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The diversity of multidrug-resistant bacteria in bloodstream infection from Indonesian patients

Muhammad Evy Prastiyanto[1], Annisa Nurul Hikmah[1], Ayu Rahmawati Sulistyaningtyas[1*], Sri Darmawati[1], Afifah Khairunnisa[1], Budi Santosa[1], Haily Liduin Koyou[2], Ahmad Naqib[2], Mohd Nazil Salleh[2]

1- Department of Medical Laboratory Technology, Faculty of Nursing and Health Science, Universitas Muhammadiyah Semarang.

2- Medical Laboratory Technology, University College MAIWP International (UCMI), Malaysia

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ABSTRACT

Background: Multidrug-resistant bacteria cases are increasing globally, including in Indonesia. Bloodstream infection (Bacteremia) is a term that represents the presence of bacteria in a patient's blood. Blood cultures have become one of the most critically important and frequently performed tests in the clinical microbiology laboratory. **Aim:** Determining the prevalence of multidrug-resistant (MDR) bacterial isolates in bloodstream infection patients in Indonesia. **Methods**: Over three years (January 2020 to December 2022), a cross-sectional study was conducted at Tugurejo Hospital in Semarang, Indonesia, to collect 184 bacterial isolates from patients with bloodstream infections. The initial identification involves Gram staining and colony morphology assessment, biochemical assays, and antimicrobial susceptibility testing utilizing the VITEK®2 Compact system. **Results**: The most identified bacterial isolate was *Staphylococcus aureus* (73.9 %), followed by *Klebsiella pneumoniae* (10.9 %), *Acinetobacter* sp. (8.7 %), and *Escherichia coli* (6.4 %). The overall prevalence of MDR bacterial isolates was >80 %, with the highest resistance observed in *Staphylococcus aureus* to benzylpenicillin (91.2%), *Klebsiella pneumoniae*, and *Escherichia coli* to ampicillin (100 % and 91.9 %) and *Acinetobacter* sp. to Cefazolin (100 %). **Conclusion**: Our study revealed that the presence of MDR pathogens in Bloodstream Infection was noteworthy. The findings of this study would assist in the decision-making process regarding Bloodstream Infection treatment.

Introduction

Bloodstream infections (BSIs), commonly referred to as bacteremia, represent a critical public health concern due to their association with significant morbidity and mortality rates across diverse populations. These infections can arise from various sources, including healthcare-associated procedures, community-acquired infections, and the presence of indwelling medical devices, leading to severe complications such as sepsis and septic shock, which can result in multi-organ failure and death [1]. Research on bloodstream infections (BSIs) has been conducted across various countries, revealing significant variations in incidence rates and causative pathogens; for instance, a study in Finland reported an increase in BSI incidence from 150 to 309 cases per 100,000 population between 2004 and 2018, while a comprehensive analysis in Sweden highlighted a high incidence rate of 307 per 100,000 person-years from 2006 to 2019,

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* *Corresponding author:* Ayu Rahmawati Sulistyaningtyas
E-mail address: *ayurs@unimus.ac.id*

underscoring the global public health challenge posed by these infections and the need for continued surveillance and intervention strategies [2,3]

Several causes of BSIs are bacterial invasion through open wounds, needle punctures, hemodialysis equipment, catheters, ventilators, and contamination from the hospital environment [4]. Bacteremia is linked to the highest hospitalization death rates [5]. The Intensive Care Unit (ICU) is a high-risk area for bacteremia [6]. A study reported that 27 blood samples from ICU patients were bacteremia [7]. Applying a central venous catheter (CVC) for patients in the ICU is one of the main factors in bacteremia. Bacteremia from ICU patients is usually associated with other diseases such as pneumonia, urinary tract infection (UTI), skin and soft tissue infection, and surgical site infection [8].

Antibiotics are typically used to treat bacteremia. However, long-term and improper use of antibiotics can cause bacteria to become resistant to them and develop multidrug resistance (MDR), which makes treating infections more difficult [9]. The burgeoning crisis of MDR bacteria in Indonesia necessitates urgent attention, driven by the alarming rise in antibiotic misuse and its profound implications for public health [10,11]. Several studies explored herbal alternatives, such as mushrooms [12], plant [13–16] and bacteria from marine isolates [17,18].

