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Prevalence, etiology, and antibiotic resistance profiles of bacterial bloodstream infections in a tertiary care hospital in Northern India: A 4-year study

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Abstract:

INTRODUCTION: Bloodstream infections (BSIs) can lead to life-threatening sepsis and are globally associated with high morbidity and mortality. Although BSIs require immediate antimicrobial treatment, their prevalence, etiology, and antimicrobial susceptibilities differ from one country to other. There is a dearth of such data from India. Here, we report the 4-year etiologic data on BSI in trauma patients admitted to a tertiary care referral hospital in New Delhi, India.

MATERIALS AND METHODS: A retrospective study was conducted at the trauma center between January 2013 and December 2016. The routine microbiological data on bacterial BSI were recorded and determined retrospectively from the laboratory records. Antimicrobial susceptibility profiles were statistically analyzed.

RESULTS: A total of 2017 bacterial strains isolated from blood culture samples were included for microbiological analysis. During the study, the median age of the patients varied from 30 to 35 years, with the percentage of females in the study population varying from 17% to 19%. The predominant pathogens were Gram-negative bacteria, with *Acinetobacter* species, followed by *Klebsiella* species being the most commonly isolated organisms throughout the 4 years of study. Among Gram-positive isolates, *Staphylococcus* species were the leading pathogens (11%–15%).

CONCLUSIONS: A detailed analysis of prevalence, etiology of BSIs in India and its resistance profile is crucial for appropriate antibiotic use, clinical management, and formulation of antibiotic policies and preventive measures.

Key words:

Antimicrobial profile, blood stream infections, etiology, Gram-negative bacteria, Gram-positive bacteria, trauma patients

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Introduction

Bloodstream infections (BSIs) range from self-limiting infections to life-threatening sepsis and are an important cause of sepsis-related morbidity and mortality worldwide.[1] Studies have revealed that the annual numbers of BSI episodes ranged from 1,213,460 to 1,381,590 in Europe and 575.462–677.389 in North America with large annual numbers of BSI-associated deaths.[2] In a developed setting, the inhospital mortality rates are observed to be at least 40%.[3] Data on the profile of BSI from low- and middle-income countries like India are limited.[4]

The epidemiology and pathogen profile of BSIs vary between regions.[5] This

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considerable unevenness between hospitals and health-care centers in different countries requires constant analysis of local trends. Many bacterial pathogens have developed resistance to most of the antibiotics and are creating a serious health crisis with many economic and social inferences all over the worlds.[6]

The changing epidemiology and susceptibility patterns of microorganisms in India threaten the effectiveness of most, if not all; antibiotics frequently used to prevent and treat bacterial infections.[7] In addition to the increasing resistance to even the last resort drugs such as colistin from across the globe, the situation is getting graver because of the absence of any new drugs in the pipeline.[8,9]

There is a dearth of detailed studies and data on prevalence, etiology, and antibiotic resistance profiles of bacterial BSIs in India. Such data are crucial for enabling clinicians to improve the empirical treatment and administer appropriate antimicrobial therapy. In addition, it is vital to recognize and track the source of all BSIs to prioritize and implement preventive measures.

India is a developing economy and a hotspot for emerging infectious diseases. Rates of antibiotic resistance, an important reason of treatment failure and subsequent mortality are also alarming in India. However, the epidemiology of BSI in Indian adults is not well studied and thus requires constant surveillance of bloodstream infections.

With this background, the present study was conducted to analyze various organisms causing BSI and their prevalence and antibiotic resistance pattern, which would ultimately aid in decreasing the hospital stay and cost of treatment which would consequently reduce mortality. This article reports a 4-year retrospective analysis of BSI data at a tertiary referral center in India.

Materials and Methods

Study design and data collection

This is a retrospective, cohort study of patients with bacterial BSI admitted to our tertiary care trauma center between January 1, 2013, and December 31, 2016.

