



Bioscientia Medicina: Journal of Biomedicine & Translational Research

Journal Homepage: www.bioscmed.com

Overview of Bacterial Profile of Bloodstream Infections in the Intensive Care Unit (ICU): Single Center Observational Study at Dr. M. Djamil General Hospital, Padang, Indonesia

Rara Puspita Impelleren¹, Dwi Yulia^{2*}, Yoshie Anto Chicamy²

¹Clinical Pathology Resident, Department of Clinical Pathology, Faculty of Medicine, Universitas Andalas, Padang, Indonesia

²Departement of Clinical Pathology Laboratory Medicine, Faculty of Medicine, Universitas Andalas/Dr. M. Djamil General Hospital, Padang, Indonesia

ARTICLE INFO

Keywords:

Blood cultures
Bloodstream infections
Bacteria

*Corresponding author:

Dwi Yulia

E-mail address:

dwiyulia@med.unand.ac.id

All authors have reviewed and approved the final version of the manuscript.

<https://doi.org/10.37275/bsm.v8i8.1055>

ABSTRACT

Background: Bloodstream infection (BSI) is a condition characterized by positive blood cultures in patients who have systemic infections. Bloodstream infections have developed into a threat to public health worldwide with high mortality rates in intensive care settings. This study aims to determine the bacterial profile of BSI in the intensive care unit (ICU) of Dr. M. Djamil General Hospital Padang. **Methods:** This study is a retrospective descriptive study with a cross-sectional design from secondary data at the Microbiology and Medical Records Installation Laboratory of Dr. M. Djamil General Hospital Padang. All blood samples from patients aged ≥ 18 years in the ICU who are suspected of being infected will be cultured and identified with VITEK 2 in 2022. **Results:** A total of 243 blood samples consisted of 126 men (52%) and 117 women (48%) with the largest age range being 41-60 years (48%). The diagnosis of BSI was found in 94% with the most common comorbidities being malignancy (42%) and stroke (15%). The most common bacterial bloodstream infections were found in the ICU of Dr. M. Djamil General Hospital Padang., namely Gram-positive bacteria (66%) and coccus (66%). The most common type of bacteria identified with the VITEK 2 automatic tool is *Staphylococcus hominis*. Multidrug-resistant organisms (MDRO) found in this study were 8% with the most common causes, namely extended spectrum B-lactamase (ESBL). Blood samples in this study found bacteria due to contamination by 38%. **Conclusion:** The BSI bacterial profile found was mostly in the ICU of Dr. M. Djamil General Hospital Padang is a Gram-positive bacterium, coccus-shaped, *Staphylococcus hominis* and ESBL. Blood cultures found bacteria contaminated by 38%.

1. Introduction

Bloodstream infection (BSI) is a condition characterized by positive blood cultures in patients who experience symptoms of systemic infection, either primary (from an unidentified source) or secondary (from an identified source).¹ Bloodstream infections have developed into a threat to public health worldwide. Bloodstream infections globally occur in 31.5 million people with deaths reaching 5.3 million per year.² Research conducted in intensive care units

in 16 countries on the Asian continent, including Indonesia, showed that the patient mortality rate due to BSI reached 44.5%.⁶ The results of data observations at Dr. M. Djamil General Hospital Padang showed that there were 145 BSI patients treated in the Medicine Department in the period January 2020 to December 2021.³ The diagnosis of BSI can pose special challenges because older adults often present with nonspecific signs and symptoms of infection such as weakness, anorexia, malaise, or confusion, which can

be considered a manifestation of underlying comorbidity. The most common clinical symptom of BSI, fever, may be absent in one-third of patients with BSI. This reflects age-related changes both in body temperature regulation and in the biological response to infection.^{2,4}

