ORIGINAL RESEARCH REPORT

ESKAPE Pathogens in Hospitalized Patients: A Comprehensive Profiling of Infections and Characteristics at Universitas Airlangga Hospital, Surabaya, Indonesia

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ABSTRACT

Background: Infections pose a significant threat in Indonesia, particularly in healthcare settings where healthcare-associated infections (HAIs) are prevalent. At a hospital in Jakarta, the prevalence of ESKAPE pathogens was reported to be 69.8%. However, detailed data on the infection profiles of these pathogens remain scarce. This underscores the importance of studying ESKAPE pathogenic bacteria to better understand their characteristics. **Objective:** This study aimed to determine the infection profile of ESKAPE pathogens in hospitalized patients at Universitas Airlangga Hospital, Surabaya, Indonesia in 2022. **Material and Method:** This descriptive observational study employed a retrospective design using secondary data from non-ICU inpatients at Universitas Airlangga Hospital infected with ESKAPE pathogens in 2022. Total sampling was applied to eligible medical records. **Result:** The study included 119 specimens from inpatients infected with ESKAPE pathogens that met the inclusion and exclusion criteria. Of these, 78% were Gram-negative bacterial infections, with *Klebsiella pneumoniae* being the most prevalent (29%). Sputum was the most commonly collected specimen (49%). Most patients were male (57%), aged 56–65 years (29%), and had no comorbidities (46%). Additionally, 63% of patients had used invasive devices during hospitalization. The majority were admitted to low-care inpatient wards. The primary clinical features were neurological complaints (29%) and respiratory disorders (37%), predominantly associated with *Klebsiella pneumoniae*. **Conclusion:** ESKAPE infections were primarily caused by *Klebsiella pneumoniae*, a Gram-negative bacterium, most frequently identified in sputum samples. The predominant clinical manifestations were decreased consciousness and respiratory disorders. Affected patients were mainly male, aged ≥56 years, hospitalized in low-care wards, with a history of invasive device use and no comorbidities.

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Highlights

1. This study found that ESKAPE pathogenic infections at Universitas Airlangga Hospital were dominated by Gram-negative bacteria, particularly *Klebsiella pneumoniae*, with sputum as the most commonly collected specimen providing valuable data for infection control strategies.
2. Most patients exhibited significant clinical manifestations involving neurological disorders, with the respiratory system being the most affected information that may enhance the effectiveness of patient management in the hospital.

BACKGROUND

Infectious diseases are illnesses caused by microorganisms, including bacteria (Ministry of Health of The Republic of Indonesia, 2021). In developing countries like Indonesia, they pose a serious threat, potentially leading to illness, complications, and even death. The transmission of infectious diseases frequently occurs in healthcare facilities, particularly hospitals, and is referred to as nosocomial infections or healthcare-associated infections (HAIs). Nosocomial infections are a major concern in healthcare due to their high prevalence and significant impact on patient outcomes.

The full impact of nosocomial infections is difficult to quantify. However, it is estimated that over 24% of affected patients develop sepsis (a bloodstream bacterial infection), and 52.3% of intensive care unit (ICU) patients die each year due to these infections. Mortality rates increase two to threefold in cases involving antimicrobial-resistant infections (World Health Organization, 2022). The prevalence of nosocomial infections in developing countries ranges from 3.5% to 12%, while in Indonesia, the incidence is around 15.74%, with reported variations between 4.8% and 15.5% (Rahmawati & Dhamanti, 2021).

One of the most common groups of pathogens responsible for nosocomial infections globally is known as the ESKAPE pathogens (Irzal, et al., 2021). The acronym ESKAPE stands for *Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa,* and *Enterobacter species* (Mulani, et al., 2019). These organisms are categorized as Multidrug-Resistant Organisms (MDROs), meaning they are resistant to at least one antibiotic in three or more classes of antibiotics, and they represent a serious global health threat (Estiningsih, et al., 2016).

