INTRODUCTION

The Intensive Care Unit (ICU) is a special care unit that provides comprehensive care and life support for patients who are seriously ill. The Intensive Care Unit's main function is to care for emergency patients and support the vital organs of patients undergoing elective surgery or interventional procedures at high risk.1-3

On average, patients in the ICU are immunocompromised patients who are susceptible to nosocomial infections. Cleanliness in the ICU plays a role in the occurrence of nosocomial infections in the ICU. Nosocomial infections are infections acquired within 48 hours of the patient receiving treatment at a health service and ≤ 30 days after returning home.4 Infections need to be differentiated between infections acquired from the community or nosocomial infections. Although the onset of more than 48 hours does not always mean a nosocomial infection while the patient is in the ICU, the causative microorganism does not come from the microbial ecology of a nosocomial infection. Still, it is a normal bacterial flora from the patient’s body.5,6

The intensive care unit is a unit that cares for patients with a high risk of infection, while viral infections are one of the predisposing factors for someone being easily infected with bacteria. Based on several studies, the germs that cause infections in the ICU are Pseudomonas aeruginosa and Klebsiella pneumonia, which causes Ventilatory Acquired Pneumonia (VAP), Enterobacter agglomerans causes sepsis (bacteremia), Enterobacter cloacae causes various nosocomial infections such as bacteremia and urinary tract infections and the Gram-negative cocci Staphylococcus sp causes bacteremia.7-9

The coronavirus disease 2019 (COVID-19), first discovered in Wuhan, China, has attracted worldwide attention over the last few years. Data in Indonesia shows that as of July 9th, 2022, as many as 6,108,729 people were confirmed positive for COVID-19, and 156,785 people died.1 The COVID-19 pandemic has had a lot of influence on the health sector. Viral infection is one of the predisposing factors that makes it easy for someone to become infected with bacteria, which results in a high incidence of nosocomial infections.

ABSTRACT

Background: The intensive care unit (ICU) is a unit that cares for patients with a high risk of infection, while viral infections are one of the predisposing factors for someone being easily infected with bacteria. This research aims to see a picture of germ patterns before, during and after the COVID-19 pandemic.

Methods: This research is descriptive with a retrospective approach. The research sample used secondary data from microbial culture results of clinical specimens (blood, sputum, pus, urine, etc.) from ICU patients for the period 2019-2022 at the Clinical Pathology Laboratory of Dr. Wahidin Sudirohusodo Hospital, Makassar. Data is grouped into Gram-positive and Gram-negative bacteria, based on the highest order, and presented as tables and graphs.

Results: There were 440 isolates, 80 Gram-positive isolates (18%) and 360 Gram-negative isolates (82%). The five most common types of isolates were dominated by the Gram-negative group in the last 4 years, respectively: Burkholderia cepacia 92 (21%), Acinetobacter baumannii 89 (20%), Klebsiella pneumoniae 91 (20%), Pseudomonas aeruginosa 58 (13%), Pseudomonas aeruginosa 37 (8%), and Enterobacter cloacae 37 (8%), and Staphylococcus aureus 89 (20%). The majority of isolates identified were obtained from blood, as many as 192 (44%), sputum 136 (31%), pus 52 (12%) and urine 8 (2%). Bacteremia was the largest cause of infection by Burkholderia cepacia, 91 (47%), while sputum was dominated by Acinetobacter baumannii 49 (26%).

Conclusion: The germ pattern in the ICU before, during, and after Gram-negative bacteria dominated the COVID-19 pandemic. Bacteremia is the largest proportion of causes of infection.

Keywords: Germ patterns, Gram-positive bacteria, Gram-negative bacteria, COVID-19 pandemic, ICU.

