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Original Research Article

Antibiotic Resistance Profiles in Septicaemia: A Retrospective Study of Gram-Positive and Gram-Negative Bacteria

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ABSTRACT

Septicaemia, a severe systemic inflammatory response caused by bloodstream bacterial infection, is frequently associated with gram-negative bacteria and high morbidity and mortality. Antibiotic resistance complicates treatment, necessitating research on resistance patterns to guide empirical therapy. This study aimed to investigate the aetiology of septicaemia and its associated antibiotic resistance patterns in patients at PKU Muhammadiyah Surakarta Hospital, Indonesia. A retrospective analysis of patients treated for bacterial infections (January–December 2022) was conducted using blood culture and antibiotic therapy data. Bacterial susceptibility was assessed via the BacT/Alert Blood Culture System, and statistical analysis was performed using SPSS version 25. Among 51 patients, 51% were male, and 84.3% were aged >65 years. Comorbidities included diabetes mellitus (15.7%) and hypertension (9.8%), with a mortality rate of 58.8%. Gram-positive bacteria predominated (66.7%), primarily *Staphylococcus aur*eus (49.0%), while gram-negative bacteria accounted for 33.3%, predominantly *Escherichia coli* (13.7%). *S. aureus* showed resistance to 17 antibiotics but remained susceptible to imipenem and vancomycin; *E. coli* exhibited significant multidrug resistance. These findings highlight the prevalence of Gram-positive pathogens and substantial Gram-negative resistance in septicaemia, underscoring the need for targeted antibiotic strategies to improve outcomes and combat resistance.

Keywords: Antibiotics Resistance Patterns, Gram-positive Bacteria, Gram-negative Bacteria, Septicaemia, Mortality

Introduction

Septicaemia is a systemic inflammatory response syndrome resulting from pathogenic bacterial invasion and proliferation in the bloodstream, accompanied by toxin release. Prolonged septicaemia can progress to multiple organ dysfunction and failure.[1] While both Gram-positive and Gram-negative bacteria may induce this condition, Gram-negative pathogens predominate, accounting for approximately 60–70% of cases.[2,3] The most prevalent Gram-negative causative organisms include *Klebsiella, Enterobacter, Escherichia coli (E. coli), Pseudomonas aeruginosa*, and *Neisseria* species.[4] Gram-positive bacteria, such as *Streptococcus*, *Staphylococcus aureus (S.aureus)*, and *Streptococcus pneumoniae.* also contribute to septicaemia. This condition frequently occurs in healthcare settings, particularly among postoperative patients, intensive care unit (ICU) patients requiring ventilator support, and elderly individuals with indwelling catheters. [5]

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Globally, septicaemia was associated with about 48.9 million cases and 11 million deaths in 2017.[6] A 2012 study conducted at the intensive care unit of Cipto Mangunkusumo Hospital in Jakarta over a one-month period found that 23 out of 84 patients were diagnosed with severe septicaemia, yielding a mortality rate of 47.8%.[7] A study investigating the relationship between gender and susceptibility to septicaemia have indicated that males exhibit a higher propensity for developing the condition.[8] Additionally, the majority of septicaemia cases are attributed to individuals aged 65 and older.[9] The condition is frequently comorbid with a variety of chronic diseases, such as chronic obstructive pulmonary disease, heart failure, diabetes mellitus, chronic kidney disease, malignancies, haematological disorders, HIV/AIDS, and systemic lupus erythematosus (SLE).[10] Age, pre-existing comorbidities, and the therapeutic strategies implemented substantially impact patients' prognoses.[8] The administration of antibiotics is a primary treatment for septicaemia. The antibiotics most frequently employed in the management of septicaemia include penicillins, cephalosporins, aminoglycosides, glycopeptides, lincosamides, tetracyclines, fluoroquinolones, and carbapenems.[11] The critical imperative to address antimicrobial resistance (AMR) underscores the importance of rational antibiotic use.[12–14] Bacterial plasmids and the ability to form biofilms can act as significant barriers, preventing antibiotics from effectively reaching target bacteria and thereby contributing to the development of antibiotic resistance.[15,16] Data from the national antimicrobial resistance survey by the Ministry of Health in 2016 indicate that multidrug-resistant organisms (MDRO), particularly *E.coli* and *Klebsiella pneumoniae* that produce extended-spectrum beta-lactamase (ESBL), exhibit resistance rates ranging from 50% to 82%.[17] Consequently, the selection of empirical antibiotics should be guided by the resistance