The rise of MDRO resistance is occurring much faster than the development of new antibiotics (World Health Organization, 2022). As a result, infections caused by ESKAPE pathogens are becoming increasingly difficult to manage, leading to higher risks of transmission, severe illness, and mortality. This trend also threatens to undermine progress in modern medicine. The economic burden of MDRO infections is projected to reach USD 100 trillion, equivalent to approximately IDR 1,496,865 trillion (World Health Organization, 2022). Given these challenges, early identification and prevention of ESKAPE pathogen infections are crucial. Unfortunately, research on ESKAPE infections in Indonesia remains limited.

OBJECTIVE

This study aimed to determine the infection profile and characteristics of ESKAPE pathogenic bacteria in hospitalized patients at Universitas Airlangga Hospital in 2022.

MATERIAL AND METHOD

This descriptive observational study utilized secondary data from hospitalized patients at Universitas Airlangga Hospital, Surabaya, Indonesia, who were infected with ESKAPE pathogens. Conducted retrospectively, the study included medical records of non-ICU inpatients from 2022, with collected data encompassing age, gender, medical history, ward type, clinical manifestations, affected organ systems, and pathogen characteristics. Data collection was carried out through total sampling of all eligible medical records.

The study was conducted in the inpatient wards and microbiology laboratory of Universitas Airlangga Hospital, Surabaya, between July 2023 and February 2024. Data were processed using Microsoft Excel 2016 (Microsoft Corp., Redmond, WA, USA) and presented in tables and graphs to display frequencies and percentages, followed by descriptive analysis.

The study complied with ethical guidelines set by the Health Research Ethics Committee of Universitas Airlangga Hospital, with protocol number UA-02-23178, approved on 11-09-2023.

RESULT

Characteristics of ESKAPE pathogenic bacteria

In this study, 119 data that fit the criteria were obtained. Based on the data obtained, Gram-negative bacteria were the predominant pathogens infecting inpatients, accounting for 93 cases (78%), while Gram-positive bacteria were responsible for 21 cases (18%). A total of 5 cases (4%) involved co-infection with both Gram-negative and Gram-positive bacteria.

Regarding bacterial species and specimen sources, *Klebsiella pneumoniae* was the most frequently isolated pathogen (29%), including 17 cases (49%) of ESBL-producing strains. This was followed by *Pseudomonas aeruginosa* (28%), *Acinetobacter baumannii complex* (20%), *Staphylococcus aureus* (18%), *Enterobacter spp.* (14%), and Enterococcus faecalis (3%). Patients could be infected with more than one bacterial species.

Table 1. Characteristics of ESKAPE pathogenic bacteria.

Characteristics of bacteria	n (%)
Gram stain	
Gram-negative	93 (78%)
Gram-positive	21 (18%)
Gram-negative and Gram-positive	5 (4%)
Species	
Klebsiella pneumoniae	35 (29%)
Klebsiella pneumoniae ESBL	17 (49%)
Pseudomonas aeruginosa	33 (28%)
Acinetobacter baumannii complex	24 (20%)
Acinetobacter baumannii	16 (67%)
Staphylococcus aureus	22 (18%)
Enterobacter spp	17 (14%)
Enterobacter aerogenes	1 (6%)
Enterobacter cloacae complex	16 (94%)
Enterococcus faecalis	4 (3%)
Specimen	
Sputum	58 (49%)
Tissues/Wounds	35 (29%)
Urine	14 (12%)
Blood	8 (7%)
Urogenital swab	4 (3%)
Cerebrospinal fluid (CSF)	2 (2%)
Abdominal fluid	3 (3%)

n = total sampling

Specimens were collected from sputum (49%), tissue/wound samples (29%), urine (12%), blood (7%), urogenital swabs (3%), cerebrospinal fluid (CSF) (2%), and abdominal fluid (3%). In some cases, multiple samples were taken from a single patient, and more than one bacterial species could be isolated from a single specimen.

