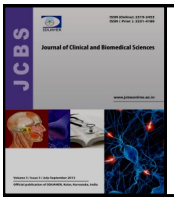

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Original Article

Profile of Blood Stream Infections in Paediatric Patients in Rural Tertiary Care Hospital

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Abstract

Background: Blood stream infections (BSI) are the major cause of morbidity and mortality worldwide. It is often associated with hospitalization, and management involving invasive therapeutic and diagnostic procedures. Timely detection and identification of blood-borne pathogens, would reduce mortality, and turnaround time and improve patient management. **Aims:** 1. To identify the common pathogens causing bacteremia in different age group in pediatric patients. 2. To identify the risk factors and other screening parameters associated with bacteremia. 3. To study the turnaround time using automated BacT/Alert 3D system **Settings and Design:** Observational study done in a rural tertiary care Hospital, Tamaka, Kolar. **Meterials and Methods:** A total of 176 paired blood culture samples were collected from paediatric patients admitted signs and symptoms of sepsis and PUO in pediatric wards during February 2012 – August 2013 The samples were collected under strict aseptic precautions before starting of antibiotics. Blood cultures were processed by BacT/Alert 3D system (bioMerieux). Growth was identified by the standard microbiological techniques and antibiotic and antifungal susceptibility testing were done according to CLSI guidelines. **Statistical analysis used: Results:** Among the blood cultures processed, 41.5% were identified as pathogens, 0.5% as contaminants and 58% had no growth. Most of the positive blood cultures were detected within 24 hours. Bacteremia was more common among neonates (69.9%).The most common organisms isolated were, Staphylococcus aureus (17.8%), followed by Candida krusei (12.3%), Candida tropicalis (10.9%), C.albicans (10.9%), and Klebsiella species (9.6%). The predominant sepsis screening parameters in the positive cultures were CRP and tachypnea. The most common risk factors observed were birth asphyxia, preterm babies and low birth weight. **Conclusion:** BSI are more common among neonates and The BacT/Alert 3D system is useful in detecting the infective organisms early and the paired samples are necessary us in confirming the pathogens from contaminants.

Key-words: Blood stream infection, Bacteriological profile, neonatal septicemia, Bac T/Alert, pediatric BSI

Introduction

Blood culture remains the most valuable tool in the diagnosis of blood stream infections. Many remarkable improvements have been made in an attempt to reduce the time to isolate pathogens from blood. Advancements in the use of liquid media linked with automation technology have enhanced the ability of laboratories to provide faster blood culture results. Bacteremia is one of the leading causes of death and the age adjusted death rate has risen by 78% over the past two decades.[1] Due to the high morbidity and mortality associated with bacteremia, the rapid detection and identification of microorganisms from blood remain critical for clinical microbiology laboratory. This study was undertaken to identify the common pathogens causing bacteremia among pediatrics patients along with risk factors and associated screening parameters and also the turnaround time using automated BacT/Alert 3D system (bioMerieux).

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Materials and Methods

A total of 176 paired blood culture samples were collected from patients admitted with signs and symptoms of sepsis and PUO in pediatric wards during Febrauary 2012 – August 2013 at R.L. Jalappa Hospital, Kolar. The samples were collected with strict aseptic precautions before starting antibiotics. Two blood samples were collected from two different sites and incubated in BacT/Alert 3D system (bioMerieux) which works on the principle of color-

imetry. The volume of 1-2 ml from infants and 2-3 ml from pediatric patients were obtained and inoculated into BacT/Alert bottles accordingly. The machine gives a signal if there is any growth. The positively flagged bottle was then removed from the system and subjected for gram staining and subcultured onto Blood agar, Mac-conkey agar and Chocolate agar respectively which is further incubated at 37^0C for 18-24 hours for growth.

Gram stain smear report was conveyed immediately to the treating physicians for preliminary management of cases. The growth on the culture plate was identified by the standard microbiological techniques and antibiotic sensitivity was done by Kirby-Bauer disk diffusion method according to CLSI guidelines.[2] The Candida species seen in gram stain was subcultured onto SDA and Chrome agar. Species identification was done by germ tube test and growth on chrome agar. Antifungal susceptibility testing was done as per CLSI.[3] The culture bottles which did not yield any growth even after 7 days were reported as no growth. The organism was recognized as pathogens, if the same organism with the same sensitivity pattern were obtained in paired blood cultures. The organism was considered as a contaminant, if it was isolated in only one of the paired blood culture bottles or if the mixed growth was detected.

