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Research Article

BACTERIOLOGICAL PROFILE OF CLINICALLY SUSPECTED SEPTICEMIA AMONG NEONATES AND THE ANTIBIOTIC SUSCEPTIBILITY PATTERN OF THEIR ISOLATES: A CROSS-SECTIONAL STUDY IN A TERTIARY CARE HOSPITAL OF JHARKHAND

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ABSTRACT

Objectives: Neonatal septicemia is a generalized bacterial infection that occurs during the first 4 weeks of life and is one of the four primary causes of neonatal mortality and morbidity in India. This study aims to determine the bacteriological profile and antibiotic sensitivity patterns of isolates from blood cultures of suspected septicemic neonates in a tertiary care hospital.

Methods: Two hundred and twenty-eight blood samples were collected and processed from patients in accordance with standard protocol. The antibiotic susceptibility of the isolates was determined by the disk diffusion method according to Clinical and Laboratory Standards Institute recommendations.

Results: Blood culture results were positive in 44.7% of the patients. Late-onset sepsis was present in 53.92%, and early-onset sepsis was observed in 46.08% of the cases. The best overall sensitivity among Gram-negative isolates was to Amikacin, followed by Gentamycin and Meropenem. Gram-positive isolates had sensitivity to Chloramphenicol, tetracycline, Linezolid, Tetracycline, Vancomycin, and Piperacillin.

Conclusion: The most common causes of newborn sepsis in this study were Gram-negative organisms (*Klebsiella pneumoniae*, *Escherichia coli*, and *Citrobacter freundii*) and Gram-positive organisms (*Staphylococcus aureus*), the majority of which are antibiotic-resistant.

Keywords: Neonatal septicemia, Bacteriological profile, Antibiotic sensitivity pattern, Early onset of neonatal sepsis, Late onset of neonatal sepsis, Blood culture, Clinical and Laboratory Standards Institute

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INTRODUCTION

Neonatal sepsis is defined as blood stream invasion by microorganisms, which may lead to septic shock and systematic inflammatory response syndrome, and this is a cause of neonatal morbidity and mortality all over the world. Septicemia literally means "sepsis of blood". It is a condition in which there is an active presence of multiplying bacteria in the blood stream and the formation of toxic products in the blood.

Neonatal sepsis is diagnosed during the first 28 days of life and is further subclassified as early-onset neonatal sepsis (EONS) if signs and symptoms of sepsis emerge within the first 3 days (72 h). EONS illness is caused primarily by bacteria acquired before and during delivery. *Group B streptococcus*, *Escherichia coli*, Coagulase-negative *Staphylococcus*, *Staphylococcus aureus*, and other bacterial pathogens cause EONS. Late-onset neonatal sepsis (LONS) occurs when clinical symptoms of sepsis appear between the ages of 4 and 28 days (72 h–28 days) [1-4]. Gram-positive bacteria cause late-onset sepsis, but it can also be caused by Gram-negative bacteria, fungi, and viruses. The most frequent Gram-negative species is *E. coli* and the most lethal is *Pseudomonas. aeruginosa* [5].

In India, the incidence of neonatal and clinical sepsis (17,000/1000 live births) is the highest in the world [6,7]. The case fatality rate of sepsis among neonates ranges from 25% to 65% in India [8,9]. Antibiotic resistance has become a global threat, and the spectrum of organisms that cause neonatal sepsis has changed over time and varies from region to region. This is due to the changing pattern of antibiotic use and changes in lifestyle. Reports of multidrug-resistant bacteria causing neonatal sepsis in developing countries are increasing, particularly in intensive care units. The clinical signs and symptoms of neonatal sepsis are subtle and non-specific, making early diagnosis difficult and leading to a high rate of empiric antibiotic utilization, which could contribute to the selection and spread of antimicrobial-resistant strains of bacteria. Knowing the causative agents of neonatal sepsis and their antimicrobial sensitivity patterns could enable us to choose appropriate therapy for neonatal sepsis. Targeted antibiotic therapy plays a significant role in reducing antimicrobial resistance and preventing morbidity and mortality [10].

Hence, in view of the changing prevalent isolates, it has been decided to take up a study of the bacteriological profile of clinically suspected septicemia among neonates and the antibiotic susceptibility pattern of their isolates. No such study has been done in East Singhbhum, Jharkhand. This will help to rationalize therapy and evaluate the common management program.