In sputum specimens, the most commonly found bacterium was *Klebsiella pneumoniae* (32%). *Acinetobacter baumannii* was most frequently found in blood specimens (25%), while *Pseudomonas aeruginosa* was predominant in urine specimens (33%). *Staphylococcus aureus* was most commonly isolated from urogenital swabs (40%) and was also found in tissue/pus specimens (33%), along with *Pseudomonas aeruginosa* (33%). In CSF specimens, only *Acinetobacter baumannii* (50%) and *Klebsiella pneumoniae* (50%) were found. In abdominal fluid specimens, *Staphylococcus aureus* (33%), *Pseudomonas aeruginosa* (33%), and *Enterobacter spp*. (33%) were each identified.

Profile of hospitalized patients infected with ESKAPE pathogenic bacteria

The data show that the majority of patients infected with ESKAPE pathogenic bacteria were male, accounting for 68 patients (57%), while females comprised 51 patients (43%).

In terms of age distribution, most patients were categorized as late elderly (29%), followed by senior citizens (26%), early elderly (18%), early adulthood (11%), late adolescence (5%), middle adulthood and toddler age groups (each 4%), and early adolescence (2%). No cases were recorded in the childhood category.

Table 2. Profile of hospitalized patients infected with ESKAPE pathogenic bacteria.

Characteristics of patients	n (%)
Gender	
Male	68 (57%)
Female	51 (43%)
Age	
Late elderly (56-65 y.o)	35 (29%)
Senior citizen (>65 y.o)	32 (26%)
Early elderly (46-55 y.o.)	21 (18%)
Early adulthood (26-35 y.o.)	13 (11%)
Late adolescence (17-25 y.o.)	6 (5%)
Middle adulthood (36-45 y.o.)	5 (4%)
Toddler (0-5 y.o.)	5 (4%)
Early adolescence (12-16 y.o.)	2 (2%)
Childhood (5-11 y.o.)	0 (0%)
Comorbidities	
Diabetes Mellitus	46 (39%)
Hypertension	15 (13%)
Tuberculosis	4 (3%)
Malignancy	2 (2%)
HIV	2 (2%)
Not recorded	55 (46%)
The Use of Invasive Devices	
Not using	75 (63%)
Urinary catheter	36 (30%)
Ventilator	21 (18%)
Central Venous Catheter (CVC)	10 (8%)
Inpatient Wards	
RSUA	104 (87%)
Low-care wards (IRNA)	74 (71%)
High-care units (HCU & Stroke unit)	30 (29%)
RSKI	15 (13%)
Low-care wards (IRNA)	14 (93%)
High-care units (HCU)	1 (7%)

n = total sampling

Legends: HIV: Human Immunodeficiency Virus; IRNA: Instalasi Rawat Inap (Inpatient Wards); HCU: High-care Unit; RSUA: Rumah Sakit Universitas Airlangga (Universitas Airlangga Hospital); RSKI : Rumah Sakit Khusus Infeksi (Part of Universitas Airlangga Hospital which specializes in infectious diseases).

Regarding comorbidities, 46 patients (39%) had Diabetes Mellitus, 15 (13%) had hypertension, 4 (3%) had tuberculosis, 2 (2%) had malignancy, and 2 (2%) had HIV. Meanwhile, 55 patients (46%) had no comorbidities. Some patients presented with multiple comorbidities.

Use of invasive devices was noted in some patients, with urinary catheters being the most common (30%), followed by ventilators (18%) and central venous catheters (CVCs) (8%). The majority of patients (63%) did not use any invasive devices. It is possible for patients to have used more than one type of invasive device or none at all.

Regarding inpatient wards, patients were distributed between two hospital divisions: RSUA and RSKI. Of the 119 patients, 87% were treated at RSUA—mostly in low-care wards (71%)—while 13% were admitted to RSKI, predominantly in low-care wards (93%).

