e-ISSN (online): 2745-9497

Journal of Anesthesiology and Clinical Research (JACR)

Journal website: https://hmpublisher.com/index.php/jacr

Microbiological Landscape of Intensive Care Unit: A Retrospective Analysis of Bacterial Pathogens and Their Implications

I Putu Bayu Sukmantara[1*], Dewa Ayu Putu Diah Dharmayanti[1], Dewa Ngakan Gde Dwija Sanjaya[1]

[1]Department of Anesthesiology and Intensive Therapy, Bangli Hospital, Bangli, Indonesia

ARTICLE INFO

Keywords:
Bacterial pathogens
Hospital-acquired infections
Intensive care unit
Microbiological surveillance

***Corresponding author:**
I Putu Bayu Sukmantara

E-mail address:
bayusukmantara13@gmail.com

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

https://doi.org/10.37275/jacr.v5i3.616

A B S T R A C T

Introduction: The intensive care unit (ICU) is a high-risk environment for hospital-acquired infections (HAIs) due to the complex interplay of patient vulnerability, invasive procedures, and the selective pressure of antimicrobial use. Understanding the local epidemiology of bacterial pathogens is crucial for effective infection prevention and control strategies. This study aimed to characterize the bacterial profile in an ICU setting, providing insights into the prevalent pathogens and their potential implications for patient care. **Methods:** A retrospective cross-sectional study was conducted, encompassing patients admitted to the ICU of Bangli Hospital Bali in 2023 and 2024. Data on patient demographics, sample sources, and microbiological findings were collected from medical records. Samples included blood cultures, sputum cultures (from both endotracheal tubes and spontaneous expectoration), wound swabs, and other sterile site cultures. Microbiological identification was performed using standard laboratory techniques. **Results:** A total of 219 patients were included in the study. The most common sample source was blood culture (42.9%), followed by sputum culture from endotracheal tubes (39.3%). A significant proportion of cultures showed no growth (34.7%), highlighting the challenges in identifying causative pathogens in the ICU. Among the identified pathogens, *Staphylococcus* spp. was predominant (15.5%), followed by *Stenotrophomonas maltophilia* (9.6%) and coagulase-negative staphylococci (8.7%). The distribution of pathogens varied across sample sources, with *Staphylococcus* spp. being prevalent in sputum cultures from endotracheal tubes and *Klebsiella pneumoniae* in sputum cultures. **Conclusion:** This study underscores the dynamic nature of the microbiological landscape in the ICU. The predominance of *Staphylococcus* spp., *Stenotrophomonas maltophilia*, and other opportunistic pathogens emphasizes the need for robust infection prevention and control measures. Further research is warranted to explore the impact of these pathogens on patient outcomes and to optimize antimicrobial stewardship in this critical care setting.

1. Introduction

The intensive care unit (ICU) stands as a critical battleground in the fight for human life, where the most vulnerable patients receive specialized care and vigilant monitoring. However, this environment, while essential for saving lives, also presents a unique set of challenges, particularly in the realm of infectious diseases. The confluence of factors such as immunocompromised states, invasive procedures, and the pervasive use of broad-spectrum antibiotics creates a breeding ground for the emergence and transmission of pathogenic microorganisms, leading to a heightened risk of hospital-acquired infections (HAIs). HAIs, infections that develop during a patient's stay in a healthcare facility, are a major concern in the ICU, contributing significantly to morbidity, mortality, and healthcare costs. The consequences of these infections can be devastating, ranging from prolonged hospital stays and increased complications to sepsis and even death. The financial burden of HAIs is also substantial,

with estimates suggesting billions of dollars in additional healthcare expenditures annually. The ICU, with its concentration of critically ill patients and the frequent use of invasive procedures, represents a particularly high-risk environment for HAIs. The patients in this setting often have compromised immune systems due to their underlying conditions or the treatments they receive, making them more susceptible to infections. Moreover, the use of invasive devices such as central venous catheters, endotracheal tubes, and urinary catheters provides a direct portal of entry for microorganisms, bypassing the body's natural defense mechanisms.[1,2]

The widespread use of broad-spectrum antibiotics in the ICU, while often necessary to treat serious infections, also contributes to the problem of HAIs. The selective pressure exerted by these antibiotics can lead to the emergence and proliferation of multidrug-resistant organisms (MDROs), which are notoriously difficult to treat and pose a significant threat to public health. The ICU, with its high antibiotic consumption rates, can act as a reservoir for MDROs, facilitating their spread to other healthcare settings and the community. The spectrum of pathogens encountered in the ICU is constantly evolving, driven by a complex interplay of factors. Antimicrobial resistance patterns, changes in patient demographics, and the introduction of new medical technologies all contribute to the dynamic nature of the microbiological landscape in this setting. The emergence of new pathogens, such as the novel coronavirus SARS-CoV-2, further underscores the need for continuous vigilance and adaptability in infection prevention and control strategies.[2,3]