Different environments have been shown to have different profiles of susceptibility and spectra of bacterial pathogens [11]. While antibiotic abuse in animals and humans rapidly speeds up the development of antibiotic resistance, antibiotic resistance occurs naturally over time. Certain antibacterial processes, such as those involved in the creation of cell walls, nucleic acids, ribosomal function, proteins, folate metabolism, and cell membrane function, are frequently inhibited, leading to the emergence of resistance to antibiotics. One of the main causes of antibiotic access and misuse is also a lax enforcement of antimicrobial laws. Antibiotics are generally over-the-counter in poor nations without a prescription [19,20]. The UK forecasts 10 million annual deaths [21]. The MDR patients, usually associated with immunocompromised conditions, who are easily targeted for hospital-acquired disease, have led to the further distribution of MDR [22,23]. Another study also reported 46 out of 58 isolates were primary bacteremia MDR (26%), and 58% secondary bacteremia [7].

The MDR organisms can cause severe and lethal human infections such as Methicillin-resistant *Staphylococcus aureus* (MRSA), vancomycin-resistant enterococci, and certain gram-negative bacilli. A study by [24,25] reported that *Enterococcus faecium, Enterobacter* sp., *Klebsiella pneumoniae,* and *Staphylococcus aureus* have been proposed for most nosocomial infections. Regarding gram-negative bacteria, the most common MDR bacteria are extended-spectrum β-lactamases (ESBL) [26]. Therapy for infections brought on by bacteria that produce ESBLs (extended-spectrum β-lactamases), which hydrolyze clinically significant drugs, is getting harder as these bacteria become more prevalent [27]. Millions of individuals are in danger of antibiotic-resistant diseases because, in many parts of Southeast Asia and other parts of the world, ESBL-producing bacteria are estimated to make up more than 50% of the population [28]. Coagulase-negative *Staphylococci* are commonly found in joints. On the other hand, *Escherichia coli, Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* are the most frequently found ESBL-producing Gram-negative bacteria [29,30]. This study aimed to look into the variety of multidrug-resistant bacteria that cause bacteremia in Central Java, Indonesia. This study also looked at rates of antibiotic resistance and the overall diversity of bacteria in the bloodstream according to age, gender, and gram strain.

Materials And Methods

Study site, period, and Sample collection

Bacteria identification from the blood samples of patients with bloodstream infections was conducted from January 2020 to December 2022 at the Microbiology Laboratory, Tugurejo Hospital, Semarang, Indonesia, Semarang, Indonesia. This study was accepted under EC number 120/KEPK.EC/VI/2023 from Tugurejo Hospital Ethics Committee. This study enrolled 184 patients in total suffering from bloodstream infections, all of whom had not received any antibiotic treatment. Blood specimens were collected according to the protocols, inoculated into blood agar and MacConkey agar (both from Merck, Darmstadt, Germany), and incubated overnight at 37±2°C.

Identification and antimicrobial susceptibility pattern analysis.

The isolated bacteria were identified preliminarily based on the type of colony, margin, elevation, size, shape, and color. Using the VITEK®2 Compact (bioMérieux, Craponne, France) equipment, all isolates were identified, and the resistance pattern was assessed. A total of 17 antibiotics were tested for Gram-negative bacteria, including aminopenicillins (AM: ampicillin, AMC: amoxicillin+clavulanic acid); 1st generation cephalosporin (CZO: cefazolin); 2nd generation cephalosporin (FAM: ampicillin+sulbactam); 3rd generation cephalosporins (CAZ: ceftazidime, CTX: cefotaxime, CRO: ceftriaxone); 4th generation cephalosporin (CEF: cefepime); aminoglycosides (GM: gentamicin); penicillins (PIP: piperacillin); monobactam (AZM: aztreonam); carbapenems (ETP: ertapenem; MEM: meropenem); fluoroquinolone (CIP: ciprofloxacin); glycylcycline (TGC: tigecycline); nitrofuran (NIT: nitrofurantoin); sulfonamides-trimethoprim (SXT: trimethoprim + sulfamethoxazole).

