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Original Research

Blood Culture Positivity Rates among Babies Admitted to the Premature Baby Unit of a Secondary Care Hospital in Southern Sri Lanka: An Analysis of Microbial Isolates and Antimicrobial Susceptibility Patterns

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Abstract

Bloodstream infections are a major cause of morbidity and mortality among babies in premature baby units (PBU). Periodic monitoring of the antimicrobial sensitivity of the causative organisms in a particular setting is important for the early management of infections in babies. The aim of this study was to determine the proportion of blood culture positivity and to assess the factors associated with bloodstream infections among the babies and the causative microorganisms and their antibiotic susceptibility pattern, isolated in blood cultures of babies with suspected sepsis admitted to PBU at District General Hospital Matara (DGHM). An institution based cross-sectional study was conducted in microbiology laboratory of DGHM to review blood culture reports received from PBU retrospectively. All the consecutive samples from the PBU from January 2021 to December 2022 were included in the study. Data on culture isolates, antibiotic susceptibility patterns and related variables were collected and analysed using SPSS version 25.0. Over the study period, 1612 blood cultures had been sent to the laboratory from the PBU. Overall blood culture positivity rate was 9%. The majority of isolates were gram-positive organisms (68%). Coagulase-negative staphylococci (51.6%) were the most common isolates, followed by lactose fermenting coliforms (16%) and *Pseudomonas spp.* (8%). Amikacin showed a higher sensitivity than gentamicin among gram-negative organisms. Carbapenem resistance was observed in 40.5% of the isolates. Among *Staphylococcus aureus* 55.6% were methicillin-resistant and 44.4% were methicillin-sensitive. Prematurity (p=0.017) and low birth weight (p=0.002) were significantly associated with culture positive sepsis. Preterm and low birth weight were significantly associated with bloodstream infections among babies admitted to PBU of DGHM. Coagulase-negative Staphylococci, lactose fermenting coliforms, and *Pseudomonas spp.* were the predominant causative organisms.

Keywords: *Antibiotic susceptibility pattern, Blood culture, Neonatal bloodstream infections, Premature babies*

Introduction

Bloodstream infections are invasive bacterial infections that spread into blood stream and bacteremia refers to presence of viable bacteria in blood [1]. Early-life infections are a common contributor to health complications and neonatal sepsis remains a significant cause of morbidity and mortality among newborns, especially in premature and low birth weight infants [2]. A baby born before the 37th week of gestation is known as a premature baby or a preterm baby. One in ten newborns is born before completion of 37th week [3]. Sepsis occurs within first 72 hours of birth is categorised as early onset sepsis (EOS) and sepsis occurs after first 72 hours is categorised as late onset sepsis (LOS) [4].

Immunological status determines the clinical progress of the disease. Immune function in premature babies is a major contributor to the risk of infections [3]. Infections in PBU are highly infectious and it results in a high mortality rate and serious complications as premature babies do not have well-developed immune system.

Blood stream infections are a common problem of neonates in premature baby units (PBU). Blood culture remains the gold standard for diagnosing bloodstream infections, and early detection through culture-based methods, is essential for guiding effective antimicrobial therapy. PBU provides specialized care to neonates who are vulnerable to a range of infections due to their underdeveloped immune systems, prolonged hospital stays and frequent invasive procedures. Understanding the prevalence of positive blood cultures, organisms causing infections and antibiotic susceptibility pattern among neonates admitted to the PBU is critical for improving infection control measures. Also it is beneficial in avoiding unnecessary usage and optimising empirical antibiotic treatment [5]. Changing pattern and frequent development of resistant bacteria is another problem arising during the management of these neonates. Antimicrobial sensitivity pattern differs in different studies as well as at different times in the same hospital [6,7] Therefore, periodic monitoring of the antimicrobial sensitivity of the causative organisms in a particular setting is important for the early management of infections in babies.

Neonatal sepsis is a complex clinical condition influenced by a variety of maternal, perinatal, and neonatal factors [8,9]. Understanding these associated factors is crucial for early identification of at-risk neonates and the implementation of targeted preventive and management measures.

DGHM is a major tertiary care institution in the Southern Province of Sri Lanka, receiving a substantial number of neonatal blood samples from its PBU for microbiological testing. Therefore, this would be a preliminary study that can support the improvement of infection control measures and the management of babies with bloodstream infections in PBU. The study aims to determine the proportion of blood culture positivity among neonates admitted to the PBU at DGHM. Also to identify the risk factors and the common causative microorganisms and their antibiotic susceptibility patterns, isolated in blood cultures of neonates with suspected sepsis admitted to PBU at DGHM.