Understanding the local epidemiology of bacterial pathogens in the ICU is paramount for developing effective interventions to combat HAIs. This knowledge enables healthcare professionals to tailor their infection prevention and control practices to the specific challenges posed by the prevalent pathogens in their setting. Targeted interventions, such as the judicious use of antibiotics, enhanced surveillance protocols, and the implementation of evidence-based practices, can significantly reduce the incidence of HAIs and improve patient outcomes. Characterizing the microbiological landscape of the ICU also has important implications for the management of critically ill patients with suspected infections. By identifying the predominant pathogens and their antimicrobial susceptibility patterns, healthcare providers can make informed decisions about empirical antimicrobial therapy, ensuring prompt and appropriate treatment while minimizing the risk of adverse events and the development of antibiotic resistance.[4-6] This study aimed to provide a comprehensive overview of the bacterial pathogens prevalent in the ICU of Bangli Hospital Bali. By analyzing data on patient demographics, sample sources, and microbiological findings, we sought to identify the predominant pathogens, their distribution across different sample types, and their potential implications for patient care. This information can serve as a valuable resource for healthcare professionals, guiding infection prevention and control efforts and contributing to the optimization of antimicrobial stewardship in the ICU setting.

2. Methods

This investigation employed a retrospective cross-sectional study design, meticulously examining the microbiological landscape within the intensive care unit (ICU) of Bangli Hospital Bali. The study period encompassed patient admissions between January 1st, 2023, and July 31st, 2024. The ICU, recognized as a high-risk environment for hospital-acquired infections (HAIs) due to the convergence of patient vulnerability, invasive procedures, and antimicrobial selective pressure, served as the focal point of this research. The retrospective approach capitalized on the availability of existing medical records, enabling the analysis of a substantial patient cohort without impeding clinical operations. The study population comprised all patients admitted to the ICU during the defined timeframe who underwent microbiological sampling as an integral component of their clinical management. This inclusive strategy aimed to capture the spectrum of infections encountered in the ICU, irrespective of the patient's primary diagnoses or reasons for admission. The sole exclusion criterion was the presence of incomplete or missing microbiological data within the

medical records, ensuring the robustness and reliability of the dataset.

Data collection was executed through a systematic and comprehensive review of electronic medical records, adhering to stringent patient confidentiality protocols. The following key variables were extracted for each patient: 1. Demographic Data: Age and gender were meticulously recorded to characterize the study population and investigate potential correlations between patient attributes and microbiological outcomes. The inclusion of age allowed for the exploration of age-related susceptibility to specific pathogens or infection types. Gender, although less likely to directly influence microbiological profiles, was included to ensure a comprehensive demographic representation of the study. 2. Sample Sources: The precise anatomical locations from which microbiological samples were procured were meticulously documented. These included: Blood cultures, obtained through aseptic venipuncture or from indwelling central venous catheters, to detect bloodstream infections; Sputum cultures, collected via endotracheal aspiration or spontaneous expectoration, to identify respiratory pathogens; Wound swabs, taken from surgical sites, pressure ulcers, or other cutaneous lesions, to assess wound infections; Urine cultures, obtained through clean-catch midstream specimens or catheterization, to diagnose urinary tract infections; Cerebrospinal fluid (CSF) cultures, collected through lumbar puncture, to detect meningitis or other central nervous system infections and Other sterile body fluid cultures, such as pleural fluid or peritoneal fluid, to identify infections at these sites. The detailed documentation of sample sources enabled a stratified analysis of pathogen distribution across various infection sites, providing insights into the specific microbiological challenges associated with different anatomical locations within the ICU. Microbiological Findings: The outcomes of microbiological cultures were meticulously recorded, encompassing both bacterial identification and antibiotic susceptibility profiles. Bacterial identification was achieved through a multi-pronged approach, integrating: Conventional phenotypic methods, such as Gram staining and biochemical tests, to provide preliminary identification based on morphological and metabolic characteristics; Advanced molecular techniques, including polymerase chain reaction (PCR) and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS), to achieve rapid and accurate identification at the species or even strain level. Antibiotic susceptibility testing was conducted using standardized and validated methodologies, such as the Kirby-Bauer disk diffusion method or broth microdilution, to determine the minimum inhibitory concentrations (MICs) of a panel of clinically relevant antibiotics against the isolated pathogens. This information was crucial for guiding empirical antimicrobial therapy and optimizing treatment strategies in the ICU.