The clinical manifestations of atypical BSI, apart from aging, are also influenced by other factors. Prolonged treatment of systemic inflammatory diseases and tumors using glucocorticoid and immunosuppressant drugs can blunt the biological response to infection and attenuate the clinical manifestations of BSI. Symptoms of systemic inflammation and other comorbidities such as neoplasms or chronic respiratory failure can mimic fever, dyspnea, or other symptoms of infection. This may prevent physicians from recognizing the possible development of BSI and mistakenly attributing the clinical picture to an underlying medical condition, thereby delaying the administration of adequate antimicrobial treatment.⁵ Another important risk factor for the development of in-hospital BSI is the placement of a central venous catheter (CVC) and ventilator. Device type indwelling Others that are frequently used in patients and can be a predisposing factor for the development of BSI are patients with prosthetic joints, prosthetic heart valves, cardiac electronic devices, and urinary catheters.⁶ *Staphylococcus aureus*, species *Enterococcus*, *Escherichia coli*, *Coagulase Negative Staphylococci* (CoNS), *Klebsiella pneumoniae* and *Klebsiella oxytoca*, *Pseudomonas aeruginosa*, *Acinobacter baumannii*, species *Enterobacter*, species *Proteus*, and species *Bacteroides* are some pathogens involved in 80-87% Healthcare Associated Infections (HCAI) and 16-20% of these pathogens are included in the phenotype multidrug-resistant (MDR). Blood culture is considered as gold standard in establishing a diagnosis of BSI at this time.⁵ Antimicrobial therapy appropriate to the most likely pathogen should be administered early and empirically while awaiting blood culture results. Empiric antimicrobial therapy should be reassessed once blood culture results are

available (usually within 48-72 hours of blood draw)¹⁰. This study aims to assess the characteristics of BSI bacteria in the ICU of Dr. M. Djamil General Hospital Padang.

2. Methods

This study is a retrospective descriptive study with a cross-sectional design that aims to determine the bacterial profile of bloodstream infections in the ICU of Dr. M. Djamil General Hospital Padang. The research was carried out at the Microbiology and Medical Records Installation Laboratory of Dr. M. Djamil General Hospital Padang. The study population was all blood samples from patients aged ≥ 18 years in the ICU at Dr. M. Djamil General Hospital Padang, who were suspected of being infected, were then cultured and identified using VITEK 2. The sample was part of the population that met the inclusion and exclusion criteria. Inclusion criteria were blood samples from BSI patients aged ≥ 18 years with positive blood culture results who were treated in the ICU at Dr. M. Djamil General Hospital Padang from January 2022 to December 2022. Exclusion criteria are taking blood samples in one place, the results of identifying bacteria that come out of an automatic tool using non/low reactive and unidentified and incomplete data.

Research specimens are blood culture samples carried out in a microbiology laboratory. Blood culture examination using the VITEK 2 automatic tool. Research data was obtained from two secondary data, namely medical record data and microbiology laboratory data. Data from medical records to obtain data on the characteristics of research subjects including gender, age, diagnosis of bloodstream infections, and comorbidities. Data on Gram staining, bacterial morphology, pathogens/contaminants, bacterial identification, and MDRO (multiple drug resistance) were obtained from microbiology laboratory data. The analysis data is processed descriptively to describe the germ profile of bloodstream infections. Data is processed and presented in the form of graphs and tables.

3. Results

The characteristics of the research subjects for bacterial bloodstream infections in the ICU who were included in this study can be seen in Table 1. The characteristics in Table 1 show that the majority of research subjects found bacteria in bloodstream

infections in the ICU of Dr. M. Djamil General Hospital Padang aged 41 - 60 years (49%) with male gender (52%). The diagnosis of bloodstream infection was found in medical record data in 229 cases (94%). The most common comorbidities found were malignancies in 130 cases (42%).

Table 1. Characteristics of BSI bacterial research subjects in the ICU of Dr. M. Djamil General Hospital Padang.

