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Original Research Article

Study on microbial profile and antibiotic resistance patterns in culture-proven neonatal sepsis: a three-year retrospective analysis from Rajarajeswari Medical College and Hospital, Bangalore, India

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ABSTRACT

Background: Neonatal sepsis remains a significant cause of morbidity and mortality, particularly in developing countries, due to varying microbial patterns and rising antimicrobial resistance. Continuous surveillance of causative organisms and their antibiotic susceptibility is essential for effective management. The objective of the study was to analyze the microbial profile and antibiotic resistance patterns in culture-proven neonatal sepsis cases in a tertiary care hospital.

Methods: A retrospective observational study was conducted over a period of three years (January 2023 to January 2026) in Rajarajeswari Medical College and Hospital, Bangalore. A total of 75 neonates with clinically suspected sepsis were included based on predefined inclusion and exclusion criteria. Blood culture reports, demographic details, and antibiotic susceptibility patterns were collected from hospital records. Microbial identification and antibiotic sensitivity testing were performed using standard microbiological methods in accordance with CLSI guidelines. Data were analyzed using descriptive and inferential statistics.

Results: Among the 75 neonates, 61.33% were male and 85.33% presented with early-onset sepsis. The culture positivity rate was 36.00%. *Klebsiella pneumoniae* (44.44%) was the most common pathogen, followed by coagulase-negative *Staphylococcus* (18.52%) and *Pseudomonas spp*. (14.81%). Gram-negative organisms (59.26%) predominated over gram-positive organisms (40.74%). High sensitivity (100%) was observed for cefotaxime, ceftazidime, amikacin, meropenem, vancomycin, and linezolid. However, high resistance was noted for penicillin (70.83%), ampicillin (66.67%), and high-level gentamicin (75.00%). Multidrug resistance was observed in 66.67% of isolates. No statistically significant association was found between demographic factors and culture positivity ($p>0.05$).

Conclusion: Neonatal sepsis in the present study was predominantly caused by gram-negative organisms with a high prevalence of multidrug resistance. While higher-generation antibiotics remain effective, increasing resistance to first-line drugs highlights the need for antibiotic stewardship, regular surveillance, and institution-specific treatment guidelines.

Keywords: Antimicrobial resistance, Antibiotic sensitivity, Neonatal sepsis, *Klebsiella pneumoniae*, Multidrug resistance

INTRODUCTION

Neonatal sepsis remains a major global health concern and is one of the leading causes of morbidity and mortality among newborns, particularly in low- and middle-income countries where healthcare resources and infection control practices may be limited. It is estimated to contribute to a significant proportion of neonatal deaths worldwide, emphasizing the urgent need for early diagnosis, appropriate management, and preventive strategies.[1] Neonatal sepsis is broadly classified into early-onset sepsis, which occurs within the first 72 hours of life and is commonly associated with maternal and perinatal factors, and late-onset sepsis, which typically occurs after 72 hours and is often linked to hospital-acquired infections and invasive procedures. The clinical presentation of neonatal sepsis is often nonspecific, including symptoms such as poor feeding, lethargy, temperature instability, and respiratory distress, making timely diagnosis challenging and frequently leading to empirical antibiotic therapy.[2]

The microbial etiology of neonatal sepsis varies significantly across different geographical regions and healthcare settings, necessitating continuous local surveillance to guide effective empirical treatment. Gram-negative organisms have increasingly been reported as predominant pathogens in many developing regions, with organisms such as *Klebsiella pneumoniae, Pseudomonas species,* and *Escherichia coli* contributing substantially to the disease burden.[3] Gram-positive organisms, including coagulase-negative *Staphylococcus* and *Staphylococcus aureus*, also play a significant role, particularly in hospital-acquired infections associated with invasive devices and prolonged hospital stays. The variability in microbial patterns underscores the importance of institution-specific data to optimize antimicrobial therapy and improve clinical outcomes.[4]