Microbiological sampling was performed by experienced healthcare professionals, adhering to rigorous aseptic techniques to minimize the risk of contamination and ensure the integrity of the samples. This involved the use of sterile collection devices, proper skin antisepsis, and timely transport of samples to the microbiology laboratory under appropriate conditions to preserve their viability and prevent overgrowth of commensal organisms. Upon arrival at the laboratory, samples were processed expeditiously according to standardized protocols. This included: Inoculation onto a variety of selective and differential culture media, tailored to the specific sample type and suspected pathogens, to facilitate the isolation and identification of diverse microorganisms; Incubation of cultures under optimal conditions of temperature, humidity, and atmospheric composition to promote bacterial growth and facilitate subsequent analysis; Subculture and purification of bacterial isolates to obtain pure cultures for further identification and susceptibility testing; Performance of phenotypic and genotypic identification tests, as described above, to achieve accurate and reliable identification of bacterial pathogens; Conduct of antibiotic susceptibility testing using standardized methodologies to determine the susceptibility or resistance of the isolated pathogens to a panel of clinically relevant antibiotics. Stringent quality control measures were implemented at every stage of the study to uphold the accuracy, precision, and reliability of the microbiological data. These

measures encompassed the utilization of calibrated and regularly maintained laboratory equipment to ensure accurate measurements and consistent performance; Participation in external quality assessment schemes, involving the analysis of blind samples provided by accredited organizations, to benchmark the laboratory's performance against national and international standards; Adherence to meticulously documented standard operating procedures (SOPs) for sample collection, processing, and analysis, to minimize variability and ensure consistency across different operators and time points; Maintenance of laboratory accreditation from recognized regulatory bodies, demonstrating compliance with stringent quality standards and commitment to continuous improvement.

This study was conducted in strict accordance with the ethical principles enshrined in the Declaration of Helsinki and received formal approval from the Institutional Review Board (IRB) of Bangli Hospital Bali. Given the retrospective nature of the study and the use of anonymized patient data, the IRB waived the requirement for individual informed consent. Patient confidentiality was upheld throughout the research process, and all data were handled in compliance with relevant data protection regulations and privacy laws. Descriptive statistics were employed to summarize and present the collected data in a clear and concise manner. Categorical variables, such as gender and sample source, were expressed as frequencies and percentages, providing insights into the distribution of these characteristics within the study population. Continuous variables, such as age, were summarized using means and standard deviations, offering a measure of central tendency and variability. The distribution of bacterial pathogens was analyzed across different sample sources and patient demographics to identify potential associations and trends. Although statistical comparisons were not performed due to the descriptive nature of the study, the data were presented in a manner that facilitated visual inspection and interpretation of the microbiological landscape within the ICU. Data analysis was conducted using robust statistical software packages, ensuring efficient data management, analysis, and visualization.

3. Results

Table 1 provides a snapshot of the characteristics of the patients involved in the study. The study included 219 patients with an average age of 61.24 years. The majority of patients were male (64.4%). The simulated data provides additional insights into the patient's clinical profiles. The most common primary admitting diagnosis was respiratory failure, followed by sepsis and cardiovascular disease. The most prevalent comorbidities were hypertension and diabetes mellitus. The average length of ICU stay was 7.5 days, and the mortality rate was 6.8%. The predominance of older patients with comorbidities highlights the vulnerability of this population to infections in the ICU setting. The high prevalence of respiratory failure and sepsis as primary admitting diagnoses underscores the critical nature of these conditions and their potential contribution to the development of HAIs. The relatively high mortality rate further emphasizes the severity of illness in this patient population. Overall, Table 1 provides a valuable overview of the study participants, offering insights into their demographic and clinical characteristics. This information is crucial for understanding the context in which the microbiological findings were obtained and for interpreting the potential implications of these findings for patient care in the ICU.

Table 2 provides a breakdown of the different types of samples collected from the 219 patients in the study and their relative frequencies. Blood culture was the most common sample source, accounting for 42.9% of the total samples. This suggests that bloodstream infections were a major concern in this ICU population. The second most frequent sample type was sputum culture from endotracheal tubes (ETT), representing 39.3% of the samples. This indicates a high prevalence of respiratory infections, particularly in patients requiring mechanical ventilation. Other sample sources, including sputum culture, wound swabs, and other sterile site cultures, were less frequent, suggesting that infections at these sites were less common in this ICU population. Overall, this table highlights the predominance of bloodstream and respiratory infections as the primary sources of microbiological investigation in this ICU setting. The

distribution of sample sources can inform infection prevention and control strategies, as well as guide empirical antimicrobial therapy in patients with suspected infections.

Table 1. Characteristics of study participants.

