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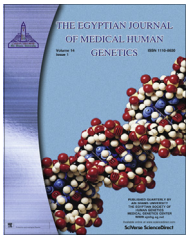

ORIGINAL ARTICLE

Comparison of broad range 16S rDNA PCR to conventional blood culture for diagnosis of sepsis in the newborn

Nehal I. Draz [a], Shereen E. Taha [a,*], Nancy M. Abou Shady [b], Yara S. Abdel Ghany [a]

[a] *Medical Microbiology and Immunology Department Faculty of Medicine, Ain Shams University, Cairo, Egypt*
[b] *Pediatrics Department, Faculty of Medicine, Ain Shams University, Cairo, Egypt*

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Abstract Neonatal sepsis is a significant cause of morbidity and mortality in neonates. The gold standard for detecting bacterial sepsis is blood culture. However, it has low sensitivity and a reporting delay of approximately 48–72 h. Molecular assays for the detection of bacterial DNA represent possible new diagnostic tools for early identification of a bacterial cause. This study aimed at comparing a broad range 16S rDNA PCR to conventional blood culture for detecting bacterial DNA in blood samples from neonates with suspected sepsis. Fifty neonates with suspected sepsis, admitted at Neonatal Intensive Care Unit of Ain Shams University Hospitals, were included in this study. From each neonate, a minimum of 2–3 ml blood was collected by standard sterile procedures, 1 ml for conventional blood culture and 1–2 ml EDTA blood for PCR. The isolated microorganisms were identified by conventional microbiological methods. Thirty neonates (60%) gave positive blood culture results. The most frequently isolated microorganisms were *Staphylococcus aureus* (n = 17, 56.7%), followed by Coagulase negative *Staphylococci* (n = 7, 23.3%), *Escherichia coli* (n = 4, 13.3%), and *Candida* spp. (n = 2, 6.7%). Twenty-eight (56%) neonates gave positive bacterial blood culture while 35 (70%) neonates gave positive PCR results. Considering the blood culture as the gold standard in diagnosis of bacterial neonatal sepsis, the sensitivity, specificity, positive predictive value and negative predictive value of PCR in detecting bacteremia relative to blood cultures were 20/28 (71.42%), 7/22 (31.81%), 20/35 (57.14%) & 7/15 (46.66%), respectively.

In conclusion, PCR approach appears to be a relatively easy, reliable and valuable complementary method for diagnosis of neonatal sepsis for samples obtained during antimicrobial treatment especially when routine cultures remain negative. *Staphylococci* spp. has played an important role

* Corresponding author. Tel.: +20 1119997002.
E-mail address: cherrytaha73@yahoo.com (S.E. Taha).
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in causing neonatal sepsis. So, implementation of simple infection control measures such as hand washing, barrier nursing and promotion of clean deliveries should be considered to reduce neonatal sepsis.

1. Introduction

Neonatal sepsis or septicaemia is a clinical syndrome characterized by systemic signs of circulatory compromise (e.g., poor peripheral perfusion, pallor, hypotonia, poor responsiveness) caused by invasion of the bloodstream by bacteria in the first month of life. In the pre-antibiotic era neonatal sepsis was usually fatal. Case fatality rates in antibiotic treated infants now range between 5% and 60% with the highest rates reported from the lowest income countries [1].

The World Health Organization (WHO) estimates that 1 million deaths per year (10% of all under-five mortality) are due to neonatal sepsis and that 42% of these deaths occur in the first week of life [2]. In particular, neonates with low birth weight show relatively high morbidity and mortality [3].

There are risk factors for neonatal sepsis including poverty and poor environmental conditions. Also, prolonged rupture of membranes, preterm labour, maternal pyrexia, unhygienic intrapartum and postnatal care, low birth weight and prelacteal feeding of contaminated foods and fluids [4].