Characteristics	Frequency	Percentage
Age (years)		
18-40	52	21
41-60	118	49
>60	73	30
Gender		
Male	126	52
Female	117	48
Diagnosis of BSI		
Yes	229	94
No	14	6
Comorbid		
Pneumonia	7	2
ARDS	42	13
CKD	8	3
DM type 2	30	10
Hypertension	12	4
Malignancy	130	42
Liver disorders	10	3
Stroke	47	15
ROSC	3	1
MOFS	3	1
Infection	17	5
COPD	2	1
No comorbidities	2	1

Table 2 shows that there are 150 samples of pathogenic bacteria. There were 99 samples (66%) classified as Gram-positive bacteria. These bacteria have thick and stiff cell walls, making them easy to stain with Gram stain. For example, *Staphylococcus aureus* and *Streptococcus pneumoniae* bacteria. There were 51 samples (34%) that were classified as Gram-negative bacteria. These bacteria have thinner and more flexible cell walls, making them difficult to stain with Gram stain. For example, *Escherichia coli* and *Salmonella typhi* bacteria. There were 51 samples (34%) that had bacillus morphology, namely rod-shaped. Bacilli are generally Gram-positive bacteria, but there are also some Gram-negative bacilli. For

example, *Bacillus subtilis* and *Escherichia coli* bacteria. There were 99 samples (66%) that had coccus morphology, namely round shape. Coccus are generally Gram-positive bacteria, but there are also some Gram-negative coccus. For example, *Staphylococcus aureus* and *Streptococcus pneumoniae* bacteria. There are 93 bacteria, apart from 150 pathogenic bacteria, which are categorized as contaminants. Contaminants are microorganisms that are not expected to be present in the sample and can affect the analysis results. In this study, contaminants likely came from the environment or other patient samples.

Table 2. Overview of bacterial types, morphology, and status.

Variable	Frequency	Percentage
Types of bacteria		
Gram-positive	99	66
Gram-negative	51	34
Morphology		
Basil	51	34
Coccus	99	66
Status		
Pathogens	150	62
Contaminants	93	38

Table 3 shows that 150 samples were analyzed and 35 different types of bacteria were identified. There were 35 different types of bacteria isolated from the samples, indicating a high level of bacterial diversity in this study. *Staphylococcus lugdunensis* (35 isolates, 23.3%) was the most dominant bacteria, followed by *Staphylococcus haemolyticus* (10 isolates, 6.7%), *Staphylococcus hominis* (16 isolates, 10.7%), and *Escherichia coli* (9 isolates, 6.0%). Other bacterial isolates found in this study included *Achromobacter denitrificans*, *Achromobacter xylosoxidans*, *Acinobacter baumannii*, *Bordetella hinzii*, *Chromobacterium violaceum*, *Citrobacter freundii*, *Citrobacter koseri*, *Dermacoccus nishinomiyaensis*, *Elizabethkingia meningoseptica*, *Enterobacter cloacae* complex, *Enterococcus faecalis*, *Enterococcus faecium*, *Klebsiella pneumoniae*, *Kocuri a kristinae*, *Kocuria rosea*, *Micrococcus luteus*, *Pseudomonas alcaligenes*, *Pseudomonas aeruginosa*, *Pseudomonas fluorescens*, *Sphingomonas paucimobilis*, *Staphylococcus aureus*, *Staphylococcus capitis*, *Staphylococcus chromogenes*, *Staphylococcus cohnii urealyticum*, *Staphylococcus epidermidis*, *Staphylococcus sapro phyticus*, *Staphylococcus warneri*, *Staphylococcus xylosus*, *Streptococcus thoraltensis*, and *Yersinia pseudotuberculosis*. The findings of this study indicate that *Staphylococcus lugdunensis* is the most frequently isolated bacteria from the clinical samples analyzed. This can be important information for

choosing the right antibiotic in the treatment of infections caused by this bacteria.