A total of 16 antibiotics were tested for Gram-positive bacteria, including penicillin (BENPEN: benzylpenicillin, OXA: oxacillin); 3rd generation cephalosporins (CTX: cefotaxime); aminoglycosides (GM: Gentamicin); fluoroquinolone (CIP: ciprofloxacin; LEV: levofloxacin, MXF: moxifloxacin); macrolides (ERY: erythromycin); lincosamides (DA: clindamycin); oxazolidinones (LNZ: linezolid); glycylcyclines (TGC: tigecycline); sulfonamides-trimethoprim (SXT: trimethoprim+ sulfamethoxazole); tetracyclines (TET: tetracycline); nitrofurans (NIT: nitrofurantoin); rifamycin (RIF: rifampicin); and glycopeptides (VAN: vancomycin)

Results

Distribution of the bacteria from Bloodstream infections

In this study, we found 73.92% (n=136) Gram-positive bacteria and 26.08% (n=48) Gram-negative bacteria. Our data indicated that *Staphylococcus aureus* (73.9 %), followed by *Klebsiella pneumoniae* (10.9 %), *Acinetobacter* sp. (8.7 %), and *Escherichia coli* (6.4 %) were the most common bacteria causing bloodstream infections **(Figure 1).**

Antibiotic resistance pattern of Gram-negative and Gram-positive bacteria

More than 90% of *Klebsiella pneumoniae*, and *Escherichia coli* showed high resistance to ampicillin (100% and 91.9%). While *Acinetobacter* sp. showed resistance to Cefazolin (100%) **(Table 1).** Over 70% of *Staphylococcus aureus* isolates showed high resistance to Penicillin (benzylpenicillin: 91.2%, and oxacillin: 79.4%)**.** In contrast, *Staphylococcus aureus* showed low resistance (less than 5%) to glycylcyclines (tigecycline), nitrofurans (NIT: nitrofurantoin), glycopeptides (VAN: vancomycin), and oxazolidinones (LNZ: linezolid) **(Table 2).**

Multidrug-resistance (MDR) profiles of isolates

MDR percentages were calculated for each bacterium based on 184 isolates. Overall, 82.6% (n=152) were MDR (resistant to three or more antibiotic classes), while 17.39%(n=32) had a non-MDR profile **(Table 3 and Table 4).** Out of the total Gram-negative isolates (n=48), *Klebsiella pneumoniae* (90%, n=18), *Acinetobacter* spp. (68.8%, n=11), and *Escherichia coli* (66.7%, n=8) had the highest MDR prevalence, contributing to 77.1% of all MDR cases (n=37) (Table 3). Among the total number of Gram-positive isolates (n=136), the MDR rate for *Staphylococcus aureus*. was the highest at 84.6% (n=115) **(Table 4)**

Table 1. Antibiotic resistance pattern of Gram-negative bacteria.

Bacteria	AM	FAM	PIP	CAZ	CZO	CTX	CRO	CEF	AZM	AMC	ETP	MEM	GM	CIP	TGC	NIT	SXT
Acinetobacter sp. (n= 16)	-	11	11	13	16	14	14	10	-	3	-	11	10	11	5	-	6
Percentage (%)	-	68.8	68.8	81.3	100.0	87.5	87.5	62.5	-	18.8	-	68.8	62.5	68.8	31.3	-	37.5
Escherichia coli (n= 12)	11	9	1	5	7	7	7	2	7	-	-	-	5	9	-	1	9
Percentage (%)	91.7	81.8	8.3	41.7	58.3	58.3	58.3	16.7	58.3	-	-	-	41.7	75.0	-	8.3	75.0
Klebsiella pneumonia (n=20)	20	16	9	15	16	16	16	7	16	1	1	1	14	12	3	15	15
Percentage (%)	100.0	80.0	45.0	75.0	80.0	80.0	80.0	35.0	80.0	5.0	5.0	5.0	70.0	60.0	15.0	75.0	75.0

Note: (-) were not examined.
aminopenicillins (AM: ampicillin, AMC: amoxicillin+clavulanic acid); 1st generation cephalosporin (CZO: cefazolin); 2nd generation cephalosporin (FAM: ampicillin+sulbactam); 3rd generation cephalosporins (CAZ: ceftazidime, CTX: cefotaxime, CRO: ceftriaxone); 4th generation cephalosporin (CEF: cefepime); aminoglycosides (GM: gentamicin); penicillins (PIP: piperacillin); monobactam (AZM: aztreonam); carbapenems (ETP: ertapenem; MEM: meropenem); fluoroquinolone (CIP: ciprofloxacin); glycylcycline (TGC: tigecycline); nitrofuran (NIT: nitrofurantoin); sulfonamides-trimethoprim (SXT: trimethoprim + sulfamethoxazole)

Table 2. Antibiotic resistance pattern of Gram-positive bacteria.