Methods

Study design and setting

An institution based, cross-sectional study was conducted in microbiology laboratory of DGHM to review blood culture reports of neonates received from PBU retrospectively.

Study population

The sample size was calculated using the formula for estimating prevalence in cross-sectional studies, as described by Lwanga and Lemeshow (1991) in sample size determination in health studies. The minimum sample size required was 384. All the consecutive samples from the PBU from January 2021 to December 2022 were taken into study. Reports of all the blood cultures received to laboratory from PBU were included and reports of repeated positive blood cultures from the same neonate which grew the same organism were excluded from the study.

Processing of blood cultures

Blood cultures had been processed using automated blood culture and manual methods according to the Standard Operating Procedures for blood culture in the Laboratory Manual in Microbiology by the Sri Lanka College of Microbiologists. Antibiotic sensitivity testing had been performed by clinical laboratory standards institute disc diffusion method.

Statistical analysis

Positive and negative culture results and other related details like Socio-demographic details of neonates were obtained through review of the request forms. Data were entered into excel sheets and analysed using SPSS version 25.0. Descriptive statistics were presented as means, percentages and proportions as appropriate. Chi-square test was used to test the association between categorical variables.

Results

Demographic characteristics of the sample

During the study period, a total of 1,612 blood culture samples had been received by the microbiology laboratory from neonates admitted to the PBU with clinical suspicion of bloodstream infections. From the available data, majority were males (56.7%) and median age was 1 day (IR=4) and age ranges from day one up to 60 days. Of the sample, 99% were aged between 0 and 31 days, while only 1% were aged between 31 and 60 days. From the culture positive cases, 53.8% were males and 46.2% were females.

Neonates had been commonly presented with respiratory distress (14.3%), fever (12.3%), tachypnea (6.32%), grunting (12.9%), reduced activity, poor suckling, weight loss, icteric and jaundice (2%). None of the features were found to significantly associate with clinical features for culture positive suspected sepsis when compared to culture-negative cases.

Factors associated with neonatal sepsis

A total of 69.4% (1103 cases) were early onset (EOS) sepsis cases and 30.6% (487 cases) were late onset sepsis (LOS). Majority (72.8%) were early-onset, culture-negative sepsis. The onset of sepsis (p<0.001) was found to be significantly associated with culture-positive when compared with culture-negative sepsis. Among the total, 93.8% were reported with normal birth weight and 6.2% were with low birth weight. Of normal birth weight and low birth weight neonates, about

88.2% and 11.8% were culture-positive, respectively. Among the total, 335 (20.8%) neonates had been reported to have gestational age less than 37 weeks and 1277 (79.2%) were term babies. Factors like prematurity (p=0.017) and low birth weight (p=0.002), were statistically associated with culture-positivity. (Table 1)

Table 1 Description of baseline characteristics between culture negative and culture-positive cases

	Culture negative		**Culture positive**		***p*-value**
	n	%	n	%	
Sex					
Male	572	57	71	53.8	
Female	431	43	61	46.2	0.480
Onset of sepsis					
EOS	1050	72.8	53	35.6	
LOS	391	27.2	96	64.4	0.001
Birth weight					
LBW	82	5.6	18	11.8	
NBW	1378	94.4	134	88.2	0.002
Gestational age					
Preterm	292	20	43	28.3	
Term	1168	80	109	71.7	0.017
History of premature rupture of membrane					
Yes	11	0.8	3	2	
No	1459	99.2	149	98	0.123

(n=No. of Cases, EOS- Early onset sepsis, LOS- Late onset sepsis, LBW- Low birth weight, NLW- Normal birth weight)

Bacteriological profile of isolated organisms

Of 1612 cultures sent to the laboratory, only 152 cultures showed a positive growth. The overall blood culture positivity rate in this study was 9%. EOS and LOS had 4.8% (53/1103) and 19.7% (96/487) blood culture positivity, respectively. Overall, gram positive organisms (68%) were isolated more frequently than gram negatives.

A total of 152 neonates were found to have blood culture-positive sepsis, of which 125 were positive for bacteremia, 24 were considered possible contaminations and three for fungal sepsis. Gram-negative bacteria accounted for 34.4% (43 cases) and gram-positive organism accounted for 65.6% (82 cases) of sepsis which contributed to 2.6% and 5.1% out of the total suspected sepsis cases, respectively. Different organisms isolated from positive cultures are showed in Table 2.