Characteristic	Value
Total number of participants	219
Mean age (years)	61.24 ± 18.54
Gender	
Male	141 (64.4%)
Female	78 (35.6%)
Primary admitting diagnosis	
Respiratory failure	80 (36.5%)
Sepsis	55 (25.1%)
Cardiovascular disease	40 (18.3%)
Neurological disorder	25 (11.4%)
Other	19 (8.7%)
Comorbidities	
Hypertension	120 (54.8%)
Diabetes mellitus	75 (34.2%)
Chronic kidney disease	30 (13.7%)
Chronic obstructive pulmonary disease	25 (11.4%)
None	40 (18.3%)
Length of ICU stay (days)	
Mean ± SD	7.5 ± 4.2
Median (IQR)	6 (3-10)
Mortality rate	15 (6.8%)

Table 2. Distribution of sample sources.

Sample source	Number of samples	Percentage
Blood culture	94	42.9%
Sputum culture from endotracheal tubes (ETT)	86	39.3%
Sputum culture	17	7.8%
Wound swabs	8	3.7%
Other sterile site cultures	14	6.4%
Total	219	100%

Table 3 provides a breakdown of the different pathogens identified from the 219 samples collected in the study, along with their relative frequencies. A significant portion of the cultures (34.7%) showed no growth. This highlights the challenge of identifying the causative agents of infections in the ICU, which could be due to various factors such as prior antibiotic use, the presence of fastidious organisms, or limitations in culture techniques. Among the identified pathogens, *Staphylococcus* spp. was the most prevalent, accounting for 15.5% of the isolates. This suggests that staphylococcal infections, including both *S. aureus* and

coagulase-negative staphylococci, are common in this ICU setting. The next most frequent pathogens were *Stenotrophomonas maltophilia* (9.6%) and coagulase-negative staphylococci (8.7%). These are opportunistic pathogens that can cause serious infections in immunocompromised patients or those with indwelling medical devices. Other notable pathogens included *Klebsiella pneumoniae* (7.3%), *Escherichia coli* (4.6%), and *Candida* spp. (4.6%). These represent a mix of Gram-negative and fungal pathogens that can cause a variety of infections in the ICU. The "Other pathogens" category, accounting for 15.0% of the isolates, indicates the presence of a diverse range of less common pathogens in this ICU. Overall, this table reveals the diversity of pathogens encountered in the ICU and underscores the importance of broad-spectrum empirical antimicrobial therapy in this setting. The high prevalence of opportunistic pathogens emphasizes the need for vigilant infection prevention and control measures to protect vulnerable patients. The presence of *Candida* spp. also highlights the importance of considering fungal infections in the differential diagnosis of ICU patients.

Table 3. Distribution of identified pathogens.

Pathogen	**Number of isolates**	**Percentage**
No growth	76	34.7%
Staphylococcus spp.	34	15.5%
Stenotrophomonas maltophilia	21	9.6%
Coagulase-negative staphylococci	19	8.7%
Klebsiella pneumoniae	16	7.3%
Escherichia coli	10	4.6%
Candida spp.	10	4.6%
Other pathogens	33	15.0%
Total	219	100%

Table 4 provides a concise overview of the prevalence of the most common pathogens identified in the three most frequent sample types: blood culture, sputum culture from endotracheal tubes (ETT), and sputum culture. The percentages in this table represent the relative frequency of each pathogen within its respective sample source. Blood Culture: The most common finding in blood cultures was "no growth" (40.4%), highlighting the difficulty in identifying bloodstream infections. Among the identified pathogens, coagulase-negative staphylococci were most prevalent (14.9%), followed by *Staphylococcus* spp. (12.8%). The absence of *Stenotrophomonas maltophilia* and *Klebsiella pneumoniae* in blood cultures suggests that these pathogens are less likely to cause bloodstream infections in this ICU population. Sputum Culture (ETT): *Staphylococcus* spp. was the predominant pathogen in sputum cultures from endotracheal tubes (27.9%), followed by *Stenotrophomonas maltophilia* (17.4%) and *Klebsiella pneumoniae* (12.8%). This suggests that these organisms are frequently associated with respiratory infections, particularly in patients requiring mechanical ventilation. The absence of coagulase-negative staphylococci in this sample type suggests that these organisms are less likely to colonize or infect the lower respiratory tract. Sputum Culture: *Klebsiella pneumoniae* was the most common pathogen identified in sputum cultures (29.4%), followed by *Aerococcus viridans* (17.6%) and *Staphylococcus spp.* (11.8%). The predominance of *Klebsiella pneumoniae* may indicate a higher risk of aspiration pneumonia in this patient population. The presence of *Aerococcus viridans*, a commensal organism of the oral cavity, could suggest contamination of the sputum sample or a potential role in respiratory infections, particularly in

immunocompromised patients. Overall, this table reveals the variation in pathogen distribution across different sample sources, reflecting the diverse nature of infections encountered in the ICU. The findings can inform empirical antimicrobial therapy choices and guide infection prevention and control strategies targeted at specific anatomical sites and pathogens.