Clinical features of ESKAPE pathogenic bacterial infections

The data indicate that patients may present with more than one clinical feature. Various clinical manifestations were observed: 29% of patients reported neurological complaints, 18% were postoperative, 18% experienced shortness of breath, 15% had fever, 11% had cough, 9% reported pain, and 1% had diarrhea. Additionally, 24% of patients had unrecorded or unspecified symptoms.

Table 3. Clinical features of ESKAPE pathogenic bacterial infections.

Clinical features	n (%)
Neurological complaints	35 (29%)
Postoperative	22 (18%)
Shortness of breath	22 (18%)
Fever	18 (15%)
Cough	13 (11%)
Pain	11 (9%)
Diarrhea	1 (1%)
Other	28 (24%)

n = total sampling

Organ system manifestations infected with ESKAPE pathogenic bacteria

This variable includes seven organ system divisions, with the respiratory system being the most commonly affected (37%), followed by the nervous system (20%), integumentary system (16%), urogenital system (15%), circulatory system (6%), and digestive system (6%).

Within these systems, the predominant bacteria were as follows: *Klebsiella pneumoniae* was most common in the respiratory system (36%) and nervous system (27%); *Staphylococcus aureus* predominated in the integumentary system (49%); *Pseudomonas aeruginosa* was the leading pathogen in both the urogenital system (30%) and circulatory system (37%). In the digestive system, *Klebsiella pneumoniae* and *Enterobacter* spp. were equally prevalent, each accounting for 29% of isolates.

Table 4. Organ system manifestations infected with ESKAPE pathogenic bacteria.

Organ system	n (%)
Respiratory system	44 (37%)
Nervous system	24 (20%)
Integumentary system	19 (16%)
Urogenital system	18 (15%)
Circulatory system	7 (6%)
Digestive system	7 (6%)

n = total sampling

DISCUSSION

Characteristics of ESKAPE pathogenic bacterial infections

Based on Gram staining

In this study, the most dominant ESKAPE pathogenic bacteria infecting RSUA inpatients were Gram-negative bacteria. This finding aligns with the study by Alhumaid, et al., (2021) in Saudi Arabia, which reported that 71.9% of bacteria isolated from healthcare-associated infections (HAIs) were Gram-negative. However, studies by Hamdiyati, et al., (2016) in Bali and Belete, et al., (2019) in Ethiopia found a higher prevalence of Gram-positive bacteria, ranging from 68% to 70%. These differences may be attributed to variations in the types of diseases affecting patients across different regions.

Moreover, there is a lack of focused research specifically on ESKAPE pathogenic bacteria; most previous studies have investigated bacteria in general rather than exclusively targeting ESKAPE pathogens (Karyanti & Faisha, 2022). It is also important to note that four out of the six ESKAPE bacteria are Gram-negative, which naturally leads to a predominance of Gram-negative isolates (Domalaon, et al., 2018). Among the ESKAPE group, *Enterococcus faecium* and *Staphylococcus aureus* are Gram-positive, while the other four species are Gram-negative. In this study, *Enterococcus faecium* was not detected in any specimens; however, due to its genetic similarity with Enterococcus faecalis, data from *E. faecalis*, also a Gram-positive bacterium, were used as a substitute (Horner, et al., 2021).

Based on their species

In this study, the most commonly isolated species was *Klebsiella pneumoniae*, accounting for 29% of cases. As a Gram-negative bacterium, this finding is consistent with the predominance of Gram-negative ESKAPE pathogens identified through Gram staining. According to Ashurst & Dawson, (2025), *Klebsiella pneumoniae* is a common cause of nosocomial bacterial infections. They also noted that the carriage rate of *K. pneumoniae* is significantly higher in hospitalized patients compared to the community.

Several factors influence the colonization and infection by *Klebsiella pneumoniae*, including admission to intensive care units, prolonged use of invasive devices, inadequate infection control measures, immunocompromised status, and extended use of broad-spectrum antibiotics (Ashurst & Dawson, 2025). A study by Wyres & Holt, (2018) reported that the widespread distribution of *Klebsiella pneumoniae* increases exposure to antimicrobial agents and bacterial contact, thereby facilitating the amplification and spread of antimicrobial resistance genes.

