MGMJMS

10.5005/jp-journals-10036-1082

ORIGINAL ARTICLE

Blood Culture and Sensitivity Profile Study in a Tertiary Medical Hospital in Kolkata, West Bengal: 7 Years' Experience

[1]Ashis K Saha, [2]Kausik Munsi, [3]Payodhi Dhar

ABSTRACT

Aims and objectives: To identify the prevalence of bacteremia and the spectrum of antimicrobial sensitivity in our community, because it will guide the clinician to institute proper antimicrobial therapy.

Background: Bacteremia originates from either intravascular sites or extraVascular sites. In case of bloodstream infection, either Gram-positive or Gram-negative bacteria are responsible. Of these bacterial isolates, Gram-negative bacteria are responsible for higher mortality and morbidity. Since 20 to 30 years, coagulase-negative Staphylococci are responsible for most infection.

Materials and methods: In this retrospective study, blood samples were collected aseptically from 11,581 patients and were injected into the bottles containing bile-broth and brain-heart infusion broth and allowed to be incubated at 37°. Then subculture was done on blood agar, chocolate agar, as well as MacConkey agar media and was kept for 7 days or till the appearance of growth of the organism. After identification of isolates, Kirby Bauer disk diffusion test on Mueller-Hinton agar II was performed to detect antimicrobial sensitivity.

Results: Our study documented 8.58% positive cultures in the last 7 years. Gram-negative bacterial isolates were significantly higher than Gram-positive isolates (64.19% *vs* 34.80%, p = 0.00). Lowest number of positivity was seen in *Morganella* (0.40%) followed by *Proteus* (0.50%) and *Enterococcus faecium* (0.90%) in ascending order. Males were significantly more culture positive than females (549/994 *vs* 445/994, p = 0.00). Most common bacterial isolates were (coagulase negative Staphylococci) CoNS (239, 24.04%) followed by *Klebsiella* including ESBL (extended spectrum beta-lactamase), carbapenamase producer (234, 23.74%) and *Escherichia coli* (110, 11.06%). *E. coli* was >75% sensitive to imipenem group, polymyxin B (98.18%), colistin (96.36%), and amikacin (80.9%). Coagulase negative *Staphylococci* showed more than 60% sensitivity to levofloxacin (76.98%), amikacin (82.84%), tigecycline (87.44%), vancomycin (94.45%), teicoplanin (91.63%), linezolid (91.21%), gentamicin (76.56%), netilmicin (74.47%), and tetracycline (75.31%). *Klebsiella* (non-ESBL and carbapenemase producer) was highly sensitive to polymyxin B (93.06%), colistin (91.90%), meropenem (65.31%), and imipenem (94.73%). Extended spectrum beta-lactamase-producing *Klebsiella* showed increased sensitivity to meropenem (89.47%), imipenem (94.73%), ertapenem (81.57%), polymyxin B, and colistin (97.36% each).

Conclusion: Positive cultures were 8.58% in the last 7 years. Gram negative bacterial isolates were significantly higher. Males were more culture positive. Most common bacterial isolates were CoNS followed by *Klebsiella* species and *E. coli*. Gram-negative bacterial isolates were highly sensitive to piperacillin, cefoperazone, imipenem, meropenem, aminoglycoside group of antibiotics, tigecycline, polymyxin B and colistin. Gram-positive bacterial isolates were sensitive to piperacillin, cefoparazone, vancomycin, teicoplanin, linezolid and clindamycin. *Salmonella typhi* were sensitive to ampicillin, cefoparazone, cefepime, azithromycin, chloramphenicol, and fluoroquinolones. *Acinetobacter* showed > 50% sensitivity to cefepime and *Pseudomonas* showed > 50% sensitivity to cefotaxime and levofloxacin. So to prevent resistance of bacterial isolates, a proper antibiotic guideline should be maintained.

Keywords: Blood culture and sensitivity, Coagulase negative *Staphylococcus*, *E. coli*, Gram-positive and Gram-negative bacterial isolates, *Klebsiella*, Tertiary care hospital.

How to cite this article: Saha AK, Munsi K, Dhar P. Blood Culture and Sensitivity Profile Study in a Tertiary Medical Hospital in Kolkata, West Bengal: 7 Years' Experience. MGM J Med Sci 2016;3(1):18-25.