*Corresponding author:
Mustamsil
Clinical Pathology Residency Programme, Faculty of Medicine, Universitas Hasanuddin, Dr. Wahidin Sudirohusodo Hospital, Makassar, Indonesia;
mustamsi06@gmail.com

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Patterns of germs before, during and after the COVID-19 pandemic in Intensive Care Unit (ICU) patients at Dr. Wahidin Sudirohusodo, Makassar, Indonesia

Mustamsil*, Irdan Handayani1, Nursin Abdul Kadir2,3

1Clinical Pathology Residency Programme, Faculty of Medicine, Universitas Hasanuddin, Dr. Wahidin Sudirohusodo Hospital, Makassar, Indonesia;
2Department of Clinical Pathology, Faculty of Medicine, Universitas Hasanuddin, Dr. Wahidin Sudirohusodo Hospital, Makassar, Indonesia;
3Department of Clinical Pathology, Labuang Baji Hospital, Makassar, Indonesia.

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in the Intensive Care Unit (ICU) of hospitals.\textsuperscript{10-12} In patients infected with COVID-19, it was reported that there were bacteria in the high-priority category with a high frequency of risk. In Wuhan, China, \textit{Acinetobacter baumannii} was the most frequently reported bacteria, followed by \textit{Klebsiella pneumoniae} (75.5\% carbapenem-resistant).\textsuperscript{12} A total of 108 pediatric inpatients with pneumonia in Dhaka, Bangladesh, underwent blood culture and found the pathogen to be predominantly Gram-negative bacteria (\textit{Pseudomonas}, \textit{Escherichia coli}, \textit{Salmonella enterica}, and \textit{Klebsiella pneumoniae}) and resistant to all empirical antibiotics that are routinely used such as ampicillin, gentamicin, ciprofloxacin, and ceftriaxone.\textsuperscript{13,14} The research results show that many germs with different germ patterns are still found in the ICU. To update findings from previous research and regarding germ patterns that can cause nosocomial infections in the ICU room during the COVID-19 pandemic, the author is interested in knowing about the description of germ patterns in patients treated in intensive care before, during and after the COVID-19 pandemic at Dr. Wahidin Sudirohusodo Hospital, Makassar.

**METHODS**

The research design used was descriptive research with secondary data from 440 medical records collected retrospectively during February - May 2023 for the microbial culture of clinical specimens (blood, sputum, pus, urine, etc.) of adult ICU, NICU, PICU, CVCU) patients for 1 year. 2019-2022 at the Clinical Pathology Laboratory of RSUP dr. Wahidin Sudirohusodo Makassar is in ICU patients using the total sampling method. The inclusion criteria for this study include: 1) Child and adult patients treated at the intensive care installation at RSUP dr. Wahidin Sudirohusodo in February and May 2023, and 2) Have microbial culture/isolate results from the patient’s medical records. Meanwhile, the exclusion criteria in this study were samples with incomplete or missing data.

The germ pattern of ICU patients in this study is a description of the distribution pattern of germ types based on the type of specimen examined, the pattern of resistance or sensitivity of germs to antimicrobials, and to assess whether there has been a shift in the pattern of germs that cause infection, resistance and sensitivity patterns over time. Different (germ patterns before, during and after the COVID-19 pandemic) in all germ examinations of patients treated in the Intensive Care Unit. Germ pattern data is collected and analyzed using the WHO standardized system (WHO Net). ICU patient microbial isolates are taken from materials in the form of blood, urine, sputum, pus and other materials belonging to patients being treated in the ICU and identified using standard microbiology methods.

Gram-positive bacteria found in blood samples, urine, sputum, pus, bronchoalveolar lavage, and feces were identified using standard microbiology procedures. Gram-positive is found when there are bacteria in the form of purple bacilli or cocci that absorb color from crystal violet on microscopic gram staining and biochemical examination (catalase, oxidase or coagulase tests), and their growth is found in the culture medium. Meanwhile, Gram-negative bacteria found in blood, urine, sputum, pus, bronchoalveolar lavage, and feces are identified using standard microbiology procedures. Gram-negative is found if there are bacteria in the form of pink bacilli or diplococci that absorb color from safranin on microscopic examination and are positive on biochemical tests (fermentation and oxidase tests) growth is found in the culture media.