Our trauma center is a 186-bedded tertiary referral center. As a result, the hospital receives patients both directly from the community and transferred from hospitals in the region. The study was approved by the local Institute Ethics Committee. All positive blood cultures with recognized bacterial pathogens among patients who were hospitalized during the study were included in the study. The routine microbiological profile was recorded for all the clinical samples received in the laboratory.

Blood samples were sent in BacTAlert (BioMérieux, France) bottles upon clinical suspicion of BSI. Bottles that signaled positive were then subculture on blood, MacConkey, and chocolate agar. These plates were incubated aerobically at 37°C and examined after 18–24 h. Bacterial identification was done by the Vitek II system. Antimicrobial susceptibility was done by Vitek II and disc diffusion technique as per Clinical and Laboratory Standards Institute (CLSI) guidelines. For Gram-negative isolates, disc diffusion testing was performed for the following antimicrobials for each isolate: Amikacin (30 μg), cefepime (30 μg), cefoperazone/sulbactam (75/30 μg), cefoxitin (30 μg), ceftazidime (30 μg), chloramphenicol (30 μg), ciprofloxacin (5 μg), imipenem (10 μg), netilmicin (30 μg), piperacillin/tazobactam (100 μg/10 μg), tigecycline (15 μg), and trimethoprim-sulfamethoxazole (1.25/23.75 μg). For Gram-positive isolates, disc diffusion testing was performed for the following antimicrobials for each isolate: amikacin (30 μg), amoxicillin (20 μg), amoxicillin/clavulanic acid (20/10 μg), ampicillin (10 μg), ampicillin/sulbactam 10/10 μg), cefoxitin (30 μg), ciprofloxacin (5 μg), clindamycin (2 μg), colistin (10 μg), co-trimoxazole (1.25/23.75 μg), erythromycin (15 μg), gentamicin (10 μg), Levofloxacin (5 μg), linezolid (30 μg), Netilmicin (30 μg), Nitrofurantoin (30 μg), Oxacillin (1 μg), Penicillin (10 U), Rifampicin (30 μg), Teicoplanin (30 μg), Tetracycline (30 μg), and Vancomycin (30 μg). Antibiotic susceptibilities were performed using CLSI guidelines with breakpoints from 2017.[10]

Data entry and statistical analysis

Data were entered into an indigenously developed automated surveillance system and analyzed using Stata/SE 12.1 (Stata Corp, LP, USA). In cases where there were multiple blood cultures positive with the same pathogen, only the 1st positive blood culture was included in this study. Standard descriptive statistics were calculated for categorical (in percentage) and continuous variables (median and interquartile, interquartile range). *P* value was calculated using Chi-square test for a row-by-column contingency table with appropriate degrees of freedom. $P < 0.05$ was considered statistically significant.

Results

Study population's demographics

After exclusion of blood cultures positive with contaminants, as per standard definitions, 1983 positive bacterial blood cultures were recorded between January 2013 and December 2016, from which a total of 2017 bacteria were isolated.

The median age of the patients varied from 30 to 35 years, with the percentage of females in the study population being 17%–19% [Table 1]. The range of patient-age largely lied between 24 and 54 years during the study. Among the 1983 positive blood samples 1009 (51%), 902 (45%), 17 (1%), 23 (1%), and 32 (2%), were recovered respectively from surgical Intensive Care Units (ICUs), neurosurgical ICUs, orthopedic ICUs, emergency department, and follow-up outpatients.

Analysis of microbiological dataset

During the 4-year study, a total of 1983 blood samples of BSI patients were received in the laboratory, and more than one bacterium were isolated from 1.5% (29/1983) of these blood samples. A total of 2017 bacterial isolates were identified with 82% (1646/2017) with Gram-negative bacteria isolated and 18% (371/2012) Gram-positive bacteria. Gram-negative bacteria were the most common cause of bloodstream infection in adults presenting to our tertiary referral hospital during all 4 years (78%–85%). *Acinetobacter* species was the most commonly isolated bacteria in 2013, 2015, and 2016. *Enterobacteriaceae* were the most commonly isolated group of organisms among the study cases in all the 4 years except for 2014, when 26% of the total isolated bacteria were *Burkholderia* spp. This was a part of an outbreak (under publication). The predominant *Enterobacteriaceae* was *Klebsiella* spp. throughout the study, followed by *Escherichia coli* and *Serratia* spp in 2013 and 2015 and 2014 and 2016 respectively. Non*enterobacteriaceae* were observed to be 43%–58% of the total bacteria isolated during the study period. Among Gram-positive isolates, *Staphylococcus* species were the leading pathogen (11%–15%), followed by *Enterococcus* spp. (4%–7%) [Table 2].