METHODS

Study design and duration

A hospital-based cross-sectional study was conducted from June 2022 to December 2022.

Setting and places

This was Neonatal Intensive Care Unit (NICU) at the Department of Pediatrics and the Department of Microbiology, MGM Medical College Hospital, Jamshedpur, Jharkhand.

Study population
All the neonates admitted who did not receive any antibiotics at the NICU with clinically proven sepsis were included in the study.

Sample size
Sample sizes were calculated based on prevalence reports of neonatal sepsis from different studies ranging from 2.7% to 17% [11]. Where 17% prevalence (P), 5% margin of error (D), 95% confidence interval, Z scores: 1.96 were taken. The sample size was calculated using the formula N = P (1-p) Z2/E2. The sample size is estimated to be a total of 217 patients. It has been rounded off to 220. We collected 228 samples.

Inclusion criteria
Clinically proven sepsis (i.e., neonates with poor activity, fever, refusal of feed, lethargy, tachypnea, tachycardia, birth asphyxia, prematurity, low birth weight, etc.) neonates were enrolled in the study.

Exclusion criteria
The following criteria were included in the study:
1. Neonates with an age >28 days or neonates on antibiotics before the collection of blood were excluded from the study
2. Non-consenting mother or guardian
3. Patients undergoing treatment (with a critically ill condition) and refusing an investigation were excluded.

Data collection and laboratory investigation
Signed informed consent was obtained from each participant (Parents) before inclusion. All clinical data were collected from the NICU Bed Head Ticket. Blood samples of these neonates were collected with strict aseptic precautions. 1–2 mL venous blood was inoculated into blood culture bottle containing 20 mL of sterile Brain Heart Infusion. The samples were processed by standard bacteriological procedure [12]. Antimicrobial susceptibility testing was performed by Kirby–Bauer disk diffusion susceptibility method in accordance to Clinical Laboratory Standards Institutes guidelines [13].

Data analysis
The Epi Info (statistical software for epidemiology) software was used to analyze the data.

Ethics consideration
Ethical approval was taken from the Institution Ethics committee of MGM Medical College, Jamshedpur (IEC Number: IEC/10/22 Dated: May 07, 2022).

RESULTS AND DISCUSSION

During the research period, 228 neonates were admitted with clinical sepsis. Out of 228 cases, 102 (44.7%) had positive blood cultures (culture-proven sepsis) and 126 (55.3%) had negative blood cultures (suspected sepsis). In the present study, the incidence of late-onset sepsis 55 (53.92%) was greater than that of early-onset sepsis 47 (46.08%) among the 102 cases with positive culture-proven sepsis (Tables 1 and 2). Sepsis was caused by Gram-negative bacteria rather than Gram-positive bacteria (Table 3).

Common isolates identified
The most common organism isolated was *S. aureus* and was present in 40 cases (39.21%), *Klebsiella pneumoniae* 31 cases (30.39%), *E. coli* in 17 cases (16.66%), *Citrobacter freundii* in 11 cases (10.78%), *Pseudomonas aeruginosa* in 2 cases (1.96%), and *Enterococcus faecium* in 1 case (0.98%) (Tables 4 and 5).

Among 61 (62.22%) Gram-negative bacilli 31 (50.8%) were *K. pneumoniae*, 17 (27.9%) *E. coli*, 11 (18.0%) *C. freundii*, and 2 (3.3%) were *P. aeruginosa* (Table 6).

Among 41 Gram-positive bacilli, 40 (97.6) were *S. aureus*, and 1 (2.4%) were *Enterococcus faecalis*. The number 21 (51.21%) of early-onset sepsis was high under Gram-positive bacteria. Among Gram-negative and-negative organism, *K. pneumoniae* and *S. aureus* were the most common isolates (Tables 6 and 7).

Susceptibility pattern of Gram-positive bacteria isolates (Table 8)
Most of the Gram-positive bacteria isolates were from LONS, possibly being hospital acquired infections. *S. aureus* bacteria were highly 100% resistant rate to Penicillin-G, Amoxicillin, Cephalexin, Ciprofloxacin Cefazolin and Cefuroxime, and Azithromycin, used at NICU. *S. aureus* bacteria showed better susceptibility patterns for Vancomycin, Tetracycline, Chloramphenicol, and Linezolid.