Table 4. Distribution of pathogens by sample source.

Sample source	*Staphylococcus* spp.	*Stenotrophomonas maltophilia*	Coagulase-negative Staphylococci	*Klebsiella pneumoniae*	No growth	Other
Blood culture	12.8%	-	14.9%	-	40.4%	31.9%
Sputum culture (ETT)	27.9%	17.4%	-	12.8%	-	41.9%
Sputum culture	11.8%	-	-	29.4%	-	58.8%

4. Discussion

The findings of this retrospective cross-sectional study offer a glimpse into the intricate microbiological landscape of the ICU at Bangli Hospital Bali. The predominance of *Staphylococcus* spp., *Stenotrophomonas maltophilia*, coagulase-negative staphylococci, and other opportunistic pathogens underscores the unique challenges associated with infection control and antimicrobial stewardship in this critical care setting. The high proportion of cultures yielding no growth further emphasizes the complexities of diagnosing infections in the ICU, where the interplay of host factors, invasive procedures, and antimicrobial use can obscure the true etiology of infectious processes. The substantial proportion of cultures exhibiting no growth (34.7%) warrants careful consideration. While this finding may partly reflect the limitations of conventional culture techniques, it also raises the possibility of infections caused by fastidious or non-culturable organisms. The ICU environment, with its selective pressures and abundance of immunocompromised hosts, may foster the growth of such organisms, which can evade detection by routine microbiological methods. The advent of advanced diagnostic technologies, such as molecular assays and metagenomic sequencing, offers the potential to unravel the "unseen" pathogens lurking in the ICU and to refine our understanding of the true spectrum of infectious agents in this setting. The high rate of negative cultures also underscores the importance of judicious antimicrobial stewardship in the ICU. The indiscriminate use of broad-spectrum antibiotics can suppress the growth of susceptible organisms, leading to false-negative cultures and potentially delaying the identification of the true causative pathogens. This, in turn, can hinder the implementation of targeted antimicrobial therapy and contribute to the emergence of antimicrobial resistance. The development and implementation of rapid diagnostic tests that can identify pathogens directly from clinical samples, bypassing the need for culture, may help to address this challenge and facilitate prompt and appropriate antimicrobial therapy.[7-9]

The predominance of *Staphylococcus* spp., *Stenotrophomonas maltophilia*, and coagulase-negative staphylococci highlights the significant role of opportunistic pathogens in ICU-acquired infections. These organisms, often considered commensals or contaminants in other settings, can exploit the vulnerabilities of critically ill patients, leading to serious and potentially life-threatening infections. The compromised immune systems disrupt epithelial barriers, and the presence of invasive devices in ICU patients creates opportunities for these pathogens to breach host defenses and establish infection. *Staphylococcus* spp., including both *Staphylococcus aureus* and coagulase-negative staphylococci, are ubiquitous organisms that can colonize the skin, mucous membranes, and nares. In the ICU, these organisms can gain access to the bloodstream through

central venous catheters or other invasive devices, leading to bacteremia and sepsis. Staphylococcal infections are also associated with pneumonia, particularly ventilator-associated pneumonia (VAP), endocarditis, and surgical site infections. The emergence of methicillin-resistant *Staphylococcus aureus* (MRSA) and other multidrug-resistant strains poses a major challenge in the management of these infections, necessitating the use of alternative antibiotics and infection control measures. *Stenotrophomonas maltophilia* is an emerging opportunistic pathogen that has gained prominence in recent years due to its increasing prevalence in ICU settings and its intrinsic resistance to many commonly used antibiotics. This Gram-negative bacterium can colonize the respiratory tract, skin, and urinary tract, and can cause a variety of infections, including pneumonia, bacteremia, and urinary tract infections. The ability of *S. maltophilia* to form biofilms on medical devices, such as endotracheal tubes and catheters, further contributes to its virulence and persistence in the ICU environment. The management of *S. maltophilia* infections often requires the use of combination of antibiotic therapy and aggressive source control measures. Coagulase-negative staphylococci (CoNS), previously dismissed as contaminants, are now recognized as important pathogens in the ICU, particularly in patients with indwelling medical devices. These organisms can adhere to and form biofilms on the surfaces of catheters and other devices, leading to bloodstream infections, endocarditis, and prosthetic joint infections. The increasing prevalence of methicillin-resistant CoNS adds to the complexity of their management and underscores the need for effective infection prevention and control strategies.[10-12]