Results

Out of 176 pediatric patients enrolled in our study, 73 (41.5%) were identified as pathogens and only 1 (0.5%) as a contaminant. The culture positivity was highest in neonates (69.9%) than the other age group. Majority of positive blood cultures (63%) were detected within 24 hours, among which 9.6% were within 12 hours and 30.1% were between 12-18 hours, 23.3% between 18-24 hours, 30.1% growth were detected between 24-36 hours and 4.1% by 36-48 hours, whereas 2.7% were detected after 48 hours. The organisms which were detected after 48 hours was *Salmonella typhi.*

The predominant sepsis screening parameters in the positive cultures were CRP (71.2%) and tachypnea (71.2%), followed by tachycardia (69.9%), fever (52.1%), leukocytosis (30.14%) and leukopenia (16.44%). The most common risk factors identified among the culture positives were birth asphyxia, preterm babies, low birth weight with 27.4% each, followed by ventilated babies (22%), respiratory infections (9.58%), cardiac infections, CNS infections and PROM with 6.85% each. The least risk factors were umbilical sepsis, diabetes, acute renal failure, skin and soft tissue infection, Necrotising enterocolitis with 1.40% respectively.

The most common organism isolated were *Staphylococcus aureus* (*S.aureus*) with (17.8%), followed by *Candida krusei* (12.3%), *Candida tropicalis* (10.9%), *C.albicans* (10.9%), *Klebsiella species* (9.6%), *Enterococci*, *Salmonella species*, *Pseudomonas aeruginosa* with equal occurrence of 5.5%, and *Streptococcus viridans*, *Enterobacter species* and *Acinetobacter species* with each (4.1%). The least common isolates were *CONS, E.coli, Citrobacter species, Haemophilus influenza* and *Candida parapsilosis* with equal occurrence of (2.74%). (Table 1)

Majority of the *Candida species* isolated in pediatric patients were among the neonates (88.5%). A outbreak of *Candida species* was detected in SNICU during the study period, which was brought under control by proper hand washing. The risk factors for candidemia were ventilation (46.2%), LBW (42.3%), preterm babies (30.8%), prolonged antibiotics and prolonged stay in hospital (11.5%), followed by equal occurrence of diabetes, necrotising enterocolitis, acute renal failure each having 3.9%.

The antimicrobial resistance pattern of gram positive and gram negative organisms is shown in the table 2 & 3 respectively. We observed more resistance among *S.aureus* and *Gram negative organisms*. The incidence of MRSA among the *S.aureus* isolates was 69.2% and inducible clindamycin resistance was seen in 38.5%. Among the gram negative organisms 24% of them were ESBL producers, 12% were AMP C producers and 4% were Carbapenemase producers. 60.3% of them recovered with appropriate antibiotic therapy as per the culture report and the mortality rate in our study was 13.7%.

Discussion

Neonatal septicaemia can be caused by a wide range of bacteria and fungi.[4] Prompt detection and treatment with appropriate antibiotics plays an important role in reducing the morbidity and mortality among neonates. In the present study culture positivity rate was seen in 41.5% among the paired blood culture samples enrolled, which is consistent with the studies by Meremikwu et al.[5] (48.9%), Rekha S.[6] (50.4%) and Roy et al.[7] (48.1%). The other studies by Osazuwa et al.[8] Schaffner et al.[9] Have reported 28.2% and 20% of blood culture positives respectively. The variation in the blood culture positivity is related to different factors like number and volume of blood taken as reported by Lee et al.[10] The system and type of

blood culture medium used are the other factors affecting the final bacterial yield.[11] The lower level of bacteremia can also be explained due to collecting blood samples after administration of antibiotics.[11,12,13] And over dilution of the small quantity of blood in the broth.[13] The contamination rate in our study was 0.5%, whereas in the study by Kumhar et al.[4] It was observed as 12.5%. Rahbar et al.[14] Stated that one important source of contamination of blood culture is the insufficient asepsis during blood sampling. Ideally contamination rate should not surpass 2-3% in a hospital.[15] We followed strict aseptic precautions which could possibly be the reason for lower contamination rate.