Tables 3 and 4 display the rates of antibiotic resistance of Gram-negative and Gram-positive isolates. Very high levels of antibiotic resistance were seen across all genera of family *Enterobacteriaceae* which was found to be statistically significant for all the antimicrobials tested. Similar trends were observed among the non*Enterobacteriaceae* [Table 3]. Discordant resistant profiles between disc diffusion and Vitek II were obtained with colistin (results not reported here). Statistically significant antibiotic resistance to amoxicillin-clavulanic acid ($P < 0.000$), ampicillin ($P = 0.021$), clindamycin ($P = 0.035$), co-trimoxazole ($P = 0.005$), gentamicin ($P < 0.000$), levofloxacin ($P = 0.006$), oxacillin ($P < 0.000$), penicillin ($P = 0.001$), and rifampicin ($P = 0.001$) was observed among Gram-positive bacteria [Table 4].

Table 1: Characteristics of the clinical study population

	Year			
	2013	2014	2015	2016
Total, *n* (%)	459	621	406	497
Age, median (IQR)	30 (24-43)	30 (25-54)	35 (25-50)	31 (23-45)
Female sex, *n* (%)	80 (17)	105 (17)	77 (19)	84 (17)
Surgical ICUs, *n* (%)	188 (41)	215 (35)	263 (65)	343 (69)
Neurosurgical ICUs, *n* (%)	248 (54)	392 (63)	134 (33)	128 (26)
Orthopedic ICUs, *n* (%)	12 (3)	0	2 (0.5)	3 (0.6)
Emergency department, *n* (%)	4 (0.9)	8 (1.3)	4 (1)	15 (3)
Follow-up OPDs, *n* (%)	7 (1.5)	6 (1)	3 (0.7)	8 (2)

IQR = Interquartile range, ICUs = Intensive Care Units, OPDs = Outpatient departments

Table 2: Etiology of bacterial bloodstream infections

Pathogen	2013 (*n*=484), *n* (%)	2014 (*n*=621), *n* (%)	2015 (*n*=411), *n* (%)	2016 (*n*=501), *n* (%)
Gram-negative isolates				
Enterobacteriaceae				
Enterobacter species	11 (2)	13 (2)	0	5 (1)
Escherichia coli	24 (5)	25 (4)	28 (7)	26 (5)
Klebsiella species	51 (11)	50 (8)	101 (25)	106 (21)
Proteus species	4 (0.8)	9 (1)	5 (1)	5 (1)
Providencia species	10 (2)	13 (2)	0	3 (0.6)
Salmonella species	6 (1)	6 (1)	0	13 (2.5)
Serratia species	13 (3)	35 (6)	0	35 (7)
Non-*Enterobacteriaceae*				
Acinetobacter species	97 (20)	132 (21)	122 (30)	135 (27)
Aeromonas species	1 (0.2)	0	0	0
Burkholderia species	19 (4)	162 (26)	9 (2)	25 (5)
Stenotrophomonas species	34 (7)	34 (6)	28 (7)	13 (2.5)
Pseudomonas aeruginosa	87 (18)	30 (5)	40 (8)	38 (8)
Other Gram-negative bacteria[#]	19 (4)	19 (3)	0	5 (1)
Gram-positive isolates				
Enterococcus species	34 (7)	26 (4)	28 (7)	37 (7)
Staphylococcus species	74 (15)	67 (11)	50 (12)	54 (11)
Streptococcus species	0	0	0	1 (0.2)