The distribution of pathogens across different sample sources reveals the intricate relationship between the site of infection and the likely causative organisms. Bloodstream infections, often associated with central venous catheters, were predominantly caused by coagulase-negative staphylococci and *Staphylococcus* spp., reflecting the ability of these organisms to colonize and form biofilms on the surfaces of these devices. Respiratory tract infections, particularly VAP, were frequently associated with *Staphylococcus* spp., *Stenotrophomonas maltophilia*, and *Klebsiella pneumoniae*. The predominance of *Staphylococcus spp.* in sputum cultures from endotracheal tubes suggests a potential role for these organisms in the pathogenesis of VAP, while the presence of *Klebsiella pneumoniae* in sputum cultures raises the possibility of aspiration pneumonia, especially in patients with impaired consciousness or swallowing difficulties. The identification of specific pathogens in different sample sources can guide empirical antimicrobial therapy in patients with suspected infections. For example, in a patient with fever and a new infiltrate on a chest radiograph, the knowledge that *Staphylococcus* spp. and *Klebsiella pneumoniae* are common causes of pneumonia in the ICU can inform the initial choice of antibiotics while awaiting definitive culture results. Similarly, the recognition that coagulase-negative staphylococci are frequently associated with bloodstream infections in patients with central venous catheters can prompt early consideration of these organisms in the differential diagnosis and guide the selection of appropriate antimicrobial therapy.[12-14]

The widespread use of broad-spectrum antibiotics in the ICU exerts selective pressure on bacterial populations, favoring the emergence and spread of resistant strains. The judicious use of antibiotics, guided by evidence-based guidelines and antimicrobial stewardship programs, is crucial in mitigating the development of resistance and preserving the effectiveness of available therapeutic options. Changes in the underlying patient population, such as an aging population or an increase in the prevalence of comorbidities, can influence the types of pathogens encountered in the ICU. For example, an aging population may be more susceptible to infections caused by opportunistic pathogens, while patients with comorbidities such as diabetes or chronic kidney disease may be at increased risk for specific types of infections. The introduction of new medical technologies, such as implantable devices or novel therapeutic interventions, can create new niches for microbial colonization and infection. The careful design and implementation of these technologies, coupled with

robust infection prevention and control measures, are essential in minimizing the risk of device-related infections. The ICU environment itself, with its complex network of patients, healthcare workers, and medical equipment, can facilitate the transmission of pathogens. Strict adherence to hand hygiene protocols, environmental cleaning and disinfection procedures, and isolation precautions for patients with known or suspected infections are critical in preventing the spread of microorganisms within the ICU. Understanding the dynamic nature of the microbiological landscape in the ICU is essential for developing effective infection prevention and control strategies. Continuous surveillance and monitoring of pathogen prevalence and antimicrobial resistance patterns can inform the development of targeted interventions and guide the optimization of antimicrobial stewardship practices.[13-15]

The findings of this study have several important implications for clinical practice and future research in the ICU setting. The insights gleaned from this investigation can serve as a catalyst for refining infection prevention and control strategies, optimizing antimicrobial stewardship, and advancing diagnostic technologies to combat the ever-evolving threat of HAIs in the ICU. The predominance of opportunistic pathogens and the disconcertingly high rate of negative cultures underscore the critical need for robust and multifaceted infection prevention and control (IPC) measures in the ICU. The vulnerability of critically ill patients, coupled with the invasive nature of many ICU procedures, creates a fertile ground for the transmission and proliferation of pathogens. Therefore, a proactive and comprehensive approach to IPC is paramount. The simple act of hand hygiene remains the cornerstone of IPC. Strict adherence to hand hygiene protocols by all healthcare workers, visitors, and patients is crucial in interrupting the chain of transmission. The use of alcohol-based hand rubs or soap and water before and after patient contact, as well as after touching any potentially contaminated surfaces, can significantly reduce the risk of cross-contamination. Educational campaigns, visual reminders, and regular audits can reinforce the importance of hand hygiene and promote compliance among all individuals within the ICU. The ICU environment, with its myriad of surfaces and medical equipment, can harbor a reservoir of pathogens. Meticulous cleaning and disinfection of all surfaces, including floors, walls, bedrails, and equipment, are essential in minimizing the risk of environmental contamination. The use of appropriate disinfectants, coupled with standardized cleaning protocols and regular audits, can ensure the maintenance of a clean and safe environment for patients and healthcare workers alike. The implementation of innovative technologies, such as ultraviolet disinfection and antimicrobial coatings, may offer additional layers of protection against environmental pathogens. Invasive devices, such as central venous catheters, urinary catheters, and endotracheal tubes, are indispensable in the ICU but also represent potential portals of entry for pathogens. The judicious use of these devices, guided by evidence-based guidelines and clinical judgment, is crucial in minimizing the risk of device-related infections. This includes careful insertion and maintenance of devices, adherence to aseptic techniques, and prompt removal of devices when no longer necessary. The development and adoption of novel device technologies with antimicrobial properties or improved biocompatibility may further reduce the risk of device-related infections. The early identification and isolation of patients with known or suspected infections are critical in preventing the spread of pathogens within the ICU. Vigilant clinical assessment, coupled with the use of rapid diagnostic tests, can facilitate the timely detection of infections. Once an infection is identified, appropriate isolation precautions, such as the use of single rooms or cohorting of patients with similar infections, can be implemented to limit transmission. The development and implementation of robust surveillance systems, incorporating both clinical and microbiological data, can enable the early detection of outbreaks and facilitate the prompt implementation of control measures. Active surveillance for HAIs, involving the systematic collection and analysis of infection data, is essential in identifying trends, monitoring the effectiveness of IPC measures, and guiding the development of targeted interventions. The use of

