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Original Article

BACTERIOLOGICAL PROFILE AND ANTIBIOGRAM PATTERN IN ISOLATES FROM NEONATAL SEPSIS IN A TERTIARY CARE HOSPITAL

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ABSTRACT

Objective: To determine the microbiological profile and their Antibiogram pattern in isolates from neonatal sepsis.

Methods: This study was conducted from October 2022 to January 15th 2023. Total 663 blood samples received from NICU, which were processed in the department of microbiology Andhra Medical College, Visakhapatnam. Organisms were identified by conventional methods and an antibiotic susceptibility test was done by Kirby Bauer disc diffusion method as per CLSI guidelines.

Results: Out of 663 samples 200 (30.16%) are culture positives, in which males are more affected than females, that is 103 (51.5%). Among the culture positives, the most predominant isolate was *klebsiella species* 106 (53%) followed by *pseudomonas 28 (14%) Escherichia coli 28 (14%) Acinetobacter 24 (12%), MRSA 11 (0.05%), MSSA* 3(0.015%). Regarding its antibiogram, *klebsiella species and Escherichia coli* were most sensitive to penicillins+beta lactamase inhibitors (83%), fluroquinolones (75%) and aminoglycosides (75%), respectively. *Pseudomonas, Acinetobacter* was sensitive to penicillins+betalactamase inhibitors (100%) and aminoglycosides (72%). Gram-positive organisms were mostly sensitive to vancomycin, linezolid, aminoglycosides (MRSA) and cefoxitin (MSSA). There was widespread resistance to third-generation cephalosporins (77.77%) among gram-negative organisms.

Conclusion: Gram negative bacteria are the most common cause of neonatal sepsis and *klebsiella species* are the predominant pathogens. These gram negative bacteria were resistant to cephalosporins. Antibiogram helps as a guide to antimicrobial therapy and resistance to antibiotics, as it is the common problem that causes ineffectiveness of empirical treatment.

Keywords: Neonatal sepsis, Bacterial isolates, Multidrug resistance, Antibiotic sensitivity.

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INTRODUCTION

Septicaemia is the significant cause of morbidity and mortality in the neonates and is responsible for 30-50% of total neonatal deaths each year in developing countries. It is estimated that up to 20% of neonates develop sepsis and approximately 1% die of sepsis [1]. Neonatal sepsis is a clinical syndrome which is characterized by signs and symptoms of infection, which may or may not be accompanied by bacteremia within the first month of life. Neonatal sepsis can be classified into early onset sepsis (EOS) and late-onset sepsis (LOS) based on the timing of onset of sepsis-EOS presenting within 72 h of birth and LOS presenting 72 h after birth. The importance of this classification. It helps to guide antibiotic therapy by implying differences in the mode of transmission and the predominant causative organisms [2]. EOS is caused mainly by bacteria transmitted from mothers to neonates during the intrapartum period, these are bacteria prevalent either in the maternal genital tract or in the area of delivery. LOS is caused by postnatal acquisition of the pathogens, caused by the bacteria which thrive in the external environment of the hospital or home. There is a gradually increasing trend of multi-drug resistant (MDR) pathogens in tertiary care neonatal intensive care units (NICU) and special newborn care units (SNCUs) all over India [3]. Multi-drug resistance was defined as the acquired resistance to at least one agent in three or more antimicrobial categories as per the Centers for Disease Control and Prevention (CDC) guidelines [4]. Strict antibiotics stewardship program will enable us to counteract multi-drug resistance patterns of emerging pathogens [3].

The aim of my study is to determine the microbiological profile and their antibiogram pattern in isolates from neonatal sepsis.

MATERIALS AND METHODS

This study was conducted on blood samples received in microbiology laboratory from NICU in Andhra Medical College over a period of four months (from October 2022 to February 2023). In the study period, a total of 663 blood samples were received from the neonates for Bacterial culture and sensitivity.

Sample collection

2 ml of blood for culture was drawn in sterile syringe after skin preparation by a two-step process with 70% alcohol and povidone-iodine application and then dried for 1 min. Blood was collected aseptically and incubated in blood culture bottle containing 10 ml of Brain Heart Infusion Broth (BHIB). These bottles were incubated at 37 °C temperature under aerobic conditions in the incubator maximum for 7 d. Subculture were made on Blood agar and Mac-conkey's agar daily from 1st to 7th day. If growth was observed further subcultures were not done and processed according to standard microbiological techniques which includes Gram staining, colony characteristics and biochemical properties. Blood culture broth which showed no microbial growth after 7 d were reported as culture negative [5]. Criteria for antimicrobial sensitivity testing used were as per Clinical Laboratory Standard Institute guidelines (CLSI) [6]. Antimicrobial sensitivity testing was done on Muller Hinton Agar (MHA) by Kirby Bauer disc diffusion method.

RESULTS

Total 663 blood sample reports were studied. Out of 663 samples 200 (30.16%) are culture positives, in which males are more effected than females that is 103 (51.5%). Early onset sepsis 137 (68.5%) was more common in our setup than late 63 (31.5%). Among the culture positives the most predominant isolate was *Klebsiella* species 106 (53%) followed by *Pseudomonas* 28 (14%) *Escherichiacoli*28 (14%) *Acinetobacter* 24 (12%), *Methicillin Resistant Staphylococcus Aureus* 11 (0.05%), *Methicillin Sensitive Staphylococcus Aureus* 3(0.015%) (fig. 1).