Source of support: Nil

Conflict of interest: None

[1]Associate Professor, [2]Assistant Professor, [3]Junior Resident

[1-3]Department of General Medicine, KPC Medical College and Hospital, Jadavpur, Kolkata-700089, West Bengal

Corresponding Author: Ashis K Saha, Associate Professor Department of General Medicine, KPC Medical College and Hospital, P-5, Block-B, Lake Town, Kolkata-700089, West Bengal India, Phone: +919433006157, e-mail: asissaha2008@gmail.com

INTRODUCTION

Episodic bacterial colonization in blood circulation is called bacteremia.[1] This bloodstream infection may be life threatening in few circumstances leading to septic shock and eventually death. Bloodborne infection is a major cause of morbidity and mortality.[2] In 1899, Brill reported the first case of bacteremia due to bacillus pyocyaneus (which is now known as *Pseudomonas aeruginosa*). After 10 years, 40 cases were reported worldwide and 30 more cases were documented in the next 15 years.[3] There are two types of bloodstream infections: first one is intravascular – it originates from cardiovascular system, e.g., infective endocarditis, mycotic aneurysm, catheter insertion. Second one is extravascular – it originates from extravascular sites, like lung, lymphatic system, kidney, bones, etc.[4] Malaria and bloodstream infection are clinically indistinguishable when a patient comes with fever, even the World Health Organization has failed to identify and distinguish these two cases.[5-8] In case of bacterial infection, Gram-negative bacteria are responsible for more mortality than infection due to Gram-positive bacteria. Over the past 20 to 30 years, *Escherichia coli* and staphylococcal infection continue to be the most common causative organisms, but recently, bacterial spectrum has changed. Nowadays, there is substantial increase in bloodstream infection due to coagulase negative *Staphylococcus*.[9] *Staphylococcus epidemidis* is responsible for infection in pediatric population followed by incidence of *Staphylococcus aureus* infection. There is also increasing frequency of changes in antimicrobial resistance of microbial isolates throughout the world.[10,11] For example, there is emerging resistance to fluoroquinolones and broad spectrum cephalosporins in Enterobacteriaceae, oxacillin in Staphylococci, vancomycin in Enterococci, and penicillin in Streptococci.[10,12] So, to prevent mortality, rapid and reliable detection of bacteria is essential worldwide and it can be accomplished by doing blood culture in proper time and in proper condition. This will guide the physicians to introduce proper antibiotic in adequate doses. In this study, our aim was (1) to identify the prevalence of microbes in our patients, (2) to study the spectrum of antimicrobial sensitivity to these microbes by performing *in vitro* culture sensitivity test, because it will guide the clinician to institute the proper antimicrobial therapy.[13]

MATERIALS AND METHODS

This was a retrospective study of 7 years period (2009 to 2015) in KPC Medical College and Hospital, Kolkata, West Bengal. This study was started only after getting permission from our local ethical committee.

Study Populations

Patients with respiratory tract infection, urinary tract infection, infective endocarditis, large abscesses in different areas of the body, osteomyelitis, ventilator-associated pneumonia, catheter-induced infection were recruited for the study.

Sample Size

A total of 11,581 blood cultures were performed, of which 994 cultures were positive.

Method of Culture

Blood samples were collected aseptically using sterile needle and syringe from the patients before antibiotic administration. But in case of patients getting antibiotics, prior to next schedule dose blood sample was collected. In case of adult and pediatric patients, 5 and 2 ml blood was collected respectively.[4]

Processing of Specimen

Aseptically collected blood was injected into the bottles containing bile broth and brain-heart infusion broth and allowed to be incubated at 37°. Blood bottles were examined periodically at regular intervals for any evidence of bacterial growth, hemolysis, turbidity, and any gas production. Then subculture was done on blood agar, chocolate agar, as well as MacConkey agar media and was kept for 7 days or till the appearance of growth of the organism.[14] Then the colonies were processed for a series of tests for identification of isolates based on motility test, Gram stain, and biochemical tests. After identifying the isolates, Kirby Bauer disk diffusion test on Mueller-Hinton agar II was performed to detect antimicrobial sensitivity according to recommendation of Clinical and Laboratory Standard Institute.[15] In each culture plate, antibiotic disk (oxoid) was applied and kept for 24 hours in 35°C. Antibiotic zones were measured and interpreted accordingly.

Statistical Analysis

The data were analyzed by using software Statistical Package for the Social Sciences (SPSS) version 18. A value of $p < 0.05$ was accepted as significant.

RESULTS

Total number of positive cultures was 994 out of total blood sent for culture of 11,581, percentage of positivity being 8.58%. Among the 7 years' study, in 2014 and 2015, the percentages of positive blood cultures were highest (17–16.49% respectively). Again in these 2 years, males showed significantly positive cultures as compared with females (102 *vs* 67 in 2014 and 95 *vs* 69 in 2015, $p = 0.00$). Similar result was demonstrated in 2011 (89 in males *vs* 46 in females, $p = 0.00$). Again, in total study, males were significantly positive than females (549 *vs* 445, $p = 0.00$) (Table 1).