One of the most critical challenges in the management of neonatal sepsis is the rising trend of antimicrobial resistance (AMR), which has emerged as a serious global public health threat. The widespread and often indiscriminate use of antibiotics has accelerated the development of resistant strains, limiting the effectiveness of commonly used antimicrobial agents.[5] High resistance rates to first-line antibiotics such as penicillin and ampicillin have been increasingly documented, necessitating the use of broader-spectrum antibiotics such as carbapenems, aminoglycosides, and glycopeptides. However, the increased reliance on these higher-generation antibiotics further contributes to the cycle of resistance, posing a significant therapeutic dilemma.[6]

Multidrug-resistant (MDR) organisms, defined as pathogens resistant to at least one agent in three or more antimicrobial classes, are increasingly being reported in neonatal intensive care units. These organisms are associated with higher morbidity, prolonged hospital stays, increased healthcare costs, and higher mortality rates.[7] The emergence of MDR pathogens such as resistant *Klebsiella pneumoniae* and *Pseudomonas* species has made treatment more complex and has highlighted the need for stringent infection control practices and antimicrobial stewardship programs. In addition, neonates are particularly vulnerable to infections due to their immature immune systems, underdeveloped physical barriers, and frequent exposure to invasive procedures such as catheterization and mechanical ventilation.[8]

Blood culture remains the gold standard for the diagnosis of neonatal sepsis, although it has limitations including low sensitivity and delayed results.[9] Despite these limitations, culture-based identification of pathogens and their antibiotic susceptibility patterns is essential for targeted therapy and for monitoring trends in antimicrobial resistance.[10] Understanding the local microbial profile and resistance patterns is therefore crucial for guiding empirical antibiotic selection and improving neonatal outcomes. The present study was undertaken to analyze the microbial profile and antibiotic resistance patterns in culture-proven neonatal sepsis cases over a defined period in a tertiary care hospital setting. The study aims to provide valuable insights into the prevailing bacterial pathogens, their susceptibility patterns, and the burden of multidrug resistance, thereby contributing to evidence-based clinical decision-making and the development of effective antibiotic policies. The findings are expected to support the implementation of targeted interventions, including infection prevention strategies and rational antibiotic use, ultimately helping to reduce neonatal morbidity and mortality.

METHODS

Study design

The present study was conducted as a retrospective observational study aimed at evaluating the microbial profile and antibiotic resistance patterns in neonates diagnosed with sepsis. A retrospective design was considered appropriate as it allowed the analysis of previously recorded clinical, microbiological, and laboratory data over a defined period. The study focused on culture-confirmed cases to ensure diagnostic accuracy and reliability of findings.

Study setting

The study was carried out at a tertiary care teaching hospital, which included a well-equipped neonatal intensive care unit (NICU) and a microbiology laboratory with advanced diagnostic facilities. The hospital catered to both inborn and outborn neonates and served as a referral center for surrounding regions. The microbiology laboratory followed standard protocols for culture and sensitivity testing.

Study duration

The study was conducted over a period of three years, from January 2023 to January 2026. This duration was selected to ensure an adequate sample size and to observe trends in microbial distribution and antibiotic resistance over time.

Inclusion criteria

Neonates aged 0–28 days with clinical suspicion of sepsis, neonates with culture-confirmed sepsis, neonates admitted to or born in the study hospital and availability of complete medical and laboratory records were included.

Exclusion criteria

Exclusion criteria included neonates with incomplete or missing clinical data, cases with contaminated blood culture reports, neonates who received antibiotics prior to sample collection (if records were unclear) and duplicate records of the same patient.

Study sampling

A consecutive sampling technique was adopted in this study. All eligible neonates who met the inclusion criteria during the study period were included. This method minimized selection bias and ensured that all relevant cases were analyzed.

Study sample size

The sample size was determined using Fisher's formula for estimating proportions, considering the prevalence of neonatal sepsis from previous literature. Based on the calculated value, a minimum sample size of 76 was obtained. However, after applying inclusion and exclusion criteria, a total of 75 neonates were included in the final analysis.