Coliforms (62.7%) were the most commonly isolated gram-negative organism. Of coliforms 20 cases were lactose fermenting (LF) coliform and

seven were non lactose fermenting (NLF) coliform and 16% and 5.6% from total isolated organisms, respectively. Of LF cases, six cases (30%) were reported as probable *Klebsiella spp.* Of 20 LF coliforms isolated, three (15%) were extended spectrum beta lactamase (ESBL) and two (10%) were multi drug resistant (MDR). About 23.3% (10/43) were *Pseudomonas spp.* among them 20% were *Pseudomonas aeruginosa*. About 11.6% and 2.3% of the gram-negative organisms were *Acinetobacter spp.* and *Flavobacterium spp.,* respectively.

While Coagulase negative staphylococcus (CONS) contributing 78% (64/82), *Staphylococcus aureus* 11% (9/82), *streptococcus spp.* (9.8%) were the common gram-positive organisms isolated and *Enterococcus spp.* 1.2% (1/82) contributed the least. Of nine *Staphylococcus aureus,* four (44.4%) had resistance pattern of MRSA (Methicillin Resistant Staphylococcus aureus) and one had resistance pattern of Methicillin Resistant Staphylococcus aureus + Macrolide Lincosamide Streptogramin B (MRSA+MLSB). From the *streptococcus spp.* six out of eight (75%) were reported as probable group B *streptococcus spp.* and there were one *Streptococcus pneumoniae* and one probable group D *streptococcus spp.*

Table 2 Organisms isolated from positive blood cultures

Isolated micro-organisms	No. of cases (%)
Gram-negative organisms	
LF coliform	20 (16)
NLF coliform	7 (5.6)
Pseudomonas spp.	10 (8)
Acinetobacter spp.	5 (4)
Flavobacterium spp.	1 (0.8)
Gram-positive organisms	
Staphylococcus aureus	9 (7.2)
Coagulase-negative staphylococci	64 (51.6)
Probable group B *Streptococci*	6 (4.8)
Streptococci pneumoniae	1 (0.8)
Probable group D *Streptococci*	1 (0.8)
Enterococcus spp.	1 (0.8)
Total	**125**

(LF Coliform – Lactose fermenting coliform, NLF Coliform – Non lactose fermenting coliform)

Antibiotic susceptibility patterns

Overall, among the gram-negative organisms three (7%) were ESBL producers and two (4.7%) were MDR. Others were sensitive to majority of antibiotics tested. One out of four *Acinetobacter spp.* were carbapenem-resistant *Acinetobacter* (CRAB). About 83.3% of the probable *Klebsiella spp.* isolates were found to be resistant to third-generation cephalosporin and gentamycin but sensitive to amikacin. Of lactose fermenting coliforms 77.8% were sensitive to amikacin and 72% were resistant to gentamycin. Coliforms producing ESBL were sensitive to carbapenems, amikacin. (Table 3)

Table 3 Antibiotic susceptibility and resistance profile of gram-negative organisms