Table 1: Year-wise male and female distribution of bacterial isolates

		Sex		
Years	*Total cases (994)*	*Males*	*Females*	*p-value*
2009	105 (10.56%)	53	52	0.89
2010	129 (12.97%)	71	58	0.10
2011	135 (13.58%)	89	46	0.00
2012	151 (15.19%)	74	77	0.72
2013	141 (14.18%)	65	76	0.19
2014	169 (17%)	102	67	0.00
2015	164 (16.49%)	95	69	0.00
		549	445	0.00

Table 2: Sex-wise distribution of bacterial isolates

Bacterial isolates	*Males*	*Percentage*	*Females*	*Percentage*	*p-value*
Escherichia coli (110) (11.06%)	54	49.09	56	50.90	0.78
Coagulase negative *Staphylococcus* (239) (24.04%)	120	43.93	119	49.79	0.92
Klebsiella (173) (17.40%)	105	60.69	68	39.30	0.00
Klebsiella (ESBL) (38) (3.82%)	25	65.57	13	34.21	0.00
Klebsiella (CARB) (25) (2.51%)	15	60	10	40	0.15
Morganella (4) (0.40%)	3	75	1	25	0.15
Proteus (5) (0.50%)	2	40	3	60	0.52
Enterococcus faecium (9) (0.90%)	6	66.66	3	33.33	0.15
Staphylococcus (86) (8.65%)	45	52.32	41	47.67	0.54
Citrobacter (22) (2.21%)	14	63.63	8	36.36	0.07
Nonfermenting Gram negative bacilli (73) (7.34%)	49	67.12	24	32.87	0.00
Enterococcus (12) (1.20%)	6	50	6	50	1
Acinetobacter (58) (5.83%)	26	44.82	32	55.17	0.26
Pseudomonas (75) (7.54%)	37	49.33	38	50.66	0.47
Salmonella (41) (4.12%)	28	68.29	13	31.70	0.00
Burkholderia cepacia (24) (2.41%)	14	58.33	10	41.66	0.24

ESBL: Extended spectrum beta-lactamase

In this study, percentage of positive cultures was highest in coagulase negative *Staphylococcus* (CoNS) (24.04%) cases, followed by *Klebsiella* (17.04%) and *E. coli* (11.06%), whereas lowest number of positivity was seen in *Morganella* (0.40%) followed by *Proteus* (0.50%) and *Enterococcus faecium* (0.90%) in ascending order. Again in case of culture positivity of *Klebsiella*, *Klebsiella* (extended spectrum beta-lactamase, ESBL producer), nonfermenting Gram-negative bacilli, and *Salmonella typhi* incidence of males were significant than in females (105 *vs* 68, 25 *vs* 13, 49 *vs* 24, and 28 *vs* 13 respectively, p = 0.00) (Table 2). In our study, the total number of Gram-positive bacteria was 346 and Gram-negative bacteria was 644, with p-value of 0.00 (Table 3).

Table 3: Total Gram-positive and negative bacteria

Gram-positive bacteria	*Gram-negative bacteria*	
Coagulase negative *Staphylococcus* (239)	*E. coli* (110) *Klebsiella* (173)	p-value
Enterococcus faecium (9)	*Klebsiella* (ESBL) (38)	
Staphylococcus (86)	*Klebsiella* (CARB) (25)	
Enterococcus (12)	*Proteus* (5)	
	Citrobacter (22)	
	Nonfermenting Gram negative bacilli (73)	
	Acinetobacter (58)	
	Pseudomonas (75)	
	Salmonella (41)	
	Burkholderia cepacia (24)	
	Morganella (4)	
Total = 346	Total = 648	0.00

ESBL: Extended spectrum beta-lactamase

Escherichia coli was > 75% positive to imipenem group, polymyxin B (98.18%), colistin (96.36%), amikacin (80.9%), and between 60 and 74% to other aminoglycoside group of drugs and piperacillin (69.09%). Coagulase negative Staphylococci showed more than 60% positivity to levofloxacin (76.98%), amikacin (82.84%), tigecycline (87.44%), vancomycin (94.45%), teicoplanin (91.63%), linezolid (91.21%), gentamicin (76.56%), netilmicin (74.47%), and tetracycline (75.31%). *Klebsiella* (non-ESBL and carbapenemase producer) was highly sensitive to polymyxin B (93.06%), colistin (91.90%), meropenem (65.31%), and imipenem (94.73%), whereas ESBL-producing *Klebsiella* showed increased sensitivity to meropenem (89.47%), imipenem (94.73%), ertapenem (81.57%), with highest positivity to polymyxin B and colistin (97.36% each). But carbapenemase-producing Klebsiella was 100% positive only to polymyxin B and colistin. *Staphylococcus aureus* was highly sensitive to vancomycin (96.51%), linezolid (97.67%), teicoplanin (89.53%), clindamycin (82.55%), tetracycline (82.55%), gentamicin (80.23%) and 100% resistant to polymyxin B and colistin. *Acinetobacter* showed high sensitivity to only polymyxin B (84.48%) and colistin (82.75%), meropenem (62.06%), and imipenem (62.06%). *Pseudomonas* bacteria showed high sensitivity to piperacillin (80%), cefoperazone (66.68%), imipenem (92%), meropenem (70%), gentamicin (78.66%), amikacin (81.33%), netilmicin and tobramycin (76% each), fluoroquinolones (ciprofloxacin 76%, levofloxacin 89.33%), polymyxin B (94.66%), and colistin (92%). Lastly, *Salmonella typhi* was highly sensitive to chloramphenicol (73.17%), ciprofloxacin (73.1%), levofloxacin (75.60%), imipenem (90.24%), ceftriaxone (32.68%), piperacillin (75.60%), and cefotaxime (73.17%) (Tables 4A to D).

