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Original Article

# 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 the resistant ones for treatment efficacy.

**Methods:** This is a retrospective 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 used VITEK 2.0.

**Results:** 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%), *Pseudomonas aeruginosa* (11.0%), and *Acinetobacter baumannii* (9.0%). 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 are 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, Pseudomonas aeruginosa,* and *Acinetobacter baumannii* to carbapenems were 8.0%, 13.0%, 53.0%, and 61.0%, respectively.

**Conclusion:** Gram-negative is the most common microorganism found in pleural empyema. The multiresistant bacteria toward an antibiotic 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 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 pneumonia*.[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 et al., 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]

Understanding the bacteria responsible for pulmonary empyema through pleural fluid 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 identify bacterial and antibiotic sensitivity profiles from pleural fluid samples in Pekanbaru hospitals

## METHODS

This study was a descriptive retrospective 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. 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), are deliberately not included or 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. 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 at 79.7%. Gram-positive bacteria at 12.18% and some cases involving fungi. Among gram-positive bacteria, *Klebsiella pneumoniae* was the predominant causative agent at 18.5%, followed by *Escherichia coli* at 12.0%, *Pseudomonas aeruginosa* at 11%, *Acinetobacter baumannii* at 9.0%, *Enterobacter cloacae* at 7.0%, and *Stenotrophomonas maltophilia* at 6.5%. Among the gram-negative bacterial group, the most frequently identified organism was *Staphylococcus aureus* at 6.09%, followed by *Enterococcus faecalis* at 2.0%. Fungal pathogens were also detected, *with Candida albicans* accounting for 5.5% and *Aspergillus sp.* for 1.5% of cases (Table 1).

Table 1. Distribution of Microorganisms Causing Empyema.

| NO | ORGANISM | NUMBER OF ISOLATES | PRESENTATION |
|---|---|---|---|
| | **GRAM NEGATIVE BACTERIA** | **157** | 79.7% |
| 1 | *Klebsiella Pneumonia* | 37 | 18.8% |
| 2 | *Escherichia coli* | 24 | 12.2% |
| 3 | *Pseudomonas aeruginosa* | 22 | 11.2% |
| 4 | *Acinetobacter baumannii* | 18 | 9.1% |
| 5 | *Enterobacter cloacae* | 14 | 7.1% |
| 6 | *Stenotrophomonas maltophilia* | 13 | 6.6% |
| 7 | *Salmonella sp.* | 3 | 1.5% |
| 8 | *Achromobacter xylosoxidans* | 2 | 1.0% |
| 9 | *Aeromonas hydrophila/caviae* | 2 | 1.0% |
| 10 | *Bukholderia cepacia* | 2 | 1.0% |
| 11 | Others | 20 | 10.2% |
| | ***GRAM POSITIVE BACTERIA*** | **27** | 12.2% |
| 1 | *Staphylococcus aureus* | 12 | 6.1% |
| 2 | *Enterococcus faecalis* | 4 | 2.0% |
| 3 | *Enterococcus faecium* | 1 | 0.5% |
| 4 | *Enterococcus avium* | 1 | 0.5% |
| 5 | *Enterococcus casseliflavus* | 1 | 0.5% |
| 6 | *Enterococcus gallinarum* | 1 | 0.5% |
| 7 | *Streptococcus agalactiae* | 1 | 0.5% |
| 8 | *Streptococcus intermedius* | 1 | 0.5% |
| 9 | *Streptococcus pluranimalium* | 1 | 0.5% |
| 10 | *Staphylococcus haemolyticus* | 1 | 0.5% |
| | ***FUNGI*** | **16** | 8.1% |
| 1 | *Candida Albicans* | 11 | 5.6% |
| 2 | *Aspergillus sp.* | 3 | 1.5% |
| 3 | *Candida tropicalis* | 1 | 0.5% |
| 4 | *Candida lipolytica* | 1 | 0.5% |

Regarding antibiotic sensitivity, *Klebsiella pneumoniae* exhibited the highest sensitivity to amikacin at 100.0%, followed by meropenem at 92.0%, ertapenem at 83.0%, and tigecycline at 86.0%. The resistance rate of *Klebsiella pneumoniae* to third and fourth-generation cephalosporins was 75.0% and 60.0%, respectively, while the resistance rate to the meropenem group was 8.0%. *Escherichia coli* exhibits high sensitivity to several antibiotics, including amikacin and tigecycline, with sensitivity rates of 100% for both. It also demonstrates good sensitivity to carbapenem antibiotics, specifically ertapenem (91.0%) and meropenem (87.0%). However, *Escherichia coli* displays resistance to third-generation cephalosporins, such as ceftriaxone, with a resistance rate of 75.0% (Table 2).