Study parameters

The parameters assessed in the study included demographic variables such as age at presentation, sex, and onset of sepsis. Microbiological parameters included type of bacterial isolates, gram staining characteristics, and distribution of organisms. Antibiotic-related parameters included sensitivity patterns, resistance patterns, and identification of multidrug-resistant organisms. Additional parameters included culture positivity rate and association of demographic factors with culture results.

Study procedure

Data were retrieved from hospital records and microbiology laboratory databases. Blood samples had been collected aseptically from neonates suspected of sepsis prior to initiation of antibiotic therapy. The samples were processed using automated blood culture systems such as BACTEC or BacT/ALERT. Positive cultures were further subjected to organism identification using standard biochemical methods. Antibiotic susceptibility testing had been performed using the Kirby-Bauer disk diffusion method, and results were interpreted according to Clinical and Laboratory Standards Institute (CLSI) guidelines. Multidrug resistance was defined as resistance to at least one agent in three or more antimicrobial classes.

Study data collection

Relevant data including demographic details, clinical findings, laboratory results, and microbiological reports were collected from patient case records and hospital databases. A structured data collection form was used to extract and record information systematically. Data related to bacterial isolates, antibiotic sensitivity, and resistance patterns were specifically obtained from microbiology records.

Data analysis

The collected data were entered into Microsoft Excel and analyzed using statistical package for the social sciences (SPSS) version 23. Descriptive statistics such as frequencies and percentages were used to summarize categorical variables. Continuous variables were expressed as mean and standard deviation. Associations between categorical variables were assessed using the chi-square test, and a p value of less than 0.05 was considered statistically significant.

Ethical considerations

Ethical approval for the study was obtained from the Institutional Ethics Committee prior to data collection. As the study was retrospective in nature, patient consent was waived; however, confidentiality and anonymity of patient data were strictly maintained. All data were used solely for research purposes, and no identifying information was disclosed. The study adhered to ethical principles in biomedical research involving human participants.

RESULTS

A total of 75 neonates with clinical suspicion of sepsis were included in this retrospective analysis. The demographic characteristics of the study population are presented in Table 1.

Among the 75 neonates included in the study, 46 (61.33%) were male and 29 (38.67%) were female. With respect to the timing of presentation, 64 neonates (85.33%) presented with early-onset sepsis, while 11 neonates (14.67%) presented with late-onset sepsis. The mean age at presentation was 1.79±1.93 days (Table 1).

Among the 27 culture-positive cases, *Klebsiella pneumoniae* was the most frequently isolated organism, accounting for 12 isolates (44.44%). *Coagulase-negative Staphylococcus* (CONS) was isolated in 5 cases (18.52%), followed by *Pseudomonas spp.* in 4 cases (14.81%), *Enterococcus spp.* in 3 cases (11.11%), *Staphylococcus aureus* in 2 cases (7.41%), and *Streptococcus spp.* in 1 case (3.70) (Table 2).

Among the 27 bacterial isolates, Gram-negative organisms accounted for 16 isolates (59.26%), while gram-positive organisms accounted for 11 isolates (40.74%) (Table 3).

The highest sensitivity rates (100.00%) were observed for cefotaxime, ceftazidime, amikacin, netilmicin, meropenem, ertapenem, vancomycin, teicoplanin, linezolid, piperacillin-tazobactam, chloramphenicol, aztreonam, and novobiocin. Doxycycline demonstrated a sensitivity rate of 91.30%, followed by cotrimoxazole (80.00%) and imipenem (77.78%). Cephalexin and clindamycin showed sensitivity rates of 73.91% and 73.68%, respectively.

Table 1: Demographic characteristics of the study population (n=75).

Characteristic	Category	Frequency (N)	Percentage (%)
Sex	Male	46	61.33
	Female	29	38.67
Age at presentation	Early onset (≤72 hours)	64	85.33
	Late onset (>72 hours)	11	14.67
Age (days)	Mean±SD	1.79±1.93	—

Table 2: Distribution of bacterial isolates in culture-positive cases (n=27).