Table 4A: Antibiotic sensitivity of bacterial isolates

Organism	*PEN*	*AMOX*	*OX*	*AMC*	*PIP*	*CES*	*CEFU*	*CFT*	*TIC*
Escherichia coli (110)	0	4 (3.63%)	1 (0.9%)	26 (23.63%)	76 (69.09%)	64 (58.18%)	12 (10.9%)	12 (10.9%)	3 (2.72%)
CoNS (239)	4 (1.67%)	20 (8.36%)	77 (32.21%)	111 (46.44%)	156 (65.27%)	10 (4.18%)	48 (20.08%)	4 (1.67%)	5 (2.09%)
Klebsiella (173)	0	5 (2.89%)	2 (1.15%)	25 (14.45%)	69 (39.88%)	57 (32.94%)	11 (6.35%)	30 (17.34%)	10 (5.78%)
Klebsiella (ESBL) (38)	0	0	0	0	18 (47.36%)	15 (39.47%)	0	0	0
Klebsiella (CARB) (25)	0	0	0	0	0	0	0	0	0
Morganella (4)	0	0	0	0	3 (1.2%)	1 (4%)	0	1 (4%)	0
Proteus (5)	0	0	0	0	2 (40%)	4 (80%)	0	0	0
Enterococcus faecium (9)	0	1 (11.11%)	0	2 (22.22%)	2 (22.22%)	1 (11.11%)	0	1 (11.11%)	1 (11.11%)
Staphylococcus (86)	6 (6.97%)	23 (26.74%)	48 (55.81%)	53 (61.62%)	57 (66.27%)	4 (4.65%)	33 (35.37%)	14 (16.27%)	1 (1.16%)
Citrobacter (22)	0	3 (13.63%)	1 (4.54%)	4 (18.18%)	16 (72.72%)	12 (54.54%)	3 (13.63%)	7 (31.81%)	5 (22.72%)
Nonfermenting Gram negative bacilli (73)	0	2 (2.73%)	1 (1.36%)	4 (5.47%)	62 (84.93%)	47 (64.38%)	3 (4.10%)	6 (82.19%)	7 (9.58%)
Enterococcus (12)	0	3 (25%)	0	8 (66.66%)	9 (75%)	1 (8.33%)	1 (8.33%)	1 (8.33%)	1 (8.33%)
Acinetobacter (58)	0	1 (1.72%)	0	6 (10.34%)	22 (37.93%)	16 (27.58%)	3 (5.17%)	7 (12.06%)	9 (15.51%)
Pseudomonas (75)	0	0	0	2 (2.66%)	60 (80%)	50 (66.66%)	0	4 (53.33%)	11 (14.66%)
Salmonella (41)	0	5 (12.19%)	0	24 (58.53%)	31 (75.60%)	24 (58.53%)	2 (4.87%)	30 (73.17%)	9 (21.95%)
Burkholderia cepacia (24)	0	1 (4.16%)	0	1 (4.16%)	20 (83.33%)	9 (37.5%)	1 (4.16%)	2 (8.33%)	0

Table 4B: Antibiotic sensitivity of bacterial isolates

Organism	*CXT*	*CFZ*	*CTRX*	*CFP*	*AZ*	*ER*	*AZT*	*ERT*	*IMP*	*CEFO*
E. coli (110)	46 (41.18%)	22 (20%)	26 (23.63%)	22 (20%)	5 (4.54%)	0	17 (18.70%)	83 (75.45%)	98 (89.09%)	0
CoNS (239)	52 (21.75%)	6 (2.51%)	76 (31.79%)	36 (15.06%)	52 (21.75%)	80 (33.47%)	38 (15.89%)	37 (15.48%)	104 (43.51%)	2 (0.83%)
Klebsiella (173)	58 (33.52%)	20 (11.56%)	31 (17.91%)	25 (14.45%)	15 (8.67%)	0	16 (9.24%)	102 (58.95%)	118 (68.20%)	2 (1.15%)
Klebsiella (ESBL) (38)	25 (65.78%)	0	0	0	0	0	0	31 (81.57%)	36 (94.73%)	0
Klebsiella (CARB) (25)	0	0	0	0	0	0	0	0	0	0
Morganella (4)	0	2 (50%)	1 (25%)	0	0	0	0	1 (25%)	3 (75%)	0
Proteus (5)	1 (20%)	0	0	0	0	0	0	4 (80%)	4 (80%)	0
Enterococcus faecium (9)	1 (11.11%	1 (11.11%)	1 (11.11%)	0	1 (11.11%)	0	0	1 (11.11%)	2 (22.22%)	0
Staphylococcus (86)	14 (16.27%)	1 (1.16%)	55 (63.95%)	38 (44.18%)	31 (36.04%)	55 (63.95%)	26 (30.23%)	16 (18.60%)	21 (24.41%)	1 (1.16%)
Citrobacter (22)	5 (22.72%)	4 (18.18%)	6 (27.27%)	3 (13.63%)	2 (9.09%)	1 (4.54%)	4 (18.18%)	20 (90.90%)	21 (95.45%)	0
Nonfermenting Gram negative bacilli (73)	3 (4.10%)	7 (9.58%)	11 (15.06%)	8 (10.95%)	9 (12.32%)	1 (1.36%)	4 (5.47%)	23 (31.50%)	68 (33.15%)	1 (1.36%)
Enterococcus (12)	0	2 (16.66%)	2 (16.66%)	1 (8.33%)	2 (16.68%)	5 (41.66%)	4 (33.33%)	3 (25%)	9 (75%)	0
Acinetobacter (58)	3 (5.17%)	7 (12.06%)	10 (17.24%)	5 (86.20%)	7 (12.06%)	0	2 (3.44%)	13 (22.41%)	36 (62.06%)	1 (1.72%)
Pseudomonas (75)	1 (1.33%)	28 (37.33%)	3 (4%)	27 (36%)	5 (6.66%)	0	24 (32%)	8 (10.66%)	69 (92%)	25 (33.33%)
Salmonella (41)	3 (7.31%)	12 (29.26%)	38 (32.68%)	23 (56.09%)	26 (63.41%)	0	19 (46.34%)	13 (31.70%)	37 (90.24%)	2 (4.87%)
Burkholderia cepacia (24)	1 (4.16%)	3 (12.5%)	2 (8.33%)	5 (20.88%)	2 (8.33%)	0	4 (16.66%)	5 (20.88%)	16 (66.66%)	0