Based on the specimen taken

In this study, various specimens were collected, with sputum being the most common specimen type (49%). This finding corresponds with the predominance of *Klebsiella pneumoniae* among the ESKAPE bacterial infections identified. Infection by *Klebsiella pneumoniae* is typically confirmed through analysis of body fluids such as blood, urine, and sputum (Tarina & Kusuma, 2017). According to surveillance data on multidrug-resistant organisms (MDRO) in Indonesian hospitals, *Klebsiella pneumoniae* was most frequently isolated from sputum specimens (41.3%), followed by urine, pus, and blood samples (Association of Indonesian Clinical Pathology and Laboratory Medicine Specialists, 2018).

Distribution of ESKAPE pathogenic bacteria

Based on the patient's gender

This study found that 57% of patients with ESKAPE infections were male, while 43% were female. This finding aligns with Li, et al., (2021), who reported that males comprised 61.1% of patients with ESKAPE infections. However, their study focused exclusively on burn patients. In contrast, Pandey, et al., (2021) observed a predominance of female patients, with 55.1% (249 patients) female and 44.9% (203 patients) male.

Based on the patient's age

The age distribution of patients with ESKAPE pathogenic bacterial infections was predominantly in the late elderly group (56–65 years), comprising 35 patients (29%). This was comparable to the elderly group (>65 years), which included 32 patients (26%). These findings aligned with Pandey et al., (2021), who reported that the majority of patients infected with ESKAPE bacteria were aged 61–70 years. The higher prevalence in these age groups may be attributed to various physical and psychological changes, as well as the presence of chronic diseases common among older adults (Raudhoh & Pramudiani, 2021).

Based on the patient's comorbidities

In this study, comorbidity data were often missing from patient medical records. As many as 55 patients had no documented comorbidities. This absence may be due to either the actual lack of comorbid conditions or incomplete medical record documentation. Among recorded comorbidities, diabetes mellitus was the most prevalent, affecting 46 patients (39%), followed by hypertension in 15 patients (13%). These findings are consistent with those of Founou, et al., (2018), who reported that individuals with compromised immune systems, such as those with cardiovascular disease, diabetes, chronic kidney disease, or malignancy are particularly vulnerable to infections. Additionally, (Li, et al., 2022) highlighted an association between diabetes and infections caused by ESKAPE pathogenic bacteria.

Based on the use of invasive devices

In this study, 63% of patients did not use invasive devices, which may reflect either the absence of such devices or incomplete documentation in medical records. Among invasive devices, urinary catheters were the most commonly used, present in 30% of patients. Hariati, et al., (2019) reported that 43.9% of patients with urinary tract infections, predominantly caused by *Escherichia coli*, had urinary catheters. Although urinary catheter use carries a risk of infection, Bennett, et al., (2018) found that catheter insertion was not statistically significant as a risk factor. Nevertheless, invasive devices remain a significant risk factor for healthcare-associated infections (HAIs). Bennett, et al., (2018) further identified endotracheal tubes (ETTs) as the most significant risk factor for HAIs, with urinary catheters and central venous catheters (CVCs) also contributing to infection risk. The duration of invasive device use is a critical factor, as prolonged exposure increases the likelihood of microbial entry and infection. It should be noted that this study excluded ICU patients; thus, the findings may not be generalizable to ICU populations.

Based on inpatient ward

This study collected data from the medical records of inpatients at RSUA and RSKI hospitals. Patients in both hospitals were categorized into high-care units and low-care wards. Within the high-care category, only data from the High Care Unit (HCU) and stroke unit were included. Patients from the ICU were excluded. Most patients in both hospitals were treated in low-care wards, accounting for 71% at RSUA and 93% at RSKI. According to Masoud, et al., (2022), ICU patients have a higher risk of infection with ESKAPE pathogenic bacteria compared to those in general inpatient wards. This finding is supported by Ayobami, et al., (2022). While patients in low-care wards can also be infected with ESKAPE bacteria, their risk is lower than that of ICU patients.