The bacteria that cause neonatal sepsis are acquired shortly before, during, and after delivery. They can be obtained directly from mother's blood, skin, or vaginal tract before or during delivery or from the environment during and after delivery. *Streptococcus agalactiae* (Group B streptococcus, GBS) is the most common cause of neonatal sepsis in many countries; gram negative bacilli (*Escherichia coli, Klebsiella* spp., *Pseudomonas* spp., *Acinetobacter* spp.) and gram-positive cocci (such as *Staphylococcus aureus* and *Staphylococcus epidermidis*) are other important causes [5].

Sepsis is a serious disease. A fast and correct diagnosis, followed by rapid treatment, plays an important role in the reduction of infant mortality resulting from sepsis [6]. However, diagnosing neonatal sepsis is difficult since being exposed to known risk factors for sepsis is not a necessity, clinical signs are often vague, and laboratory parameters are unspecific [7].

Elevation of C-reactive protein (CRP) has been a useful marker of sepsis in many studies. Initiation of broad-spectrum systemic antibiotic treatment is based only on the suspicion of sepsis since no early definitive diagnostic test is yet available [8].

Conventional blood culture is considered the gold standard in the aetiological diagnosis of neonatal bacterial sepsis [9]. However, obtaining sufficiently large amounts of blood for culture from neonates is often difficult, and it often takes 48–72 h to obtain a preliminary positive result [10].

Antigen detection techniques allow rapid detection and identification of microorganisms without culturing. The most commonly used commercially available test is the latex agglutination assay, which is based on specific agglutination by bacterial cell wall antigens of antibody coated latex particles. However, these tests can only detect specific organisms such as *S. agalactiae* and are associated with high false positive and negative rates [11]. New urinary antigen tests for pneumococcus are more encouraging but are also associated with false positives from pneumococcal carriage [12].

Detection of bacterial DNA in blood samples of neonates is suggested to represent a rapid and sensitive supplement to blood culture in diagnosing bacterial sepsis in neonates [7]. Polymerase chain reaction (PCR) amplification of highly conserved DNA sequences found in all bacteria would permit fast and sensitive determination of the presence of bacteria in clinical specimens [13]. There are a few studies on the use of universal primer PCR on blood samples of neonates with suspected sepsis, and they have shown promising results. Unlike blood culture, PCR does not depend on the viability of bacteria. It is hypothesized that PCR results may remain positive in septicemic neonates even after antibiotic drug therapy. There are no clinical data on this issue, but animal data suggest that a positive PCR result persists after starting antibiotic therapy [8].

The rapid and accurate detection of bacteraemia in newborn infants might have a significant impact in shortening hospital stays within the neonatal intensive care unit (NICU) as well as reducing the costs to the health care system [14].

The aim of this study was to compare a broad range 16S rDNA PCR done on whole blood samples without prior enrichment to conventional blood culture for detecting bacterial DNA in blood samples from neonates with suspected sepsis.

2. Patients and methods

The study was approved by the Hospital Ethics Committee of Ain Shams University Hospitals (ASUHs) and an informed consent was taken from the authorized person in Neonatal Intensive Care Units (NICUs) and from the neonates' parents. This study was conducted on 50 neonates with clinical or laboratory findings suggestive of sepsis admitted at NICUs of ASUHs during the period from May 2012 till August 2012. Full history taking, thorough clinical examination and routine laboratory investigations were done to all neonates with suspected sepsis.

2.1. Specimens

From each neonate, a minimum of 2–3 ml blood was collected by standard sterile procedures, 1 ml for conventional blood culture and 1–2 ml EDTA blood for PCR.

2.2. Bacterial culture

The blood culture bottles (paediatric diphasic medium supplied by Himedia, India) were incubated for at least 7 days aerobically at 37 °C. Blood from bottles showing positive growth was subcultured after overnight incubation and after 48 h on blood agar medium, MacConkey's agar medium and Sabouraud agar medium. They were considered negative in case of

no growth on blood culture bottles for one week. Identification of the isolated organisms was done according to Collee et al. [15] based on colonial morphology, microscopic examination of Gram stained films and biological activity of the isolated organisms.