Table 4C: Antibiotic sensitivity of bacterial isolates

Organism	*MER*	*GEN*	*TOB*	*NET*	*AMK*	*NLX*	*NF*	*CIP*	*OF*	*LEV*
E. coli (110)	95 (86.36%)	76 (69.09%)	74 (67.27%)	82 (74.54%)	89 (80.90%)	0	0	40 (36.36%)	36 (32.72%)	56 (50.90%)
CoNS (239)	61 (25.52%)	183 (76.56%)	98 (41%)	178 (74.47%)	198 (82.84%)	0	10 (4.18%)	134 (56.06%)	140 (58.57%)	184 (76.98%)
Klebsiella (173)	113 (65.31%)	78 (45.08%)	77 (44.50%)	70 (40.46%)	88 (50.86%)	0	0	50 (28.90%)	42 (24.27%)	66 (38.15%)
Klebsiella (ESBL) (38)	34 (89.47%)	16 (42.10%)	17 (44.73%)	18 (47.36%)	23 (60.52%)	0	0	11 (28.94%)	9 (23.68%)	14 (36.84%)
Klebsiella (CARB) (25)	0	1 (4%)	1 (4%)	1 (4%)	1 (4%)	0	0	0	0	0
Morganella (4)	2 (50%)	2 (50%)	2 (50%)	2 (50%)	2 (50%)	0	0	3	0	3 (75%)
Proteus (5)	4 (80%)	2 (40%)	2 (40%)	2 (40%)	2 (40%)	0	0	0	2 (40%)	2 (40%)
Enterococcus faecium (9)	1 (11.11%)	1 (11.11%)	0	0	1 (11.11%)	0	0	0	0	0
Staphylococcus (86)	17 (19.76%)	69 (80.23%)	18 (20.93%)	61 (70.93%)	64 (74.41%)	0	0	59 (68.60%)	59 (68.60%)	64 (74.41%)
Citrobacter (22)	19 (86.36%)	13 (59.09%)	14 (63.63%)	13 (59.09%)	15 (68.18%)	0	0	11 (50%)	11 (50%)	18 (81.81%)
Nonfermenting Gram negative bacilli (73)	67 (91.78%)	46 (63.01%)	43 (58.90%)	46 (63.01%)	49 (67.12%)	3 (4.10%)	0	54 (73.97%)	42 (57.53%)	62 (84.93%)
Enterococcus (12)	2 (16.66%)	8 (66.66%)	2 (16.66%)	1 (8.33%)	2 (16.66%)	0	0	8 (66.66%)	3 (25%)	8 (66.66%)
Acinetobacter (58)	36 (62.06%)	21 (36.20%)	19 (32.75%)	19 (32.75%)	22 (37.93%)	0	0	23 (39.65%)	7 (12.06%)	31 (53.44%)
Pseudomonas (75)	70 (93.33%)	59 (78.66%)	57 (76%)	57 (76%)	61 (81.33%)	0	1 (1.33%)	57 (76%)	37 (49.33%)	67 (89.33%)
Salmonella (41)	28 (68.29%)	4 (9.75%)	3 (7.31%)	3 (7.31%)	3 (7.31%)	17 (41.46%)	1 (2.43%)	30 (73.17%)	22 (53.65%)	31 (75.60%)
Burkholderia cepacia (24)	16 (66.66%)	9 (37.5%)	7 (29.16%)	7 (29.16%)	8 (33.33%)	0	0	15 (62.5%)	3 (12.5%)	17 (70.83%)