[#]*Morganella* species, *Pantoea* species, *Achromobacter* species, *Chryseobacterium* species, *Elizabethkingia* species, *Ralstonia pickettii, Sphingomonas paucimobilis*

Discussion

Among all types of nosocomial infections, BSIs prove to be potentially the most grave and expensive. Patients admitted to ICUs have an even higher risk of nosocomial BSIs than those admitted to other types of units. Although the causative agents are affected by a number of factors; predominantly the focus of infection, comorbidities such as chronic diseased conditions, immunodeficiency, other than geographic, socioeconomic and environmental factors, important insights can be gained from the analyses of the microbiological profile of BSIs as most cases reflect severe illness and the bacteria detected are usually the causative agents of the disease. The unprecedented antimicrobial resistance to antimicrobials like colistin has breached one of the last lines of defense against such infections with multidrug-resistant bugs.[9]

Table 3: Resistance among Gram-negative bacteria from bloodstream infections

Family	Genus	Year	Antibiotics tested (number of resistant strains [%])											
			Amikacin	Cefepime	Cefoperazone Sulbactam	Cefoxitin	Ceftazidime	Chloramphenicol	Ciprofloxacin	Imipenem	Netilmicin	Piperacillim -tazobactam	Tigecycline	Trimethoprim/ sulphamethoxazole
Enterobacteriaceae	*Enterobacter*	2013	0	3 (27)	3 (27)	8 (73)	9 (82)	7 (63)	4 (36)	4 (36)	7 (64)	8 (73)	3 (27)	11 (100)
		2014	2 (15)	7 (54)	2 (15)	12 (92)	7 (54)	7 (54)	3 (23)	0	2 (15)	0	7 (54)	6 (46)
		2015	0	0	0	0	0	0	0	0	0	0	0	0
		2016	2 (40)	1 (20)	3 (60)	NA	4 (80)	1 (20)	4 (75)	1 (20)	2 (40)	4 (80)	0	NA
	Escherichia	2013	9 (38)	23 (96)	15 (63)	18 (75)	24 (100)	15 (63)	23 (96)	20 (83)	16 (67)	22 (92)	5 (21)	24 (100)
		2014	10 (40)	24 (96)	14 (56)	15 (60)	24 (96)	8 (32)	25 (100)	8 (32)	10 (40)	15 (60)	1 (4)	19 (76)
		2015	11 (39)	27 (96)	18 (64)	NA	28 (100)	7 (25)	28 (100)	2 (7)	11 (39)	23 (82)	0	NA
		2016	14 (54)	23 (85)	15 (58)	NA	25 (96)	10 (38)	25 (96)	11 (42)	12 (46)	15 (58)	1 (4)	0
	Klebsiella	2013	44 (86)	49 (96)	44 (86)	50 (98)	49 (96)	34 (67)	36 (71)	26 (51)	22 (43)	36 (71)	18 (35)	51 (100)
		2014	29 (58)	40 (80)	32 (64)	37 (74)	39 (78)	14 (28)	34 (68)	30 (60)	28 (56)	33 (66)	7 (14)	33 (66)