*Pseudomonas aeruginosa* demonstrates 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, *Pseudomonas aeruginosa* shows lower sensitivity to other third-generation cephalosporins, notably ceftazidime (50.0%), and resistance to ceftriaxone. The resistance rate of *Pseudomonas aeruginosa* to the meropenem group is 53.0%. *Acinetobacter baumannii* displays good sensitivity to tigecycline (83.0%), followed by trimethoprim/sulfamethoxazole and amikacin, each with a sensitivity of 61.0%. However, it exhibits resistance to ampicillin-sulbactam and meropenem, both at 61.0%. The resistance rate of *Acinetobacter baumannii* to third-generation cephalosporins is notably high at 67.0% (Table 2).

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

*Staphylococcus aureus* displays high sensitivity to several antibiotics, including linezolid, tigecycline, and vancomycin, each with a sensitivity rate of 100.0%. Additionally Quinupristin/Dalfopristin exhibits a high sensitivity rate of 92.0%. Notably, the prevalence of *Methicillin-Resistant Staphylococcus aureus* (MRSA) is substantial at 58.0% (Table 2).

Table 2: Antibiotic resistance pattern

| NO | Antibiotics | Sensitivity to antibiotics (n(%)) | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | *K. Pneumonia* (n=37) | *E. coli* (n=24) | *P. aeruginosa* (n=22) | *A. baumannii* (n=18) | *E. cloacae* (n=14) | *S. maltophilia* (n=13) | *S. aureus* (n=12) |
| 1 | Amikacin | 37(100) | 23(100) | 22(76) | 18(61) | 14(100) | | |
| 2 | Ampicillin | 37(0) | 24(4) | 22(0) | 18(0) | 14(0) | | 1(0) |
| 3 | Ampicillin/ Sulbactam | 37(10) | 24(20) | 22(0) | 18(50) | 14(7) | | 12(42) |
| 4 | Azithromycin | | | | | | | 4(75) |
| 5 | Aztreonam | 37(32) | 22(36) | 19(21) | 4(0) | 14(50) | | |
| 6 | Cefazolin | 37(19) | 24(17) | 22(0) | 18(6) | 14(7) | | 12(42) |
| 7 | Cefepime | 37(40) | 23(52) | 21(52) | 18(33) | 14(79) | | 12(42) |
| 8 | Cefoxitin | | | | | | | 12(42) |
| 9 | Ceftazidime | 37(37) | 24(41) | 22(50) | 18(33) | 14(57) | | 12(42) |
| 10 | Ceftriaxone | 36(25) | 24(25) | 22(0) | 18(0) | 14(50) | | 12(42) |
| 11 | Ciprofloxacin | 36(44) | 22(27) | 21(76) | 18(39) | 14(72) | | 12(50) |
| 12 | Clarithromycin | | | | | | | 5(80) |
| 13 | Clindamycin | | | | | | | 12(75) |
| 14 | Doxycycline | | | | | | | 1(100) |
| 15 | Ertapenem | 37(89) | 23(91) | | | 14(79) | | 12(42) |
| 16 | Erythromycin | | | | | | | 12(83) |
| 17 | Gentamicyn | 37(48) | 23(52) | 21(61) | 18(50) | 14(79) | | 12(83) |
| 18 | Imipenem | | | | | | | 12(42) |
| 19 | Levofloxacin | | | | | | | 11(64) |
| 20 | Linezolid | | | | | | | 12(100) |
| 21 | Meropenem | 37(92) | 23(87) | 21(47) | 18(39) | 14(72) | | 12(42) |
| 22 | Moxifloxacin | | | | | | | 12(67) |
| 23 | Oxacillin MIC | | | | | | | 12(42) |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| 24 | Piperacillin/ Tazobactam | 37(59) | 22(73) | 20(45) | 18(22) | 14(71) | | 12(42) |
| 25 | Quinupristin /Dalfopristin | | | | | | | 12(92) |
| 26 | Tetracycline | | | | | | | 12(58) |
| 27 | Tigecycline | 37(86) | 23(100) | 22(0) | 18(83) | 14(100) | | 12(100) |
| 28 | Trimethoprim/ Sulfamethoxazole | 34(38) | 23(43) | 22(0) | 18(61) | 14(72) | 13(54) | 11(82) |
| 29 | Vancomycin | | | | | | | 12(100) |