Bacteria	OXA	CTX	BENPEN	GM	CIP	MXF	LEV	TGC	TET	NIT	SXT	VA	ERY	LNZ	RIF	DA
Staphylococcus aureus (n= 136)	108	62	124	52	78	74	78	1	59	6	62	6	99	4	50	84
Percentage (%)	79.4	45.6	91.2	38.2	57.4	54.4	57.4	0.7	43.4	4.4	45.6	4.4	72.8	2.9	36.8	61.8

Penicillin (BENPEN: benzylpenicillin, OXA: oxacillin); 3rd generation cephalosporins (CTX: cefotaxime); aminoglycosides (GM: Gentamicin); fluoroquinolone (CIP: ciprofloxacin; LEV: levofloxacin, MXF: moxifloxacin); macrolides (ERY: erythromycin); lincosamides (DA: clindamycin); oxazolidinones (LNZ: linezolid); glycylcyclines (TGC: tigecycline); sulfonamides-trimethoprim (SXT: trimethoprim+ sulfamethoxazole); tetracyclines (TET: tetracycline); nitrofurans (NIT: nitrofurantoin); rifamycin (RIF: rifampicin); and glycopeptides (VAN: vancomycin)

Table 3. Gram-negative bacteria isolated from blood infections with an MDR pattern.

Bacteria	R0 (%)	RI (%)	R2 (%)	R3 (%)	R4 (%)	R5 (%)	R6 (%)	R7 (%)	R8 (%)	R10 (%)	MDR (%)
Acinetobacter spp	0 (0.0)	1 (6.3)	4 (25.0)	1 (6.3)	0 (0.0)	0 (0.0)	1 (6.3)	6 (37.5)	3 (18.8)	0 (0.0)	11 (68.8)
Escherichia coli	1 (8.3)	0 (0.0)	3 (25.0)	0 (0.0)	0 (0.0)	4 (33.3)	4 (33.3)	0 (0.0)	0 (0.0)	0 (0.0)	8 (66.7)
Klebsiella pneumoniae	0 (0.0)	1 (5.0)	1 (5.0)	1 (5.0)	2 (10.0)	1 (5.0)	4 (20.0)	2 (10.0)	7 (35.0)	1 (5.0)	18 (90.0)
Gram-negative bacteria	1 (2.1)	2 (4.2)	8 (16.7)	2 (4.2)	2 (4.2)	5 (10.4)	9 (18.8)	8 (16.7)	10 (20.0)	1 (2.1)	37 (77.1)

R0: Sensitive to every chosen lass of antibiotic; R1: Willing to resist at least one type of antibiotic; R2: Willing to resist at least two type of antibiotics; R3: Willing to resist at least three classes of antibiotics; R4: Willing to resist at least four classes antibiotics; R5: Willing to resist at least five classes antibiotics; R6: Willing to resist at least six classes antibiotics; R7: Willing to resist at least seven classes antibiotics; R8: Willing to resist at least eight classes antibiotics; R9: Willing to resist at least nine classes antibiotics; R10: Willing to resist at least ten classes antibiotics; MDR: Resistant to a minimum of three classes of antibiotics.

Table 4. Gram-positive bacteria isolated from blood infections with an MDR pattern.