Table 4 shows that 150 samples were analyzed and 12 samples (8.0%) were identified as MDRO. ESBL (extended spectrum beta lactamases): The most common type of MDRO found (6 samples, 4.0%). ESBL is an enzyme produced by bacteria and makes it resistant to broad-spectrum beta-lactam antibiotics, including penicillins and cephalosporins. CRE (carbapenem resistant enterobacterales): Found in 5 samples (3.3%). CRE is a bacterium that is resistant to carbapenems, broad-spectrum antibiotics that are a last resort for the treatment of severe gram-negative bacterial infections. MRSA (Methicillin Resistant *Staphylococcus aureus*): Found in 1 sample (0.7%). MRSA is a strain of *Staphylococcus aureus* that is resistant to methicillin, an antibiotic commonly used to treat staphylococcal infections. VRE (vancomycin resistant *Enterococci*): Not found in analyzed samples (0.0%). VRE is an enterococcal bacterium that is resistant to vancomycin, a glycopeptide antibiotic used to treat severe gram-positive bacterial infections. The findings of this study indicate that the prevalence of MDRO in the analyzed clinical sample was 8.0%. This shows that infections caused by MDRO can be a serious health problem because this bacteria is resistant to many commonly used antibiotics.

Table 3. Characteristics of bacterial isolates.

Bacterial isolation	Frequency	Percentage
<i>Achromobacter denitrificans</i>	1	0.70%
<i>Achromobacter xylosoxidans</i>	1	0.70%
<i>Acinobacter baumannii</i>	4	2.70%
<i>Bordetella hinzii</i>	3	2.00%
<i>Chromobacterium violaceum</i>	1	0.70%
<i>Citrobacter freundii</i>	1	1.10%
<i>Citrobacter koseri</i>	1	0.70%
<i>Dermacoccus nishinomiyaensis</i>	2	1.30%
<i>Elizabethkingia meningoseptica</i>	1	0.70%
<i>Enterobacter cloacae</i> complex	5	3.30%
<i>Enterococcus faecalis</i>	1	0.70%
<i>Enterococcus faecium</i>	5	3.30%
<i>Escherichia coli</i>	9	6.00%
<i>Klebsiella pneumoniae</i>	9	6.00%
<i>Kocuria kristinae</i>	6	4.00%
<i>Kocuria rosea</i>	1	0.70%
<i>Micrococcus luteus</i>	3	2.00%
<i>Pseudomonas alcaligenes</i>	3	2.00%
<i>Pseudomonas aeruginosa</i>	4	2.70%
<i>Pseudomonas fluorescens</i>	5	3.30%
<i>Sphingomonas paucimobilis</i>	2	1.30%
<i>Staphylococcus aureus</i>	1	0.70%
<i>Staphylococcus capitis</i>	1	0.70%
<i>Staphylococcus chromogenes</i>	1	0.70%
<i>Staphylococcus cohnii urealyticum</i>	1	0.70%
<i>Staphylococcus epidermidis</i>	7	4.70%
<i>Staphylococcus haemolyticus</i>	10	6.70%
<i>Staphylococcus hominis</i>	16	10.70%
<i>Staphylococcus lugdunensis</i>	35	23.30%
<i>Staphylococcus saprophyticus</i>	1	0.70%
<i>Staphylococcus warneri</i>	1	0.70%
<i>Staphylococcus xylosus</i>	3	2.00%
<i>Streptococcus thoraltensis</i>	4	2.70%
<i>Yersinia pseudotuberculosis</i>	1	0.70%
Total	150	100.0%

Table 4. Overview of multiple drug-resistant organisms.

Variable	Frequency	Percentage
MDRO		
CRE (Carbapenem Resistant Enterobacterales)	5	3.3
MRSA (Methicillin Resistant <i>Staphylococcus aureus</i>)	1	0.7
ESBL (Extended Spectrum Beta Lactamases)	6	4.0
VRE (Vancomycin Resistant <i>Enterococci</i>)	0	0.0
Number of MDROs	12	8.0
Non-MDRO		
Number of Non-MDROs	138	92.0
Total	150	100.0