Table 4D: Antibiotic sensitivity of bacterial isolates

Organism	*COT*	*CHLO*	*NIF*	*TET*	*TIG*	*CLIN*	*VAN*	*TEI*	*LID*	*POL*	*COL*
E. coli (110)	50 (45.45%)	55 (50%)	3 (2.72%)	38 (34.45%)	87 (79.90%)	0	0	0	0	108 (98.18%)	106 (96.36%)
CoNS (239)	116 (48.53%)	170 (71.12%)	0	180 (75.31%)	209 (87.44%)	153 (64.01%)	226 (94.45%)	219 (91.63%)	218 (91.21%)	11 (4.60%)	11 (4.60%)
Klebsiella (173)	62 (35.83%)	67 (38.72%)	0	73 (42.19%)	134 (77.45%)	1 (0.57%)	0	2 (1.15%)	1 (0.57%)	161 (93.06%)	159 (91.90%)
Klebsiella (ESBL) (38)	15 (39.47%)	21 (55.26%)	0	18 (47.36%)	32 (84.21%)	0	0	0	0	37 (97.36%)	37 (97.36%)
Klebsiella (CARB) (25)	1 (4%)	3 (12%)	0	10 (40%)	21 (84%)	0	0	0	0	25 (100%)	25 (100%)
Morganella (4)	3 (75%)	1 (25%)	0	3 (75%)	3 (75%)	0	0	0	0	1 (25%)	1 (25%)
Proteus (5)	0	3 (60%)	0	0	0	0	0	0	0	0	0
Enterococcus faecium (9)	1 (11.11%)	6 (66.66%)	0	5 (55.55%)	6 (66.66%)	0	7 (77.77%)	7 (77.77%)	7 (77.77%)	1 (11.11%)	1 (11.11%)
Staphylococcus (86)	54 (62.79%)	59 (68.60%)	1 (1.15%)	71 (82.55%)	60 (69.76%)	71 (82.55%)	83 (96.51%)	77 (89.53%)	84 (97.67%)	0	0
Citrobacter (22)	7 (31.81%)	13 (59.09%)	1 (4.54%)	12 (54.54%)	17 (77.27%)	0	0	0	0	22 (100%)	22 (100%)
Nonfermenting Gram negative bacilli (73)	55 (75.34%)	12 (16.43%)	0	24 (32.87%)	26 (35.61%)	2 (2.73%)	3 (4.10%)	2 (2.73%)	3 (4.10%)	20 (27.39%)	22 (30.13%)
Enterococcus (12)	2 (16.66%)	4 (33.33%)	0	5 (41.66%)	3 (25%)	1 (8.33%)	8 (66.66%)	7 (58.33%)	8 (66.66%)	3 (25%)	3 (25%)
Acinetobacter (58)	20 (34.48%)	14 (24.13%)	2 (3.44%)	22 (37.93%)	35 (60.34%)	0	0	0	0	49 (84.48%)	48 (82.75%)
Pseudomonas (75)	12 (16%)	3 (4%)	0	4 (5.33%)	6 (8%)	0	0	0	0	71 (94.66%)	69 (92%)
Salmonella (41)	22 (53.65%)	30 (73.17%)	0	12 (29.26%)	8 (19.51%)	1 (2.43%)	1 (2.43%)	0	1 (2.43%)	16 (39.02%)	16 (39.02%)
Burkholderia cepacia (24)	18 (75%)	3 (12.5%)	0	4 (16.66%)	7 (29.16%)	0	0	0	0	1 (4.16%)	1 (4.16%)

CoNS: Coagulase negative *Staphylococcus*; ESBL: Extended spectrum beta-lactamase; PEN: Penicillin; AMOX: Amoxycillin; OX: Oxacillin; AMC: Ampicillin; PIP: Piperacillin; CES: Cefoperazone + Sulbactum; CEFU: Cefuroxime; CFT: Cefotaxime; TIC: Ticarcillin; CXT: Cefoxitin; CFZ: Ceftazedime; CTRX: Ceftriaxone; CFP: Cefepime; AZ: Azithromycin; ER: Erythromycin; AZT: Aztreonum; IMP: Imipenem; CEFO: Cefoperazone; MER: Meropenem; GEN: Gentamicin; TOB: Tobramycin; NET: Netelmycin; AMK: Amikacin; NLX: Nalidixic acid; NF: Norfloxacin; CIP: Ciprofloxacin; OF: Ofloxacin; LEV: Levofloxacin; COT: Cotrimoxazole; CHLO: Chloramphenicol; NIF: Nitrofurantoin; TET: Tetracycline; TIG: Tigicycline; CLIN: Clindamycin; VAN: Vancomycin; TEI: Teicoplanin; LID: Linezolid; POL: Polymyxin; COL: Colistin

DISCUSSION

Our study revealed blood culture sensitivity of 8.58%, which was nearly half of the value as shown in the studies of Mehta et al (16.8%),[16] Qureshi and Aziz (16.6%),[17] and Devi et al (16.8%).[18] This low rate of positivity may be due to reasons like proper clinical care, proper antibiotic administration prior to admission in the tertiary care hospital, and most importantly prohibition over-the-counter antibiotic therapy.