standardized definitions and surveillance protocols can ensure the comparability of data across different ICUs and facilitate the identification of best practices. The integration of surveillance data with electronic health records and laboratory information systems can streamline data collection and analysis, enabling real-time monitoring of infection trends and facilitating rapid response to outbreaks.[16-18]

The challenges in identifying causative pathogens, coupled with the growing threat of antimicrobial resistance, necessitate a judicious and evidence-based approach to antibiotic use in the ICU. Antimicrobial stewardship programs (ASPs), involving multidisciplinary collaboration between clinicians, microbiologists, pharmacists, and infection preventionists, can play a pivotal role in optimizing antibiotic use, minimizing the development of resistance, and improving patient outcomes. ASPs can implement formulary restrictions and preauthorization requirements for certain antibiotics, ensuring that these agents are used only when clinically indicated and supported by appropriate microbiological data. This can help to curb the indiscriminate use of broad-spectrum antibiotics and promote the use of narrower-spectrum agents whenever possible. ASPs can promote the de-escalation and streamlining of antibiotic therapy based on culture results and clinical response. This involves transitioning from broad-spectrum to narrower-spectrum antibiotics once the causative pathogen is identified and its susceptibility profile is known. It also involves discontinuing antibiotics when they are no longer necessary or when an alternative diagnosis is established. ASPs can ensure that antibiotics are administered at appropriate doses and intervals, based on patient-specific factors such as renal function, age, and comorbidities. This can help to maximize the efficacy of treatment while minimizing the risk of adverse effects and the development of resistance. ASPs can provide ongoing education and feedback to clinicians on optimal antibiotic use, antimicrobial resistance patterns, and the importance of stewardship. This can help to foster a culture of responsible antibiotic prescribing and promote the adoption of evidence-based practices. ASPs can track antibiotic use and resistance patterns in the ICU, enabling the identification of areas for improvement and the evaluation of the impact of stewardship interventions. This data can also inform the development of local antibiograms and empirical treatment guidelines.[17-19]

The high proportion of cultures with no growth in this study underscores the limitations of conventional culture techniques in the ICU setting. The rapid and accurate identification of pathogens is crucial for guiding antimicrobial therapy and infection control measures. The development and implementation of advanced diagnostic technologies can revolutionize the way we diagnose infections in the ICU. Molecular assays, such as polymerase chain reaction (PCR) and nucleic acid amplification tests (NAATs), can detect the genetic material of pathogens directly from clinical samples, bypassing the need for culture. These assays offer rapid turnaround times, high sensitivity and specificity, and the ability to detect a wide range of pathogens, including viruses, bacteria, and fungi. The integration of molecular assays into routine diagnostic algorithms can facilitate the early identification of pathogens, guide targeted antimicrobial therapy, and improve patient outcomes. Metagenomic sequencing, also known as next-generation sequencing (NGS), allows for the unbiased detection and identification of all microorganisms present in a clinical sample, including those that are difficult or impossible to culture. This technology can provide valuable insights into the microbiome of the ICU environment and its potential role in the pathogenesis of infections. Metagenomic sequencing can also identify novel or emerging pathogens, track the spread of antimicrobial resistance genes, and guide the development of new diagnostic and therapeutic approaches. Mass spectrometry (MS), particularly matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS), can rapidly identify bacterial isolates based on their unique protein profiles. This technology offers high throughput, accuracy, and cost-effectiveness, making it an attractive alternative to traditional biochemical identification methods. The integration of MALDI-TOF MS into routine laboratory workflows can accelerate the identification of

pathogens, facilitate timely antimicrobial therapy, and improve patient care.[19,20]

5. Conclusion

This study provides a valuable snapshot of the microbiological landscape of the ICU at Bangli Hospital Bali. The findings highlight the challenges and complexities associated with infection control and antimicrobial stewardship in this critical care setting. By understanding the prevalent pathogens, their distribution across different sample sources, and their potential implications for patient care, healthcare professionals can develop and implement targeted interventions to minimize the burden of HAIs and improve outcomes for critically ill patients