		2015	64 (63)	99 (98)	70 (69)	NA	92 (91)	64 (63)	96 (95)	43 (43)	60 (59)	78 (77)	13 (13)	NA
		2016	101 (95)	99 (94)	98 (92)	NA	103 (97)	64 (60)	103 (97)	68 (64)	105 (99)	83 (78)	13 (12)	86 (81)
	Proteus	2013	3 (75)	4 (100)	3 (75)	4 (100)	4 (100)	0	4 (100)	4 (100)	1 (25)	4 (100)	0	NA
		2014	9 (100)	9 (100)	2 (22)	3 (33)	9 (100)	9 (100)	9 (100)	3 (33)	9 (100)	2 (22)	9 (100)	9 (100)
		2015	1 (20)	1 (20)	0	NA	0	4 (80)	1 (20)	0	1 (20)	4 (80)	0	NA
		2016	5 (100)	2 (40)	1 (20)	NA	5 (100)	2 (40)	5 (100)	2 (40)	5 (100)	1 (20)	3 (60)	NA
	Providencia	2013	7 (70)	6 (60)	7 (70)	9 (90)	8 (80)	5 (50)	8 (80)	5 (50)	4 (40)	9 (90)	5 (50)	10 (100)
		2014	12 (92)	12 (92)	11 (85)	7 (54)	12 (92)	9 (69)	12 (92)	12 (92)	12 (92)	1 (8)	1 (8)	5 (38)
		2015	0	0	0	0	0	0	0	0	0	0	0	0
		2016	0	0	0	NA	0	0	0	0	0	0	NA	NA
	Salmonella	2013	0	0	0	0	4 (67)	0	4 (67)	2 (33)	0	3 (50)	0	6 (100)
		2014	0	0	0	1 (17)	0	0	1 (17)	0	0	0	0	1 (17)
		2015	0	0	0	0	0	0	0	0	0	0	0	0
		2016	2 (15)	1 (8)	2 (15)	NA	0	1 (8)	2 (15)	0	0	0	0	0
	Serratia	2013	3 (23)	3 (23)	8 (62)	12 (92)	7 (54)	7 (46)	6 (45)	7 (54)	6 (46)	8 (62)	2 (15)	NA
		2014	26 (74)	0	5 (14)	10 (29)	28 (80)	9 (26)	12 (34)	12 (34)	25 (71)	1 (3)	8 (23)	0
		2015	0	0	0	0	0	0	0	0	0	0	0	0
		2016	28 (80)	2 (77)	14 (40)	NA	30 (86)	14 (40)	22 (63)	1 (3)	30 (86)	12 (34)	9 (26)	0
	P value		<0.001	<0.001	<0.0001	0.000	0.043	0.0032	<0.0001	0.0024	<0.0001	<0.0001	0.0004	<0.0001
	df		3	3	3	3	3	3	3	3	3	3	3	3
Non -*Enterobacteriaceae*	*Acinetobacter*	2013	77 (79)	93 (96)	64 (66)	0	93 (96)	59 (61)	57 (59)	37 (38)	54 (56)	46 (47)	29 (30)	97 (100)
		2014	112 (85)	11 (86)	112 (85)	132 (100)	121 (92)	15 (11)	124 (94)	107 (81)	104 (79)	109 (83)	4 (3)	NA
		2015	108 (89)	120 (98)	107 (88)	NA	119 (98)	120 (98)	121 (99)	117 (96)	65 (53)	120 (98)	23 (19)	121 (99)
		2016	124 (92)	126 (93)	123 (91)	NA	129 (96)	134 (99)	130 (96)	124 (92)	103 (76)	125 (93)	23 (17)	135 (100)
	Aeromonas	2013	1 (100)	1 (100)	1 (100)	1 (100)	1 (100)	1 (100)	1 (100)	1 (100)	1 (100)	1 (100)	1 (100)	1 (100)
		2014	0	0	0	0	0	0	0	0	0	0	0	0
		2015	0	0	0	0	0	0	0	0	0	0	0	0
		2016	0	0	0	0	0	0	0	0	0	0	0	0
	Burkholderia	2013	NA	14 (74)	NA	4 (21)	14 (74)	10 (53)	9 (47)	6 (32)	6 (32)	4 (21)	9 (47)	19 (100)
		2014	NA	12 (7)	NA	145 (90)	4 (2)	NA	NA	53 (33)	NA	NA	7 (4)	NA

Contd...

Table 3: Contd...