4. Discussion

The characteristics of the subjects in this study were assessed using descriptive analysis. The characteristics assessed were age, gender, BSI diagnosis, and comorbidities. Statistical analysis shows that the majority of patients in the ICU who

have positive blood culture results are aged 41-60 years. Martinez and Wolk's research also found that age over 40 years was a risk factor for BSI and the worst outcomes occurred in patients over 85 years of age due to the presence of previous comorbidities and a reduced immune system.⁷ The gender of patients

with positive blood cultures in this study was predominantly male (52%). Bloodstream infections occur more often in men than women.⁷ Smith et al research also found that cases of BSI with positive cultures were mostly experienced by men (58%)⁵. Positive blood culture examination in patients in the ICU at Dr. M. Djamil General Hospital Padang found that the most common diagnosis was bloodstream infection at 94%. The diagnostic approach to identify BSI is a microbiological procedure. Blood culture is considered as gold standard in establishing the current diagnosis of BSI. Blood cultures were obtained from a minimum of two sites to minimize contamination. A blood culture examination should be carried out before administering antibiotics.^{8,9} The most common comorbidities found in cases of bloodstream infections in the ICU at Dr. M. Djamil General Hospital Padang are malignancy and stroke. Comorbidities and complications can be predisposing factors for BSI. The use of cytotoxic drugs in cancer patients is largely responsible for suppressing the patient's immune system and making them susceptible to BSI.⁷ Bedridden patients with stroke are also at high risk of developing skin ulcers, with infection superimposed continued by Gram-positive bacteria and Gram-negative bacteria.¹⁰

Gram staining results were often found in blood cultures of patients in the ICU at Dr. M. Djamil General Hospital Padang is a Gram-positive coccus bacterium. Gram-positive bacteria have increased in prevalence with increasing age in BSI cases.¹¹ Studies conducted in Southeast Asia and China have similar distributions of Gram-positive and Gram-negative bacteria in the etiology of bloodstream infections in adults.² Saavedra et al research found that the most common bacteria causing BSI were Gram-positive with a prevalence of 216 cases while Gram-negative was 187 cases.⁵ In contrast to Martinez and Wolk's research which found that almost 90% of the etiology of BSI was caused by Gram-negative bacilli.⁷ Kim Research *et al* (2021) also found that there were more Gram-negative bacteria (68.9%) than Gram-positive bacteria (26.4%).¹² The most common bacteria

identified in this study were: *Staphylococcus hominis* (23%) and *Staphylococcus haemolyticus* (11%). The results of this study are in line with previous studies, the most common cause of BSI bacteria is Gram-positive coccus, but the species are different.¹³⁻¹⁵

Research findings show a high prevalence of Gram-positive coccus bacteria in blood cultures of ICU patients at Dr. M. Djamil General Hospital Padang is a significant health issue. This phenomenon deserves comprehensive analysis to understand the underlying factors and their implications for clinical practice. The group of gram-positive bacteria is characterized by thick and stiff cell walls, composed of peptidoglycan and teichoic acid. This structure allows retention of Gram dye, producing a purple color in microscopic preparations. Examples of Gram-positive coccus bacteria commonly found in bloodstream infections (BSI) are *Staphylococcus aureus*, *Streptococcus pneumoniae*, and *Enterococcus faecalis*. Various factors contribute to the increased prevalence of Gram-positive cocci in elderly patients with BSI. First, a weakened immune system with age makes individuals more susceptible to infections. Second, comorbidities that often accompany old age, such as heart disease, diabetes, and chronic lung disease, can worsen the body's ability to fight infections. Third, excessive use of broad-spectrum antibiotics can trigger drug resistance and encourage the growth of Gram-positive bacteria. Gram-positive coccus bacteria are the main causative agents of BSI, especially in patients with sepsis. Mechanisms of pathogenicity are diverse, including direct invasion of the bloodstream, toxin production, and activation of systemic inflammatory responses. Common symptoms of BSI include fever, chills, tachycardia, and hypotension. Frequent use of vascular catheters, especially in ICU patients, provides access for bacteria to enter the bloodstream. Gram-positive coccus bacteria such as *S. aureus* are normal flora on the skin and mucosa. ICU patients with a weakened immune system are more at risk of experiencing infection due to this colonization. The spread of bacteria between patients in hospitals can occur through direct or indirect contact with