## 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. 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 100.0% 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, gentamicyn is the best antibiotic for treating *Pseudomonas aeruginosa* with a sensitivity of 100.0%.[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* has 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 has a* good sensitivity to amikacin, which is 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 is* 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 states that *Acinetobacter baumannii* has a high level of resistance to third-generation cephalosporins, each of which is 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 betalactam 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 anibiotic.[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 suggest that there are two antibiotics that have good sensitivity against *Stenotrophomonas maltophilia* bacteria, namely minocycline and trimethoprim or sulfamethoxazole, minocycline can be an alternative if there is 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.

The high level of resistance to various antibiotics caused by various microbes requires supervision and regulation through the strengthening 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.

**LIMITATION**

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

**CONCLUSION**

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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**REFFERENCE**

1. Perhimpunan Dokter Paru Indonesia. Panduan umum praktik klinis penyakit paru dan pernapasan [Internet]. 2021st ed. Jakarta; Available from: https://pamki.or.id/download/buku-surveilans-resistansi-antibiotik-rumah-di-indonesia-tahun-2021/?wpdmdl=1467&refresh=6476044f85b1a168545595
2. Arnold DT, Hamilton FW, Morris TT, Suri T, Morley A, Frost V, et al. Epidemiology of pleural empyema in English hospitals and the impact of influenza. Eur Respir J. 2021 Jun;57(6):2003546.
3. Garvia veronica, paul manju. Empyema [Internet]. Treasure Island (FL): StatPearls Publishing LLC.; 2023. Available from: https://www.ncbi.nlm.nih.gov/books/NBK459237/
4. Hassan S, Ahmed Z, Agha S, Dasari V, Stewart J, Smolderen K, et al. The Updated Estimate Of Prevalence, Mortality And Hospital Length Of Stay In Patients With Parapneumonic Empyema In The US: Distribution Of Health Outcomes Across Various Demographic GroupS. CHEST. 2019 Oct 1;156(4):A425–6.
5. Lehtomäki A, Nevalainen R, Ukkonen M, Nieminen J, Laurikka J, Khan J. Trends in the Incidence, Etiology, Treatment, and Outcomes of Pleural Infections in Adults Over a Decade in a Finnish University Hospital. Scand J Surg. 2020 Jun;109(2):127–32.
6. Hassan M, Cargill T, Harriss E, Asciak R, Mercer RM, Bedawi EO, et al. The microbiology of pleural infection in adults: a systematic review. Eur Respir J. 2019 Sep;54(3):1900542.
7. Atif M, Naseem M, Sarwar S, Mukhtar S, Malik I, Hassan MRU, et al. Spectrum of Microorganisms, Antibiotic Resistance Pattern, and Treatment Outcomes Among Patients With Empyema Thoracis: A Descriptive Cross-Sectional Study From the Bahawal Victoria Hospital Bahawalpur, Punjab, Pakistan. Front Med. 2021 Aug 6;8:665963.
8. Sharma DA. Bacteriological Profile in Pleural fluid and its antibiotic susceptibility pattern among patients admitted in tertiary care teaching hospital in Solapur, Maharashtra. International Journal of Medical and Health Research.
9. Habibie YA, Hamdani K. Bacteriological Profile of Pleural Empyema: Surgical Management Plays an Important Role in Comprehensive Treatment. Aceh Experiences. Heart, Lung and Circulation. 2018;27:S559.
10. McCauley L, Dean N. Pneumonia and empyema: causal, casual or unknown. Journal of Thoracic Disease. 2015;7(6).
11. Anggraini D, Sholihin UH, Savira M, Djojosugito FA, Irawan D, Rustam RP. Prevalensi dan Pola Sensitivitas Enterobacteriaceae Penghasil ESBL di RSUD Arifin Achmad Pekanbaru. JKB. 2018 Feb 28;47–52.
12. Perhimpunan Dokter Spesialis Mikrobiologi (PAMKI). Surveilans resistensi antibiotik Rumah Sakit di Iindonesia Tahun 2021. 2021. 84 p.
13. Kawamura K, Nagano N, Suzuki M, Wachino J ichi, Kimura K, Arakawa Y. ESBL-producing

