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ANTIMICROBIAL RESISTANCE PATTERN OF CLINICAL BACTERIAL ISOLATES AT THE EAST KALIMANTAN PROVINCIAL HEALTH LABORATORY, 2024

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Abstrak

Meningkatnya kejadian infeksi akibat bakteri resisten antimikroba telah menjadi masalah kesehatan masyarakat yang serius di Indonesia, sementara data mengenai pola resistansi di Kalimantan Timur, khususnya Samarinda, masih terbatas. Penelitian ini bertujuan menggambarkan pola resistansi antimikroba pada isolat bakteri klinis yang diperiksa di UPTD Laboratorium Kesehatan Provinsi Kalimantan Timur tahun 2024 melalui studi observasional deskriptif menggunakan data sekunder hasil kultur dan uji kepekaan antibiotik terhadap 201 isolat bakteri klinis periode Januari–Desember 2024. Analisis dilakukan secara deskriptif dalam bentuk tabulasi dan persentase. Dari seluruh isolat positif, 54,4% merupakan bakteri Gram-negatif dan 45,6% Gram-positif, dengan Escherichia coli sebagai bakteri yang paling banyak ditemukan (24,4%), diikuti Staphylococcus haemolyticus (7,0%) dan Pseudomonas aeruginosa (7,0%). Uji kepekaan menunjukkan bahwa E. coli memiliki sensitivitas tinggi terhadap meropenem (98%) dan amikasin (100%), sementara Staphylococcus aureus menunjukkan resistansi oksasilin sebesar 30,8% yang mengindikasikan keberadaan MRSA. Mekanisme resistansi utama meliputi produksi β-laktamase (21,7%), ESBL (40,6%), dan MRSA (37,7%). Temuan ini menunjukkan keberagaman pola kepekaan bakteri terhadap antibiotik di wilayah Samarinda dan memberikan gambaran awal yang penting bagi penguatan program surveilans resistansi antimikroba secara berkelanjutan.

Kata Kunci: Resistansi antimikroba, Isolat bakteri klinis, Pola kepekaan antibiotik, Samarinda

Abstract

The rising incidence of infections caused by antimicrobial-resistant bacteria has become a serious public health concern in Indonesia, yet data on resistance patterns in East Kalimantan, particularly in Samarinda, remain limited. This study aimed to describe antimicrobial resistance patterns among clinical bacterial isolates examined at the East Kalimantan Provincial Health Laboratory (UPTD Labkes) in 2024 through a descriptive observational design using secondary data from culture results and antibiotic susceptibility testing of 201 clinical isolates collected from January to December 2024. Data were analyzed descriptively using tabulation and percentage distribution. Of all positive isolates, 54.4% were Gram-negative bacteria and 45.6% were Gram-positive, with Escherichia coli being the most frequently identified species (24.4%), followed by Staphylococcus haemolyticus (7.0%) and Pseudomonas aeruginosa (7.0%). Susceptibility testing indicated that E. coli exhibited high sensitivity to meropenem (98%) and amikacin (100%), whereas Staphylococcus aureus demonstrated oxacillin resistance of 30.8%, suggesting the presence of MRSA. The predominant resistance mechanisms detected included β-lactamase production (21.7%), ESBL (40.6%), and MRSA (37.7%). These findings highlight substantial variability in bacterial susceptibility patterns in Samarinda and provide an essential baseline for strengthening continuous antimicrobial resistance surveillance efforts.

Keywords: *Antimicrobial resistance, Clinical bacterial isolates, Antibiotic susceptibility patterns, Samarinda*

INTRODUCTION

Antimicrobial resistance (AMR) has emerged as a serious global health threat, reducing the effectiveness of antibiotics and contributing to increased morbidity, mortality, and healthcare costs.[12] By 2050, AMR is projected to cause more than 10 million deaths annually if no effective mitigation strategies are implemented.[1] In developing countries such as Indonesia, the burden is amplified by high infectious disease prevalence and limited antibiotic stewardship.[3]

National reports indicate a significant rise in resistance among key bacterial pathogens over the past decade, particularly toward β-lactams, quinolones, and aminoglycosides.[3] Irrational antibiotic use and inconsistent implementation of stewardship policies further accelerate the spread of resistance.[4] Although several studies highlight the growing AMR burden in major Indonesian hospitals, systematic data from non-metropolitan regions remain limited, including for East Kalimantan.