2.3. Polymerase chain reaction (PCR)

The EDTA blood samples for PCR were wrapped and stored in the refrigerator for until 72 h to be divided into plasma and cell fractions and stored at −70 °C until analysis. DNA extraction was done by using QIAGEN DNA extraction Kit® (QIAGEN, USA), for purification of DNA from cells. PCR reactions were set up to amplify bacterial DNA using the primer 5′TGAAGAGTTTGATCATGGCTCAG3′ combined with primer 5′TCGTTGCGGGACTTAACC3′ (Molbiol, Germany). The primers reacted with highly conserved regions of the bacterial 16S rRNA gene to provide PCR products of approximately 1100 basepairs [7]. Each PCR reaction (50 µl) consisted of 25 µl of a 2× QIAGEN HotStar Taq® Master Mix, 2 µl of each primer, and 11 µl of RNase-free water and 10 µl template DNA. Cycling conditions, with use of thermal cycler (Thermo PxE 0.21, England), included a 5 min denaturing step at 94 °C followed by 35 cycles of 20 s at 94 °C, 20 s at 58 °C and 60 s at 72 °C and final extension of 10 min at 72 °C. Identification of amplified products was done by gel electrophoresis according to Voytas [16]. The amplicons (2 µl) (added to a Loading buffer: bromophenol blue with sucrose) was analysed by electrophoresis on 2% agarose gels and ethidium bromide staining in tris–acetate-EDTA (TAE) running buffer compared with negative control (water) and positive control (*E. coli*) in each run. They were visualized on a UV transilluminator (365 wave length). Qiagen gel pilot 100 bp Plus (cat no. 239045) used as molecular weight ladder (Fig. 1).

2.4. Statistical analysis

Data were presented as count and percent. The sensitivities, specificities, positive predictive values (PPV) and negative predictive values (NPV) of PCR compared to blood culture were calculated as described by Ilstrup [17].

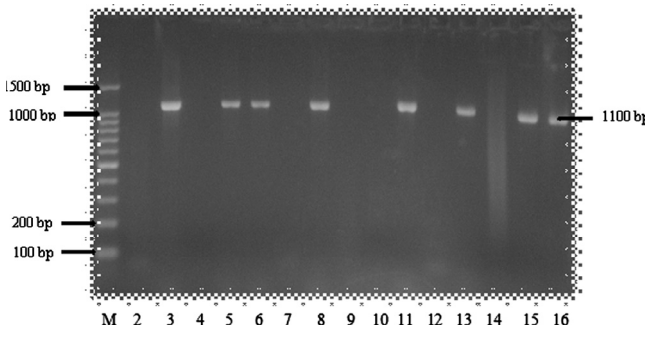

Figure 1 Agarose gel electrophoresis indicating the presence of broad range 16S rRNA gene (1100 bp). Lane M: molecular size marker; Lane 2: negative control; Lane 3: positive control; Lanes 5, 6, 8, 11, 13, 15 & 16: correspond to the positive bacterial DNA yield; Lanes 4, 7, 9, 10, 12 & 14: correspond to the negative bacterial DNA yield.

3. Results

This study was conducted on 50 neonates with suspected sepsis admitted at NICU of ASUHs. The age of neonates ranged from one to fifty days. They were 30 males (60%) and 20 (40%) females making the male: female ratio 3:2. Thirty-six (72%) were full term while the remaining fourteen (28%) were preterm. Seventy percent of neonates (n = 35) were delivered by spontaneous vaginal delivery and 30% (n = 15) were delivered by caesarean section (CS). Among the fifty neonates, 26 were diagnosed as early onset sepsis (52%) and 24 (48%) as late onset sepsis as shown in Table 1. Some laboratory findings of the study group are shown in Table 2.

Fever (n = 38, 76%) was the most common presenting fetal symptom (or sign) followed by respiratory and feeding problems (n = 13, 26% each), then central nervous system (CNS) problems and tachycardia (n = 7, 14% each), low birth weight (LBW) (n = 3, 6%), anaemia, jaundice and abdominal distention (n = 2, 4% each) while renal problems (n = 1, 2%).