Table 1: Distribution of blood culture positive and negative

Blood culture	Frequency	
Culture positive (Culture proven sepsis)	102 (44.7)	Chi-square = 228.0 p = 0.000
Culture negative (Suspected sepsis)	126 (55.3)	
Total	228	

Table 2: Distribution of onset of sepsis as per culture proven sepsis (*n* = 102)

Onset of sepsis	Frequency	Percent
Early onset of sepsis	47	46.08
Late onset of sepsis	55	53.92
Total	102	100.0

Table 3: Distribution of Gram-negative and Gram-positive bacteria (*n* = 102)

Isolated bacteria	Frequency	Percent
Gram-negative bacteria	61	59.80
Gram-positive bacteria	41	40.20
Total	102	100.0

Table 4: Distribution of bacterial isolates with their relative frequency (*n* = 102)

Isolated organism	Frequency	Percent
Citrobacter freundii	11	10.78
Escherichia coli	17	16.66
Enterococcus faecium	1	0.98
Klebsiella pneumoniae	31	30.39
Pseudomonas aeruginosa	2	1.96
Staphylococcus aureus	40	39.21
Total	102	100%

Table 5: Distribution of isolated organism as per onset of sepsis (*n* = 102)

Isolated organism	Sepsis category (%)		Total (%)
	Early onset of sepsis	Late onset sepsis	
Citrobacter freundii	7 (14.9)	4 (7.3)	11 (4.8)
Escherichia coli	8 (17.0)	9 (16.4)	17 (7.5)
Enterococcus faecium	1 (2.1)	0 (0.0)	1 (0.4)
Klebsiella pneumoniae	11 (23.4)	20 (36.4)	31 (13.6)
Pseudomonas aeruginosa	0 (0.0)	2 (3.6)	2 (0.9)
Staphylococcus aureus	20 (42.6)	20 (36.4)	40 (17.5)
Total	47	55	102

p = 0.000, Pearson Chi-square = 241.185

The resistance rates *E. faecium* against Penicillin-G, Amoxicillin, Cefuroxime, Chloramphenicol, Linezolid, and Vancomycin were (100%). Moreover, better susceptibility patterns for Tetracycline, Piperacillin, Cefazolin, Amoxicillin-Clavulanic acid, and Co-trimxazole.

Best overall sensitivity among Gram-positive isolates had sensitivity of 26% to Tetracycline, 24% to Vancomycin, 20% Chloramphenicol, and 12% to Linezolid.

Suscebility pattern of Gram-negative bacteria isolates (Table 9)
Most *C. freundii* were sensitive to Amikacin, Meropenem, ciprofloxacin, Gentamycin, Cefuroxime, and Cefotaxime and resistant to Tobramycin, Gemifloxacin, Piperacillin + Tazobactum, Cefoperazone + Sulbactam, Cefpodoxime, Cefpirome, and Ticarcillin-Clavulanic Acid.

Escherichia coli were usually sensitive to Meropenem, Gentamycin, Amikacin, and Ofloxacin. *E. coli* was 80% resistant to first-line, second-line, and third-line drugs.

The antibiotic sensitivity pattern showed that the most commonly isolated organism, *Klebsiella pneumoniae*, was highly sensitive to Gentamycin, Cefuroxime, Ceftriaxone, Piperacillin Tazobactum, Imipenem, and 3rd generation Amikacin. Where *Klebsiella pneumoniae* was resistant to Nalidixic acid, Cefixime, Cefdinir, Ceftazidime, Ticarcillin-Clavulanic acid, Moxifloxacin, Cefprozil, Ceftizoxime, Cefpodoxime, Cefoperazone-Sulbactam, and Gemifloxacin.

P. aeruginosa was highly sensitive to Cilastatin and 100% resistant to all listed drugs.

Best overall sensitivity among Gram-negative isolates was to Meropenem (77%), Amikacin (63.9%), Gentamycin (47.5%), Ofloxacin (24.6%), Cefuroxime, and Ciprofloxacin (23.6%), followed by Ceftriaxone (1.7%) and Norfloxacin (16.4%).