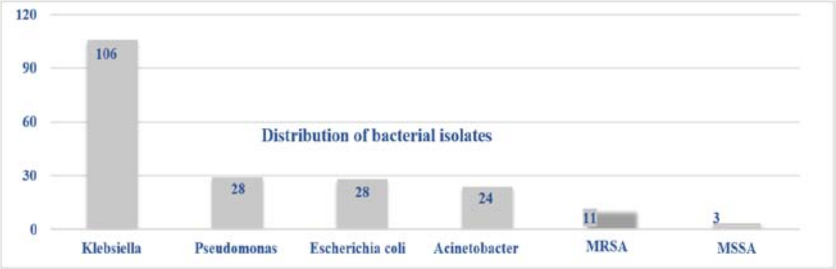

Fig. 1: Distribution of bacterial isolates

Regarding its antibiogram, *Klebsiella* and *Escherichiacoli* were sensitive to Pencillins+Betalactamase inhibitors (83.5%), Carbapenems (83%) Fluroquinolones (75%) and Aminoglycosides (75%). *Pseudomonas and Acinetobacter,* were sensitive to Pencillins+Betalactamase inhibitors (100%), Carbapenems (75%), Aminoglycosides (72%) (table 1). Gram-positive organism *staphylococcus aureus* was sensitive to vancomycin (100%), linezolid (95%), aminoglycosides (81%), Tigecycline (88%) (table 2). There was widespread resistance to third generation cephalosporins (77.77%) among Gram-negative organisms.

Table 1: Antibiotic sensitivity pattern of isolated gnb organisms

Antimicrobial drugs	Isolated organisams			
	Klebsiella, n= 106	**Escherichia coli, n= 28**	**Pseudomonas n=28**	**Acinetobacter, n=24**
Piperacillin+tazobactum	92 (87.2%)	23 (82%)	28 (100%)	24 (100%)
Ciprofloxacin	74 (70%)	22 (78.5%)	16 (57.1%)	15 (62.5%)
Meropenem	87 (83%)	24 (85%)	22 (78.5%)	21 (87%)
Amikacin	69 (66.6%)	24 (85%)	20 (71.4%)	14 (58%)
Cefotaxime	21 (20%)	4 (14.28%)	--	--
Cotrimoxazole	42 (40%)	11 (39.2%)	--	--
Ceftazidime	---	--	14 (50%)	3 (12%)

Table 2: Antibiotic sensitivity pattern of isolated gpc organisms

Antimicrobial drugs	Staphylococcus aureus (n=14)
Vancomycin	14 (100%)
Linezolid	13 (95%)
Tigecycline	12 (88%)
Gentamicin	11 (81%)
Cefoxitin	7 (50%)
Ciprofloxacin	5 (40%)

DISCUSSION

The emergence of anti-biotics-resistant bacteria and its dissemination is exacerbated by inappropriate antimicrobial consumption and precarious living condition. The most common organisms associated with neonatal sepsis vary with time of infections and geographical location. Therefore, information on the bacteriological profile of neonatal sepsis and effective antimicrobials for its treatment are important to combat with neonatal morbidity and mortality issues [7].

Gram negative bacteria (93%) were the most common organisms isolated in the present study. Similar observations have been made by others; Manjula Dutta *et al.* 67.94%) [8] Mythri B. A *et al.* (62.34%) [2] and Bipin Gupta *et al.* [9]. These gram negative bacteria were resistant to third-generation cephalosporins [10].

In our study the predominant pathogen isolated was *Klebsiella* species among Gram-negative organisms and *Methicillin Resistant Staphylococcus* Aureus among Gram-positive organisms. Various other studies have been compared in following (table 3).

Table 3: Comparison of bacterial pathogens isolated with other studies

Studies	Total culture positives (n)	Total gram negative organisams isolated	Total gram positive organisams isolated	Pre-dominant isolate
Our study	200	186(93%)	14(7%)	Klebsiella
Dr. Manjula Dutta *et al.*	156	118(75.6%)	32(20.5%)	Klebsiella
Dr. Mythri B. A *et al.*	154	96(62.3%)	58(37.6%)	Klebsiella

CONCLUSION

In present study gram gram-negative bacteria are the most common cause of neonatal sepsis and *klebsiella* species are the predominant pathogens and they were resistant to third-generation cephalosporins preterm and low birth weight neonates are more susceptible to neonatal sepsis. Gram negative organisms were the commonly isolated organisms. This study emphasizes that empirical therapy for suspected neonatal septicemia should cover both Gram-negative and Gram-positive organisms particularly *Klebsiella* species and *Staphylococcus Aureus,* which were more prevalent in this region. There is also need for regular periodic surveillance of the causative organisms of neonatal sepsis as well as their antibiotic susceptibility patterns to curtail the inappropriate use of antibiotics and the emergence of resistant strains and review the hospital antibiotic policy from time to time.

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AUTHORS CONTRIBUTIONS

First author of the study Dr. K. Urmila devi contributed conceptual design, literature search, and collected the data. The second author contributed data analysis statistical analysis and wrote the first draft of the manuscript and guided in the literature review. Third author corrected the final draft of the manuscript.

CONFLICTS OF INTERESTS

There are no conflicts of interest.

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