A total of 50 blood culture samples were taken, out of which 34 (68%) were positive, while the remaining 16 (32%) were negative. *S. aureus* was the most frequent bacterium isolated (n = 17) followed by Coagulase negative *staphylococci* (CoNS) (n = 7), *E. coli* (n = 4), *Diphtheroid* spp. (n = 4), *Candida* spp. (n = 2). Thirty isolates (*S. aureus,* CoNS, *E. coli* & *Candida* spp.) were considered clinically significant pathogens while the remaining four *Diphtheroid* spp. were considered as contaminants of blood culture as we did a single blood culture for each neonate and they rarely cause disease in the neonates. Seventeen out of the thirty blood culture proved sepsis were males (56.7%), while the remainder 13 were females (43.3%).

The frequency of Gram-positive cocci, Gram-negative bacilli and fungi of all clinically significant isolates was (n = 24, 80%), (n = 4, 13.3%) and (n = 2, 6.7%) respectively. The percentages of most frequently isolated microorganisms

Table 1 Demographic characteristics of the study group.

Characteristics	Number
Gender (Male/Female)	30/20
Preterm/Term	14/36
Type of delivery (Normal/CS)	35/15
Birth weight (LBW/NBW)	3/47
Onset of sepsis (Early/Late)	26/24

CS = Caesarean section; LBW = Low birth weight; NBW = normal birth weight; Early onset sepsis < 48 h after birth; late onset sepsis ⩾48 h after birth.

Table 2 Some laboratory findings of the study group.

Laboratory finding	Mean ± SD
WBCs ($\times 10^3/\mu L$)	11.8 ± 2.4
HGB (g/dL)	12.35 ± 1.61
Platelet ($/mm^3$)	203.925 ± 23.203
CRP (mg/L)	42.47 ± 6.539

WBCs = white blood cells; HGB = haemoglobin; CRP = C-reactive protein.

Table 3 Microbiological profile found in blood culture from neonates according to onset of sepsis & gestational age.

Microorganism	Onset of sepsis		Gestational age	
	EOS (n = 18) N (%)	LOS (n = 12) N (%)	Full Term (n = 22) N (%)	Preterm (n = 8) N (%)
S. aureus	10 (55.6%)	7 (58.3%)	13 (59.2%)	4 (50%)
CoNS	4 (22.2%)	3 (25%)	6 (27.3%)	1 (12.5%)
E. coli	4 (22.2%)	0 (0%)	2 (9%)	2 (25%)
Candida spp.	0 (0%)	2 (16.7%)	1 (4.5%)	1 (12.5%)

EOS = early onset sepsis; LOS = Late onset sepsis; N = number; CoNS = coagulase negative *staphylococci*.

Table 4 Day wise organism profile during the study period.

Microorganism	D1 (n = 13) N (%)	D2 (n = 5) N (%)	D3 (n = 7) N (%)	D4 (n = 2) N (%)	D5 (n = 3) N (%)
S. aureus	6 (46.1%)	4 (80%)	4 (57.1%)	1 (50%)	2 (66.7%)
CoNS	4 (30.8%)	0 (0%)	2 (28.6%)	0 (0%)	1 (33.3%)
E. coli	3 (23.1%)	1 (20%)	0 (0%)	0 (0%)	0 (0%)
Candida spp.	0 (0%)	0 (0%)	1 (14.3%)	1 (50%)	0 (0%)

D = day; N = number; CoNS = Coagulase negative *staphylococci*.

were as follows: *S. aureus* was the most common pathogen (n = 17, 56.7% of total clinically significant isolates, 70.8% of isolated Gram-positive cocci), followed by Coagulase negative *staphylococci* (CoNS) (n = 7, 23.3% of total clinically significant isolates, 29.2% of isolated Gram-positive cocci), *E. coli* (n = 4, 13.3% of total clinically significant isolates, 100% 0f isolated Gram negative bacilli) and *Candida* spp. (n = 2, 6.7% of total clinically significant isolates, 100% of isolated fungi).