Data is grouped into Gram-positive and Gram-negative bacteria, based on the highest order, and presented as tables and graphs. Data were analyzed with Microsoft Excel and SPSS version 20.0 for Windows.

**RESULTS**

This research was conducted at Dr. Wahidin Sudirohusodo Hospital, Makassar, regarding germ patterns found in the ICU. This research was carried out by collecting data on germ/bacterial culture results before, during and after the COVID-19 pandemic at Dr. Wahidin Sudirohusodo Hospital, Makassar, Indonesia.

### Table 1. The number of Gram-positive and Gram-negative microbial isolates in ICU patients at Dr. Wahidin Sudirohusodo Hospital, Makassar, Indonesia

<table>
<thead>
<tr>
<th>Bacteria Group</th>
<th>2019</th>
<th>2020</th>
<th>2021</th>
<th>2022</th>
<th>Total</th>
<th>%</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gram-Positive</td>
<td>12</td>
<td>13</td>
<td>26</td>
<td>29</td>
<td>80</td>
<td>18.20</td>
</tr>
<tr>
<td>Gram-Negative</td>
<td>88</td>
<td>44</td>
<td>111</td>
<td>117</td>
<td>360</td>
<td>81.80</td>
</tr>
<tr>
<td>Total</td>
<td>100</td>
<td>57</td>
<td>137</td>
<td>146</td>
<td>440</td>
<td>100.00</td>
</tr>
</tbody>
</table>

### Table 2. Number of isolates based on specimen type

<table>
<thead>
<tr>
<th>Specimen Year</th>
<th>2019</th>
<th>2020</th>
<th>2021</th>
<th>2022</th>
<th>Total</th>
<th>%</th>
</tr>
</thead>
<tbody>
<tr>
<td>Blood</td>
<td>46</td>
<td>27</td>
<td>59</td>
<td>60</td>
<td>192</td>
<td>43.60</td>
</tr>
<tr>
<td>Sputum</td>
<td>15</td>
<td>18</td>
<td>57</td>
<td>64</td>
<td>154</td>
<td>35.00</td>
</tr>
<tr>
<td>Pus</td>
<td>31</td>
<td>8</td>
<td>5</td>
<td>10</td>
<td>54</td>
<td>12.30</td>
</tr>
<tr>
<td>Urine</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>7</td>
<td>8</td>
<td>1.80</td>
</tr>
<tr>
<td>Bronchial lavage</td>
<td>4</td>
<td>0</td>
<td>7</td>
<td>0</td>
<td>11</td>
<td>2.50</td>
</tr>
<tr>
<td>Body Tissue</td>
<td>0</td>
<td>3</td>
<td>4</td>
<td>2</td>
<td>9</td>
<td>2.00</td>
</tr>
<tr>
<td>Other Body Fluids</td>
<td>3</td>
<td>1</td>
<td>5</td>
<td>3</td>
<td>12</td>
<td>2.80</td>
</tr>
<tr>
<td>Total</td>
<td>100</td>
<td>57</td>
<td>137</td>
<td>146</td>
<td>440</td>
<td>100.00</td>
</tr>
</tbody>
</table>
Figure 1. Germ patterns graphic of ICU patients for 2019-2022.

Table 3. The most common type of isolate in ICU patients at RSUP dr. Wahidin Sudirohusodo for the period 2019 - 2022