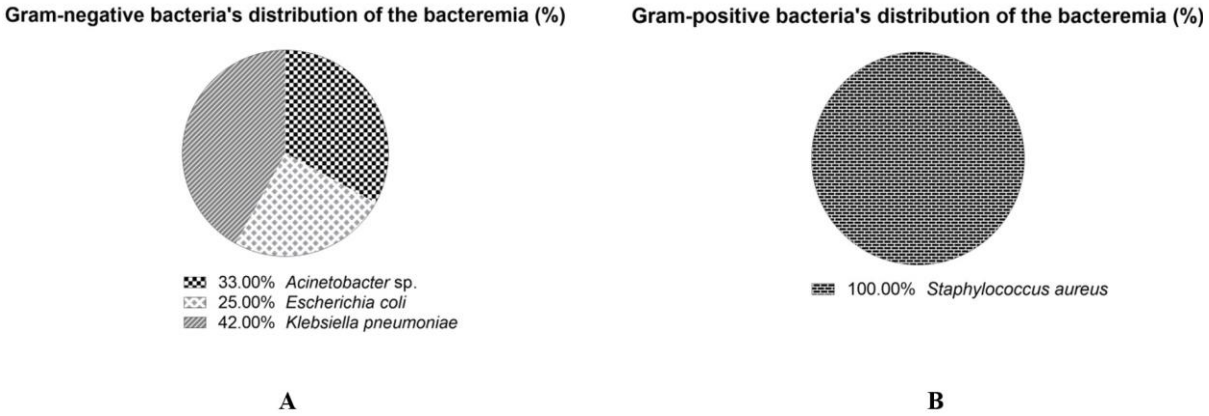
Bacteria	R0 (%)	RI (%)	R2 (%)	R3 (%)	R4 (%)	R5 (%)	R6 (%)	R7 (%)	R8 (%)	R9 (%)	R10 (%)	R11 (%)	R12 (%)	MDR (%)
Staphylococcus aureus	1 (0.7)	11 (8.1)	9 (6.6)	10 (7.4)	6 (4.4)	16 (12.5)	17 (12.5)	26 (19.1)	18 (13.2)	15 (11.0)	5 (3.7)	1 (0.7)	1 (0.7)	115 (84.6)

R0: Sensitive to every chosen lass of antibiotic; R1: Willing to resist at least one type of antibiotic; R2: Willing to resist at least two type of antibiotics; R3: Willing to resist at least three classes of antibiotics; R4: Willing to resist at least four classes antibiotics; R5: Willing to resist at least five classes antibiotics; R6: Willing to resist at least six classes antibiotics; R7: Willing to resist at least seven classes antibiotics; R8: Willing to resist at least eight classes antibiotics; R9: Willing to resist at least nine classes antibiotics; R10: Willing to resist at least ten classes antibiotics; MDR: Resistant to a minimum of three classes of antibiotics

Table 5. MDR bacteria distribution according to criteria.

		N	MDR	NONMDR
			(n) (%)	(n)
Age	0-9	65	51 (78.5)	14 (21.5)
	10-19	8	7 (87.5)	1 (12.5)
	20-29	12	8 (66.7)	4 (33.3)
	30-39	5	5 (100.0)	0 (0.0)
	40-49	18	16 (88.9)	2 (11.1)
	50-59	31	26 (83.9)	5 (16.1)
	≥60	45	39 (86.7)	6 (13.3)
Gender	Female	94	77 (81.9)	17 (18.1)
	Male	90	75 (83.3)	15 (16.7)
Gram Strain	Negative	48	37 (77.1)	11 (22.9)
	Positive	136	115 (84.6)	21 (15.4)

Figure 1. Distribution of the bloodstream infection, A: Gram-negative bacteria, B: Gram-positive bacteria



Discussion

This study has determined the variety of MDR bacteria in blood infections as well as the list of microorganisms frequently linked to blood infections in Semarang. Indonesia. The independent variables of this study are age, Gender, and Gram staining. According to our research. Bacteria from blood infection patients who are young, old, or teenagers have a higher likelihood of developing into MDR than bacteria from other age groups. Compared to bacteria-isolated children (0-9 years). isolates from patients aged 30-39 years have a higher likelihood of developing multidrug-resistant strains. Additionally, isolates of blood samples from adult patients revealed a comparatively greater proportion of MDR (86.7%).

In this study, 16 (33.3%) were found *Acinetobacter* sp. This percentage is higher than the test conducted by Carena et al (2020) on a cancer patient who reported *Acinetobacter* sp., 3.4% out of 394 isolates. The previous study reported that *Acinetobacter* sp. increased in bacteremia infection and pneumonia [31]. Antibiotic-resistant bacteria naturally develop resistance to medicines. which means that their existence can be detrimental to civilization [32]. Multiple isolates in the current investigation were discovered to be MDR to more than three classes of antibiotics. there are 11 out of 16 isolates (*Acinetobacter* sp.), 8 out of 12 isolates (*Escherichia coli*), and 18 out of 20 isolates (*Klebsiella pneumoniae*). A pattern of MDR of Amoxicillin/ Clavulanic Acid (18.8%) in total MDR isolates of *Acinetobacter* sp., 3 of 16 total isolates. *Acinetobacter* is a gram-negative coccobacillus pathogen that can be found frequently in hospitals and other healthcare settings [33]. The natural reservoirs and sites of colonization of *Acinetobacter* sp. are human skin and mucous membranes, and they are also able to survive in a dry environment.