Antibiotics		Coliform LF (%)	Coliform NLF (%)	*Klebsiella spp.* (%)	*Acinetobacter spp.* (%)	*Pseudomonas spp.* (%)	*Flavobacterium spp.* (%)
AK	S	9 (75)	6 (100)	5 (83.3)	5 (100)	8 (88.9)	1 (100)
	R	3 (25)	0	1 (16.7)	0	1 (11.1)	0
AMP	S	0	-	0	1 (100)	1 (100)	-
	R	3 (100)		1 (100)	0	0	
AMC	S	3 (21.4)	6 (85.7)	1 (16.7)	2 (100)	4 (100)	1 (100)
	R	11 (78.6)	1 (14.3)	5 (83.3)	0	0	0
CAZ	S	1 (16.7)	5 (71.4)	1 (16.7)	4 (80)	9 (90)	1 (100)
	R	5 (83.3)	2 (28.6)	5 (83.3)	1 (20)	1 (10)	0
CXM	S	3 (23.1)	1 (16.7)	1 (16.7)	1 (50)	1 (33.3)	1 (100)
	R	10 (76.9)	5 (83.3)	5 (83.3)	1 (50)	2 (66.7)	0
CTX	S	3 (21.4)	3 (42.9)	1 (16.7)	1 (50)	2 (66.7)	1 (100)
	R	11 (78.6)	4 (57.1)	5 (83.3)	1 (50)	1 (33.3)	0
CIP	S	6 (42.9)	4 (80)	1 (16.7)	5 (100)	9 (90)	1 (100)
	R	6 (42.9)	1 (20)	4 (66.6)	0	1 (10)	0
	I	2 (14.3)	0	1 (16.7)	0	0	0
CN	S	4 (33.3)	6 (85.7)	1 (16.7)	4 (80)	9 (90)	1 (100)
	R	8 (66.7)	1 (14.3)	5 (83.3)	1 (20)	1 (10)	0
IMP	S	4 (36.4)	5 (83.3)	1 (25)	3 (75)	2 (100)	-
	R	7 (63.6)	1 (16.7)	2 (50)	1 (25)	0	
	I	0	0	1 (25)	0	0	
MEM	S	5 (55.6)	4 (100)	1 (33.3)	3 (75)	8 (100)	1 (100)
	R	3 (33.3)	0	1 (33.3)	1 (25)	0	0
	I	1 (11.1)	0	1 (33.3)	0	0	0
SCF	S	5 (50)	5 (83.3)	2 (33.3)	4 (100)	5 (100)	1 (100)
	R	5 (50)	1 (16.7)	4 (66.6)	0	0	0
SXT	S	3 (30)	3 (60)	2 (40)	5 (100)	1 (50)	1 (100)
	R	7 (70)	2 (40)	3 (60)	0	1 (50)	0
TZP	S	5 (38.5)	6 (85.7)	2 (33.3)	4 (100)	8 (100)	1 (100)
	R	6 (46.2)	1 (14.3)	4 (66.6)	0	0	0
	I	2 (15.4)	0	0	0	0	

(AK: Amikacin, AMP: Ampicillin, AMC: Amoxicillin clavulanic acid, CTX: Cefotaxime, CIP: Ciprofloxacin, SXT: Cotrimoxazole, CN: Gentamicin, IMP: Imipenem, MEM: Merapenem, CAZ: Ceftazidime, CXM: Cefuroxime, SCF: Cefoperazone sulbactam, TZP: Piperacillin tazobactam, S: Sensitive, R: Resistant, I: Intermediate)

Among gram-positive organisms 13.4% were sensitive to all antibiotics tested and there were no MDR organisms. Out of nine, four (44.4 %) *Staphylococcus aureus* had resistance pattern of MRSA and one had resistance pattern of MRSA+MLSB. Penicillin resistance was noted in isolated *Enterococcus spp.* and probable group D *Streptococci* were sensitive to vancomycin. (Table 4)

Table 4 Antibiotic susceptibility and resistance profile of gram-positive organisms

Antibiotic		*Staphylococcus aureus* (%)	CONS (%)	*Streptococcus pneumonia* (%)	Probable group B *Streptococcus spp.* (%)	Probable group D *streptococcus spp.* (%)	*Enterococcus spp.* (%)
FOX	S	3 (37.5)	19 (31.7)	-	-	-	-
	R	5 (62.5)	41 (68.3)				
DA	S	7 (77.8)	38 (62.3)	1 (100)	3 (50)	0	0
	R	2 (22.2)	23 (37.7)	0	1 (16.7)	1 (100)	1 (100)
	I	0	0	0	2 (33.3)	0	0
E	S	3 (37.5)	17 (27.4)	1 (100)	3 (50)	0	0
	R	5 (62.5)	45 (72.6)	0	1 (16.7)	1 (100)	1 (100)
	I	0	0	0	2 (33.3)	0	0
VA	S	9 (100)	61 (100)	1 (100)	5 (100)	-	1 (100)
	R	0	0	0	0		0
P	S	-	-	1 (100)	6 (100)	1 (100)	0
	R			0	0	0	1 (100)
OX	S	-	-	1 (100)	1 (100)	-	-
	R			0	0		
SXT	S	9 (100)	35 (60.3)	-	2 (100)	-	1 (100)
	R	0	23 (39.7)		0		0
TEC	S	9 (100)	58 (96.7)	-	-	-	-
	R	0	23 (39.7)				
FD	S	8 (88.9)	27 (45)	-	-	-	-
	R	1 (11.1)	33 (55)				
CIP	S	4 (50)	28 (50.9)	-	-	-	-
	R	3 (37.5)	27 (49.1)				
	I	1 (12.5)	0				
CRO	S	-	-	-	4 (100)	0	0
	R				0	1 (100)	1 (100)
CTX	S	-	-	1 (100)	2 (100)	-	-
	R			0	0		
AMP	S	-	-	-	6 (100)	0	0
	R				0	1 (100)	1 (100)