In our study, incidence of Gram negative isolates was significantly high as compared with Gram-positive isolates (648, 65.19% *vs* 346, 34.80%, p = 0.00). It is compared with the study done by Irenge Leonid et al (Gram-negative isolate 104, 61.2% *vs* Gram-positive isolates 66, 38.8%, p = 00).[19] But on the contrary, study done by Moyo et al as well as studies done in Tanzania and other African countries showed prevalence of Gram-positive bacterial isolates over Gram-negative isolates (82% Gram-positive *vs* 17.9% Gram-negative bacteria).[9,20,21] Other studies in the developing countries similarly showed significant prevalence of Gram-positive bacterial isolates in bloodstream infections.[8,9,22,23]

There was no significant difference in gender involvement with respect to bacterial isolates in the studies done by Jombo et al (89/1260 *vs* 111/1910, p > 0.05)[24] and Devi et al (males *vs* females = 48.93% *vs* 51.06%, p > 0.05).[18] But in our study males showed significant positive bacterial isolates as compared with females (549/994 *vs* 445/994, p = 0.00).

Our study showed the most commonly isolated bacteria as CoNS (239/994, 24.04%) followed by *Klebsiella* including ESBL and carbapenemase producer (236/994, 23.74%) and *E. coli* (110/994, 11.06%). Coagulase negative *S.* are the most common blood culture contaminant and very much responsible for nosocomial bloodstream infection. Since only one blood sample is usually obtained from one patient for blood culture, it is not possible to determine whether the result is due to skin contamination or really true bacteremia. But recovery of CoNS may be due to other factors like use of prolonged intravascular device, prolonged stay in hospital, or underlying comorbidities. So, our findings are consistent with many surveillance studies.[9,18,21,25] Warren et al[26] detected CoNS as a significant cause of bloodstream infection. In a study done by Jombo et al,[24] commonest blood culture isolates were *Staphylococcus aureus* (22.7%) followed by *Klebsiella* species (20.2%) and third being *E. coli* (15.3%). Similar result was obtained in the study in Yobe state, Nigeria, and also documented in Slovakia where common bacterial isolates were *E. coli*, *Staphylococcus*, and *Klebsiella* species.[27,28] Again, in a study in Warsaw, Poland, *E. coli* and *Klebsiella* were the 1st and 2nd commonest, third being *Proteus*.[29] So, in any tertiary care hospital, at least two samples of blood should be taken for culture to determine whether it is true CoNS bacteremia or it is merely contamination. One should also consider that blood should be collected very aseptically.

Our study considered penicillin, amoxicillin, oxacillin, ampicillin, cefuroxime, cefotaxime, ticarcillin, ceftriaxone, ceftazedime, cefoxitin, cefepime, azithromycin, erythromycin, aztreonam, cefoperazone, nalidixic acid, fluoroquinolone group of drugs, nitrofurantoin, tetracycline, clindamycin, vancomycin, teicoplanin, and linezolid showing low sensitivity (<50%) to Gram-negative bacilli except *Salmonella* (>50% sensitive to ampicillin, cefotaxime, cefepime, azithromycin, fluoroquinolones, and chloramphenicol), acinetobacter (>50% sensitive to cefepime) and *Pseudomonas* (>50% sensitive to cefotaxime, levofloxacin). On the contrary, these Gram-negative bacilli were very much sensitive to piperacillin, cefoperazone, imipenem, meropenem, aminoglycoside group of antibiotics, tigecycline, polymyxin B, and colistin. Gram-positive isolates were sensitive to piperacillin, cefoperazone, vancomycin, teicoplanin, and linezolid. This was similar to the study done by Jombo et al,[24] who showed 0 to 50% sensitivity to penicillin, ampicillin, cloxacillin, tetracycline, cotrimoxazole, and chloramphenicol. In our study, each recovered agent showed resistance to at least four antimicrobial agents, which underscores the depth of antibiotic resistance in contemporary medical practice. This resistance of Enterobacteriaceae has been shown in different studies in Brazil, Vietnam, as well as South Africa.[30-32] This resistance is probably due to plasmid-mediated beta-lactamase production. *Staphylococcus* in our study demonstrated sensitivity of > 60% to amoxicillin, piperacillin, ceftriaxone, erythromycin, aminoglycoside group of drugs (except tobramycin), fluoroquinolone group of antibiotics, cotrimoxazole, chloramphenicol, tetracycline, tigecycline, and clindamycin and ≥ 90% sensitivity to vancomycin, teicoplanin, and linezolid. This finding was contrary to the studies done in Asia Pacific, Germany, and Nigeria.[33-35] Again in the study done by Jombo et al,[24] *S. aureus* showed > 90% sensitivity to fluoroquinolone group of antibiotics, 63 to 70% sensitivity to aminoglycoside group of antibiotics (similar to our study), but 0% sensitivity to chloramphenicol (which is contrary to our study). But studies done by Qureshi and Aziz[17] as well as by Devi et al[18] showed nearly 100% sensitivity to vancomycin and linezolid, which is nearly similar to our study (vancomycin 96.5%, linezolid 97.67%).