The distribution of the clinically significant microorganisms isolated from positive blood culture according to onset of sepsis is demonstrated in Table 3. There were 18 (60%) neonates with early onset sepsis (EOS) and 12 (40%) with late onset sepsis (LOS). *S. aureus* (n = 10, 55.6%) was the most common organism isolated in neonates with EOS, followed by CoNS and *E. coli* (n = 4, 22.2% each). As regards LOS, *S. aureus* (n = 7, 58.3%) was also the most common organism isolated followed by CoNS (n = 3, 25%), while the least common were *Candida* spp. (n = 2, 16.7%).

The distribution of organisms isolated by gestational age is shown in Table 3. *S. aureus* (n = 4, 50%) and *E. coli* (n = 2, 25%) were the predominant organisms isolated in preterm neonates while *Candida* spp. and CoNS (n = 1, 12.5% each) were less predominantly isolated. As regards full term neonates, *S. aureus* (n = 13, 59.2%) and CoNS (n = 6, 27.3%) were the predominant organisms isolated while *E. coli* (n = 2, 9%) and *Candida* spp. (n = 1, 4.5%) were less predominantly isolated.

Table 4 shows day wise organism profile during the study period. The most commonly isolated organism among neonates who developed sepsis in day 1, day 2, day 3, day 4 and day 5 was *S. aureus* (n = 6, 4, 4, 1& 2) respectively, followed by CoNS in day 1, day 3 & day 5 (n = 4, 2 & 1) respectively, *E. coli* in day 1 & day 2 (n = 3 & 1) respectively, while the least isolated organisms were *Candida* spp. in day 3 & day 4 (n = 1 each). The number of neonates who developed sepsis was n = 13 (43.3%) at day 1, followed by n = 7 (23.3%) at day 3, n = 5 (16.7%) at day 2, n = 3, (10%) at day 5 and they were n = 2, (6.7%) at day 4.

Table 5 The correlation between PCR results and gestational age at onset of sepsis.

PCR	Early onset sepsis		Late onset sepsis		Total
	Preterm	Full term	Preterm	Full term	
Positive	7	13	3	12	35
Negative	1	5	3	6	15

PCR = polymerase chain reaction.

Table 6 The correlation between PCR and bacterial blood culture results.

		Blood culture		Total
		Negative	Positive	
PCR	Negative	7	8	15
	Positive	15	20	35
Total		22	28	50

PCR = polymerase chain reaction.

A total of 50 blood samples obtained from neonates admitted to the NICU for suspected sepsis were analysed by PCR for broad-range 16S rRNA gene. 16S rDNA PCR analysis of blood samples from the 50 neonates revealed 35 (70%) samples positive for the presence of bacterial DNA, while 15 (30%) revealed negative results. Table 5 demonstrates the relation between PCR results and gestational age at onset of sepsis.

Table 6 illustrates the relation between PCR and blood culture results after exclusion of *Diphtheroid* spp. contaminants in blood culture bottles (n = 4) and the two cultures that yielded *Candida* spp. as they were considered as negative for bacterial cultures.

Twenty-eight neonates gave positive bacterial blood culture with isolation of clinically significant microorganisms, while 35

Table 7 The relation of risk factors with PCR and blood culture results.

Risk factor		PCR		Blood Culture	
		Positive (n = 35)	Negative (n = 15)	Positive (n = 30)	Negative (n = 20)
PROM	Positive	9	1	10	0
	Negative	26	14	20	20
Maternal UTI	Positive	10	1	5	6
	Negative	25	14	25	14
Maternal fever	Positive	8	3	7	4
	Negative	27	12	23	16
Vaginal infection	Positive	1	1	1	1
	Negative	34	14	29	19
Diabetes mellitus	Positive	0	2	1	1
	Negative	35	13	29	19
Difficult labour	Positive	3	0	0	2
	Negative	32	15	30	18
Preterm labour	Positive	10	4	8	6
	Negative	25	11	22	14
Foul meconium	Positive	1	0	1	0
	Negative	34	15	29	20
Multiple pregnancies	Positive	2	0	0	2
	Negative	33	15	30	18