Bacterial isolate	Frequency (N)	Percentage (%)
Klebsiella pneumoniae	12	44.44
Coagulase-negative *staphylococcus* (CONS)	5	18.52
Pseudomonas spp.	4	14.81
Enterococcus spp.	3	11.11
Staphylococcus aureus	2	7.41
Streptococcus spp.	1	3.70
Total	27	100.00

Amoxiclav and gentamicin both demonstrated 68.18% sensitivity. Ciprofloxacin showed 60.00% sensitivity, while cefuroxime showed 42.86% sensitivity. Erythromycin, ampicillin, and penicillin showed lower sensitivity rates of 37.50%, 33.33%, and 29.17%, respectively. High-level gentamicin showed the lowest sensitivity at 25.00% (Table 4).

Table 3: Distribution by gram staining characteristics (n=27).

Gram classification	Frequency (N)	Percentage (%)
Gram-negative	16	59.26
Gram-positive	11	40.74
Total	27	100.00

The highest resistance rates were observed for high-level gentamicin (75.00%), followed by penicillin (70.83%) and ampicillin (66.67%). Erythromycin showed a resistance rate of 62.50%, while cefuroxime showed 57.14% resistance. Ciprofloxacin demonstrated a resistance rate of 40.00%. Gentamicin and amoxiclav showed resistance rates of 31.82% and 31.82%, respectively.

Cephalexin and clindamycin showed resistance rates of 26.09% and 26.32%, respectively. Imipenem demonstrated a resistance rate of 22.22%, while cotrimoxazole showed 20.00% resistance. Doxycycline showed a low resistance rate of 8.70%. No resistance (0.00%) was observed for cefotaxime, ceftazidime, amikacin, netilmicin, meropenem, ertapenem, vancomycin, teicoplanin, linezolid, piperacillin-tazobactam, chloramphenicol, aztreonam, and novobiocin (Table 5).

Table 4: Antibiotic sensitivity pattern of bacterial isolates (n=27).

Antibiotic class	Antibiotic	Sensitivity (%)
Cephalosporins	Cefotaxime	100.00
	Ceftazidime	100.00
	Cephalexin	73.91
	Cefuroxime	42.86
Aminoglycosides	Amikacin	100.00
	Gentamicin	68.18
	Netilmicin	100.00
	High-level Gentamicin	25.00
Carbapenems	Meropenem	100.00
	Imipenem	77.78
	Ertapenem	100.00
Glycopeptides	Vancomycin	100.00
	Teicoplanin	100.00
Oxazolidinones	Linezolid	100.00
Penicillins	Ampicillin	33.33
	Penicillin	29.17
	Piperacillin-Tazobactam	100.00
	Amoxiclav	68.18
Fluoroquinolones	Ciprofloxacin	60.00
Macrolides	Erythromycin	37.50
Others	Chloramphenicol	100.00
	Cotrimoxazole	80.00
	Clindamycin	73.68
	Doxycycline	91.30
	Aztreonam	100.00
	Novobiocin	100.00

Table 5: Antibiotic resistance pattern of bacterial isolates (n=27).

Antibiotic class	Antibiotic	Resistance (%)
Cephalosporins	Cefotaxime	0.00
	Ceftazidime	0.00
	Cephalexin	26.09
	Cefuroxime	57.14
Aminoglycosides	Amikacin	0.00
	Gentamicin	31.82
	Netilmicin	0.00
	High-level Gentamicin	75.00
Carbapenems	Meropenem	0.00
	Imipenem	22.22
	Ertapenem	0.00
Glycopeptides	Vancomycin	0.00
	Teicoplanin	0.00
Oxazolidinones	Linezolid	0.00
Penicillins	Ampicillin	66.67
	Penicillin	70.83
	Piperacillin-Tazobactam	0.00
	Amoxiclav	31.82
Fluoroquinolones	Ciprofloxacin	40.00
Macrolides	Erythromycin	62.50
Others	Chloramphenicol	0.00
	Cotrimoxazole	20.00
	Clindamycin	26.32
	Doxycycline	8.70
	Aztreonam	0.00
	Novobiocin	0.00