Table 6: Distribution of bacteriological profile of Gram-negative clinical isolates as per onset of sepsis (*n* = 61)

Isolated pathogens	Early onset of sepsis (%)	Late onset of sepsis (%)	Total (%)
Citrobacter freundii	7 (26.9)	4 (11.4)	11 (18.0)
Escherichia coli	8 (30.8)	9 (25.7)	17 (27.9)
Klebsiella pneumoniae	11 (42.3)	20 (57.1)	31 (50.8)
Pseudomonas aeruginosa	0 (0.0)	2 (5.7)	2 (3.3)
Total	26	35	61

Table 7: Distribution of bacteriological profile of Gram-positive clinical isolates as per onset of sepsis (*n* = 41)

Isolated pathogens	Early onset of sepsis (%)	Late onset of sepsis (%)	Total (%)
Enterococcus faecium	1 (4.8)	0 (0.0)	1 (2.4)
Staphylococcus aureus	20 (95.2)	20 (100.0)	40 (97.6)
Total	21	20	41

In the NICU, septicemia is the main cause of baby mortality and morbidity. Infection rates in the NICU range from 2.7% to 17% [11]. The blood culture positivity rate in neonatal septicemia cases in this study is 44.7%, which is comparable to other studies [14-20]. Lower rates of occurrence were 2.1% [21] and 8.9% [22]. The incidence rates were 82.35% [23] and 56.67% [24], respectively.

The variation in neonatal septicemia culture positivity rate could be attributed to changes in sample size, prior antibiotic administration (self-medication) before to sample collection, infection with anaerobes and fungal pathogens, and effective control of nosocomial infection dissemination.

Positive blood culture results the late onset of sepsis (53.92%) was higher than the early onset of sepsis (46.08%). Other studies [25,26] found a higher prevalence of late-onset sepsis. The late onset of sepsis is caused by the postnatal acquisition of infections produced by bacteria that thrive in the external environment of the hospital and other delivery settings. One probable explanation for the high rate of late-onset septicemia is that medical staffs do not comprehend the need of cleanliness, sanitation, and the use of aseptic procedures in ICUs.

Gram-negative organisms were detected in the majority of cases (59.80%), which is consistent with the findings of prior research [27-29].

According to National neonatal-perinatal database statistics, Gram-negative pathogens caused neonatal sepsis [25,30]. *K. pneumoniae* was the most frequent pathogen in this study, accounting for 30.39% [31] of newborn sepsis, followed by *S. aureus* (39.51% [31]), *E. coli* (16.66% [32]), and *C. freundii* (10.78% [23]). The most prevalent Gram-positive organism was discovered to be *S. aureus*. In both EONS and

Table 8: Antibiotic sensitivity and resistant pattern of Gram-positive organisms

Set of antibiotic disk	Drug code	Isolated organisms			
		Enterococcus faecium		*Staphylococcus aureus*	
		Resistant	Sensitive	Resistant	Sensitive
		Count (n%)	Count (n%)	Count (n%)	Count (n%)
Penicillin-G	P	1 (100)	0 (0.0)	40 (100)	0 (0.0)
Amoxicillin	AMX	1 (100)	0 (0.0)	39 (97.5)	1 (2.5)
Amoxicillin-Clavulanic acid	AMC	0 (0.0)	1 (100)	37 (92.5)	3 (7.5)
Co-trimoxazole	SXT	0 (0.0)	1 (100)	37 (92.5)	3 (7.5)
Cephalexin	CFM	0 (0.0)	1 (100)	40 (100)	0 (0.0)
Cefazolin	CFZ	0 (0.0)	1 (100)	40 (100)	0 (0.0)
Cefuroxime	XM	1 (100)	00.0)	40 (100)	0 (0.0)
Erythromycin	EM	1 (100)	0 (0.0)	39 (97.5)	1 (2.5)
Chloramphenicol	C	1 (100)	0 (0.0)	20 (50.0)	20 (50)
Ciprofloxacin	CI	1 (100)	0 (0.0)	38 (95.0)	2 (5.0)
Ofloxacin	OF	1 (100)	0 (0.0)	36 (90.0)	4 (10)
Piperacillin	PI	0 (0.0)	1 (100)	35 (87.5)	5 (12.5)
Azithromycin	AZ	1 (100)	0 (0.0)	39 (97.5)	1 (2.5)
Tetracycline	TE	0 (0.0)	1 (100)	15 (37.5)	25 (62.5)
Linezolid	LZ	1 (100)	0 (0.0)	28 (70.0)	12 (30)
Vancomycin	VA	1 (100)	0 (0.0)	16 (40.0)	24 (60)

Table 9: Antibiotic sensitive and resistant pattern of Gram-negative organisms

Antibiotic disk	Isolates organisms							
	Drug Code	*Citrobacter freundii*		*Escherichia coli*		*Klebsiella pneumoniae*		*Pseudomonas aeruginosa*	
		Resistant	Sensitive	Resistant	Sensitive	Resistant	Sensitive	Resistant	Sensitive
		Count (n%)	Count (n%)	Count (n%)	Count (n%)	Count (n%)	Count (n%)	Count (n%)	Count (n%)
Norfloxacin	NOR	6 (54.5)	5 (45.5)	15 (88.2)	2 (11.8)	28 (90.3)	3 (9.7)	2 (100)	0 (0.0)
Aztreonam	AT	9 (81.8)	2 (18.2)	17 (100)	0 (0.0)	29 (93.5)	2 (6.5)	2 (100)	0 (0.0)
Cefotaxime	CTX	6 (54.5)	5 (45.5)	17 (100)	0 (0.0)	29 (93.5)	2 (6.5)	2 (100)	0 (0.0)
Ceftriaxone	CRO	7 (63.6)	4 (36.4)	15 (88.2)	2 (11.8)	25 (80.6)	6 (19.4)	2 (100)	0 (0.0)
Nalidixic acid	NA	11 (100)	0 (0.0)	17 (100)	0 (0.0)	31 (100)	0 (0.0)	2 (100)	0 (0.0)
Nitrofurantoin	NI	11 (100)	0 (0.0)	17 (100)	0 (0.0)	31 (100)	0 (0.0)	2 (100)	0 (0.0)
Cefuroxime	XM	6 (54.5)	5 (45.5)	14 (82.4)	3 (17.6)	25 (80.6)	6 (19.4)	2 (100)	0 (0.0)
Gentamycin	GM	3 (27.3)	8 (72.7)	7 (41.2)	10 ((58.8)	20 (64.5)	11 (35.5)	2 (100)	0 (0.0)
Amikacin	AK	1 (9.1)	10 (90.9)	8 (47.1)	9 (52.9)	11 (35.5)	20 (64.5)	2 (100)	0 (0.0)
Ciprofloxacin	CI	5 (45.5)	6 (54.5)	15 (88.2)	2 (11.8)	25 (80.6)	6 (19.4)	2 (100)	0 (0.0)
Ofloxacin	OF	4 (36.4)	7 (63.6)	13 (76.5)	4 (23.5)	27 (87.1)	4 (12.9)	2 (100)	0 (0.0)
Cefixime	FIX	7 (63.6)	4 (36.4)	17 (100)	0 (0.0)	31 (100)	0 (0.0)	2 (100)	0 (0.0)
Cefdinir	CD	6 (54.5)	5 (45.5)	17 (100)	0 (0.0)	31 (100)	0 (0.0)	2 (100)	0 (0.0)
Ceftazidime	CAZ	8 (72.7)	3 (27.3)	16 (94.1)	1 (5.9)	29 (93.5)	2 (6.5)	2 (100)	0 (0.0)
Ticarcillin-Clavulanic acid	TCC	11 (100)	0 (0.0)	16 (94.1)	1 (5.9)	29 (93.5)	2 (6.5)	2 (100)	0 (0.0)
Meropenem	MP	2 (18.2)	9 (81.8)	2 (11.8)	15 (88.2)	8 (25.8)	2 (74.2)	2 (100)	0 (0.0)
Levofloxacin	LE	8 (72.7)	3 (27.3)	17 (100)	0 (0.0)	29 (93.5)	2 (6.5)	2 (100)	0 (0.0)
Moxifloxacin	MXF	10 (90.9)	1 (9.1)	17 (100)	0 (0.0)	31 (100)	0 (0.0)	2 (100)	0 (0.0)
Cefprozil	FP	11 (100)	0 (0.0)	17 (100)	0 (0.0)	31 (100)	0 (0.0)	2 (100)	0 (0.0)
Cefpirome	CE	11 (100)	0 (0.0)	17 (100)	0 (0.0)	31 (100)	0 (0.0)	2 (100)	0 (0.0)
Ceftazidime	CZ	10 (90.9)	1 (9.1)	17 (100)	0 (0.0)	31 (100)	0 (0.0)	2 (100)	0 (0.0)
Cefpodoxime	CPD	11 (100)	0 (0.0)	17 (100)	0 (0.0)	31 (100)	0 (0.0)	2 (100)	0 (0.0)
Cefoperazone + Sulbactam	CS	11 (100)	0 (0.0)	16 (94.1)	1 (5.9)	29 (93.5)	2 (6.5)	2 (100)	0 (0.0)
Piperacillin + Tazobactum	P/T	11 (100)	0 (0.0)	17 (100)	0 (0.0)	26 (83.9)	5 (16.1)	2 (100)	0 (0.0)
Sparfloxacin	SO	11 (100)	0 (0.0)	17 (100)	0 (0.0)	30 (96.8)	1 (3.2)	2 (100)	0 (0.0)
Gemifloxacin	GEM	10 (90.9)	1 (9.1)	17 (100)	0 (0.0)	30 (96.8)	1 (3.2)	2 (100)	0 (0.0)
Imipenem	I	11 (100)	0 (0.0)	17 (100)	0 (0.0)	29 (93.5)	2 (6.5)	2 (100)	0 (0.0)
Cilastatin	S	11 (100)	0 (0.0)	17 (100)	0 (0.0)	31 (100)	0 (0.0)	0 (0.0)	2 (100)
Tobramycin	To	11 (100)	0 (0.0)	17 (100)	0 (0.0)	30 (96.8)	1 (3.2)	2 (100)	0 (0.0)