<table>
<thead>
<tr>
<th>Gram Negative (n=324)</th>
<th>n</th>
<th>% Total</th>
<th>% GN</th>
</tr>
</thead>
<tbody>
<tr>
<td>Burkholderia cepacia</td>
<td>92</td>
<td>21.00</td>
<td>26.00</td>
</tr>
<tr>
<td>Acinetobacter baumannii</td>
<td>89</td>
<td>20.00</td>
<td>25.00</td>
</tr>
<tr>
<td>Klebsiella pneumoniae ss. pneumoniae</td>
<td>58</td>
<td>13.00</td>
<td>16.00</td>
</tr>
<tr>
<td>Pseudomonas aeruginosa</td>
<td>37</td>
<td>8.00</td>
<td>10.00</td>
</tr>
<tr>
<td>Escherichia coli</td>
<td>37</td>
<td>8.00</td>
<td>10.00</td>
</tr>
<tr>
<td>Stenotrophomonas maltophilia</td>
<td>11</td>
<td>3.00</td>
<td>3.00</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Gram Negative (n=58)</th>
<th>n</th>
<th>% Total</th>
<th>% GP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Staphylococcus aureus ss. aureus</td>
<td>20</td>
<td>5.00</td>
<td>25.00</td>
</tr>
<tr>
<td>Staphylococcus haemolyticus</td>
<td>11</td>
<td>3.00</td>
<td>14.00</td>
</tr>
<tr>
<td>Enterococcus faecalis</td>
<td>8</td>
<td>2.00</td>
<td>10.00</td>
</tr>
<tr>
<td>Staphylococcus hominis ss. Hominis</td>
<td>8</td>
<td>2.00</td>
<td>10.00</td>
</tr>
<tr>
<td>Staphylococcus cohnii ss. urealyticum</td>
<td>6</td>
<td>1.00</td>
<td>8.00</td>
</tr>
<tr>
<td>Staphylococcus epidermidis</td>
<td>5</td>
<td>1.00</td>
<td>6.00</td>
</tr>
</tbody>
</table>

GP= Gram Positive; GN= Gram Negative

the COVID-19 pandemic, totaling 440 isolates in patients treated in the ICU/NICU/PICU/CVCU (Table 1).

Table 1 shows the number of microbial isolates identified based on Gram-positive and Gram-negative bacterial groups in ICU patients at RSUP dr. Wahidin Sudirohusodo Makassar, 440 isolates were obtained, consisting of 80 (18.20%) Gram-positive and 360 (81.80%) Gram-negative isolates.

Table 2 shows that the most identified isolates based on specimen type were blood, 192 (43.60%), 154 (35.00%) sputum, 54 (12.30%) pus, 11 (2.50%) bronchial lavage and 8 (2.00%) urine. Figure 1 shows a graph of germ patterns representing the period before the COVID-19 pandemic (2019), during the COVID-19 pandemic (2020-2021) and after the COVID-19 pandemic (2022).

Table 3 shows that the five most common isolates were *Burkholderia cepacia* 92 (21%), *Acinetobacter baumannii* 89 (20%), *Klebsiella pneumoniae* 58 (13%), *Pseudomonas aeruginosa* 37 (8%), *Escherichia coli* 37 (8%), and *Staphylococcus aureus* was the 6th largest with 20 (5%) of the total isolates. Bacteremia was the cause of infection, the largest being *Burkholderia cepacia* at 91 (47%), while sputum was dominated by *Acinetobacter baumannii* at 49 (26%).

**DISCUSSION**

This research was conducted at Dr. Wahidin Sudirohusodo Hospital Makassar. The research design used was descriptive research with data collected retrospectively to determine the pattern of germs or microbes using data from culture isolates/bacteria from the Clinical Pathology Laboratory of Dr. Wahidin Sudirohusodo Hospital, Makassar in the period before, during and after the Covid-19 pandemic (2019-2022 period), who was treated in the ICU/NICU/PICU/CVCU installation.

The research found a pattern of germs or bacteria; 440 isolates were obtained, consisting of 80 (18.20%) Gram-positive and 360 (81.80%) Gram-negative isolates. Identification of the most isolates based on specimen type showed 192 (43.60%), 154 (35.00%) sputum, 54 (12.30%) pus, 11 (2.50%) bronchial lavage and 8 (2.00%) urine. The five most common
types of isolates were dominated by the Gram-negative group in the last 4 year period, respectively: Burkholderia cepacia 92 (21%), Acinetobacter baumannii 89 (20%), Klebsiella pneumoniae 58 (13%), Pseudomonas aeruginosa 37 (8%), Escherichia coli 37 (8%), and Staphylococcus aureus was the 6th largest with 20 (5%) of the total isolates. Burkholderia cepacia at 91 (47%), while sputum was dominated by Acinetobacter baumannii at 49 (26%).