CONCLUSION

Our study documented 8.58% positive cultures in last 7 years. Gram negative bacterial isolates were significantly higher than Gram-positive isolates (64.19% *vs* 34.80%).

Males were significantly culture positive than females (549/994 *vs* 445/994). Most common bacterial isolates were CoNS followed by *Klebsiella* species and *E. coli*. Since CoNS is the most common contaminant of skin, to confirm true bacteremia, blood should be taken aseptically in two occasions from the same patient. Gram-negative bacterial isolates were highly sensitive to piperacillin, cefoperazone, imipenem, meropenem, aminoglycoside group of antibiotics, tigicycline, polymyxin B, and colistin. Gram-positive bacterial isolates were sensitive to piperacillin, cefoperazone, vancomycin, teicoplanin, linezolid, and clindamycin. *Salmonella typhi* was sensitive to ampicillin, cefoperazone, cefepime, azithromycin, chloramphenicol, and fluoroquinolone group of antibiotics. *Acinetobacter* showed >50% sensitivity to cefepime and *Pseudomonas* showed >50% sensitivity to cefotaxime and levofloxacin. To prevent progressive increase in antimicrobial resistance to antibiotics in different centers, a proper guideline should be set so that ultimate aim of recovery of the severely ill patients should be fulfilled.

ACKNOWLEDGMENT

We are thankful to all the Staff, Department of Microbiology and Medical Director of our college for helping us to collect the data.

REFERENCES

1. Munford, RS. Severe sepsis and septic shock. Kasper, DL.; Braunwald, E.; Fuaci, AS.; Hauser, SL.; Longo, DL.; Jameson, JL., editors. Harrison's principles and practice of internal medicine. 17th ed. Vol. 2. New York: McGraw Hill; 2008. p. 1696-1697.
2. Weinstein MP, Towns MI, Quartey SM, Mirrett S, Reimer LG, Parmigiani G, Reller LB. The clinical significance of positive blood cultures in the 1990s: a prospective comprehensive evaluation of microbiology, epidemiology and outcome of bacteremia and fungemia in adults. Clin Infect Dis 1997 Apr; 24(4):584-602.
3. Trevino, S.; Ross, D. Bacteremia and sepsis. Mahon, CR.; Lehman, DC.; Manuselis, G. Textbook of diagnostic microbiology. 3rd ed. New Delhi: Elsevier; 2007. p. 995-1009.
4. Winn W, Allen S, Janda W, Koneman E, Procop G, Schreckenberger P, Woods G, editors. Infections of blood. Koneman's color atlas and textbook of diagnostic microbiology. 6th ed. Philadelphia: Lippincott Williams and Wilkins; 2006. p. 97-105.
5. Evans JA, Adusei A, Timmann C, May J, Mack D, Agbenyega T, Horstmann RD, Frimpong E. High mortality of infant bacteremia clinically indistinguishable from severe malaria. QJM 2004 Sep;97(9):591-597.
6. Factor SH, Schillinger JA, Killer HD, Saha S, Begum H, Hossain A, Hossain M, Dewitt V, Hanif M, Khan N. Diagnosis and management of febrile children using the WHO/UNICEF guidelines for IMCI, Dhaka, Bangladesh. Bull World Health Organ 2001;79(12):1096-1105.
7. Bahwere P, Levy I, Hennart P, Donnen P, Lomoyo W, Dramaix-Wilmet M, Butzler JP, De Mol P. Community acquired bacteremia among hospitalized children in rural central Africa. Int J Infect Dis 2001;5(4):180-188.
8. Van Herp M, Praque V, Rackley E, Ford N. Mortality violence and lack of access to health care in the Democratic Republic of Congo. Disasters 2003 Jun;27(2):141-153.
9. Moyo S, Aboud S, Kasubi M, Maselle SY. Bacteria isolated from bloodstream infections at a tertiary hospital in Dares Salaam, Tanzania. Antimicrobial resistance of isolates. S Afr Med J 2010 Dec 1;100(12):835-838.
10. Ndugulile F, Jureen R, Harthug S, Urassa W, Langeland N. Extended spectrum β-lactamses among Gram-negative bacteria of nosocomial origin from a intensive care unit of a tertiary health facility in Tanzania. BMC Infect Dis 2005 Oct;5: 85-91.
11. Blomberg B, Jureen R, Manji KP, Tamim BS, Mwakagile DS, Urassa WK, Fataki M, Msangi V, Tellevik MG, Maselle SY, et al. High rate of fatal cases of pediatric septicemia caused by Gram negative bacteria with extended spectrum betailactamses in Dar es Salaam, Tanzania. J Clin Microbiol 2005 Feb;43(2): 745-749.
12. Shah AA, Hasan F, Ahmed S, Hameed. