomycin.

The data presentation followed the guidelines of the Clinical and Laboratory Standards Institute (CLSI). Both participating laboratories in this study employed control bacteria strains, including *Escherichia coli* American Type Culture Collection (ATCC) 25.922 and *Pseudomonas aeruginosa* ATCC 27853. Only the first sample was analyzed in this study in cases with multiple samples from a single patient.

The results of bacterial culture and antibiotic sensitivity tests were obtained from the VITEK 2 compact device and cross-referenced with the registration book to ensure data completeness. Data processing, including antimicrobial sensitivity patterns, was conducted using WHONET 5.6. Ethical approval for this research was granted by the Research Ethics Unit of the Faculty of Medicine and Health, Faculty of Medicine, Riau University, with reference number B/094/UN.19.5.1.1.8/UEPKK/2023

RESULTS

Examining pleural fluid cultures revealed that most cases were attributed to gram-negative bacteria (79.7%). Gram-positive bacteria was at 12.2%, while some cases involving fungi. Among gram-negative bacteria, *Klebsiella pneumoniae* was the predominant causative agent at 18.8%, followed by *Escherichia coli* at 12.2% and *Pseudomonas aeruginosa* at 11.2%. Among the gram-positive bacterial group, the most frequently identified organism was *Staphylococcus aureus* at 6.1%, followed by *Enterococcus faecalis* at 2.0%. Fungal pathogens were also detected, with *Candida albicans* accounting for 5.6% and *Aspergillus sp.* for 1.5% of cases (Table 1).

Regarding antibiotic susceptibility, *K. pneumoniae* exhibited the highest sensitivity to amikacin at 100.0%, followed by carbapenem classes such as meropenem at 92.0% and ertapenem at 89.0%. The resistance rate of *K. pneumoniae* to third and fourth-generation cephalosporins was 75.0% and 60.0%, respectively,

while the resistance rate to meropenem was 8.0%. *Escherichia coli* exhibited high susceptibility to several antibiotics, including amikacin and tigecycline, with sensitivity rates of 100% for both. It also demonstrated good sensitivity to carbapenem antibiotics, specifically ertapenem (91.0%) and meropenem (87.0%). However, *E. coli* displayed resistance to third-generation cephalosporins, such as ceftriaxone, with a resistance rate of 75.0% (Table 2).

Table 1. Distribution of Microorganisms Causing Empyema.

Organism	N	%
Gram Negative Bacteria	157	79.7
<i>Klebsiella pneumoniae</i>	37	18.8
<i>Escherichia coli</i>	24	12.2
<i>Pseudomonas aeruginosa</i>	22	11.2
<i>Acinetobacter baumannii</i>	18	9.1
<i>Enterobacter cloacae</i>	14	7.1
<i>Stenotrophomonas maltophilia</i>	13	6.6
<i>Salmonella sp.</i>	3	1.5
<i>Achromobacter xylosoxidans</i>	2	1.0
<i>Aeromonas hydrophila/caviae</i>	2	1.0
<i>Bukholderia cepacia</i>	2	1.0
Others	20	10.2
Gram Positive Bacteria	27	12.2
<i>Staphylococcus aureus</i>	12	6.1
<i>Enterococcus faecalis</i>	4	2.0
<i>Enterococcus faecium</i>	1	0.5
<i>Enterococcus avium</i>	1	0.5
<i>Enterococcus casseliflavus</i>	1	0.5
<i>Enterococcus gallinarum</i>	1	0.5
<i>Streptococcus agalactiae</i>	1	0.5
<i>Streptococcus intermedius</i>	1	0.5
<i>Streptococcus pluranimalium</i>	1	0.5
<i>Staphylococcus haemolyticus</i>	1	0.5
Fungi	16	8.1
<i>Candida Albicans</i>	11	5.6
<i>Aspergillus sp.</i>	3	1.5
<i>Candida tropicalis</i>	1	0.5
<i>Candida lipolytica</i>	1	0.5

Pseudomonas aeruginosa demonstrated favorable sensitivity to aminoglycoside antibiotics, including amikacin (76.0%) and gentamicin (61.0%). It also exhibits good sensitivity to quinolone antibiotics, particularly ciprofloxacin (76.0%). Nevertheless, *P. aeruginosa* showed lower sensitivity to other third-generation cephalosporins, notably ceftazidime (50.0%), and resistance to ceftriaxone. The resistance rate of *P. aeruginosa* to meropenem was 53.0% (Table 2).

Table 2: Antibiotic resistance pattern

Antibiotics	Sensitivity to Antibiotics						
	<i>K. Pneumonia</i> (n=37)	<i>E. coli</i> (n=24)	<i>P. aeruginosa</i> (n=22)	<i>A. baumannii</i> (n=18)	<i>E. cloacae</i> (n=14)	<i>S. maltophilia</i> (n=13)	<i>S. aureus</i> (n=12)
Amikacin	37 (100%)	23 (100%)	22 (76%)	18 (61%)	14 (100%)	0 (0%)	0 (0%)
Ampicillin	37 (0%)	24 (4%)	22 (0%)	18 (0v)	14 (0%)	0 (0%)	1 (0%)
Ampicillin/Sulbactam	37 (10%)	24 (20%)	22 (0%)	18 (50%)	14 (7%)	0 (0%)	12 (42%)
Azithromycin	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	4 (75%)
Aztreonam	37 (32%)	22 (36%)	19 (21%)	4 (0%)	14 (50%)	0 (0%)	0 (0%)
Cefazolin	37 (19%)	24 (17%)	22 (0%)	18 (6%)	14 (7%)	0 (0%)	12 (42%)
Cefepime	37 (40%)	23 (52%)	21 (52%)	18 (33%)	14 (79%)	0 (0%)	12 (42%)
Cefoxitin	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	12 (42%)
Ceftazidime	37 (37%)	24 (41%)	22 (50%)	18 (33%)	14 (57%)	0 (0%)	12 (42%)
Ceftriaxone	36 (25%)	24 (25%)	22 (0%)	18 (0%)	14 (50%)	0 (0%)	12 (42%)
Ciprofloxacin	36 (44%)	22(27)	21 (76%)	18 (39%)	14 (72%)	0 (0%)	12 (50%)
Clarithromycin	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	5 (80%)
Clindamycin	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	12 (75%)
Doxycycline	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (100%)
Ertapenem	37 (89%)	23 (91%)	0 (0%)	0 (0%)	14 (79%)	0 (0%)	12 (42%)
Erythromycin	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	12 (83%)
Gentamicyn	37 (48%)	23 (52%)	21 (61%)	18 (50%)	14 (79%)	0 (0%)	12 (83%)
Imipenem	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	12 (42%)
Levofloxacin	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	11 (64%)
Linezolid	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	12 (100%)
Meropenem	37 (92%)	23 (87%)	21 (47%)	18 (39%)	14 (72%)	0 (0%)	12 (42%)
Moxifloxacin	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	12 (67%)
Oxacillin MIC	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	12 (42%)
Piperacillin/Tazobactam	37 (59%)	22 (73%)	20 (45%)	18 (22%)	14 (71%)	0 (0%)	12 (42%)
Quinupristin/Dalfopristin	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	12 (92%)
Tetracycline	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	12 (58%)
Tigecycline	37 (86%)	23 (100%)	22 (0%)	18 (83%)	14 (100%)	0 (0%)	12 (100%)
Trimethoprim/Sulfamethoxazole	34 (38%)	23 (43%)	22 (0%)	18 (61%)	14 (72%)	13 (54%)	11 (82%)
Vancomycin	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	12 (100%)

A. baumannii displayed good sensitivity to tigecycline (83.0%), followed by trimethoprim/sulfamethoxazole and amikacin, each with a sensitivity of 61.0%. However, it exhibited resistance to ampicillin-sulbactam and meropenem of 50% and 61%, respectively. The resistance rate of *A. baumannii* to third-generation cephalosporins was notably high at 100% (Table 2).

Enterobacter cloacae demonstrated high sensitivity to aminoglycoside antibiotics, including amikacin (100.0%) and gentamicin (79.0%). It also displayed good sensitivity to tigecycline (100.0%) and ciprofloxacin (72.0%). However, it was resistant to third-generation cephalosporins at a rate of 50.0%. *S. maltophilia* exhibited good sensitivity to trimethoprim/sulfamethoxazole, with a sensitivity rate of 54.0%, making it the preferred antibiotic for this bacterium (Table 2).

Staphylococcus aureus indicated high sensitivity to several antibiotics, including linezolid, tigecycline, and vancomycin, each with a sensitivity rate of 100.0%. Additionally, quinupristin/dalfopristin displayed a high sensitivity rate of 92.0%. Notably, the prevalence of *Methicillin-resistant Staphylococcus aureus* (MRSA) was substantial at 58.0% (Table 2).

DISCUSSION

Empyema is characterized by the accumulation of pus in the pleural cavity, resulting from exudative and fibropurulent processes caused by various microorganisms. In this study, gram-negative bacteria, specifically *Klebsiella pneumoniae*, *Escherichia coli*, *Pseudomonas aeruginosa*, *Acinetobacter baumannii*, *Enterobacter*

cloacae, and *Stenotrophomonas maltophilia*, were identified as the predominant agents responsible for pulmonary empyema. These findings are consistent with research conducted by Atif et al in Pakistan and Sharma et al in India, both of whom also identified gram-negative bacteria as the most common causative agents of empyema.^{7,8}

The etiology of empyema often relies on the microbiological patterns, and it typically varies according to the geographical conditions of a given region.⁴ As study by McCauley et al in their research conducted in the United States, empyema-causing bacteria predominantly belong to the gram-positive bacterial group, specifically *S. pneumoniae*, *Haemophilus influenzae*, and *Staphylococcus aureus*. This prevalence of gram-positive bacteria is influenced by various factors, including the demographic characteristics of the local population, their immunity status, and geographic conditions, which collectively contribute to the dominance of gram-positive bacteria in the area.¹⁰

On the other hand, a separate study conducted by Hassan et al revealed that *Klebsiella pneumoniae*, a gram-negative bacterium, is typically prevalent in hot and tropical regions, such as Indonesia. This finding provides a plausible explanation for why *Klebsiella pneumoniae* emerged as the primary causative agent of empyema in the hospitals of Pekanbaru, as observed in this study.⁶ Additionally, the research conducted by Habibie et al corroborates these findings by identifying *Klebsiella pneumoniae* as the most frequently encountered bacteria in pleural fluid culture results.⁹

In this study, it is highlighted that *Klebsiella pneumoniae* exhibits the highest sensitivity to amikacin, achieving a remarkable 100% sensitivity rate. Subsequently, carbapenem antibiotics, specifically meropenem and ertapenem, also demonstrated substantial efficacy against *Klebsiella pneumoniae*, with sensitivity rates of 92.0% and 83.0%, respectively. These findings are consistent with earlier research conducted at Arifin Achmad General Hospital by Anggraini et al, which reported that *Klebsiella pneumoniae* displayed high sensitivity to both amikacin (96.7%) and meropenem (94.0%).¹¹

The prevalence of carbapenem resistance in *Klebsiella pneumoniae*, as indicated by antibiotic resistance surveillance data in Indonesia for the year 2021, was found to be higher compared to the observed resistance rate in this study. Specifically, the nationwide data showed a higher carbapenem resistance rate, while in this study, the resistance rate stood at 12.0%.¹²

In this study, *Klebsiella pneumoniae* exhibited resistance to third-generation cephalosporins, with a resistance rate of 75.0%. These findings are consistent with a prior study conducted by Anggraini et al at Arifin Achmad General Hospital, where they also reported complete resistance of *Klebsiella pneumoniae* to third-generation cephalosporins.¹¹ This study's findings indicate that *Klebsiella pneumoniae*'s resistance to cephalosporins is greater than what was reported in the nationwide antibiotic resistance surveillance data for Indonesia in 2021. Nationally, the resistance rate of *Klebsiella pneumoniae* to cephalosporins was documented at 50.0%, while the specific data for Pekanbaru revealed a higher resistance rate of 75.0% among *Klebsiella pneumoniae* isolates against ceftriaxone.¹²

The elevated resistance to cephalosporins observed in *Klebsiella pneumoniae* can be attributed to the fact that this bacterium is pathogenic and produces extended-spectrum beta-lactamase (ESBL). Third-generation cephalosporins contain oximo groups that are susceptible to hydrolysis by these ESBL-producing bacteria, rendering them ineffective against *Klebsiella pneumoniae* and contributing to the observed resistance.¹³

Escherichia coli exhibits notable sensitivity to several antibiotics, with high efficacy rates recorded for amikacin (100.0%), tigecycline (100.0%), ertapenem (91.0%), and meropenem (87.0%). This sensitivity pattern aligns with the data from antibiotic resistance surveillance in Indonesia for the year 2021, where it was reported that 88.0% of *Escherichia coli* isolates demonstrated sensitivity to carbapenems.¹²

However, this study found that *Escherichia coli* exhibited resistance to third-generation cephalosporins. This resistance can be attributed to

the fact that *Escherichia coli*, like *K. pneumoniae*, is capable of producing extended-spectrum beta-lactamase (ESBL). The presence of ESBL in these bacteria contributes to their resistance not only to cephalosporin antibiotics but also to quinolone antibiotics.¹³ The resistance level of *Escherichia coli* to third-generation cephalosporins in this study was found to be 75.0%. Comparatively, this resistance rate is slightly higher than the data from the 2021 antibiotic resistance surveillance in Indonesia, which reported that 74.0% of *Escherichia coli* isolates had developed resistance to third-generation cephalosporins.¹²

These study results are notably more positive compared to a prior study conducted by Anggraini et al at Arifin Achmad General Hospital, which reported that all *Escherichia coli* isolates were resistant to third-generation cephalosporins. In this current study, there is evidence of some degree of sensitivity among *Escherichia coli* isolates to third-generation cephalosporins, indicating a potentially improved situation regarding antibiotic resistance in this context.¹¹

Pseudomonas aeruginosa exhibits notable sensitivity to amikacin and gentamicin, with sensitivity values of 76.0% and 61.0%, respectively. These findings are in line with the research conducted by Wahyunita et al at Dr. Wahidin Sudirohusodo Hospital, which identified amikacin as the most effective antibiotic for treating *Pseudomonas aeruginosa*, achieving an impressive sensitivity rate of 95.8%.¹⁴ Meanwhile, at Hasanudin University Hospital, gentamycin is the best antibiotic for treating *Pseudomonas aeruginosa* with a sensitivity of 100%.¹⁵ *Pseudomonas aeruginosa* also has good sensitivity to quinolone antibiotics, namely ciprofloxacin, which is 76.0%. This is similar to research conducted by Anggraini et al, who found that *Pseudomonas aeruginosa* had a good sensitivity to quinolones of 48.8%.¹⁶

In this study, the observed level of resistance of *Pseudomonas aeruginosa* to carbapenems stood at 53.0%. Notably, this resistance rate is higher than the findings from previous research conducted by Anggraini et al in 2018, which reported a lower

resistance rate of 43.0% for *Pseudomonas aeruginosa* against carbapenems.¹⁶ This condition of higher resistance in *Pseudomonas aeruginosa* to carbapenems, as observed in the current study, is also notable when compared to the antibiotic resistance surveillance data in Indonesia for the year 2021. The national data indicated a lower resistance rate, with only 27.0% of *Pseudomonas aeruginosa* isolates exhibiting resistance to carbapenem-class antibiotics.¹²

Acinetobacter baumannii has a good sensitivity to amikacin of 61.0%. This is similar to previous research at Arifin Achmad General Hospital conducted by Anggraini et al showing that *Acinetobacter baumannii* had a good sensitivity to amikacin, which was 78.0%.¹⁷ The condition at the hospital in Pekanbaru is almost similar to the research by Aulia et al conducted at Dr. Soeradji Tirtonegoro General Hospital in Klaten, which found that *Acinetobacter baumannii* was still sensitive to amikacin at 54.2% and meropenem at 55.9%. However, this study has found a low sensitivity to ampicillin sulbactam at 20.7%.¹⁵

Acinetobacter baumannii is resistant to third-generation cephalosporins. This is in line with research conducted by Aulia et al in Klaten and Anggraini et al in Pekanbaru, which stated that *Acinetobacter baumannii* had a high level of resistance to third-generation cephalosporins, each of which was 96.0%.^{15,17} This can be explained through the enzymatic mechanism produced by *Acinetobacter baumannii*, namely beta-lactamase enzyme activity, which is able to hydrolyze beta-lactam antibiotics such as penicillin, cephalosporin, and carbapenem groups.¹⁸