The number of culture positivity was observed among male patients than female patients. This was similar to the findings observed by Rekha S.[6] (60.3%), Tallur et al.[16] (63.6%), Schaffner et al[9] (60%), Karki S et al.[17] (63.3%) who also showed male preponderance among the culture positives. The most common age group associated with bacteremia were neonates (69.9%). The vulnerability to infection in this age group may be due their weak immunological barrier.[8] This was similar to the other studies done by Meremikwu et al,[5] Murthy et al.[18] Rekha S.[6] And Rahbar et al.[14] Who observed higher culture positivity rates among neonates 50.78%, 52.63%, 50.4% and 54.5% respectively. We found that majority of our positive blood cultures (63%) were detected within 24 hours, among which 9.6% were detected within 12 hours and 30.1% were detected within 12-18 hours and 23.3% in 18-24 hours. The organisms which were detected after 48 hours were *Salmonella typhi (2*). Similar study by Tarai et al.[19] Who used BacT/Alert 3D system, showed most of their blood cultures (99.27%) grew within 72 hours, among which 95.8% were isolated within 48 hours and 75.81% in 24-36 hours. They also showed *Salmonella* was isolated after 48 hours which is similar to our study. We observed CRP and tachypnea as the common sepsis screening parameters, which is in concordance with Rekha S.[6] And discordance with Khinchi et al.[20] The most common risk factors observed were birth asphyxia and preterm babies which is similar to the study by Ghotaslou et al.[21]

S.aureus was the most predominant organism isolated and majority were from neonates. Similarly, studies by Iregbu et al.[12] Shrestha et al.[22] And Meremikwu et al.[5] Observed *S.aureus* as the common organism isolated among neonates. This was followed by *Candida species* with more occurrences in neonates, which is in concordance with the study by Sardana et al.[23] Who also observed highest percentage of *Candida species* among neonates. Another study by Sharma et al.[24] Observed only 4.27% of candidemia in neonates. In the present study, an outbreak of *Candida species* was detected in SNICU during the study period, which was brought under control by proper hand washing. Most of our *Candida species* were *non-albicans Candida* (NAC), which is in accordance with Sardana et al.[23] And Agarwal et al.[25] Who also showed predominance of NAC. The next common organism isolated was *Klebsiella species*. This is contrast with the other studies by Roy et al.[7] Zakariya et al.[26] Rekha et al.[5] Who observed Klebsiella species as the most common isolates.

Antimicrobial resistance has been recognized since the beginning of the antibiotic era in the mid-20th century. In our study, we observed more resistance among *S.aureus*, and *Enterobacteriaceae*. The MRSA among the *S.aureus* isolates was 69.2%. This was similar to the study done by Osazuwa et al.[8] Who observed 83.9% of MRSA, whereas contrast to the study by Kaistha et al.[27] Who observed only 11.11% were all MRSA from pediatric patients. Among the gram negative organisms 24% of them were ESBL producers, 12% were AMP C producers and 4% were Carbapenemase producers. This is in accordance with the study by Osazuwa et al.[8] Who found 26.2% of ESBL producers and discordant with the study by Fouzia et al.[28] Who observed high frequency of ESBL (94.84%). The mortality rate in our study was 13.7%. Similar mortality rate was observed in other studies by Karthikeyen et al.[29] (13.53%), Mehmat et al.[30] (16%). Non albicans candida tend to be less susceptible to azoles, particularly fluconazole.[23] Fluconazole susceptibility was not tested in our study for *C.krusei*, as it is intrinsically resistant to this drug. We did not observe resistance to azoles in our study, but resistance was observed by other studies done in India by Kumar et al.[31] Goel et al.[32] Xess et al.[33] Who observed resistance to fluconazole with 17.2%, 4.5%, and 11.7% respectively. A study by Kothari et al.[34] Observed resistance to fluconazole, itraconazole and voriconazole with 36%, 24% and 56% respectively.