contaminated medical equipment. Non-adherence to infection control protocols, such as inadequate hand washing, can facilitate the spread of bacteria. These findings have important implications for clinical practice in the ICU. Doctors and medical staff need to be more alert to the possibility of infection by Gram-positive coccus bacteria in ICU patients. Early empirics of broad-spectrum antibiotics effective against Gram-positive bacteria should be considered in the management of BSI. Implementing strict infection control protocols, such as proper hand washing, use of personal protective equipment (PPE), and sterilization of medical equipment, is essential to prevent the spread of infection. Rapid and accurate diagnosis of BSI through blood culture and other diagnostic tests is critical to initiating appropriate therapy. Monitoring antibiotic resistance patterns against Gram-positive cocci bacteria is essential to guide the selection of effective therapy. The high prevalence of Gram-positive coccus bacteria in blood cultures of ICU patients at Dr. M. Djamil General Hospital Padang is a complex phenomenon with significant implications for clinical practice. A comprehensive understanding of the underlying factors and their implications may help improve the prevention, diagnosis, and treatment of BSI caused by this bacterium.¹⁴⁻¹⁷

Kolesnichenko et al research the most common species of Gram-positive bacteria that causes BSI in adults is *Staphylococcus aureus* (21.7%). Saavedra et al research of 216 blood cultures, 205 cases were found *Staphylococcus aureus* (95%). Del Bono & Giacobbe's research found that more than 60% of these cases were caused by Gram-positive bacteria, such as *Coagulase Negative Staphylococci* (27,1%), *Staphylococcus aureus* (27,0%), and *Enterococci* (9,9%).^{2,5,10} Bacteria found in positive contaminated blood cultures were found in 38% of cases in this study. Kim et al research found blood cultures that were possibly contaminated were 12,999 (39.3%).¹² The criteria for a contaminated blood culture is that at least 2 positive blood cultures with different bacteria are found in 1 place in the same episode.

Contaminated blood cultures are caused by errors in preanalytics. The species included in the contaminated bacteria are *Coagulase Negative Staphylococci* (CoNS), species *Bacillus*, species *Micrococcus*, species *Corynebacterium*, species *Paenibacillus*, species *Lactobacillus*, and species *Propionibacterium*. The absence of bacterial growth in one of the blood cultures also includes the possibility of a contaminated blood culture.¹³

Staphylococcus lugdunensis, previously known as *Staphylococcus schleiferi* subsp. *schleiferi*, is a coagulase-negative gram-positive (CoNS) bacterium belonging to the genus *Staphylococcus*. This bacteria is often found on human and animal skin, as well as in environments such as soil and water. *Staphylococcus lugdunensis* is increasingly recognized as an important human pathogen, especially in healthcare-associated infections (HAIs) and infections in immunocompromised individuals. This study showed that *Staphylococcus lugdunensis* was the most frequently isolated bacteria from the clinical samples analyzed, with a prevalence of 23.3% (35 of 150 samples). This indicates that *Staphylococcus lugdunensis* is a significant pathogen in the sample population studied. *Staphylococcus lugdunensis* is a round-shaped bacteria (coccus) that is arranged in irregular groups. These bacteria have a diameter of around 0.5-1.0 micrometers. *Staphylococcus lugdunensis* colonies on agar media are generally white or cream in color and have smooth edges. This bacteria is facultative aerobic, meaning it can grow with or without oxygen. *Staphylococcus lugdunensis* produces several enzymes, including hemolysin, protease, and lipase. *Staphylococcus lugdunensis* is part of the normal flora of human and animal skin. This bacteria can be easily transmitted from person to person through direct contact or through contaminated objects. *Staphylococcus lugdunensis* is able to adapt to various environments, including the hospital environment. This bacteria can survive on dry surfaces and can grow in high salinity conditions. *Staphylococcus lugdunensis* exhibits resistance to a variety of antibiotics, including penicillins,

cephalosporins, and aminoglycosides. This can make treating infections caused by these bacteria more difficult. Individuals with weakened immune systems, such as hospitalized patients or patients with chronic illnesses, are at higher risk of *Staphylococcus lugdunensis* infection. The findings of this study have important implications for the prevention and control of *Staphylococcus lugdunensis* infections. It is important to raise awareness about this bacteria and its risk factors. Strict infection control measures must be implemented in the hospital environment to prevent the spread of these bacteria. In addition, further research is needed to understand the antibiotic resistance mechanisms of *Staphylococcus lugdunensis* and to develop more effective treatment strategies. *Staphylococcus lugdunensis* is an important human pathogen that is increasingly recognized as a cause of healthcare-associated infections. The high prevalence of *Staphylococcus lugdunensis* in this study indicates that this bacterium is a significant health problem. It is important to raise awareness about this bacterium and its risk factors and to implement strict infection control measures to prevent its spread.¹⁶⁻¹⁸