*Escherichia coli* and Its Rapid Rise among Healthy People. Food Safety. 2017;5(4):122–50.

14. Toka WD, Sjahril R, Hamid F. Antibiotic Susceptibility Pattern in Clinical Isolates of Pseudomonas aeruginosa. Nusantara Medical Science Journal. Nusantara Medical Science Journal. 2021;6(2):66–73.
15. Aulia A, Nurrokhman, Muhammad Mustafa. POLA KEPEKAAN Acinetobacter baumannii TERHADAP BEBERAPA ANTIBIOTIK DI RSUP DR. SOERADJI TIRTONEGORO PADA TAHUN 2012-2013 [Internet]. [Yogyakarta]: Universitas Gajah Mada; 2014. Available from: https://etd.repository.ugm.ac.id/penelitian/detail/80130
16. Anggraini D, Yulindra UG, Savira M. Prevalensi dan Pola Sensitivitas Antimikroba Multidrug Resistant Pseudomonas aeruginosa di RSUD Arifin Achmad. mkb. 2018 Mar;50(1):6–12.
17. Anggraini D, Kemal RA, Hadi U, Kuntaman K. The susceptibility pattern and distribution of blaOXA-23 genes of clinical isolate Acinetobacter baumannii in a tertiary hospital, Indonesia. J Infect Dev Ctries. 2022 May 30;16(05):821–6.
18. Kyriakidis I, Vasileiou E, Pana ZD, Tragiannidis A. Acinetobacter baumannii Antibiotic Resistance Mechanisms. Pathogens. 2021 Mar 19;10(3):373.
19. Ramirez D, Giron M. Enterobacter Infections [Internet]. Treasure Island (FL); 2023. Available from: https://www.ncbi.nlm.nih.gov/books/NBK559296/
20. Zhang H, Xu J, Xiao Q, Wang Y, Wang J, Zhu M, et al. Carbapenem-sparing beta-lactam/beta-lactamase inhibitors versus carbapenems for bloodstream infections caused by extended-spectrum beta-lactamase-producing Enterobacteriaceae: a systematic review and meta-analysis. International Journal of Infectious Diseases. 2023 Mar;128:194–204.
21. Gibb J, Wong DW. Antimicrobial Treatment Strategies for Stenotrophomonas maltophilia: A Focus on Novel Therapies. Antibiotics. 2021 Oct 9;10(10):1226.
22. Flamm RK, Shortridge D, Castanheira M, Sader HS, Pfaller MA. *In Vitro* Activity of Minocycline against U.S. Isolates of Acinetobacter baumannii-Acinetobacter calcoaceticus Species Complex, Stenotrophomonas maltophilia, and Burkholderia cepacia Complex: Results from the SENTRY Antimicrobial Surveillance Program, 2014 to 2018. Antimicrob Agents Chemother. 2019 Nov;63(11):e01154-19.
23. Anggraini D, Santosaningsih D, Kuntaman ., Ihsan M, Ridha SF. Description of Methicillin-resistant Staphylococcus aureus Infection at Arifin Achmad General Hospital, Riau Province from 2015-2019: In: Proceedings of the 1st Jenderal Soedirman International Medical Conference in conjunction with the 5th Annual Scientific Meeting (Temilnas) Consortium of Biomedical Science Indonesia [Internet]. Purwokerto, Indonesia: SCITEPRESS - Science and Technology Publications; 2020 [cited 2023 Sep 5]. p. 184–9. Available from: https://www.scitepress.org/DigitalLibrary/Link.aspx?doi=10.5220/0010489801840189

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