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patterns and bacterial profiles that are specific to the region or hospital.[18] This study aims to investigate the aetiology of septicaemia and its associated antibiotic resistance patterns in patients at PKU Muhammadiyah Surakarta Hospital, Indonesia.

Materials and Methods

Study Design

This retrospective study was conducted to compare antibiotic resistance patterns between gram-positive and gram-negative bacteria in septicaemia patients. This study was conducted at PKU Muhammadiyah Surakarta Hospital. All hospitalized patients diagnosed with bacterial infections, including diabetic ulcers, pneumonia, septicaemia, and urinary tract infections, were included. The study population comprised patients treated at the hospital between January and December 2022. Patients were selected through purposive sampling based on specific criteria, including prior antibiotic treatment and the collection of samples for blood, pus, sputum, or urine cultures.

Antibiotic Agents

The antibiotics included β-lactams such as amoxicillin (AMX), Clavulanate (AMC), ampicillin (AMP), and oxacillin (OXA), along with combinations like ampicillin/sulbactam (SAM) and piperacillin/tazobactam (TZP). Cephalosporins class used were cefadroxil (CFR), cefazolin (CZO), cefepime (FEP), cefixime (CFM), cefotaxime (CTX), cefoxitin (FOX), ceftazidime (CAZ), and ceftriaxone (CRO). Aminoglycosides such as amikacin (AMK), gentamicin (GENES), and kanamycin (KAN) were also included. Fluoroquinolones like ciprofloxacin (CIP), levofloxacin (LVX), and moxifloxacin (MFX) were used, alongside carbapenems such as imipenem (HDI) and meropenem (MEM). Other antibiotics listed were clindamycin (CLI), erythromycin (ERY), chloramphenicol (CHL), colistin sulphate (COL), doxycycline (DOX), fosfomycin (FOS), tetracycline (TCY), cotrimoxazole (SXT), and vancomycin (VAN).

Processing and Identification

Blood specimens from study participants were obtained in accordance with established microbiological protocols. All samples were transported aseptically to the microbiology department at PKU Muhammadiyah Hospital for culture and antimicrobial susceptibility testing. Blood culture bottles and blood agar plates were used to inoculate all samples. The blood culture bottles were incubated at 37°C in an incubator with 5% CO_2 for five to seven days. Each plate was incubated according to the specimen type and the expected organism. Bacterial isolates were characterised by colony morphology and haemolytic activity. Conventional techniques, such as Gram staining, catalase testing, slide coagulase testing, and tube coagulase testing, were employed.[19]

Bacterial Identification and Antimicrobial Susceptibility Testing

This study utilised the VITEK 2 Compact System BacT/Alert Blood Culture System (bioMérieux, France) for bacterial identification and antimicrobial susceptibility testing. The procedure followed the methods described by Gebremariam.[19] Data interpretation was conducted in accordance with the Clinical and Laboratory Standards Institute (CLSI) guidelines.[20]

Ethical Approval

The Health Research Ethics Committee (HREC) of the Dr. Moewardi Hospital granted ethical clearance with reference number 1083/XI/HREC/2023. All procedures were executed in accordance with pertinent guidelines and regulations, including the Declaration of Helsinki. Consent forms were obtained from all participants or their family members.

Data Analysis

Data entry and analysis were performed utilising the Statistical Package for the Social Sciences (SPSS) version 25 (IBM-SPSS Inc., Chicago, IL, USA). The gathered data were analysed utilising univariate methods, encompassing descriptive statistics, frequency distributions, and antimicrobial susceptibility testing.

Results and Discussion

Antibiotic resistance in septicaemia presents a formidable challenge in clinical practice, driven by the rising prevalence of resistant strains among both Gram-positive and Gram-negative bacterial pathogens. Research indicates that resistance patterns vary considerably, with Gram-negative bacteria, such as *Escherichia coli* and *Klebsiella pneumoniae*, frequently exhibiting high levels of multidrug resistance.[21,22] Similarly, Gram-positive bacteria, notably *Staphylococcus aureus*, commonly demonstrate resistance to widely used antibiotics.[22] This escalating resistance underscores the pressing need for targeted research to manage and mitigate the impact of antibiotic resistance in septicaemia.[23]

Study Population and Demographics

A total of 51 septicaemia patients (26 [51%] men and 20 [49%] women) were enrolled. The age distribution showed a predominance of patients over 65 years old, accounting for 84.31% of the sample, while younger age groups (0-1, 13-18, and 19-65 years) were less represented. The outcomes indicated that 41.2% of the patients survived, while 58.8% died (Table 1).

Table 1: Characteristics of Patients

Characteristics	Freq.	Percentage
Gender		
Man	26	51 %
Woman	25	49 %
Age (Year)		
0-1	1	2 %
13-18	3	5.9 %
19-65	4	7.8 %
>65	43	84.31 %
Comorbid		
Diabetes mellitus	8	15.69 %
Hypertension	5	9.8 %
Chronic kidney failure	3	5.9 %
Pneumonia	4	7.8 %
Anemia	2	3.9 %
Outcomes		
Life	21	41.2 %
Died	30	58.8 %

These findings align with a 2022 study conducted in the intensive care unit of H. Adam Malik Hospital, Medan, which reported a higher incidence of sepsis among males (59.5%) than females.[24] A nationwide study in the United States further corroborated this trend, noting that male patients accounted for 63.8% of 187,587 septic shock episodes analysed.[25] Additionally, a significant proportion of this study (84.31%) were aged over 65 years, with younger age groups less represented. This observation is consistent with a California-based study, which found that over 60% of sepsis cases occurred in patients aged over 65.[26] The heightened susceptibility of elderly patients to sepsis may be attributed to a combination of factors, including impaired immune function, the

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presence of chronic comorbidities, and age-related physiological changes that increase vulnerability to infections.[27]

The prevalent comorbidities linked to septicaemia in this study were diabetes mellitus (15.69%), hypertension (9.8%), chronic kidney disease (5.9%), pneumonia (7.8%), and anaemia (3.9%). The Centres for Disease Control and Prevention (CDC) reported similar prevalent comorbidities: diabetes mellitus (35%), cardiovascular disease (32%), chronic kidney disease (23%), and chronic obstructive pulmonary disease (20%).[28] This study revealed a high mortality rate, with 58.8% of patients succumbing to septicaemia. Gram-positive bacteria were predominant, accounting for 66.67% of cases, with *Staphylococcus aureus* being the most frequently identified pathogen. Gram-negative bacteria comprised 33.33% of cases, with *Escherichia coli* as the most common isolate. These findings align with a previous study that reported Gram-positive bacteria as the leading cause of sepsis, surpassing Gram-negative bacteria.[5] Conversely, another study reported that 67% of sepsis cases were attributed to Gram-negative bacteria, with 37% involving Gram-positive bacteria, indicating a higher prevalence of Gram-negative pathogens.[2]

Prevalence of Gram-Positive and Gram-Negative causing Septicaemia

The results on the prevalence of Gram-positive and Gram-negative bacteria causing septicaemia showed that Gram-positive bacteria are more prevalent, accounting for 66.67% of cases (Table 2). Notably, *Staphylococcus aureus* was the most frequently isolated pathogen, responsible for 49.02% of cases, followed by *Streptococcus* at 11.77% and *Staphylococcus hominis* at 5.88%. In contrast, Gram-negative bacteria comprised 33.33% of the cases, with *Escherichia coli* being the most prevalent at 13.73%. Other notable Gram-negative bacteria included *Klebsiella pneumoniae* (5.88%) and *Flavimonas oryzihabitans* (3.92%), with several other species each accounting for 1.96% of cases. This distribution underscores the significant role of Gram-positive bacteria in septicaemia cases within the study cohort.

Table 2: Bacteria that cause septicaemia

Bacteria	Freq.	Percentage
Gram-Positive		
Staphylococcus aureus	25	49.02 %
Streptococcus	6	11.77 %
Staphylococcus hominis	3	5.88 %
Total	34	66.67 %
Gram-Negative		
Escherichia coli	7	13.73 %
Klebsiella pneumoniae	3	5.88 %
Flavimonas oryzihabitans	2	3.92 %
Citrobacter koseri	1	1.96 %
Proteus mirabilis	1	1.96 %
Escherichia vulneris	1	1.96 %
Enterobacter cloacae	1	1.96 %
Acinetobacter baumannii	1	1.96 %
Total	17	33.33 %

Antimicrobial Susceptibility Profiles of Microbes

This study investigated antibiotic resistance patterns in Gram-positive bacteria isolated from 51 patients with septicaemia. The analysis focused on resistance profiles for *Staphylococcus aureus* (455 antibiotics tested), *Streptococcus* species (114 antibiotics tested), and *Staphylococcus hominis* (39 antibiotics tested). Table 3 presents a detailed breakdown of the variability in resistance patterns among these Gram-positive bacteria. *Staphylococcus aureus* demonstrated resistance to 17 antibiotics, sensitivity to 2 antibiotics, and intermediate resistance to 5 antibiotics. *Streptococcus* species exhibited resistance to 13 antibiotics, sensitivity to 3 antibiotics, and intermediate resistance to 3 antibiotics. In contrast, *Staphylococcus hominis* showed resistance to 9 antibiotics and sensitivity to 16 antibiotics.

Staphylococcus aureus showed significant resistance to multiple antibiotics, with 28% sensitivity to CAZ, 30% to CTX, 33% to CRO, 39% to CFR and LVX, and twelve additional antimicrobial agents. Notably, it retained complete (100%) sensitivity to HDI and VAN. In contrast, *Streptococcus spp*. demonstrated limited sensitivity, with only 17% to OXA and 33% to CAZ, CLI, and ERY. However, no resistance was observed to DOX, SXT, or VAN, with 100% susceptibility maintained for these antibiotics. *Staphylococcus hominis* presented a distinct resistance profile, exhibiting complete susceptibility (100%) to a broad spectrum of antibiotics, including AMX, AMC, SAM, and thirteen additional regimens. This Gram-positive bacterium displayed no resistance to any of the antibiotics tested, suggesting a more favourable therapeutic approach.

Present study revealed varied antibiotic resistance patterns among Gram-positive bacteria, with *Staphylococcus aureus* showing resistance to 17 antibiotics but retaining full sensitivity to imipenem and vancomycin. A similar study evaluating antibiotic resistance patterns in 221 sepsis patients found that gram-positive bacteria were the most common cause of sepsis, with *Staphylococcus haemolyticus* (16.3%) and *Staphylococcus aureus* (12.5%) being the most prevalent species.[22] The study reported high sensitivity of these bacteria to piperacillin-tazobactam, daptomycin, and clindamycin.[22] Another study conducted in Ethiopia also showed that Staphylococcus aureus was the most common gram-positive bacteria (26.7%) with significant resistance to gentamicin (41.7%), methicillin (66.7%), and ciprofloxacin (58.3%).[29] Further, this study showed *Streptococcus* and *Staphylococcus hominis* displayed distinct resistance profiles. This research revealed that Streptococcus exhibited resistance to 13 different antibiotics. A previous study showed that *Streptococcus sp.* was a less common cause of sepsis, including *beta-haemolytic Streptococcus* (3.61%), *Streptococcus viridans* (1.55%), and *Streptococcus pneumoniae* (1.03%).[23] This study revealed the emerging resistance of *Streptococcus sp*. to gentamicin, erythromycin, tetracycline, and ciprofloxacin (58.3%). However, this study showed *Staphylococcus hominis* has complete susceptibility to a wide range of antibiotics (17 agents). In contrast, a study evaluating the causative agent of septicaemia in cancer patients showed that the subspecies *S. hominis subsp. novobiosepticus* was uniformly resistant to penicillin, oxacillin and ciprofloxacin.[30]