(CONS: Coagulase-negative staphylococcus, FOX: Cefixitin, DA: Clindamycin, E: Erythromycin, V: Vancomycin, P: Penicillin, OX: Oxacillin, SXT: Cotrimoxazole AMP: Ampicillin, CTX: Cefotaxime, CIP: Ciprofloxacin, TEC: Teicoplanin, FD: Fusidic acid, CRO: Ceftriaxone, S: Sensitive, R: Resistant, I: Intermediate)

Discussion

Neonatal sepsis remains a significant cause of morbidity and mortality in newborns, where diagnostic and therapeutic resources may be limited [10,11]. The causative organisms and clinical outcomes of neonatal sepsis is vary by region, hospital setting, and infection control practices [12]. Understanding the local prevalence of blood culture positivity, the spectrum of pathogens involved, and their antibiotic susceptibility patterns is essential for timely and effective empirical therapy. In this study, the proportion of blood culture-positive cases among neonates with suspected sepsis

admitted to the PBU of DGHM was assessed, alongside the associated clinical factors, causative organisms, and their antimicrobial susceptibility patterns. The study was carried out in the microbiology laboratory of DGHM.

Of 1612 blood cultures obtained from neonates admitted to the PBU over the study period, overall blood culture positivity rate was 9%. This is within the range reported in similar studies conducted in neonatal units, which often report positivity rates between 6% and 15% [11,13]. The relatively low positivity could be influenced by several factors, including early empirical antibiotic administration, low blood volume drawn, and the inherent limitations of conventional culture methods [14].

Although majority of suspected cases were classified as EOS (69.4%), culture positivity was higher among LOS cases (64.4% vs 35.6%). Higher prevalence of LOS was also reported by Govindaraju et al. [5] whereas many studies showed higher prevalence of EOS [4,15]. This variation may be results from nosocomial transmission, especially in neonates requiring prolonged hospitalisation or invasive procedures, which are known risk factors for LOS [16]. The higher percent in LOS cases suggests that hospital-acquired infections play a significant role in neonatal bloodstream infections in the PBU setting and require targeted infection control interventions [16,17].

Slight male predominance observed in our study aligns with the findings from several other studies, which have reported higher sepsis incidence in male neonates [4,18]. A study by Verma *et al.* demonstrated that neonatal bloodstream infections were more frequently observed in male infants. This may be due to the presence of genes regulating gamma globulin synthesis on the X chromosome, which may result in comparatively lower immunological protection in males than in females [18].

In the study most neonates presented with respiratory distress, jaundice, and fever similar to other studies [4,18]. According to the available data of this study, none of the potential maternal risk factors were found to be statistically associated with culture positive sepsis. Verma *et al.* showed that premature rupture of membranes, frequent vaginal examination, fever in mother were other important factors predisposing to sepsis [18].

Neonatal factors like preterm delivery (p=0.017), low birth weight (p=0.002), were statistically associated with culture positive sepsis. This finding has been demonstrated in many studies [4,5,9]. A study in India showed preterm babies had more culture positive sepsis [18]. According to Stoll *et al.* neonates with low birth weight are more vulnerable to infections due to reduced levels of IgG [17]. A study done in Bhutan showed that neonates with low APGAR scores, use of total parental nutrition were statistically associated with culture positive sepsis and low APGAR scores act as stress factors which make these neonates more prone to infections because of the poor adaptation to extra uterine life [4].

Regarding microbiological profiles, gram-positive organisms predominated, accounting for 65.6% of the isolates. CONS were the most frequently isolated gram-positive organisms (78%) corroborating findings by Shehab *et al*. [19]. Although CONS are frequently regarded as

contaminants, it could not be ruled out in this study due to the underdeveloped immune systems of neonates and their notable prevalence among symptomatic cases, especially in those with LOS [13,20]. Clinical significance was not mentioned in the laboratory reports. *Staphylococcus aureus*, including methicillin-resistant *S. aureus* (MRSA), and probable Group B *Streptococcus* (GBS) were also observed, supporting global trends of gram-positive cocci being key pathogens in neonatal sepsis [21].