Conclusion

The neonates were more susceptible to BSI, with risk factors like birth asphyxia and preterm delivery. We also observed, prevalence of candidemia was more common among neonates, especially Non-albicans *Candida species*. The BacT/Alert 3D system helped us in detecting the organisms early and the paired sample helped us in confirming the pathogens from contaminants. In order to reduce the contamination rate strict aseptic techniques should be followed.

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Legend:

Table 1. Age wise distribution of organisms
Table 2. Resistance pattern of Gram positive organisms
Table 3. Resistance pattern of Gram negative organism

Table 1.

Organisms	0-1 m	1m-1y	>1 - 5y	>5-18 y	Total(73)
Gram positive organism N=22 (30.14%)					
S.aureus	9	3	0	1	13(17.8%)
CONS	0	2	0	0	2 (2.74%)
St.viridans	0	2	0	1	3 (4.1%)
Enterococci	2	1	1	0	4 (5.5%)
Gram negative organisms N=25 (34.25%)					
E.coli	1	1	0	0	2(2.74%)
Klebsiella species.	6	1	0	0	7 (9.6%)
Enterobacter species	2	0	0	1	3(4.1%)
Citrobacter species.	1	0	0	0	1(1.4%)
H.influenzae	0	1	0	0	1(1.4%)
Salmonella species.	0	0	1	3	4(5.5%)
Ps.aeruginosa	4	0	0	0	4(5.5%)
Acintobacter species	3	0	0	0	3(4.1%)
Candida species N=26 (35.62%)					
C.tropicalis	5	1	0	2	8 (11%)
C.krusei	9	0	0	0	9(12.3%)
C.albicans	8	0	0	0	8 (11%)
C.parapsilosis	1	0	0	0	1(1.4%)
Total (%)	**51 (69.9%)**	**12 (16.4%)**	**2 (2.7%)**	**8 (11%)**	**73(100%)**

Table 2.

Organism	P (%)	AMP (%)	CX (%)	AMC (%)	E (%)	CD (%)	CIP (%)	COT (%)	TE,DO (%)	LZ (%)	C (%)	GEN (%)
S.aureus **(n=13)**	100	-	69.2	69.2	92.3	53.8	46.1	76.9	23.1	0	0	46.1
CONS **(n=2)**	100	-	100	100	100	50	0	50	50	0	0	50
Enterococci **(n=4)**	100	100	-	-	50	-	50	-	25	0	-	50
Streptococci viridans **(n=3)**	0	0	-	-	100	-	66.7	66.7	33.3	0	0	0

Table 3.

Organism	*E.coli* (n=2)	*Klebsiella species*p (n=7)	*Entero bacter* spp (n=3)	*Citro bacter species* (n=1)	*Salmo nellaspecies* (n=4)	*H.influ enza* (n=1)	*Ps.aeru ginosa* (n=4)	*Acineto bacter spp* (n=3)
AMP(%)	100	100	100	100	75	0	-	-
CAZ(%)	100	85.7	100	100	-	0	100	100
CTX(%)	100	85.7	100	100	0	0	100	100
CX(%)	100	28.6	66.7	0	-	-	-	-
CTR(%)	100	85.7	100	100	0	0	-	100
CXM(%)	100	85.7	100	100	-	-	-	-
PI(%)	100	85.7	100	100	-	-	-	100
AMC,PIT(%)	100	28.6	66.7	0	-	0	0	33.3
CIP(%)	100	28.6	33.3	0	0	0	75	100
LE(%)	100	28.6	33.3	0	0	0	25	33.3
COT(%)	100	42.9	33.3	100	75	0	100	33.3
TE(%)	50	42.9	33.3	100	0	0	50	0
C(%)	0	14.3	33.3	100	0	0	-	-
AK(%)	0	14.3	0	0	-	-	0	0
GEN(%)	100	42.9	100	100	-	-	50	33.3
TB(%)	100	42.9	100	100	-	-	50	33.3
IPM,MRP, ETP(%)	50	0	0	0	-	0	0	0