Fourteen antibiotics demonstrated sensitivity rates of 100.00%, including cefotaxime, ceftazidime, chloramphenicol, amikacin, novobiocin, netilmicin, vancomycin, linezolid, teicoplanin, aztreonam, piperacillin-tazobactam, meropenem, and ertapenem. Doxycycline showed a sensitivity rate of 91.30% (Table 6). Multidrug resistance was observed in 66.67% of isolates, indicating a high burden of resistant organisms in neonatal sepsis. This finding is clinically significant and emphasizes the need for judicious use of antibiotics and strict infection control practices (Table 7). Higher MDR rates were observed in *Pseudomonas spp.*, *Staphylococcus aureus,* and *Streptococcus spp.*, all showing 100% MDR. CONS also demonstrated a high MDR rate (80%). Although *Klebsiella pneumoniae* showed a comparatively lower MDR rate (41.67%), it remained the most common isolate. The association between organism type and MDR was not statistically significant (p=0.201), possibly due to small sample size (Table 8).

Table 6: Most effective antibiotics (sensitivity ≥90%) (n=27).

Rank	Antibiotic	Sensitivity (%)
1	Cefotaxime	100.00
1	Ceftazidime	100.00
1	Chloramphenicol	100.00
1	Amikacin	100.00
1	Novobiocin	100.00
1	Netilmicin	100.00
1	Vancomycin	100.00
1	Linezolid	100.00
1	Teicoplanin	100.00
1	Aztreonam	100.00
1	Piperacillin-Tazobactam	100.00
1	Meropenem	100.00
1	Ertapenem	100.00
14	Doxycycline	91.30

Table 7: Multidrug resistance (MDR) pattern (n=27).

MDR status	Frequency (N)	Percentage (%)
MDR positive	18	66.67
MDR negative	9	33.33
Total	27	100.00

Multidrug resistance (MDR) defined as resistance to at least one agent in three or more antimicrobial classes

Culture positivity was observed in 18 out of 46 male neonates (39.13%) and 9 out of 29 female neonates (31.03%). The difference in culture positivity between sexes was not statistically significant (χ^2=0.2156, df=1, p=0.6424). With respect to age group, culture positivity was observed in 21 out of 64 neonates (32.81%) with early-onset sepsis and 6 out of 11 neonates (54.55%) with late-onset sepsis. The difference in culture positivity between age groups was not statistically significant (χ^2=1.0966, df=1, p=0.2950) (Table 9).

Table 8: Association of multidrug resistance with bacterial isolates (n=27).

Bacterial isolate	MDR positive (N)	MDR negative (N)	Total (N)	MDR rate (%)
Klebsiella pneumoniae	5	7	12	41.67
Coagulase-negative *Staphylococcus* (CONS)	4	1	5	80.00
Pseudomonas spp.	4	0	4	100.00
Enterococcus spp.	2	1	3	66.67
Staphylococcus aureus	2	0	2	100.00

Continued.

Bacterial isolate	MDR positive (N)	MDR negative (N)	Total (N)	MDR rate (%)
Streptococcus spp.	1	0	1	100.00
Total	18	9	27	66.67

Chi-square test: χ^2=7.275, df=5, p=0.201*

Table 9: Association of demographic factors with culture positivity (n=75).