The results of research on germ patterns in the ICU at Dr. Wahidin Sudirohusodo Hospital, Makassar, in 2009 found that Klebsiella pneumonia was the most common germ (28.3%), while Pseudomonas aeruginosa and Alkaligenes faecalis each accounted for only 3.3%. The incidence of antibiotic resistance is increasing, especially in the Asian continent, including Indonesia. Microbiologists agree that there is multi-antibiotic resistance to Gram-negative bacteria. Enterobacteriaceae is the most common cause of infection, especially in the ICU and often causes resistance to third-generation cephalosporin antibiotics because it is capable of producing the beta-lactamase enzyme, or what is known as extended-spectrum beta-lactamase (ESBL).

A study conducted in the ICU at Cipto Mangunkusumo Hospital, Jakarta, in 2011 aimed to determine the phenotypic characteristics of Gram-negative bacteria in the Enterobacteriaceae family. From this research, it was found that Gram-negative bacteria in the Enterobacteriaceae family are bacteria with the characteristics of producing beta-lactamase enzymes, such as ESBL, AmpC, and carbapenemase. This research used three methods to confirm the phenotypic characteristics of these three enzymes, namely the disc diffusion method for ESBL confirmation, the AmpC disk test (cefotixin-based) for AmpC confirmation, and the modified Hodge test for carbapenemase confirmation. Of the 112 isolates analyzed, it was found that Klebsiella pneumonia was the most common isolate (54.46% /61 isolates). In addition, from the double disk diffusion method, it was found that 58.42% of the isolates were ESBL producers, 1.98% were AmpC producers using the AmpC disk test (cefotixin-based), and 27.59% were carbapenemase producers using the modified Hodge test. The results of this study show that the prevalence of beta-lactamase-producing Klebsiella pneumoniae, especially ESBL, is very high. By knowing this, better control of infections can be carried out, and appropriate and rational antibiotics can be administered.

Another study was conducted in the ICU at Kariadi Hospital, Semarang. This research aims to determine the germ patterns of patients treated in the ICU at Dr. Kariadi Hospital Semarang. The research design used was descriptive research with data collected retrospectively, using ICU patients in July–December 2019 as samples. Sixty-nine ICU patients (100 sheets of germ culture results) met the inclusion and exclusion criteria and recorded the type of germ, antibiotic resistance, patient age, gender, and funding source. Of the 100 sheets of germ culture results from patients in the intensive care unit at Dr. Kariadi Hospital in the July–December 2019 period, it can be seen that the most common germs that cause infections are Enterobacter aerogenes (34%), Staphylococcus epidermidis (17%), Escherichia coli (15%), Pseudomonas aeruginosa (10%), Candida sp. (9%), and Acinetobacter spp. (8%).

In other research conducted at Hasan Sadikin Hospital, Bandung, a map of bacteria and their sensitivity to various antibiotics was created in the ICU at Hasan Sadikin Hospital, Bandung, in 2022. From this mapping, it was found that the most common bacteria in blood specimens was Pseudomonas aeruginosa (13.29%), while sputum examination showed Acinetobacter baumannii (26.53%). From body fluid examination, Staphylococcus epidermidis was found (34.78%), while urine examination showed Candida albicans (50%) and non-albicans (50%).

To find out the pattern of germs that most commonly cause infections in the ICU, it is also necessary to know about one of the diseases with the highest incidence in the ICU, namely ventilator-associated pneumonia (VAP). As previously explained, VAP is the most common form of hospital infection encountered in the ICU, especially in patients on mechanical ventilation. Ventilator-associated pneumonia (VAP) is hospital-acquired pneumonia that occurs after 48 hours of the patient receiving mechanical ventilation, either through an endotracheal tube or a tracheostomy tube. The incidence of pneumonia increases 3 to 10 times in mechanically ventilated patients. Ibrahim et al. VAP is divided into early onset, occurring within the first four days of mechanical ventilation, and late-onset, occurring five or more days after mechanical ventilation. Most VAPs begin with aspiration of oropharyngeal organisms into the distal bronchi, then biofilm formation by bacteria occurs, followed by bacterial proliferation and invasion of the lung parenchyma.

