Original Article

Assessment of prevalence of pathogens causing bacteraemia

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ABSTRACT:

Background: Bacteraemia means presence of microorganisms in circulating blood or blood stream. Septicaemia means multiplication of microorganisms and production of toxins in blood stream. The present study was conducted to assess prevalence of pathogens causing bacteraemia. **Materials & Methods:**76 patients of clinically diagnosed blood stream infections admitted in various units such as intensive care units (ICU) and health care units of both genders was recorded. The blood samples were collected and processed by standard methods. Isolation and identification of organisms was done as per standard guidelines. **Results:** Out of 76, males were 46 and females were 30. Gram positive organisms isolated were staphylococccus aureus in 22, streptococcus pyogens in 10, coagulase negative staphylococci in 6, streptococcus pneumoniae in 4 and enterococcus species in 2 cases. The difference was significant (P< 0.05). Gram negative organisms isolated were Escherichia coli in 12, Klebsiella species in 5, Enterobacter species in 4, Citrobacter species in 3, Acinetobacter species in 5, Salmonella typhi in 2 and Proteus vulgaris in 1 case. The difference was significant (P< 0.05). **Conclusion:** Gram positive organisms isolated were Escherichia coli and Klebsiella species.

Key words: Gram positive organisms, Klebsiella species, Staphylococcus aureus

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Received: 18-03-2014	Revised: 28-04-2014	Accepted: 26-04-2014

This article may be cited as: Mittal N. Assessment of prevalence of pathogens causing bacteraemia. J Adv Med Dent Scie Res 2014;2(2):205-208.

INTRODUCTION:

Bacteraemia means presence of microorganisms in circulating blood or blood stream. Septicaemia means multiplication of microorganisms and production of toxins in blood stream. Bacteraemia may be unimicrobial or polymicrobial.1 Common pathogens causing bacteraemia are Staphylococcus aureus, Coagulase Negative Staphylococci, Streptococci pneumonia, Enterococcus species, Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa, Proteus vulgaris, Enterobacter cloacae, Salmonella species etc., and rare organisms are Brucella species, HACEK groups (Haemophilus species, Actinobacillus actinomyatem comitans, Cardiobacterium hominis, Ekinella species and Kingella Kingae), Candida species etc.²

Due to symptom overlap bacteraemia is frequently misclassified as malaria and malaria is often overdiagnosed. Malaria may occur concomitantly with and has been indicated as a risk factor for bacteraemia.³ Yet, the World Health Organization's (WHO) guidelines for management of acute paediatric illness primarily focus on malaria and do not include BSIs in the diagnostic algorithm for fever in the absence of general danger signs. The timely detection of bacteraemia, followed by expeditious identification of pathogens and determination of susceptibility to antimicrobial agents can have great diagnostic and prognostic importance.⁴

Neonatal sepsis is causing 9% of fatal cases. Apart from a few well-equipped hospitals, health facilities lack microbiological diagnostic capacities necessary to diagnose bacteremia and to isolate bacterial pathogens in order to allow targeted treatment. While public interest tends to focus on malaria, tuberculosis and HIV, the morbidity and mortality burden of systemic bloodstream infections are still insufficiently investigated.⁵Prompt initiation of appropriate antimicrobial therapy is demonstrably important for preventing morbidity and mortality.6The present study was conducted to assess prevalence of pathogens causing bacteraemia.

MATERIALS & METHODS:

The present study comprised of 76patients of clinically diagnosed blood stream infections admitted in various units such as intensive care units (ICU) and health care units of both genders. The consent was obtained from all enrolled patients.

Data such as name, age, gender etc. was recorded. The blood samples were collected and processed by standard methods. Isolation and identification of organisms was done as per standard guidelines. Data thus obtained were subjected to statistical analysis. P value < 0.05 was considered significant.

RESULTS: Table I Distribution of patients

Total- 76				
Gender	Males	Females		
Number	46	30		

Table I shows that out of 76, males were 46 and females were 30.

Table II Gram positive organisms isolated from blood culture

Gram positive organisms	Number	P value
Staphylococcus aureus	22	0.02
Streptococcus pyogens	10	
Coagulase Negative staphylococci	6	
Streptococcus pneumoniae	4	
Enterococcus species	2	

Table II, graph I shows that gram positive organisms isolated were staphylococcus aureus in 22, streptococcus pyogens in 10, coagulase negative staphylococci in 6, streptococcus pneumoniae in 4 and enterococcus species in 2 cases. The difference was significant (P < 0.05).



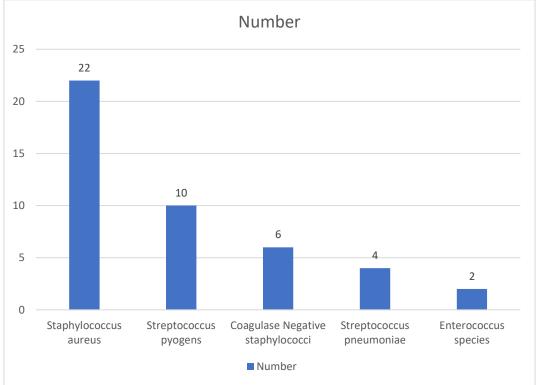
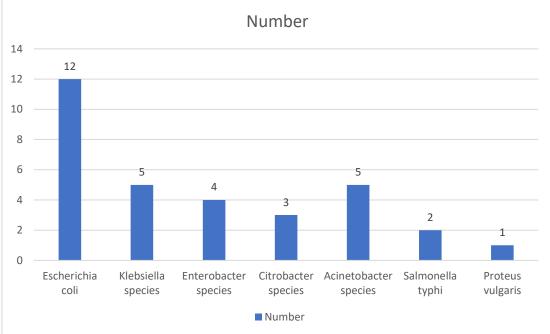