Present study also examined the antibiotic resistance profiles of Gram-negative bacteria across a diverse patient cohort, focusing on resistance patterns in *E. coli*, *Klebsiella pneumoniae*, *Flavimonas oryzihabitans*, and other bacterial species. The findings reveal considerable variation in resistance profiles among these pathogens. *Escherichia coli* displayed the highest level of resistance, with resistance to 20 antibiotics, sensitivity to 8, and intermediate resistance to 1. *Flavimonas oryzihabitans* exhibited resistance to 20 antibiotics and susceptibility to 4, while *Citrobacter koseri* demonstrated resistance to 19 antibiotics and susceptibility to only 1. Table 4 provides a detailed overview of the resistance profiles for additional species, employing a colour-coded system to denote resistance levels: red indicates resistance (sensitivity below 70%), yellow signifies intermediate sensitivity (70–90%), green represents high sensitivity (above 90%), and white denotes antibiotics not tested for a given species.

E.coli demonstrated significant resistance to multiple antibiotics, with 0% sensitivity to AMP, OXA, CFR, and six others A similar resistance profile was observed for *Flavimonas oryzihabitans*, which displayed complete (100%) resistance to AMP, OXA, TZP, and twelve other antibiotics. In contrast, *Citrobacter koseri* had only sensitive to ERY, indicating serious multiple drug resistance (MDR) approach. In contrast, *Enterobacter cloacae* showed resistance only to five antibiotics and remained sensitive to sixteen.

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Table 3: Antibiotic resistance patterns of blood specimens in septicaemia patients for gram-positive bacteria

	Antibiotic	AMX	AMC	AMP	SAM	OXA	CFR	CZO	FEP	CFM	CTX	FOX	CAZ	CRO	GENES	KAN	CIP	LVX	MFX	HDI	MEM	CLI	ERY	CHL	COL	DOX	FOS	TCY	SXT	VAN
S. aureus (n=455)	Total	24		24		23	23	23			23	23	25	24	18	7	25	18	23	2	5	25	19		7	23	7	23	23	18
	S	15		13		11	9	13			7	13	7	8	11	3	10	7	12	2	3	16	10		6	17	6	16	19	18
	%	63%		54%		48%	39%	57%			30%	57%	28%	33%	61%	43%	40%	39%	52%	100%	60%	64%	53%		86%	74%	86%	70%	83%	100 %
Streptococcus (n=114)	Total	6		6		6	6	6			6	6	6	6	6		6	6	6			6	6			6		6	6	6
	S	5		5		1	3	3			3	3	2	3	5		4	4	3			2	2			6		4	6	6
	%	83%		83%		17%	50%	50%			50%	50%	33%	50%	83%		67%	67%	50%			33%	33%			100%		67%	100%	100 %
S. hominis (n=39)	Total	1	1		1	2	1		1	1	1	1	1	1	3	1	3	2	2	1		3	3	1	1		1	2	2	2
	S	1	1		1	0	1		1	1	1	1	1	1	2	1	1	0	0	1		1	1	1	1		1	0	0	2
	%	100%	100%		100%	0%	100%		100%	100%	100%	100%	100%	100%	67%	100%	33%	0%	0%	100%		33%	33%	100%	100%		100%	0%	0%	100 %