Local laboratory observations in Indonesia have shown increasing resistance among Gram-negative bacteria such as *Escherichia coli*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa*.[3] However, in East Kalimantan particularly Samarinda published evidence on bacterial distribution and antibiotic susceptibility patterns is scarce. This gap is critical, as local AMR data are essential for informing empirical therapy and strengthening regional surveillance systems.

From a public health perspective, antibiogram data serve not only clinical purposes but also function as indicators of antibiotic governance and infection control performance.[5] High resistance to first-line antibiotics can directly influence treatment choices, length of hospitalization, and overall healthcare expenditures.[5] The lack of studies focusing on AMR patterns in provincial laboratories outside Java and Sumatra further underscores the need for localized investigations.[6]

Based on these considerations, this study aims to describe the antimicrobial resistance patterns of clinical bacterial isolates examined at the East Kalimantan Provincial Health Laboratory during January–December 2024. The analysis encompasses bacterial distribution (Gram-negative and Gram-positive), dominant species, antibiotic susceptibility profiles, and detected resistance mechanisms such as β-lactamase, ESBL, and MRSA. This research contributes to filling the evidence gap in AMR epidemiology at the provincial level and provides essential data to support local surveillance and antibiotic stewardship initiatives.

METHOD

This study employed a descriptive qualitative design to characterize antimicrobial resistance patterns among clinical bacterial isolates examined at the Provincial Health Laboratory of East Kalimantan from January to December 2024. This approach was selected to describe the resistance phenomenon naturally without variable manipulation, focusing on systematic interpretation of laboratory data, as outlined by Hall (2024)[15].

The data source consisted of secondary laboratory records automatically generated by the WHONET BD EpiCenter system. A total of 201 bacterial isolates were included, each having undergone species identification and antimicrobial susceptibility testing. Extracted variables included bacterial species, Gram classification, specimen type, antibiotics tested, and susceptibility interpretations susceptible, intermediate, resistant). Because data were digitally recorded without manual input, the risk of transcription error was minimized.

Data collection involved extraction by authorized laboratory personnel followed by verification procedures to ensure accuracy, including cross-checking specimen codes, examination dates, and automated validation outputs. Internal validation was performed through peer review by microbiology analysts and quality control officers. Data credibility, dependability, confirmability, and transferability were ensured according to the qualitative research quality criteria proposed by Tenny and Brannan (2022)[16].

Data were analyzed descriptively using Microsoft Excel through frequency distributions, percentages, and pivot tables to summarize bacterial distribution, antibiotic susceptibility patterns, and resistance mechanisms. Findings were then interpreted narratively to describe local resistance trends in East Kalimantan, following analytical guidance from Ayton (2023)[17]. All data were anonymized prior to analysis, and formal permission for data use was obtained from the Provincial Health Laboratory.

RESULT AND DISCUSSION

Table 1 shows that a total of 201 clinical specimens were culture-positive during January–December 2024, with urine being the most common specimen (47.8%), followed by pus (28.9%) and blood (11.4%). This distribution indicates that urinary tract infections and wound-related infections remain the primary sources of bacterial isolates submitted to the Provincial Health Laboratory, consistent with national findings[5].

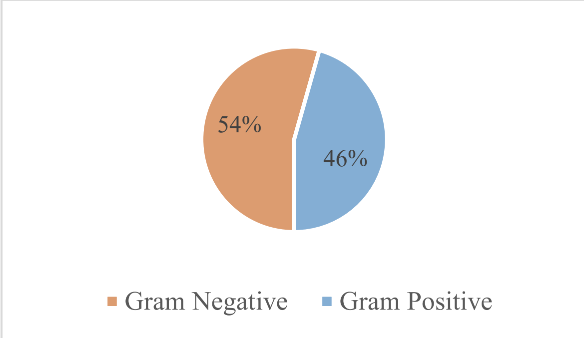
Table 1. Distribution of Clinical Specimen Types for Bacterial Culture Examination at the East Kalimantan Provincial Health Laboratory. 2024

Specimen Type	Number of Specimens (n)	Percentage (%)
Urine	96	47.8%
Pus	58	28.9%
Blood	23	11.4%
Vaginal Secretion	8	4.0%
Sputum	7	3.5%
Feces	5	2.5%
Urethral Secretion	3	1.5%
Cerebrospinal Fluid	1	0.5%
Grand Total	**201**	**100.0%**

Source: Secondary data from BD EpiCenter–WHONET system, East Kalimantan Provincial Health Laboratory, 2024.