LONS, *S. aureus* was isolated in the majority of cases [33], followed by *P. aeruginosa* (1.96%), and *E. faecium* (0.98%) [34].

In this study, both Gram-negative and Gram-positive organisms were resistant to the majority of the antibiotics drugs. In 70% of cases, Gram-negative organisms were resistant to Cephalosporins [35]. Other investigations [36] found substantial resistance to Ampicillin among *S. aureus*; however, resistance to other drugs was modest. They also reported a significant resistance to Azithromycin. However, an Indian research found 37% Ampicillin resistance [37].

Amikacin, Gentamycin, and Meropenem were shown to be the most effective against *K. pneumoniae*, *Citrobacter*, *and E. coli*, while Cilastatin was found to be the most effective against *P. aeruginosa*. The most effective antibiotics drugs against *E. faecium* were tetracycline, piperacillin, cefazolin, amoxicillin-clavulanic acid, and cotrimoxazole.

The antibiotic susceptibility pattern of all newborn sepsis isolates was investigated. The examination of drug resistance patterns revealed that, in the case of *C. freundii*, the majority of Gram-negative isolates were resistant to Tobramycin, Gemifloxacin, Piperacillin + Tazobactum, Cefoperazone + Sulbactam, Cefpodoxime, Cefpirome, and Ticarcillin-Clavulanic Acid. Maximum numbers of *E. coli* were resistant to 80% of first-line, second-line, and third-line medications. In contrast, *K. pneumoniae* was resistant to Nalidixic acid, Cefixime, Cefdinir, Ceftazidime, Ticarcillin-Clavulanic acid, Moxifloxacin, Cefprozil, Ceftrizoxime, Cefpodoxime, Cefoperazone-sulbactum, and Gemifloxacin in high quantities. *P. aeruginosa* was completely resistant to all of the drugs tested.

High resistance to Penicillin-G, Amoxicillin, Cephalexin, Ciprofloxacin, Cefazolin, Cefuroxime, and Azithromycin was observed in Gram-positive isolates (*S. aureus*). Most *E. faecalis* isolates were resistant to Penicillin-G, Amoxicillin, Cefuroxime, Chloramphenicol, Linezolid, and Vancomycin.

The current investigation found that the majority of the isolated bacteria were Multidrug-Resistant (MDR) (Tables 8 and 9). Gram-negative and Gram-positive organisms were both considerably resistant to popular antibiotic classes. Previous research [38,39] has found similar results. *K. pneumoniae* was one of the most common MDR organisms. In this investigation, the major pathogens were *Klebsiella* spp., *E. coli*, and *Citrobacter*, which are normally recognized as nosocomial pathogens [40].

CONCLUSION

S. aureus is the most common Gram-positive organism, whereas *E. coli*, *C. freundii*, *and K. pneumoniae* are the most common Gram-negative species. Antibiotic resistance was high in both Gram-positive and Gram-negative isolates. MDR strains made up a sizable majority of them.

AUTHORS' CONTRIBUTIONS

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CONFLICTS OF INTEREST

None to declare.

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Nil.

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