Family	Genus	Year	Antibiotics tested (number of resistant strains [%])											
			Amikacin	Cefepime	Cefoperazone Sulbactam	Cefoxitin	Ceftazidime	Chloramphenicol	Ciprofloxacin	Imipenem	Netilmicin	Piperacillim -tazobactam	Tigecycline	Trimethoprim/ sulphamethoxazole
Non -*Enterobacteriaceae*		2015	NA	5 (56)	NA	NA	4 (44)	NA	NA	9 (100)	NA	NA	6 (67)	NA
		2016	NA	14 (56)	NA	NA	7 (28)	NA	NA	20 (80)	NA	NA	19 (76)	NA
	Pseudomonas	2013	23 (26)	42 (48)	17 (20)	76 (87)	56 (64)	61 (70)	59 (68)	40 (46)	47 (54)	57 (66)	31 (36)	87 (100)
		2014	9 (30)	10 (33)	10 (33)	29 (97)	11 (37)	17 (57)	10 (33)	9 (30)	9 (30)	NA	21 (70)	NA
		2015	21 (53)	25 (63)	24 (60)	NA	27 (68)	29 (73)	26 (65)	18 (45)	39 (98)	NA	8 (20)	40 (100)
		2016	23 (61)	21 (55)	15 (39)	NA	22 (58)	30 (79)	27 (71)	16 (42)	29 (76)	NA	19 (50)	38 (100)
	Stenotrophomonas	2013	NA	34 (100)	NA	34 (100)	NA	22 (65)	26 (76)	20 (59)	22 (65)	23 (68)	10 (29)	34 (100)
		2014	NA	33 (97)	NA	34 (100)	NA	NA	NA	32 (94)	NA	NA	NA	NA
		2015	NA	19 (68)	NA	NA	NA	NA	NA	28 (100)	NA	NA	NA	NA
		2016	NA	13 (100)	NA	NA	NA	NA	NA	13 (100)	NA	NA	NA	NA
	Other Gram-negative bacteria[#]	2013	14 (74)	16 (84)	9 (47)	14 (74)	16 (84)	16 (84)	13 (68)	10 (53)	11 (58)	15 (79)	8 (42)	19 (100)
		2014	6 (32)	19 (100)	16 (84)	19 (100)	19 (100)	18 (95)	3 (16)	6 (32)	6 (32)	0	0	19 (100)
		2015	0	0	0	0	0	0	0	0	0	0	0	0
		2016	4 (80)	5 (100)	4 (80)	NA	5 (100)	4 (80)	5 (100)	5 (100)	5 (100)	0	5 (100)	5 (100)
	P value		<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	0.422
	df		3	3	3	3	3	3	3	3	3	3	3	3

[#] *Morganella* species, *Pantoea* species, *Achromobacter* species, *Chryseobacterium* species, *Elizabethkingia* species, *Ralstonia pickettii, Sphingomonas paucimobilis.* df = Degree of freedom, NA = Not available