Table 4: Antibiotic resistance patterns of blood specimens in septicaemia patients for gram-negative bacteria

	drugs	AMC	AMP	SAM	OXA	TZP	CFR	CZO	FEP	CFM	CTX	FOX	CAZ	CRO	AMK	GENES	KAN	CIP	LVX	HDI	MEM	CLI	ERY	CHL	COL	DOX	FOS	TCY	SXT	VAN
E. coli (n=134)	Total	7	7	6	1	5	7	1	6	6	7	1	7	6	6	5	5	6	2	7	5	1	1	6	4	1	6	6	5	1
	S	3	0	3	0	5	0	1	2	0	0	0	0	0	6	2	2	3	1	7	5	0	1	5	0	1	4	3	2	1
	%	43%	0%	50%	0%	100%	0%	100%	33%	0%	0%	0%	0%	0%	100%	40%	40%	50%	50%	100%	100%	0%	100%	83%	0%	100%	67%	50%	40%	100%
Klebsiella pneumoniae (n=62)	Total	3	3	3	1	3	3		3	3	3		3	3	3	2	3	3		3	3			3	2		3	3	3	
	S	3	0	3	0	3	1		2	2	2		2	2	3	1	3	2		3	3			2	0		3	1	2	
	%	100%	0%	100%	0%	100%	33%		67%	67%	67%		67%	67%	100%	50%	100%	67%		100%	100%			67%	0%		100%	33%	67%	
Flavimonas oryzihabit	Total	2	2	2	1	1	2		2	2	2		2	2	2	2	1	2	1	2	1		1	2			2	2	1	1
	S	1	0	2	0	0	0		0	0	0		1	0	0	1	0	0	1	0	0		0	0			1	1	1	1

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	%	50%	0%	100%	0%	0%	0%		0%	0%	0%		50%	0%	0%	50%	0%	0%	100%	0%	0%		0%	0%			50%	50%	100%	100%
Citrobacter koseri (n=20)	Total	1	1	1	1		1		1	1	1		1	1	1	1		1	1	1			1	1			1	1		1
	S	0	0	0	0		0		0	0	0		0	0	0	0		0	0	0			1	0			0	0		0
	%	0%	0%	0%	0%		0%		0%	0%	0%		0%	0%	0%	0%		0%	0%	0%			100%	0%			0%	0%		0%
Proteus mirabilis (n=21)	Total	1	1	1		1	1		1	1	1		1	1	1	1	1	1		1	1			1	1		1	1	1	
	S	0	0	0		1	0		0	0	0		0	0	1	0	0	0		1	1			1	0		1	0	0	
	%	0%	0%	0%		100%	0%		0%	0%	0%		0%	0%	100%	0%	0%	0%		100%	100%			100%	0%		100%	0%	0%	
E. vulneris (n=21)	Total	1	1	1		1	1		1	1	1		1	1	1	1	1	1		1	1			1	1		1	1	1	
	S	0	0	1		1	0		1	0	1		1	0	1	0	1	0		1	1			0	0		1	0	0	
	%	0%	0%	100%		100%	0%		100%	0%	100%		100%	0%	100%	0%	100%	0%		100%	100%			0%	0%		100%	0%	0%	
Enterobacter cloacae (n=21)	Total	1	1	1		1	1		1	1	1		1	1	1	1	1	1		1	1			1	1		1	1	1	
	S	0	0	1		1	0		1	1	1		1	0	1	1	1	1		1	1			1	0		1	1	1	
	%	0%	0%	100%		100%	0%		100%	100%	100%		100%	0%	100%	100%	100%	100%		100%	100%			100%	0%		100%	100%	100%	
A. baumannii (n=10)	Total						1	1			1	1	1		1				1	1		1				1				
	S						0	1			1	1	1		1				1	1		1				1				
	%						0%	100%			100%	100%	100%		100%				100%	100%		100%				100%				

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Acinetobacter baumannii (*A. baumannii*) also demonstrated less resistance, which only to CFR and sensitive to ten other regiments. These findings suggest that *Enterobacter cloacae* and *A. baumannii* possess narrower resistance profiles compared to other Gram-negative bacteria.