Clinical features of ESKAPE pathogenic bacterial infections

The clinical presentation in this study showed that neurological complaints were the most common, reported in 29% of patients. *Klebsiella pneumoniae* was the predominant pathogenic bacterium associated with these neurological symptoms. Besides causing pneumonia, *Klebsiella pneumoniae* can also infect the central nervous system (CNS), leading to conditions such as meningitis and brain abscesses. CNS infections often result in decreased consciousness (Public Health Agency of Canada, 2025). Although *Klebsiella pneumoniae*-induced brain abscesses are relatively rare, its role in nosocomial CNS infections should not be overlooked, particularly in Asia (Zhao, et al., 2022). Additionally, *Klebsiella pneumoniae* infections carry risks of respiratory failure, septic shock, and other complications that may contribute to altered consciousness (Chen, et al., 2024).

The exact cause of decreased consciousness in these patients remains unclear. Most were admitted to the stroke unit, with preexisting neurological diagnoses and comorbidities prior to bacterial infection. Determining whether decreased consciousness is directly due to infection can be guided by monitoring therapeutic response. Improvement following antibiotic treatment suggests infection as the cause. However, decreased consciousness itself can predispose patients to infections in various organs, as immunosuppression in such patients increases vulnerability to bacterial infections (Aleem, et al., 2025)

Organ system manifestations infected with ESKAPE pathogenic bacteria

In this study, the respiratory system was the most frequently infected organ system, accounting for 37% of cases. *Klebsiella pneumoniae*, a key pathogen in respiratory infections, urinary tract infections, nosocomial infections, and associated mortality, is well-documented for its virulence mechanisms (Paczosa & Mecsas, 2016). This bacterium produces an extracellular polysaccharide capsule that protects it from host phagocytosis, enhancing its survival. Additionally, *Klebsiella pneumoniae* can form biofilms, particularly in catheterized patients, serving as persistent infection sources. The bacterium predominantly affects immunocompromised individuals and can cause a range of severe infections including pyogenic hepatic abscess, meningitis, necrotizing fasciitis, endophthalmitis, and severe pneumonia. Its ability to evade phagocytosis contributes to lung infections and severe pneumonia. Key virulence factors include capsular polysaccharides (CPSs), lipopolysaccharides

(LPSs), fimbriae, outer membrane proteins (OMPs), and iron-binding siderophores (Abbas, et al., 2024).

Strength and limitations

This study enhances understanding of ESKAPE pathogens by providing valuable insights into their involvement in hospital-acquired infections, thereby addressing gaps in the limited literature on multidrug-resistant bacteria. However, the study has limitations is the exclusion of ICU patients restricts the ability to compare infection patterns in this high-risk group, and incomplete medical records may introduce bias, potentially affecting data accuracy and the generalizability of the findings.

CONCLUSION

In this study conducted at Universitas Airlangga Hospital, Surabaya, Indonesia infections caused by ESKAPE pathogenic bacteria were frequently identified, with Gram-negative bacteria predominating. Klebsiella pneumoniae emerged as the most prevalent species. Sputum samples were the most commonly collected specimens for bacterial culture. Among the clinical presentations, neurological complaints were most common, followed by respiratory system manifestations, which were often linked to *Klebsiella pneumoniae* infections.

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Conflict of Interest

None.

Ethic Consideration

This study adhered to ethical guidelines and received approval from the Research Ethics Committee of Universitas Airlangga Hospital (certificate number UA-02-23178, approved on 11-09-2023).

Funding Disclosure

None.

Author Contribution

DRH contributed to the conception and design, analysis and interpretation of the data, drafting of the article, critical revision of the article for important intellectual content. TPA, FS, and PDE contributed to the critical revision of the article for important intellectual content and final approval of the article.

Data Availability

None.

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