The types of infections were suppurative infections in any organ system and ocular infections. septic arthritis, respiratory infections, soft tissue infections, abscesses, and sepsis [34]. *Acinetobacter* bacteria were resistant to three or more antibiotic classes. including imipenem, Doripenem, meropenem (type 3 carbapenems), and ampicillin-sulbactam [33,35]. Our results also showed *Acinetobacter* sp. strain MDR against the type of antibiotic cephalosporin (83.8%). Carbapenem (68.8%). and Penicillin (68.8%).

Escherichia coli isolates possessed one or more serum resistance-related genes [36] . The pattern of multidrug resistance in this study showed a high percentage of *Escherichia coli* resistance to ampicillin (91.9%) was the highest percentage of other antibiotics, such as Ampicillin/sulbactam (81.8%), Trimethoprim/Sulfamethoxazole (75.0%) and Ciprofloxacin (75.0%), sulfamethoxazole-trimethoprim (45.8%). ampicillin-sulbactam (56.3%). and ciprofloxacin (35.4%) is the same as the result reported in the previous study [36]. The MDR *Escherichia coli* isolates are very common in many countries and are responsible for a range of infections of high severity and difficult to treat. *Escherichia coli* is the Gram-negative bacterium most frequently isolated in adult patients with bacteremia [37]. However, in general, *Escherichia coli* is a normal flora of the commensal gut microbiota. Moreover. some strains can cause extraintestinal infections due to specific virulence factors (VFs) [38].

Klebsiella sp. site of colonization is found in the gastrointestinal and respiratory tracts of humans. The transmission paths are usually through ingestion of contaminated water and food. droplets. and contact. Types of infection, such as sepsis. pneumonia. UTIs. intraabdominal infections. and meningitis [34]. In 2005. *K. pneumoniae* was the third most prevalent blood infection [39]. In a study conducted according to pathogens and geographical distribution, 1882 blood infections in the world were caused by *Klebsiella pneumoniae*, including 150 cases of blood infection in Asia, 551-561 cases in Europe, and 335 cases in America [40]. In this study, we found showed there are 20 blood samples contaminated with *Klebsiella pneumoniae* (41.7%)**.** and MDR bacteria, 18 isolates (90.0%). Based on the study results. antibiotics ertapenem is very sensitive to gram-negative bacteria except *Klebsiella pneumoniae*. Table 2 showed that Ampicillin had the highest percentage (100%) compared to other types of antibiotics. In addition. the MDR pattern of *Klebsiella pneumonia* in this study showed that 80.0% of isolates were MDR to Ampicillin/Sulbactam. Aztreonam and Cephalosporin antibiotics (Cefazolin, Cefotaxime, and Ceftriaxone). Out of 15 isolates (75%), *Klebsiella pneumoniae was* resistant to Ceftazidime. Nitrofurantoin and Trimethoprim/Sulfamethoxazole. Results showed that *Klebsiella pneumonia*e was also resistant to Ciprofloxacin (60.0%). 9 isolates resistant to Piperacillin (45.0%). 7 isolates resistant to Cefepime. 3 isolates were resistant to tigecycline. and only 1 isolate (5.0%) resistant to Amoxicillin/ Clavulanic Acid and Carbapenem group antibiotics (ertapenem dan meropenem). In total, 152 blood samples from patients in Saudi Arabia were positive infected *K. pneumoniae*. 53 isolates were ESBL-strain (34.87%), 55 isolates were Carbapenem-resistant (36.18%), and 44 isolates were susceptible (28.95%) [41].