Figure 1 illustrates the antimicrobial resistance patterns of Gram-positive bacteria isolated from septicaemia blood samples. We highlighted the highest resistance observed for CAZ (69%), CTX (63%), OXA (61%), CRO and (61%). Other notable resistance levels included LVX (58%), CFR (57%), CIP (56%), and 11 others. The yellow bars indicated intermediate drug resistance, such as DOX (13%), FOS (13%), and SXT (19%). However, several antibiotics (including AMC, AMP, OXA, CFM, MEM, and VAN) showed no resistance (0%), suggesting more effective therapeutic options.

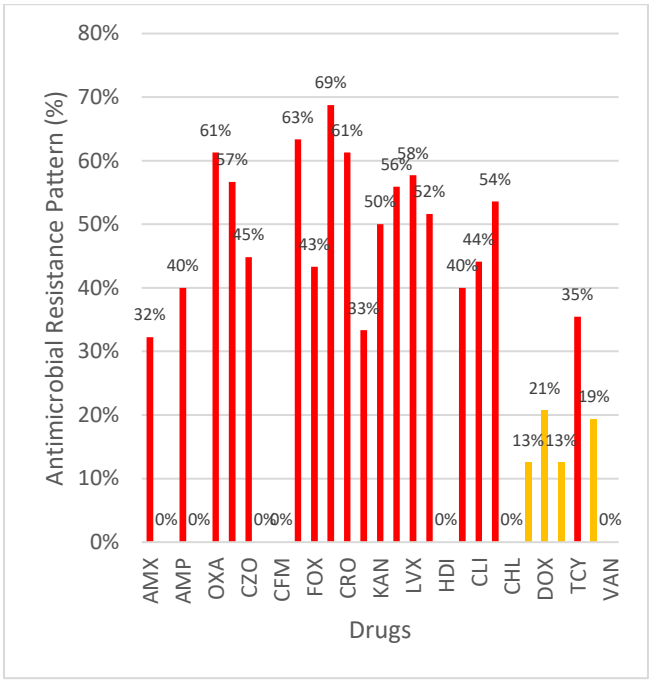

Figure 1: Antimicrobial resistance patterns of Gram-positive bacteria isolated from septicaemia blood samples.

Moreover, Figure 2 illustrates the antimicrobial resistance patterns of various antibiotics for Gram-negative bacteria. Several drugs, including AMP, OXA, and COL, demonstrated high resistance, with each displaying 100% resistance. CFR, CRO, and CFM also display significant resistance levels at 94%, 87%, and 80%, respectively. Yellow bars demonstrated moderate resistance for AMK (19%), HDI (18%), and FOS (27%). Several antibiotics, including TZP, MEM, CZO, and DOX, showed lower resistance levels at 8%, 8%, 0%, and 0%, respectively. These results highlight significant concerns regarding the efficacy of certain antibiotics, emphasising the need for cautious selection and rigorous monitoring of antimicrobial therapies.

In contrast to this study, which revealed a lower prevalence of Gram-negative bacteria, a study in Ethiopia identified them as the primary cause of septicaemia, representing 55.6% of cases.[29] Among Gram-negative bacteria in the present study, *E.coli* and *Flavimonas oryzihabitans* exhibited significant resistance, each resistant to 20 antibiotics. The Ethiopia study showed that resistance rates in *E.coli* were varying, which include GENES (25%), AMK (18%), AMP (92%), AMX (90.9%), amoxiclav (73.9%), cefuroxime (54.5%), CTX (52.9%), cefoperazone (36.8%), CIP (31.6%), CHL (39%) and TCY (33.7%).[29] However, no existing research on the antimicrobial susceptibility of *Flavimonas oryzihabitans* in cases of septicaemia was found, underscoring the originality of this study.