Under normal conditions, organisms in the oral cavity and oropharynx are dominated by S. viridans, Haemophilus species and anaerobic organisms. Saliva containing immunoglobulin A (Ig A) and fibronectin maintain the balance of oral cavity organisms so that aerobic gram-negative bacilli are rarely found. In critically ill patients due to SARS CoV-2 infection, the balance changes; the dominant organisms in the oral cavity are aerobic gram-negative bacilli and Staphylococcus aureus.

A study was carried out at the hospital. Harapan Kita, Jakarta, in 2020–2022, during the COVID-19 pandemic, on 116 respiratory tract specimens originating from VAP and non-VAP patients. The specimens consisted of 88 (75.9%) bronchial secretions, 20 (17.2%) throat secretions, 6 (5.2%) ETT tip secretions, and 2 (1.7%) pleural fluids. The results obtained were 4 specimens (3.4%) sterile, 112 positive cultures with 15 types of microorganisms causing infection in a row, the most dominant being Pseudomonas sp. (22.4%), Pseudomonas aeruginosa (18.1%), Stenotrophomonas maltophilia (9.5%), Serratia marcescens (8.6%), Enterobacter aerogenes (7.8%), Klebsiella pneumonia, Bacillus sp., and Escherichia coli (5.2%), Streptococcus haemolyticus and Staphylococcus epidermidis (3.4%), Streptococcus viridans and Staphylococcus aureus (2.6%); Candida sp. (1.7%), and Streptococcus E haemolyticus (0.9%). When grouped, 79.5% were gram-negative bacteria (Pseudomonas, S. maltophilia, Serratia marcescens, E. aerogenes, K. aureus, and others).
pneumonia, and E. coli). This study also presented bacterial patterns based on VAP onset isolates. Cultures were grouped based on the day of sampling. Cases of early-onset VAP were taken on days 1–4 of admission, and late-onset VAP was taken on days 5 or more. Of the 112 positive culture isolates, 23 early-onset VAP samples and 73 late-onset VAP samples were obtained. The most dominant early-onset VAP germ is P. aeruginosa, with the highest sensitivity to the antibiotics amikacin and ceftazidine. In late onset VAP, the most dominant is Pseudomonas sp, followed by P. aeruginosa, S. maltophilia and Serratia marcescens.

Research conducted in the ICU at Fatmawati Hospital on the relationship between empirical antibiotic use and bacterial sensitivity in the ICU at Fatmawati Hospital, Jakarta, showed that almost all bacteria were resistant to cephalixin (>75%); S. epidermidis, E. aerogenes, and Klebsiella spp were resistant to ceftazidime (>60%); E. coli was resistant to ceftriaxone (60%). This study also explained that comorbidities or complications and surgery did not show a statistically significant relationship because the severity was closely related to the length of stay. The higher the severity level, the longer the patient is hospitalized, making it possible for nosocomial infections to occur. This study also explained that the relationship between ventilator use, length of ventilator use, and the incidence of infection in the ICU is not statistically significant. This is because the average difference between the use of a ventilator and the time for taking culture samples is 2 days. As many as 42.3% of samples taken for culture tests were carried out the day after ventilator installation, so it is possible that infection has not occurred due to ventilator use. Patients who use a ventilator for more than 72 hours may be infected with VAP. Still, the analysis does not show significant results because only 13.6% of the total sample used a ventilator.