PCR = polymerase chain reaction; PROM = premature rupture of membranes; UTI = urinary tract infection.

neonates gave positive PCR results. However, 22 neonates gave a negative bacterial blood culture result and 15 neonates gave negative PCR results. Twenty neonates had positive bacterial blood culture/ PCR results, while seven of neonates had negative bacterial blood culture/ PCR results. Eight neonates with a positive bacterial blood culture had a negative PCR result, 15 neonates had a positive PCR in spite of a negative bacterial blood culture. Considering the blood culture as the gold standard in diagnosis of bacterial neonatal sepsis, the sensitivity, specificity, positive predictive value and negative predictive value of PCR in detecting bacteremia relative to blood cultures were 20/28 (71.42%), 7/22 (31.81%), 20/35 (57.14%) & 7/15 (46.66%) respectively.

Table 7 shows that premature rupture of membrane (PROM) (n = 10) was the most common risk factor found in relation to blood culture positive status followed by preterm labour (n = 8), maternal fever (n = 7), maternal urinary tract infections (UTI) (n = 5), then vaginal infection, diabetes mellitus (DM), foul meconium (n = 1 each) and difficult labour, multiple pregnancy (n = 0 each). As regards the relation between risk factors and positive PCR results, maternal UTI, preterm labour (n = 10 each) followed by PROM (n = 9), then maternal fever (n = 8), difficult labour (n = 3), multiple pregnancies (n = 2), vaginal infection, foul meconium (n = 1 each) then DM (n = 0) as shown in Table 7.

4. Discussion

Neonatal sepsis is associated with increased mortality and morbidity including neurodevelopmental impairment and prolongation of hospital stay. Clinical features of sepsis are nonspecific in neonates and a high index of suspicion is required for timely diagnosis [18]. Prompt diagnosis and effective treatment are necessary to prevent deaths and complications due to septicemia [19].

The ideal test for diagnosis of neonatal sepsis continues to be elusive [20]. Although blood culture is the currently accepted criterion standard, it may take 48 h to get a report, and previous antibiotic drug exposure often interferes with growth on blood culture [8]. Detection of bacterial DNA in blood samples of neonates is suggested to represent a rapid and sensitive supplement to blood culture in diagnosing bacterial sepsis in neonates [21]. There are a few studies on the use of universal primer PCR on blood samples of neonates with suspected sepsis and they have shown promising results. Unlike blood culture, PCR does not depend on the viability of bacteria. Animal data suggest that a positive PCR result persists after starting antibiotic therapy [8].

In this study, neonatal sepsis was predominant in males which is similar to that observed in other studies [22–24]. However, Chacko and Sohi [25] showed equal distribution among males and females. The male preponderance in neonatal septicemia may be linked to the X-linked immunoregulatory gene factor contributing to the host's susceptibility to infections in males [26],

In agreement with previous reports by several studies [22–24,27], our study showed that neonatal sepsis occurs more frequently in neonates delivered by spontaneous vaginal delivery (SVD). The higher rates of neonatal sepsis in vaginally delivered neonates may be due to the surface colonization of the neonate with the microbial flora of the birth canal during vaginal delivery [23].

In this study, EOS was diagnosed in 26 (52%) of neonates versus 24 (48%) who had LOS. Similar observations were made in other studies [22–24,28]. This could be attributed to

ascending infection following rupture of membranes or through the infected birth canal or acquired at the time of resuscitation of the newborn in the labour room. Also, immature immunological responses of the neonates in the first week of life make them more susceptible to infections in this period [29].

Among culture positive neonates in the current study, three neonates were of low birth weight and the remainder 27 were of normal birth weight. This goes in accordance with reports from previous studies [30,31]. However other studies [23,27,32] reported that sepsis was more common among low birth weight neonates.