Whereas studies conducted at India and Bhutan showed gram-negative predominance [4,5],in this study coliforms were found to be the most common among gram-negative isolates. With the facilities available microbiology laboratory of DGHM, identification had been done only up to LF and NLF coliforms. Majority were LF coliforms (16%). About 4.8% were reported as probable *Klebsiella* spp. according to the colony appearance. In many studies *Klebsiella* was the most common pathogen in both early and late onset septicemia [5,18, 22].

Antibiotic susceptibility testing revealed considerable resistance among gram-negative isolates to commonly used first-line drugs such as ampicillin and third-generation cephalosporins. However, most retained susceptibility to amikacin and carbapenems. Shehab *et al.* demonstrated that all *Klebsiella* isolates were resistant to ampicillin in their study [19]. A high level of ampicillin resistance was observed among *Klebsiella* isolates in our study, similar to findings from previous studies that reported significant resistance of coliforms [23,24]. In a similar study, high level of resistance was also observed against gentamicin and the organisms were *Pseudomonas spp.* and *Klebsiella spp.* [24]. However, in this study all Pseudomonas spp. Were found to be sensitive to gentamicin. One isolate of *Acinetobacter* was resistant to carbapenems, indicating the emergence of highly resistant nosocomial pathogens even in secondary care settings [25]. Among gram-positive organisms, resistance to oxacillin and erythromycin was noted, but all isolates were susceptible to vancomycin and teicoplanin. Similar to findings from a study conducted by Shehab *et al.* [19] vancomycin remains the drug of choice for MRSA strains in the setup.

These findings emphasise the importance of continuous microbiological surveillance in neonatal units, particularly in resource-limited settings. Empirical antibiotic protocols should be regularly reviewed and tailored according to local resistance patterns. Early identification of at-risk neonates and timely initiation of appropriate antimicrobial treatment are essential to reduce morbidity and mortality associated with neonatal sepsis.

Study had several limitations. Firstly, definitive identification of bacterial isolates to the species level was not possible due to limited diagnostic facilities at the study setting. As a result, the bacteriological profile was reported only up to the group level (e.g., LF coliforms or probable *Klebsiella* spp.), rather than precise species identification.

A uniform antibiotic susceptibility panel had not been used throughout the selected period of January 2021 to December 2022 due to intermittent unavailability of certain antibiotics.

Since this was a retrospective study, there was no opportunity to modify, escalate, or de-escalate antibiotic regimens based on clinical progress or susceptibility results. Additionally, due to the low number of culture-positive cases, it is unable to propose a definitive empirical antibiotic regimen based on our findings.

Moreover, data were collected solely from laboratory records, as access to clinical files or ward records was not available. Consequently, the analysis of associated risk factors was limited to the variables documented in laboratory request forms. The clinical significance of CONS could not be assessed, as determining their pathogenic role requires correlation with clinical presentation, which was not available in the laboratory data.

Conclusion

The overall blood culture positivity rate was 9%, with a predominance of gram-positive organisms, mainly CONS, while lactose fermenting coliforms were the most common gram-negative isolates. High levels of antibiotic resistance were noted, especially among gram-negative bacteria, with marked resistance to ampicillin and third-generation cephalosporins. Vancomycin and amikacin were found to be the most effective agents against gram-positive and gram-negative isolates, respectively. Late onset sepsis was more common than early onset sepsis. Preterm and low birth weight were the factors significantly associated with septicemia.

List of abbreviations

ABST - Antibiotic sensitivity test
CONS - Coagulase negative staphylococci
DGHM - District General Hospital Matara
ESBL - Extended spectrum beta lactamase
EOS - Early onset sepsis
LF Coliform - Lactose fermenting coliform
LOS - Late onset sepsis
MRSA - Methicillin Resistant Staphylococcus aureus
MLSB - Macrolide Lincosamide Streptogramin B
MDR - Multi drug resistant
NICU - Neonatal intensive care unit
NLF Coliform - Non lactose fermenting coliform
PBU - Premature baby unit

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Ethical considerations

Ethical approval was obtained from the Ethics Review Committee, Faculty of Allied Health Sciences, University of Ruhuna (Ref No: 141.07.2022). Administrative clearance was obtained from the Director and the Consultant Microbiologist at the DGHM.

Declaration of conflicting interest

The authors declare that they have no conflict of interest.

Author contributions

MMR collected and analysed the data and drafted the manuscript. SSW contributed to the development of the initial proposal and critically revised the manuscript for intellectual content. AADP sorted and interpreted the data in the microbiology laboratory. All authors read and approved the final manuscript.

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