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## Antimicrobial Susceptibility Profile of Isolates from Pediatric Blood Stream Infections

We describe the pathogens and their antimicrobial profile causing blood stream infections in children over a 4-year period. The commonest pathogens were: non-fermenting Gram negative bacilli other than *Pseudomonas*, *Salmonella* species, *Escherichia coli*, *Staphylococcus aureus* and *Klebsiella* species. High rates of drug-resistance were observed.

**Keywords:** *Antibiotic, Bacteremia, Resistance.*

Blood stream infections are important causes of morbidity and mortality in children [1]. Successful outcome of these infections relies on prompt and timely empiric therapy with broad spectrum antibiotics [2]. Inadequate empiric therapy results in poor outcome with increased mortality rate and emergence of antibiotic resistance [3]. Drug resistant organisms such as extended spectrum beta-lactamase (ESBL) producing organisms and Methicillin - resistant *Staphylococcus aureus* (MRSA) concern health care providers, especially in the developing countries [4]. Surveillance of prevalence and antimicrobial suscepti-

bility of pathogens is essential for empiric treatment choice in pediatric blood stream infections. We present the distribution of pathogens and their antibiotic susceptibility profile from blood cultures in children who presented with clinical features of sepsis over a 4-year period.

All children aged between 30 days and 15 years of age, who presented to Christian Medical College, Vellore from January 2010 to December 2013 with clinical features of sepsis had their blood samples drawn under aseptic condition. The specimens were inoculated and processed by BacT/ALERT system followed by Gram staining and sub-cultures on MacConkey agar and 5% sheep blood agar. Biochemical identification of the pathogen was done using standard procedures, and followed by antibiotic susceptibility testing as per standard Clinical and Laboratory Standards Institute (CLSI) guidelines. Organisms such as Coagulase negative *Staphylococcus aureus* (CONS), Diphtheroids and Aerobic spore formers (ASF) were considered contaminants and excluded from analysis.

A total of 41457 blood cultures were done during the study period with positive cultures in 4.8% ( $n=2015$ ); 3.6% ( $n=1507$ ) Gram negative bacilli (GNB) and 1.2%

**TABLE I** ANTIBIOTIC SUSCEPTIBILITY PROFILE FOR THE PREDOMINANT BACTERIA ISOLATED FROM BLOOD CULTURES

Pathogen	Number (%)	Antibiotic Susceptibility in Percentage										
		PEN/ AMP/ OXA	P/T	GEN	AK	3 <sup>rd</sup> gen. Ceph.	CIP	MER	COL	TIG	VAN	LIN
NFGNB	522 (25.9)		75		60	70		73	90			
Salmonella spp.	349 (17.3)	95 (AMP)				100	5					
<i>E. coli</i>	221 (11)		55	43	83	28	26	92	100	99		
<i>Klebsiella</i> spp.	200 (9.9)		56	44	60	31	37	78	100	91		
<i>Pseudomonas</i> spp.	128 (6.4)		91		90	90		88				
<i>Enterobacter</i> spp.	58 (2.9)		74	43	76	33	64	86	98	98		
<i>S. aureus</i>	217 (10.8)	60 (OXA)		58			32				100	100
<i>Enterococcus</i> spp.	111 (5.5)	50 (AMP)		50 (HLG)							86	100
<i>S. pneumoniae</i>	94 (4.7)	97 (PEN)				98						

PEN-Penicillin; AMP-Ampicillin; OXA-Oxacillin; P/T-Piperacillin/tazobactam; Gen-Gentamicin; AK-Amikacin; 3<sup>rd</sup> gen. Ceph.-3<sup>rd</sup> generation cephalosporin; CIP-Ciprofloxacin; MER-Meropenem; COL-Colistin; TIG-Tigecycline; VAN-Vancomycin; LIN-Linezolid; HLG-high level Gentamicin; NFGNB – Non-fermenting Gram negative bacilli other than *Pseudomonas*.

(*n*=508) Gram positive cocci (GPC). **Table I** shows the predominant pathogens and their antibiotic susceptibility profile. The other pathogens were alpha-hemolytic Streptococci (*n*=46, 2.3%), beta-hemolytic Streptococci (*n*=40, 2%) and other Gram negative bacilli (*n*=29, 1.4%). Non-fermenting Gram-negative bacteria other than *Pseudomonas* spp. (NFGNB) were commonly isolated. Further characterization showed *Acinetobacter* spp – 202, *Burkholderia cepacia* – 41, *Sphingobacterium multivorum* – 6, *Ralstonia* spp – 4 and undifferentiated NFGNB – 269.

NFGNB are increasingly being recognized as a source of healthcare associated infections [5]. The hospital-based nature of our study may be a reason for high number of NFGNB in our study. Our study also shows high rates of extended spectrum  $\beta$ -lactamase production (71%) among *E. coli* and *Klebsiella* spp. Carbapenemase producing organisms were found in 22% of *Klebsiella* spp. and 9% of *E. coli*. Among the Gram positive organisms, 40% of the *Staphylococcus aureus* were methicillin-resistant. All of them were susceptible to Vancomycin and Linezolid. Among *Streptococcus pneumoniae*, 97% were susceptible to penicillin compared to 94.1% reported by CDC in 2012 [6]. Fourteen per cent of enterococci in our study were resistant to vencomycin.

To conclude, we documented a high level of drug resistance in gram positive and gram negative bacterial isolates. Urgent efforts are needed to combat increasing drug-resistance in our country.

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