Factor	Category	Culture positive (N)	Culture negative (N)	Total (N)	Positivity rate (%)	χ^2	df	P value
Sex	Male	18	28	46	39.13	0.2156	1	0.6424
	Female	9	20	29	31.03			
Age group	Early onset	21	43	64	32.81	1.0966	1	0.2950
	Late onset	6	5	11	54.55			

DISCUSSION

The present study provided a detailed evaluation of neonatal sepsis with respect to demographic profile, microbial distribution, antibiotic sensitivity, and resistance patterns, and the findings were compared with previously reported studies to understand similarities and variations. In this study, a total of 75 neonates were included, with a clear male predominance of 61.33% compared to females (38.67%), which is consistent with the general observation that male neonates are more vulnerable to infections due to immunological and genetic factors. A similar trend of male predominance has been reported in previous studies, although exact proportions vary across settings. The majority of cases in the present study were early-onset sepsis (85.33%), with only 14.67% being late-onset, and the mean age at presentation was 1.79±1.93 days. This high proportion of early-onset sepsis is comparable to findings reported by Gurmu (2026), where early-onset sepsis accounted for 71.9% of cases, indicating the strong influence of maternal and perinatal factors in neonatal infections.[11]

The culture positivity rate in the present study was 36.00%, which falls within the range reported in earlier studies. Jadav et al reported a slightly lower culture positivity rate of 29.7%, while Sorsa observed a similar rate of 29.4%, and Gurmu reported a higher rate of 62.8% (1–3).[11,12] These variations may be attributed to differences in sample size, diagnostic methods, prior antibiotic exposure, and healthcare settings. Additionally, Karmila reported a significant proportion of culture-negative sepsis (44%), emphasizing that a considerable number of clinically suspected cases may not yield positive cultures due to low bacterial load or prior antibiotic use.[13] Thus, the present study's finding of 64.00% culture-negative cases aligns with these observations and highlights the limitations of blood culture as a diagnostic tool.

With respect to microbial distribution, the present study demonstrated a predominance of gram-negative organisms (59.26%) over gram-positive organisms (40.74%), which is consistent with findings reported by Jadav et al where gram-negative bacteria constituted 62% of isolates, and Gao et al where gram-negative organisms accounted for 59.8% of isolates.[13,14] Similarly, Gurmu reported a nearly equal distribution of gram-positive (50.8%) and gram-negative (49.2%) organisms, indicating regional variations.[11] The predominance of gram-negative organisms in the present study reflects the increasing burden of hospital-acquired infections and environmental contamination in neonatal intensive care units.

Among the bacterial isolates, *Klebsiella pneumoniae* was the most common organism in the present study, accounting for 44.44% of cases, followed by *coagulase-negative Staphylococcus* (18.52%), *Pseudomonas spp.* (14.81%), *Enterococcus spp.* (11.11%), and *Staphylococcus aureus* (7.41%). This finding is consistent with Jadav et al where *Klebsiella pneumoniae* accounted for 27% of isolates, and Gao et al where Klebsiella pneumoniae was one of the most predominant pathogens (21.9%).[12,14,1,5] Similarly, Gurmu also identified *Klebsiella pneumoniae* (22.4%) as a leading gram-negative pathogen.[11,2] However, in contrast, Sorsa reported coagulase-negative staphylococci (25%) as the most common isolate, followed by *Escherichia coli* (20.5%) and *Staphylococcus aureus* (18%), while Karmila reported coagulase-negative staphylococci (30.9%) as the predominant organism.[3,13,15] These differences highlight geographical variations in microbial patterns and emphasize the need for region-specific surveillance.

The antibiotic sensitivity pattern observed in the present study demonstrated high effectiveness of higher-generation antibiotics. A total of 14 antibiotics showed 100.00% sensitivity, including cefotaxime, ceftazidime, amikacin, netilmicin, meropenem, ertapenem, vancomycin, teicoplanin, linezolid, and piperacillin-tazobactam, while doxycycline showed 91.30% sensitivity. These findings are consistent with Jadav et al which reported that carbapenems retained the highest sensitivity among gram-negative isolates and that vancomycin and linezolid were highly effective against gram-positive organisms.[1,12] Similarly, Gurmu reported that gram-negative organisms were most susceptible to amikacin (85.8%) and carbapenems (75.8%), while gram-positive organisms showed high susceptibility to vancomycin (91.9%).[11] Sorsa also found that isolates remained susceptible to higher-line antibiotics such as vancomycin, clindamycin, and ciprofloxacin despite resistance to first-line drugs.[15] These consistent findings across studies reinforce the continued effectiveness of higher-generation antibiotics in managing severe neonatal infections.