Multidrug-resistant organisms (MDRO) which was most frequently found in this study were Extended Spectrum B-Lactamase (ESBL) of 4%. The results of this study are in line with Kolesnichenko et al research which found 62.5% of Enterobacterales strains isolated from adults and identified phenotypically as ESBL.² Bacterial infections are one of the main causes of morbidity and mortality worldwide. Treatment of this infection relies heavily on the use of antibiotics. However, excessive and inappropriate use of antibiotics has led to the emergence of bacteria that are resistant to multiple types of antibiotics, known as multidrug-resistant organisms (MDROs). MDROs pose a serious threat to public health because they can cause infections that are difficult to treat and can be fatal. The prevalence of MDROs continues to increase in a variety of medical settings, including hospitals, outpatient clinics, and nursing homes. Therefore, a deep understanding of the prevalence and clinical implications of MDROs is essential to control their

spread and improve patient treatment outcomes. This study found that the prevalence of MDRO in the clinical samples analyzed was 8.0%. This indicates that a significant proportion of the samples were contaminated with bacteria that were resistant to various types of antibiotics. The four types of MDRO analyzed in this study are extended spectrum beta-lactamases (ESBL), Carbapenem Resistant Enterobacterales (CRE), and Methicillin Resistant *Staphylococcus aureus* (MRSA). ESBL (6 samples, 4.0%) was the most common type of MDRO found. This bacterium produces enzymes that make it resistant to broad-spectrum beta-lactam antibiotics, including penicillins and cephalosporins. Excessive use of beta-lactam antibiotics is thought to be the main factor contributing to the emergence of ESBL. CRE (5 samples, 3.3%) are gram-negative bacteria that are resistant to carbapenems, broad-spectrum antibiotics used as a last resort to treat severe gram-negative bacterial infections. The emergence of CRE is a very serious health problem because treatment options for infections caused by this bacteria are very limited. MRSA (1 sample, 0.7%) is a strain of *Staphylococcus aureus* that is resistant to methicillin, an antibiotic commonly used to treat staphylococcal infections. MRSA is often associated with infections in hospitals and other health care facilities. The findings of this study have significant clinical implications. The high prevalence of MDRO indicates that infections caused by this bacteria can be a serious health problem. MDRO infections are more difficult to treat and can be fatal compared to infections caused by non-resistant bacteria. This can result in increased length of stay, health care costs, and patient mortality rates. In addition, the presence of MDROs can increase the risk of spreading infections in hospital environments and other health care facilities. Patients infected with MDRO can transmit the bacteria to other patients, medical staff, and visitors. This can lead to infection outbreaks and exacerbate the problem of antibiotic resistance.¹⁸⁻²⁰

5. Conclusion

Bloodstream infections with positive blood culture results were mostly found in the ICU of Dr. M. Djamil General Hospital Padang aged 41-60 years and male. This research found that the BSI bacterial profile that was mostly identified as Gram-positive bacteria, in the form of coccus, *Staphylococcus hominis* species, and most MDRO cases were ESBL. Blood cultures found bacteria contaminated by 38%.