Another gram-negative bacterium. *Acinetobacter* sp. is more sensitive to Amoxicillin/ Clavulanic Acid antibiotics, with an MDR of 3%, which has an antibiotic resistance rate of 100%. The Piperazine antibiotic group was sensitive to *Escherichia coli* with an MDR percentage of 8.3%. compared to *Acinetobacter* sp., which has an MDR figure of 68.8%. According to multiple earlier studies. *Staphylococcus aureus* and *Klebsiella pneumonia*e were the most common pathogens linked to blood infections [42]. We found there are 136 isolates containing *Staphylococcus aureus* in blood specimens**.** while 115 isolates were MDR (84.6%). These results were in agreement with those who found that *S. aureus* represents 52 out of 207 isolates in the blood (25.1%) [43]. *S. aureus* was a common cause of blood infection, and the population of incidents of 50: 100.000 population, with a mortality rate of 20-30% [44]. Bacteria *S. aureus* were normally present in adults' skin and the mucosa of the anterior portion of the nose and pharynx. In some countries. methicillin-resistant *Staphylococcus aureus* (MRSA) infection is up to 50% in the most common cases of vancomycin and teicoplanin [45].

Bacteremia is strongly associated with an increased risk of invasive blood infections, particularly in cancer patients, bone marrow transplant recipients, and individuals with compromised immune systems. The MDR pattern has observed that Tigecycline (TGC) was the most

potent antibiotic in terms of sensitivity against *Staphylococcus aureus* and other gram-positive bacterial species. There were no other bacteria noted in our research. But still. 1 (0.7%) *Staphylococcus aureus* was tigecycline-resistant. Furthermore. it was discovered that 91.2% of *Staphylococcus aureus* had the highest level of resistance to benzopenicillin. The antibiotic pattern showed that 78.4% of isolates were resistant to ampicillin. 45.6% isolates resistant to Ampicillin/Sulbactam. there were 38.2% isolates resistant to gentamicin. 56.4% isolates are resistant to Fluoroquinolones. 45.6% isolates resistant to Trimethoprim/Sulpfamethoxazole. there were 36.8% isolates resistant to Rifampicin. 61.8% isolates are resistant to Clindamycin. 72.8% isolates are resistant to Erythromycin. 44.4% isolates resistant to Vancomycin and Nitrofurantoin, and only 1.5% isolates resistant to Quinupristin-dalfopristin (GDA). Recent research from Colombia and India has produced comparable results. In other countries. 255 bloodstream infections in Argentina were caused by Carbapenemase-producing Enterobacterales (CPE) (21%), which were mostly *Klebsiella pneumoniae* carbapenemases (KPC) (83%) [46].

This study has shown the variety of MDR related to blood infections and provided a list of prevalent bacteria found in blood infections in Semarang. Indonesia. The data was analyzed based on variable gram staining. age. and gender. According to age**,** children (0-9 years) represent the highest proportion (35.3%) of patients with MDR bacteria from blood infections, followed by the elderly (≥60 years), which is 24.5%. and patients 50-59 years (16.8%). The data showed that isolates from people aged 30-39 were more prone to become multidrug-resistant (100%) than bacteria from other age groups. Moreover. blood samples from patients aged 40-49 years also showed a relatively high percentage (88.9%). The lowest percentage of MDR bacteria based on age was from patients 20-29 years (66.7%). Elderly patients were at high risk of nosocomial infections [47].

The distribution of patients with MDR bacteria from blood infection according to gender is shown in Table 5. Out of 184 isolates, 94 (51.1%) were from females and 90 (48.9%) from males. Similar findings were reported in another study. Characteristic bacteremia among 84 hospitalized patients in Arizona, females (69.0%) are more likely to suffer bacteremia than males (31.0%) [48]. According to the Gram stain. Our study showed that gram-positive bacteria have a higher percentage (73.92%) than gram-negative bacteria (26.08%). In addition, compared to gram-negative bacteria (77.1%), the percentage of MDR gram-positive bacteria (84.6%) was higher.

In our study, the most frequently isolated bacteria from blood infection samples were *Staphylococcus aureus, Escherichia coli, Acinetobacter* sp., and *Klebsiella pneumoniae.* These isolates show a high percentage of resistance to most commercial antibiotics, this will be a serious problem that needs attention. Eliminating the sources of resistance development for multidrug-resistant bacteria is essential to stop their spread. Our study had limitations despite some noteworthy findings, such as its reliance on data from a diagnostic facility in Semarang, Indonesia. Future studies aimed at preventing MDR in bloodstream infections must address these constraints.

Conflict of interest

There is no conflict of interest

Funding statement

None

Data availability

All data generated or analyzed during this study are included in this puplished article.

Authors' contribution

All authors made significant contributions to the work presented, including study design, data collection, analysis, and interpretation. They also contributed to the article's writing, revising, or critical evaluation, gave final approval for the version to be published.

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