Figure 2 shows that Gram-negative bacteria accounted for the majority of isolates (54.4%), predominantly *Escherichia coli* (24.4%), followed by *Klebsiella pneumoniae* and *Pseudomonas aeruginosa*. Gram-positive isolates (45.6%) were primarily *Staphylococcus aureus* and *Staphylococcus haemolyticus*. The predominance of *E. coli* in urine samples and *S. aureus* in pus specimens is consistent with typical infection patterns reported in Indonesia[12].

Based on the cumulative antibiogram in tables 3A and 3B, Gram-negative bacteria showed high susceptibility to amikacin (100%) and meropenem (≥98%) for E. coli, Klebsiella pneumoniae, and Pseudomonas aeruginosa. Conversely, high resistance was found to ciprofloxacin (0% sensitivity in E. coli and Klebsiella pneumoniae) and third-generation cephalosporins (cefotaxime, ceftazidime, cefepime ≈ 55% sensitivity). For the Gram-positive group, S. haemolyticus showed high sensitivity to vancomycin and linezolid (100%), but significant resistance to oxacillin (92.9%), confirming the potential for MR-CoNS (Methicillin-Resistant Coagulase-Negative Staphylococci). Meanwhile, Enterococcus faecalis showed 100% sensitivity to vancomycin, but total resistance to gentamicin and trimethoprim-sulfamethoxazole.



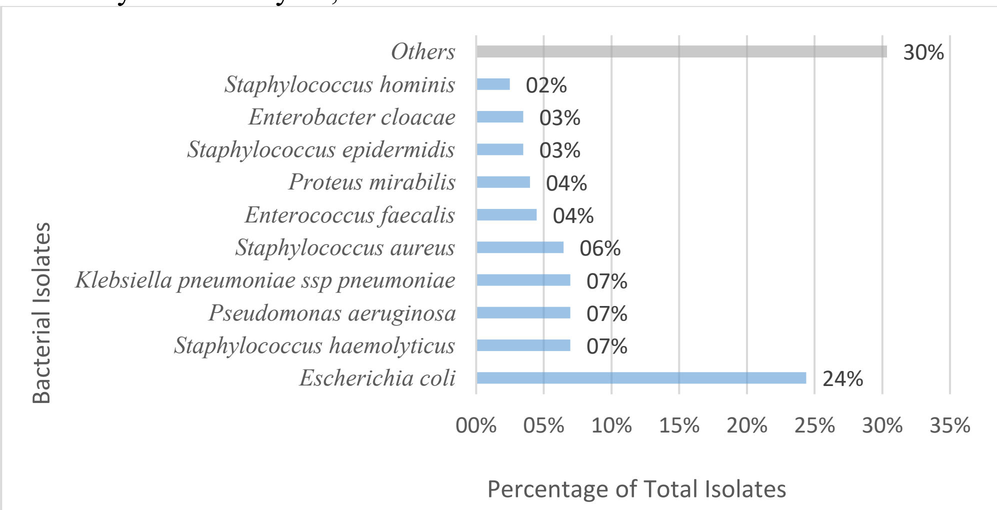


Figure 1. The Most Common Bacterial Isolates from Clinical Specimens at the East Kalimantan Provincial Health Laboratory, 2024

Table 3A. Cumulative Antibiogram (% Susceptible) — Gram-Negative Bacterial Isolates, East Kalimantan Provincial Health Laboratory, 2024