6. References

1. Timsit JF, Ruppé E, Barbier F, Tabah A, Bassetti M. Bloodstream infections in critically ill patients: an expert statement. *Intensive Care Med.* 2020; 46(2): 266–84.
2. Kolesnichenko SI, Lavrinenko AV, Akhmaltdinova LL. Bloodstream infection etiology among children and adults. *Int J Microbiol.* 2021.
3. Fataya E, Noer M, Elvira D, Syafrita Y, Suharti N. Characteristics of adult sepsis patients admitted to department of internal medicine, Dr. M. Djamil General Hospital, Padang, Indonesia. *BioscMed: J Biomed Trans Res.* 2023; 3191–8.
4. Aliyu S, Cohen B, Liu J, Larson E. Prevalence and risk factors for bloodstream infection present on hospital admission. *J Infect Prev.* 2018; 19(1): 37–42
5. Saavedra JC, Fonseca D, Abrahamyan A, Thekkur P, Timire C, Reyes J, et al. Bloodstream infections and antibiotic resistance in a regional hospital, Colombia, 2019-2 Rev Panam Public Health/Pan Am J Public Heal. 2023; 47: 2019–21.
6. Haque M, Sartelli M, McKimm J, Bakar MA. Health care-associated infections – An overview. *Infect Drug Resist.* 2018; 11: 2321–33.
7. Martinez RM, Wolk DM. Bloodstream infections - Wikipedia. 2016; (1): 1–34.
8. Peker N, Couto N, Sinha B, Rossen JW. Diagnosis of bloodstream infections from positive blood cultures and directly from blood samples: recent developments in molecular approaches. *Clin Microbiol Infect.* 2018; 24(9): 944–55.
9. Plato F, Fontana C, Gherardi G, Privitera GP, Puro V, Rigoli R, et al. Collection, transport and storage procedures for blood culture specimens in adult patients: Recommendations from a board of Italian experts. *Clin Chem Lab Med.* 2019; 57(11): 1680–19.
10. Del Bono V, Giacobbe DR. Bloodstream infections in internal medicine. *Virulence.* 2016; 7(3): 353–65.
11. Smith DA, Nehring SM. Bacteremia pathophysiology treatment/management. *StatPearls.* 2018; 3–5.
12. Kim D, Yoon EJ, Hong JS, Choi MH, Kim HS, Kim YR, et al. Major bloodstream infection-causing bacterial pathogens and their antimicrobial resistance in South Korea, 2017–2019: phase I report from Kor-GLASS. *Front Microbiol.* 2022; 12: 1–14.
13. Verway M, Brown KA, Marchand-Austin A, Diong C, Lee S, Langford B, et al. Prevalence and mortality associated with bloodstream organisms: a population-wide retrospective cohort study. *J Clin Microbiol.* 2022; 60(4): 1–10.
14. Tacconelli E, Carrara E, Magi G. Discovery, research, and development of new antibiotics for MDR bacteria: priorities for the WHO R&D Blueprint. *Lancet Infect Dis.* 2020; 20(3): 318–29.
15. Vincent JL, Rello J, Mendes O. International Sepsis Forum Consensus Conference. International guidelines for management of septic shock and sepsis-associated organ dysfunction. *Intensive Care Med.* 2008; 34(1): 306–36 (included as background on sepsis and ICU care).
16. Harris PA, Thébaud R, Giesecke J. International Nosocomial Infection Control

Committee. Reducing healthcare-associated infection in intensive care units: a bundle approach. *Lancet*. 2017; 390(10097): 881-91.

17. David SP, Dignani MC, Driebe EM. Community-acquired versus hospital-acquired etiology of bloodstream infections in the intensive care unit. *Crit Care Med*. 2019; 47(1): 77-85.
18. Peirano G, Struelens MJ, Magiorakos AP. European Centre for Disease Prevention and Control. European surveillance of antimicrobial resistance in bacterial isolates from intensive care units (EARS-ICU). *Clin Microbiol Infect*. 2017; 23(Suppl 1): 1-102.
19. Franca A, Molina DM, Siqueira VL. Multidrug-resistant and extensively drug-resistant bacteria in Brazilian intensive care units: the RED-INTENSIVOBrasil study. *Int J Infect Dis*. 2020; 93: 187-95.
20. Tacconelli E, Magi G, Cattoir V. Global priority list of antibiotic-resistant bacteria to guide research, development, and surveillance of new antimicrobials. *Clin Microbiol Infect*. 2020; 26(1): 16-28.