Table III Gram negative organisms isolated from blood culture

Gram negative organisms	Number	P value		
Escherichia coli	12	0.01		
Klebsiella species	5			
Enterobacter species	4			
Citrobacter species	3			
Acinetobacter species	5			
Salmonella typhi	2			
Proteus vulgaris	1			

Table III, graph II shows that gram negative organisms isolated were Escherichia coli in 12, Klebsiella species in 5, Enterobacter species in 4, Citrobacter species in 3, Acinetobacter species in 5, Salmonella typhi in 2 and Proteus vulgaris in 1 case. The difference was significant (P < 0.05).



Graph II Gram negative organisms isolated from blood culture

DISCUSSION

The burden of disease attributable to bloodstream infections (BSIs) is insufficiently studied where few healthcare facilities have the capacity to identify invasive diseases.^{7,8} BSIs are increasingly recognized as an important cause of hospitalisation and mortality in the region, and studies indicate that the prevalence of and mortality in bacteraemia parallels or exceeds that of malaria.^{9,10}The present study was conducted to assess prevalence of pathogens causing bacteraemia. We found that out of 76, males were 46 and females

were 30. Isendehl et al¹¹ in their study blood cultures and malaria diagnostics was performed on 372 consecutive children presenting with tachycardia. Bacterial species detection, antimicrobial susceptibility testing and molecular typing were performed. The capacity of clinical parameters to identify bacteraemia was evaluated. Results: The prevalence of bloodstream infection was 12% (46/372) and in 46% (21/46) of the infections the child was non-febrile at presentation to the hospital. The predictive value for bacteraemia was poor for all assessed clinical parameters. Staphylococcus aureus accounted for 54% (26/48) of the isolates followed by non-typhoidal Salmonella, 10% (5/48),Streptococcus pneumoniae, 8% (4/48),and Salmonella Typhi, 6% (3/48). Among S. aureus there was a large diversity of spa types and 38% produced Pantone-Valentine leukocidin. Antibiotic resistance was low, however two out of three Klebsiella pneumoniae isolates produced extended-spectrum beta-lactamases. Malaria was laboratory confirmed in only 5% of the children but 64% (237/372) received a clinical malaria diagnosis.

We found that gram positive organisms isolated were staphylococcus aureus in 22, streptococcus pyogens in 10, coagulase negative staphylococci in 6, streptococcus pneumoniae in 4 and enterococcus species in 2 cases.Karlowsky et al¹²prevalence rate in neonatal age group was 8.7% admitted in NICU. The most organisms isolated in blood culture were Pseudomonas species were (40%) followed by Klebsiella pneumoniae (20%), CoNS (20%),Streptococci species (10%) and Enterococci species (10%). A recent study shows, septicaemia continues to be a major cause of neonatal mortality and morbidity worldwide. In India, the National Neonatal Prenatal Database (NNPD) reported an incidence of 8.5 per 1000 live births for blood culture proven sepsis for the year 2002-2003. As high as 47.5% -64% incidence of bacteraemia were reported in neonates previously with gram negative organisms such as Klebsiella being the main isolate.

We observed that gram negative organisms isolated were Escherichia coli in 12, Klebsiella species in 5, Enterobacter species in 4, Citrobacter species in 3, Acinetobacter species in 5, Salmonella typhi in 2 and Proteus vulgaris in 1 case. Nielson et al¹³ found that among 1,196 hospitalized children, 19.9% (n=238) were blood culture positive. The four most frequent isolated pathogens were nontyphoidal salmonellae (NTS) (53.3%; n=129), Staphylococcus aureus (13.2%; n=32), *Streptococcus* pneumoniae (9.1%; n=22) and Salmonella ser. Typhi (7.0%; n=17). Yearly cumulative incidence of bacteremia was 46.6 cases/1,000. Yearly cumulative incidences per 1,000 of the four most frequent isolates were 25.2 (CI 21.1-29.4) for NTS, 6.3 for S. aureus. 4.3 for S. pneumoniae and 3.3 for Salmonella ser. Typhi. Wasting was positively associated with bacteremia and systemic NTS bloodstream infection. Children older than three

months had more often NTS bacteremia than younger children. Ninety-eight percent of NTS and 100% of *Salmonella* ser. Typhi isolates were susceptible to ciprofloxacin, whereas both tested 100% susceptible to ceftriaxone. Seventy-seven percent of NTS and 65% of *Salmonella* ser. Typhi isolates were multidrug resistant (MDR). Systemic bacterial infections in nearly 20% of hospitalized children underline the need for microbiological diagnostics, to guide targeted antimicrobial treatment and prevention of bacteremia. If microbiological diagnostics are lacking, calculated antimicrobial treatment of severely ill children in malaria-endemic areas should be considered.

CONCLUSION

Authors found that that gram positive organisms isolated were staphylococcus aureus and streptococcus pyogens and gram negative organisms isolated were Escherichia coli and Klebsiella species.

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Source of support: Nil

Conflict of interest: None declared

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