In the current study, fever was the most common presenting fetal symptom. This is similar to results of other studies [33,34]. However, Masood et al. [24] and Afroza and Begum [35] reported that refusal to feed was the most common presenting complaint. In the study of Shitaye, et al. [36], hypothermia was the most prevalent clinical feature of sepsis.

The present study detected that blood culture positivity rate was (30/50, 60%) which is similar to results previously reported by other authors [36–42]. However, other authors demonstrated a lower positivity rate [43–46]. These differences in positivity of blood culture result may be attributed to differences in blood volume withdrawn, blood culture techniques and exposure to antimicrobials in mother or neonate or the possibility of infection with viruses, fungi or anaerobes [47]. Also, misdiagnosis could be another factor because of some similarities between the clinical signs of sepsis with other diseases like metabolic disorders [48].

In the current study, the frequency of Gram-positive cocci, Gram-negative bacilli and fungi of all isolates was (n = 24, 80%), (n = 4, 13.3%) and (n = 2, 6.7%) respectively. Similarly, several studies have shown that the predominant aetiological agents were Gram-positive organisms [14,28,49–51]. However, other studies found that Gram negative isolates were predominant [22,31,46,52,53].

As regards the most common isolated pathogen in this study, it was *S. aureus*, which agrees with the findings of other studies [23,38,54–57]. This is in contrast to other reports by several studies [31,42,46,50,58,59]. The predominance of an organism causing septicemia in the unit can be due to selective pressure of antibiotics and organisms associated with neonatal infection, change over time and are different in different geographic areas.

Staphylococcus aureus was also the most common organism isolated in neonates with early and late onset sepsis in the current study. As regards EOS, our results were in contrast to Shitaye et al. [36] and Sundaram et al. [60] who found that *Klebsiella pneumoniae* was the predominant organism. While Khloi-Kochhar et al. [28] reported that *Staphylococcus epidermidis* was the most common organism. Our findings could be either due to the delivery room acting as a source of infection as all babies who warranted admission in NICU had a transitional period of care in the delivery room or acquired from the maternal genital tract where the colonization pattern might have changed due to the transmission of organisms from the hospital environment and the health care workers to the expectant mother [5]. As regards LOS, our findings agree with previous reports by other authors [60,61]. However, Khloi-Kochhar et al. [28] and Shitaye et al. [36] showed that CoNS were the predominant organisms.

In this study, the most common isolated organisms among neonates developed sepsis during the initial 24 h were *S. aureus* followed by CoNS, then *E. coli*. Our results go in accordance with Khloi-Kochhar et al. [28] and in contrast Mhada et al. [57]. This predominant isolation of *S. aureus* during the initial 24 h could be explained by the proportion of smaller neonates and the resultant need for intensive care and handling during the initial stabilization period [60]. An earlier report by Stoll and Fanaroff [62] raised the issue of hospital acquired EOS by CoNS with the source of infection unfound. In the current study, we did not study the genital tract colonization pattern, so, isolation of CoNS in the first 24 h of life, raises the strong suspicion of hospital acquired EOS.

In this study, broad range 16S rDNA PCR analysis of blinded blood samples from the 50 neonates with suspected sepsis revealed that 35 (70%) samples were positive for the presence of bacterial DNA, while 15 (30%) were negative. This was a higher detection rate than that by using conventional bacterial blood culture in neonatal sepsis 28/50 (56%). This improvement in bacterial detection by using PCR goes in accordance with Fujimori et al. [3], Reier-Nilsen et al. [7], Rupenthal et al. [14], Yadav et al. [63], El-Hawary et al. [64] and Abu Faddan et al. [65].

Our results showed that fifteen neonates had a positive PCR in spite of a negative bacterial blood culture. The blood cultures may have been negative due to inadequate amount of blood drawn for optimal detection of bacteria [66–68]. Kellogg et al. [69–71] found that low-level bacteraemia (< 10 cfu/ml) is far more common (up to 68%) in paediatric patients than previously believed. They concluded that it is necessary to collect up to 4.5% of the patient's blood volume (approximately4 ml/kg) in at least two blood cultures to detect low concentrations of pathogens in the blood. However, as neonates are very sensitive to even small losses of blood, collecting more than 1–2 ml of blood is not an option for this group of patients.