Other research was also carried out in the ICU at Dr. Soetomo Surabaya to identify bacterial sensitivity patterns and analyze antibiotic therapy in VAP patients. The research design was a prospective observational analysis with data collected from January to March 2013. Patients who met the inclusion criteria (diagnosed with VAP during treatment in the ICU, had microbiology culture and antibiotic sensitivity test results, and received antibiotic therapy for VAP during treatment in the ICU) were observed prospectively. Bacterial patterns and sensitivity to antibiotics were identified based on the results of culture and sensitivity tests. A total of 158 patients were on ventilators; nine met the inclusion criteria with thirty specimens (13 sputum, 17 blood). The most common bacteria found in sputum specimens from VAP patients in the ICU was Pseudomonas aeruginosa (30.8%), while in blood culture, the most common bacteria was coagulase-negative Staphylococcus (75%). Pseudomonas aeruginosa is a common cause of pneumonia in adult patients on ventilators and is susceptible to a wide spectrum of antibiotics. The source of the pathogen can also be medical personnel.

A study at Abdul Moeloek Regional Hospital, Lampung, was conducted to determine the percentage of MRSA in medical and paramedical personnel in the ICU and surgical treatment rooms at Abdul Moeloek Regional Hospital. The research design used was experimental research with a sample of 68 respondents. Samples were taken from nasal swabs, planted on Mannitol Salt Agar (MSA) media, and replanted on sheep blood agar media. The largest number of MRSA-positive samples came from the ICU, namely 13. At the same time, from the surgical treatment room, there were 6 samples, and the surgical treatment room II obtained 7 MRSA-positive samples. Factors that play a role in increasing the incidence of MRSA are the influence of dose determination (90, 4%), accuracy of treatment (90.2%), provision of anteisptics (84.9%), procedures for installing infusion cannulas (74.6%), and hand washing facilities (66.3%).

The Centers for Disease Control and Prevention (CDC) reported during the 2009 H1N1 influenza pandemic that 29 and 55% of deaths were due to secondary bacterial infections. Of five studies conducted during the 2002 SARS-CoV outbreak, 11% of cases were associated with secondary bacterial infections. Staphylococcus aureus, in particular, is isolated from hospitalized patients with SARS-CoV and influenza virus infections. Bacteria such as Streptococcus pneumoniae, P. aeruginosa K.pneumoniae, Enterobacter, Citrobacter sp, and H. influenzae are also common bacteria isolated from blood and sputum
cultures in patients with bacterial superinfections on top of respiratory viral infections.34,38,39

In this study, we found the most common types of infections in the ICU were bloodstream infections (bacteremia), pneumonia (ventilator-associated pneumonia [VAP]), urinary tract infections (UTIs), and surgical site infections (SSIs). Bacteremia is closely related to HAI infections due to the use of internal devices such as central venous catheters and so on. Apart from that, Acinetobacter baumannii is a type of bacteria that often complicates therapy because it tends to become MDR. Although there are no significant differences in germ patterns between the period before and after COVID-19, the emergence of Acinetobacter baumannii, which tends to be resistant, is an important concern for preventing infections related to HAI in hospitals.

CONCLUSION
The germ pattern in the ICU before, during, and after the COVID-19 pandemic was dominated by Gram-negative bacteria. Bacteremia is the largest cause of infection in the ICU. However, ongoing research is needed to obtain data regarding germ resistance patterns as a cause of infection in hospitals, especially in the ICU, which can be useful in patient management, especially in selecting antibiotics. It is related to the increase in antibiotic resistance in a hospital, which affects the length of therapy and patient prognosis.

CONFLICT OF INTEREST
There is no competing interest regarding the manuscript.

ETHICAL CONSIDERATION
This study has met the ethical recommendation to be carried out by the Health Research Ethics Commission, Faculty of Medicine, Universitas Hasanuddin, Dr. Wahidin Sudirohusodo Hospital, Makassar, with number: 15699/UN4.6.8/KP06.07/2023.

FUNDING
None.

AUTHOR CONTRIBUTION
All authors equally contribute to the study from the conceptual framework, data acquisition, and data analysis until reporting the study results through publication.

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