Bacteria	**Amikacin (%)**	**Gentamicin (%)**	**Cefotaxime (%)**	**Ceftazidime (%)**	**Meropenem (%)**	**Ciprofloxacin (%)**	**Trimethoprim–Sulfamethoxazole (%)**
Escherichia coli	100.0	73.5	55.1	55.1	98.0	0.0	52.1
Klebsiella pneumoniae ssp. pneumoniae	100.0	92.9	50.1	50.0	100.0	0.0	50.0
Pseudomonas aeruginosa	100.0	100.0	0.0	92.9	100.0	92.9	0.0

Table 3B. Cumulative Antibiogram (% Susceptible) — Gram-Positive Bacterial Isolates, East Kalimantan Provincial Health Laboratory, 2024

Bacteria	**Gentamicin (%)**	**Ciprofloxacin (%)**	**TrimethoprimSulfamethoxazole (%)**	**Vancomycin (%)**	**Linezolid (%)**	**Oxacillin (%)**	**Cefoxitin (%)**
Staphylococcus aureus	84.6	76.9	92.3	92.3	100.0	69.2	0.0

Staphylococcus haemolyticus	35.7	42.9	71.4	100.0	100.0	7.1	0.0
Enterococcus faecalis	0.0	55.6	0.0	100.0	55.6	-	0.0

Table 4. Distribution of Key Antimicrobial Resistance Mechanisms among Major Bacterial Isolates

Organism	Category	β-Lactamase (%)	ESBL (%)	MRSA (%)
Escherichia coli	*Gram Negative*	-	100.0	-
Klebsiella pneumoniae ssp. pneumoniae	*Gram Negative*	-	100.0	-
Staphylococcus aureus	*Gram Positive*	66.7	-	33.3
Staphylococcus haemolyticus	*Gram Positive*	7.1	-	92.9
Staphylococcus epidermidis	*Gram Positive*	66.7	-	33.3
Staphylococcus hominis	*Gram Positive*	33.3	-	66.7
Grand Total (%)		**21.7**	**40.6**	**37.7**

Note: "Grand Total (%)" represents the overall proportion of isolates showing each resistance mechanism, not cumulative or additive percentages.

β-lactamase = enzyme-mediated resistance to penicillin and cephalosporins;

ESBL = extended spectrum β-lactamase producers;

MRSA/MRCoNS = methicillin-resistant staphylococci.

Data source: BD EpiCenter – WHO-NET system, East Kalimantan Provincial Health Laboratory, January–December 2024.

Analysis of resistance mechanisms revealed that ESBL production was detected in 40.6 % of isolates, predominantly among E. coli and K. pneumoniae. β-lactamase production was found in 21.7 % of isolates, while MRSA/MR-CoNS accounted for 37.7 %. These findings highlight the significant burden of both ESBL-producing Enterobacterales and methicillin-resistant staphylococci in East Kalimantan. The presence of these mechanisms underscores the urgent need for strengthened antimicrobial stewardship and infection-control programs.

Overall, the resistance patterns observed in this study mirror national AMR trends, demonstrating declining susceptibility to commonly used antibiotics and high prevalence of ESBL and MRSA. The use of WHONET BD EpiCenter data allowed systematic characterization of local AMR patterns, providing essential evidence to guide empirical treatment decisions and inform regional surveillance efforts.

CONCLUSION

This study demonstrates that antimicrobial resistance (AMR) has become a significant public health concern in East Kalimantan, with resistance patterns closely reflecting national and global trends. Gram-negative bacteria predominated among clinical isolates, particularly *Escherichia coli*, while *Staphylococcus aureus* and *S. haemolyticus* were the most common Gram-positive species. Resistance to first-line antibiotics such as ampicillin, trimethoprim–sulfamethoxazole, fluoroquinolones, and third-generation cephalosporins was notably high, whereas carbapenems and key agents such as linezolid and vancomycin remained largely effective.

High proportions of ESBL-producing Enterobacterales, β-lactamase–mediated resistance, and methicillin-resistant staphylococci (MRSA/MR-CoNS) indicate that AMR in the region is already complex and requires strengthened surveillance and stewardship efforts. Findings from this study provide essential evidence for improving empirical antibiotic therapy, enhancing infection-prevention strategies, and supporting the development of standardized antibiotic policies within provincial healthcare facilities.

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