Furthermore, *A. baumannii* and *Enterobacter cloacae* showed narrower resistance profiles, suggesting a more tolerable course of therapy. This finding differed from a study from Ethiopia, which showed A. baumannii was resistant to GENES (11.5%), AMK (3.7%), AMP (84.2 %), AMX (83.2%), amoxiclav (80.1%), cefuroxime (75.4%), CTX (44.8%), CAZ (45.2%), cefoperazone (33.3%), CIP (19%), CHL (34.1%) and TYP (32%).[29] In a study conducted in Lebanon, *A. baumannii* also revealed broad resistance profiles, including to SXT (46.8%), minocycline (87.4%), GENES (90.9%), CIP (93.7%), TZP (94.5%), AMK (94.6%), FEP (94.6), HDI/cilastatin (94.6%), MEM (94.6%), CAZ (94.6%), DOX (94.6%), SAM (94.6%), and aztreonam (94.6%).[31] For the *E. cloacae* profile, A surveillance study in Italy from 2011 to 2019 revealed high resistance to amoxicillin/clavulanate (100%), norfloxacin (100%), CTX (90%), and CAZ (90%).[32] Another study in Switzerland reported that a majority of isolates possessed inducible or derepressed AmpC enzymes, with a high resistance to CAZ and TZP, while remaining susceptible to HDI and CIP.[33] These varied findings indicate a more challenging therapeutic landscape for the management of septicaemia.

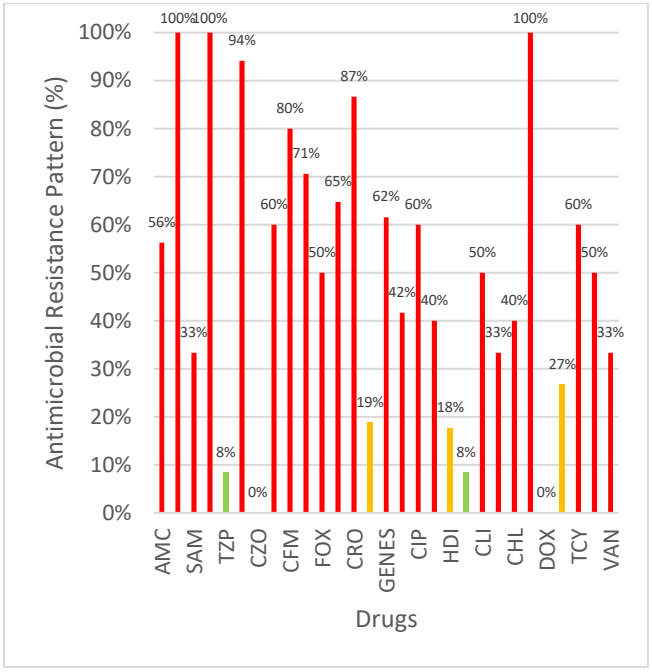

Figure 2: Antimicrobial resistance patterns of Gram-negative bacteria isolated from septicaemia blood samples.

This study has several limitations that should be considered when interpreting the results. Firstly, the relatively small sample size may limit the generalisability of the results. Secondly, the study focused solely on a specific facet of the phenomenon, leaving other pertinent factors unexamined. Lastly, the cross-sectional design precludes the establishment of causal relationships, necessitating longitudinal studies to elucidate the associations between variables comprehensively. Collectively, while this study offers valuable insights, its limitations underscore the imperative for further research to achieve a more complete understanding of the subject.

Conclusion

This study offers important details about the antibiotic resistance profiles of Gram-positive and Gram-negative bacterial pathogens in septicaemia cases. It revealed that Gram-positive bacteria were more prevalent, while Gram-negative bacteria were less common but exhibited significant multidrug resistance. The study highlights the high mortality rate associated with septicaemia, with 58.8% of patients not surviving, and underscores the challenge of antibiotic resistance, as many pathogens showed resistance to multiple antibiotics. Our findings emphasise the need for targeted antibiotic strategies to combat resistant strains and improve patient outcomes in septicaemia cases. Future research should focus on developing rapid diagnostic tools for bacterial identification and susceptibility testing, implementing comprehensive antimicrobial stewardship programs, and conducting larger multicenter longitudinal studies.

Conflict of Interest
The authors declare no conflict of interest.

Authors' Declaration
The authors hereby declare that the work presented in this article is original and that any liability for claims relating to the content of this article will be borne by them.

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