In eight neonates, included in this study, blood culture was positive (2 *S. aureus* and 6 CoNS) with a concordant negative PCR result. The result could reflect the presence of a low level of live bacteria with lower detection limit by PCR. There are no standardized clinically evaluated tests available for the detection of pathogenic nucleic acid in blood samples of neonates. One available PCR based test for detection of pathogenic DNA in blood of patients with suspected sepsis is developed by Roche, the LightCycler SeptiFast system [7]. The test detects a total of 25 pathogenic bacteria and fungi in blood samples, is standardised and commercially available in Europe. However, it is not evaluated for neonates, and a volume of blood of 3 ml is required.

However, Jordan et al. [49,72,73] showed a higher level of agreement between the two methodologies when preincubation was performed before PCR testing. They used 200–500 µl EDTA-full blood preincubated at 37 °C for 5 h before PCR-testing, and found 96% sensitivity, 99.4% specificity, and 88.9% positive and 99.8% negative predictive values for PCR compared with the culturing of 0.5–1.0 ml full blood with BACTEC 9240. However, a drawback with this procedure is that only live bacteria, able to grow in blood culture bottles will be detected. In our study we omitted the enrichment step and this might explain the difference between the two methods compared to what was reported by Connel et al. [10] and Jordan et al. [69,49].

Compared to blood culture, the gold standard for diagnosing bacterial sepsis in the newborn, sensitivity, specificity, positive predictive value and negative predictive value of PCR in the current study were 20/28 (71.42%), 7/22 (31.81%), 20/35 (57.14%), 7/15 (46.66%), respectively. A much better finding was reported by Yadav et al. [63], where sensitivity was 100%, specificity was 95.6% and negative predictive value was 100%. While, Ruppenthal et al. [14] reported that PCR had 87.9% sensitivity & 96.3% specificity. However, Elwan and Zarouk [74] detected 92.3% sensitivity, 88.2% specificity, positive 90% predictive value and 91% negative predictive value. In the study of Reier-Nilsen et al. [7], PCR revealed 66.7% sensitivity and 87.5% specificity. Abu Faddan et al. [65] reported 96.4% sensitivity, 66.6% specificity, 72.9% positive predictive value and 95.2% negative predictive value. Ohlin et al. [75] found that PCR assay yielded a sensitivity of 79%, a specificity of 90%, a positive predictive value of 59%, and a negative predictive value of 96%.

These differences could be explained by use of different primers with different sensitivities of detection and there are no standardized clinically evaluated tests available for the detection of pathogenic nucleic acid in blood samples of neonates. The conventional parameters used for the evaluation of new diagnostic tests, such as the sensitivity, specificity, positive and negative predictive values; do not appropriately reflect the quality and usefulness of a new PCR test, since there is no defined reference for evaluation of the new test. Blood has been most widely used as a ''gold standard for statistical evaluation of new PCR tests, and we therefore include these parameters to compare with other studies''. However, PCR can detect more cases of bacteremia than culture, since it can detect the DNA of nonviable microorganisms [76]. In general, it appears more appropriate to correlate PCR results not only with blood culture but also with other microbiological cultures and clinical data from the patients.

In our study, premature rupture of membrane (PROM) followed by preterm labour were the most common risk factors observed in relation to blood culture positive in agreement with results of other studies [23,25,34,77]. Also, several studies [31,78,79] found that PROM was significantly associated with positive blood culture. Leal et al. [51] reported that after logistic regression, PROM is included in risk factors for sepsis.

In conclusion, PCR approach appears to be a relatively easy, reliable and valuable complementary technique for diagnosis of neonatal sepsis for samples obtained during antimicrobial treatment especially when routine cultures remain negative. *Staphylococci* spp. has played an important role in causing neonatal sepsis. So, implementation of simple infection control measures of proven efficacy such as hand washing, barrier nursing, and promotion of clean deliveries should be considered to reduce neonatal sepsis.

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