The level of resistance of *Acinetobacter baumannii* to meropenem was 71.0%. This resistance condition is higher than previous research by Anggraini et al, which showed resistance to meropenem only reached 50.0%.¹⁷ In this study, the level of *Acinetobacter baumannii* resistance to meropenem was also higher than the antibiotic resistance surveillance data in Indonesia, which only showed 62.0% of *Acinetobacter baumannii* had carbapenem resistance.¹²

The resistance rate of *Enterobacter cloacae* to third-generation cephalosporins is 60.0%. Some researchers have warned against the use of third-generation cephalosporins against *Enterobacter cloacae*. This warning is specific to severe infection conditions caused by *Enterobacter sp.*, especially those caused by *Enterobacter cloacae* and *Enterobacter aerogenes*. This consideration is due to *Enterobacter cloacae* also producing *AmpC b-lactamases*, which can increase the risk of resistance to this type of antibiotic.¹⁹ Management for patients with third-generation cephalosporin resistance can be given in the form of carbapenem antibiotics, especially meropenem. Although *Enterobacter cloacae* produces *AmpC b-lactamases* that can hydrolyze third-generation cephalosporins, *AmpC b-lactamases* are not yet able to inhibit carbapenem antibiotics.²⁰

Stenotrophomonas maltophilia has good sensitivity to trimethoprim and sulfamethoxazole, which have a sensitivity of 54.0%. Based on global data, the sensitivity of trimethoprim and sulfamethoxazole against *Stenotrophomonas maltophilia* has a range that varies from 79.0 to 96.0%.²¹

Based on in vitro tests conducted by Flamm et al, which suggested that there were two antibiotics which had good sensitivity against *Stenotrophomonas maltophilia* bacteria, namely minocycline and trimethoprim or sulfamethoxazole, minocycline could be an alternative if there was resistance to trimethoprim or sulfamethoxazole. The standardized antibiotic sensitivity test for *Stenotrophomonas maltophilia* is only for trimethoprim or sulfamethoxazole.²²

The percentage of MRSA in this study was 58.0%. This condition is included in the high MRSA rate when compared to previous research conducted by Farhani et al, who conducted research in the 2015–2019 timeframe and found that the average MRSA rate at Arifin Achmad General Hospital was only 32.8%.²³ This MRSA rate is also higher than the antibiotic resistance surveillance data in Indonesia, which found that the MRSA percentage only reached 38.0%.¹² In this study, *S. aureus* had good sensitivity

to linezolid, tigecycline, and vancomycin. So that these antibiotics can be a therapeutic option for MRSA.

In Pekanbaru hospitals, the resistance rate is generally higher than the resistance surveillance data observed in Indonesia. This discrepancy can be attributed to the misuse and overuse of antibiotics, which have played a significant role in the emergence of antibiotic-resistant organisms. These resistant organisms are associated with an estimated 700,000 deaths annually. If the current trend continues, it is estimated that by 2050, antimicrobial resistance could result in up to 10 million deaths annually, accompanied by potential economic losses nearing 100 trillion USD, unless significant measures are promptly taken.²⁴

To prevent this, supervision and regulation are necessary through the strengthening of antimicrobial stewardship programs and infection prevention and control to reduce the level of antibiotic resistance and reduce the number and costs due to unwise antibiotic use. Strengthening antimicrobial stewardship programs has been implemented over the past few years in both of hospitals. However, its execution is not yet optimal, for instance, in terms of compliance with antibiotic usage guidelines. Both hospitals are classified as class B hospitals and serve as provincial referral hospitals, so the majority of patients are referrals from district hospitals who have received antibiotics previously.

LIMITATIONS

The limitation of this study is that not all types of antibiotics can be tested, and clinical data do not accompany the data obtained.

CONCLUSIONS

The most common microorganisms found were gram-negative bacteria, namely *Klebsiella pneumoniae*, *Escherichia coli*, *Pseudomonas aeruginosa*, and *Acinetobacter baumannii*. The prevalence of multiresistant bacteria is so high that it requires supervision to implement appropriate antibiotic administration based on local antimicrobial

patterns through strengthening antimicrobial stewardship programs.

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CONFLICT OF INTEREST

None.

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