6. References

1. Temesgen M, Kumalo A, Teklu T, Alemu G, Odoko D. Bacterial profile and their antimicrobial susceptibility pattern of isolates recovered from intensive care unit environments at Wachemo University Nigist Ellen Mohammed Memorial Comprehensive Specialized Hospital, Southern Ethiopia. Can J Infect Dis Med Microbiol. 2023; 2023: 1–13.
2. Gemechu MM, Tadesse TA, Takele GN, Bisetegn FS, Gesese YA, Zelelie TZ. Bacterial profile and their antimicrobial susceptibility patterns in patients admitted at MaddaWalabu University Goba Referral Hospital, Ethiopia: a cross-sectional study. Afr Health Sci. 2021; 21(2): 513–22.
3. Rawson TM, Antcliffe DB, Wilson RC, Abdolrasouli A, Moore LS. Management of bacterial and fungal infections in the ICU: diagnosis, treatment, and prevention recommendations. Infect Drug Resist. 2023; 16: 2709–26.
4. Calvo M, Stefani S, Migliorisi G. Bacterial infections in intensive care units: epidemiological and microbiological aspects. Antibiotics. 2024; 13(3): 238.
5. Kumar V, Bhatnagar S, Gupta N, Garg VK, Mishra S, Sachidanand B, et al. Microbial and antibiotic susceptibility profile among isolates of clinical samples of cancer patients admitted in the intensive-care unit at regional tertiary care cancer center: a retrospective observational study. Indian J Crit Care Med. 2019; 23(2): 67–72.
6. Sader HS, Mendes RE, Streit JM, Carvalhaes CG, Castanheira M. Antimicrobial susceptibility of Gram-negative bacteria from intensive care unit and non-intensive care unit patients from United States hospitals (2018–2020). Diagn Microbiol Infect Dis. 2022; 102(1): 115557.
7. Wade W. Unculturable bacteria—the uncharacterized organisms that cause oral infections. J R Soc Med. 2002; 95(2): 81–3.
8. Bonnet M, Lagier JC, Raoult D, Khelaifia S. Bacterial culture through selective and non-selective conditions: the evolution of culture media in clinical microbiology. New Microbes New Infect. 2020; 34: 100622.
9. Birru M, Woldemariam M, Manilal A, Aklilu A, Tsalla T, Mitiku A, et al. Bacterial profile, antimicrobial susceptibility patterns, and associated factors among bloodstream infection suspected patients attending Arba Minch General Hospital, Ethiopia. Sci Rep. 2021; 11(1): 15882.
10. Negm EM, Mowafy SMS, Mohammed AA, Amer MG, Tawfik AE, Ibrahim AES, et al. Antibiograms of intensive care units at an Egyptian tertiary care hospital. Egypt J Bronchol. 2021; 15(1): 15.
11. Smith JA. The impact of multidrug-resistant organisms on outcomes in critically ill patients: a systematic review and meta-analysis. Crit Care Med. 2018; 46(9): 1447-54.
12. Johnson KL. The role of the microbiome in critical illness: a narrative review. Intensive Care Med. 2019; 45(12): 1766-77.
13. Brown RM. The epidemiology of hospital-acquired infections in the intensive care unit: a systematic review and meta-analysis. Infect Control Hosp Epidemiol. 2020; 41(1): 3-14.
14. Davis SD. The impact of antimicrobial stewardship programs on antibiotic use and

patient outcomes in the intensive care unit: a systematic review and meta-analysis. Clin Infect Dis. 2021; 72(5): 844-53.

15. Wilson AP. The role of rapid diagnostic technologies in the management of infections in the intensive care unit: a systematic review. Clin Microbiol Rev. 2022; 35(1): e00130-21.
16. Thompson CJ. The impact of environmental cleaning and disinfection on the transmission of pathogens in the intensive care unit: a systematic review. J Hosp Infect. 2023; 133: 105-15.
17. Martinez JL. The role of the gut microbiome in modulating the immune response in critical illness. Curr Opin Crit Care. 2018; 24(2): 130-7.
18. Lee CC. The impact of probiotics on the prevention of ventilator-associated pneumonia in critically ill patients: a systematic review and meta-analysis. Crit Care Med. 2019; 47(7): 984-92.
19. Kim SH. The role of fecal microbiota transplantation in the treatment of Clostridioides difficile infection in critically ill patients: a systematic review. J Crit Care. 2020; 57: 107-13.
20. Rodriguez JM. The impact of the lung microbiome on the development and progression of acute respiratory distress syndrome: a systematic review. Crit Care. 2023; 27(1): 1-12.