Table 4: Resistance among Gram-positive bacteria from bloodstream infections

Genu	Year (*n*)	Antibiotics tested (number of resistant strains [%])																			
		Amikacin	Amoxicillin	Amoxicillin -Clavulanic acid	Ampicillin	Ampicillin -sulbactam	Cefoxitin	Ciprofloxacin	Clindamicin	Co -trimoxazole	Erythromycin	Gentamycin	Levofloxacin	Linezolid	Netilmycin	Nitofurantoin	Oxacillin	Penicillin	Rifampicin	Teichoplanin	Tetracyclin
Enterococcus	2013	NA	34 (100)	33 (970)	25 (74)	22 (65)	NA	NA	NA	NA	29 (85)	11 (32)	28 (82)	3 (9)	NA	19 (56)	NA	31 (91)	25 (74)	4 (12)	18 (53)
	2014	NA	26 (100)	26 (100)	26 (100)	24 (92)	NA	25 (96)	NA	NA	18 (69)	20 (77)	25 (96)	0	NA	NA	NA	26 (100)	26 (100)	7 (27)	15 (58)
	2015	NA	NA	24 (86)	25 (89)	24 (86)	NA	26 (93)	NA	NA	28 (100)	NA	26 (93)	2 (7)	NA	NA	NA	25 (89)	16 (57)	1 (40)	13 (46)
	2016	NA	NA	30 (81)	37 (100)	31 (84)	NA	32 (86)	NA	NA	36 (97)	0	33 (89)	0	NA	NA	NA	30 (81)	26 (700)	3 (8)	24 (65)
Staphylococcus	2013	37 (50)	NA	60 (81)	73 (99)	52 (70)	65 (42)	67 (91)	46 (62)	48 (65)	59 (80)	63 (85)	58 (78)	0	6 (8)	0	57 (77)	74 (100)	29 (39)	6 (8)	30 (41)
	2014	NA	NA	60 (90)	66 (99)	45 (67)	57 (39)	55 (82)	52 (78)	30 (45)	62 (93)	53 (790)	55 (82)	1 (1)	2 (3)	NA	62 (93)	67 (100)	40 (60)	1 (1)	27 (40)
	2015	NA	NA	30 (61)	49 (100)	24 (49)	35 (29)	41 (84)	27 (55)	17 (35)	34 (69)	23 (47)	33 (67)	1 (2)	2 (4)	NA	29 (59)	49 (100)	17 (35)	0	10 (20)
	2016	NA	NA	36 (67)	52 (96)	33 (61)	42 (34)	52 (96)	40 (74)	32 (59)	47 (87)	34 (63)	53 (98)	0	7 (13)	NA	36 (67)	50 (93)	26 (48)	0	7 (13)
Streptococcus	2013	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	2014	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	2015	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	2016	NA	NA	NA	NA	NA	NA	0	NA	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
P value		NA	NA	<0.000	0.021	0.414	0.096	0.625	0.035	0.005	0.170	<0.000	0.006	0.241	0.144	NA	<0.000	0.001	0.001	0.059	0.085
df		NA	NA	3	3	3	3	3	3	3	3	3	3	3	3	NA	3	3	3	3	3

df = Degree of freedom, NA = Not available

We observed a predominance of young and middle-aged adult males among patients with BSI (81%–83%). This phenomenon is similar to various studies reporting septic shock as one of the top causes of death.[4] We observed a higher proportion of males than females. The highest percentage of patients with BSI in our study were from surgical and neurosurgical ICUs.

In a previous study from the same center conducted in 2011–2012 a high prevalence of BSIs was reported. We reported a total of 316 organisms isolated from the 296 episodes of BSIs.[11] The numbers have only increased since then. *Acinetobacter* species followed by *Klebsiella* species are still the most common cause of BSI.

Gram-positive and Gram-negative bacteria showed very high resistance to most the antibiotics tested, and the statistical analysis clearly suggest that the drug resistance is undeniably significant and poses threat more-so to high-risk patients having blood culture positive.

Our study, however, has some important limitations. First, our trauma center is a tertiary referral hospital and specializes in trauma cases. Therefore, the pattern of etiology, resistance, and spectrum of clinical disease is different from that seen in other hospitals in India. Second, we have reported only the total number of organisms and not the BSI episodes. Study of BSI episodes classified into community- and hospital-acquired BSIs would have led to a more comprehensive analysis. Finally, the importance and role of certain bacteria, such as *Aeromonas* species or *Stenotrophomonas* species, which have been associated with both real and pseudobacteremia infection was not ascertained because of a lack of repeat sampling and the retrospective nature of our study.

Considering the load of BSI and the toll it is taking, especially on our young and middle-aged adult population, we are in dire need of rapid identification and antimicrobial susceptibility testing of the causative agents of bloodstream infections. Such point-of-care testing systems would promptly provide essential information to clinicians for selecting an appropriate antimicrobial therapy for patients with potentially fatal bloodstream infections. We have seen a positive impact of an intensive surveillance on the central line-associated bloodstream infections in a study conducted at our center emphasizing the need of regular and stringent surveillance of BSI.[12] Thus, a deeper understanding of the prevalence, etiology of BSIs in India, its resistance patterns and their impact on patients' outcomes is important to guide clinical management and appropriate antibiotic use.

Conclusion

We require a detailed analysis of the prevalence and etiology of BSIs and its resistance profile. It will lead to appropriate antibiotic use, clinical management, and formulation of antibiotic policies and preventive measures.

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Conflicts of interest
There are no conflicts of interest.

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