However, the present study also revealed alarming resistance patterns, particularly to commonly used first-line antibiotics. High resistance was observed for high-level gentamicin (75.00%), penicillin (70.83%), ampicillin (66.67%), erythromycin (62.50%), and cefuroxime (57.14%). These findings are comparable to Jadav et al, which reported resistance rates of 78% for ampicillin, 64% for cefotaxime, and 55% for gentamicin.[1] Similarly, Sorsa reported resistance rates of 66.7% for *E. coli* and 91% for *Klebsiella spp.* against ampicillin, along with high resistance to gentamicin.[1,3] Gurmu documented very high resistance to ampicillin (92.5%) and significant resistance to third-generation cephalosporins (65.8–93.3%).[11] These consistent findings across multiple studies highlight the declining effectiveness of first-line antibiotics and the growing challenge of antimicrobial resistance in neonatal sepsis.

A major concern identified in the present study was the high prevalence of multidrug resistance (66.67%), which is comparable to Sorsa, where 72% of isolates were multidrug-resistant, and Karmila, which reported 62.6% multidrug-resistant organisms.[3,4,13] Although slightly lower than these studies, the MDR rate in the present study remains significantly high and clinically concerning. Jadav et al reported a rising trend of multidrug-resistant organisms over time.[12] In the present study, organisms such as *Pseudomonas spp., Staphylococcus aureus*, and *Streptococcus spp.* showed 100% MDR, while coagulase-negative *Staphylococcus* showed 80% MDR and *Klebsiella pneumoniae* showed 41.67% MDR. These findings indicate that even though *Klebsiella pneumoniae* had a relatively lower MDR rate, its high prevalence makes it a major contributor to disease burden. The lack of statistically significant association between organism type and MDR (p=0.201) may be due to the limited sample size.

The association between demographic factors and culture positivity in the present study showed that males had a higher positivity rate (39.13%) compared to females (31.03%), and late-onset sepsis had a higher positivity rate (54.55%) compared to early-onset sepsis (32.81%); however, these differences were not statistically significant (p>0.05). Similar observations have been reported in previous studies, where demographic factors were not found to be strong predictors of culture positivity, although clinical and perinatal factors may play a more significant role.[2]

Overall, the findings of the present study are largely consistent with previous research, demonstrating a predominance of Gram-negative organisms, particularly *Klebsiella pneumoniae*, high sensitivity to higher-generation antibiotics, and alarming resistance to commonly used first-line drugs. The high prevalence of multidrug-resistant organisms further emphasizes the urgent need for rational antibiotic use, continuous surveillance, and strict infection control practices. These comparisons with previous studies strengthen the validity of the present findings and highlight the global and regional challenge of antimicrobial resistance in neonatal sepsis.

CONCLUSION

Neonatal sepsis remains a critical clinical challenge, particularly in tertiary care settings, with a predominance of early-onset cases and a higher susceptibility among male neonates. The study highlights the dominance of Gram-negative organisms, especially opportunistic hospital-associated pathogens, reflecting the ongoing burden of nosocomial infections. Although higher-generation antibiotics continue to demonstrate good efficacy, the increasing resistance to commonly used first-line antibiotics and the substantial presence of multidrug-resistant organisms pose serious concerns for treatment outcomes. These findings emphasize the urgent need for regular microbiological surveillance, strict infection prevention and control measures, and the implementation of effective antibiotic stewardship programs. Developing institution-specific antibiograms and promoting rational antibiotic use are essential strategies to improve neonatal outcomes and combat the growing threat of antimicrobial resistance.

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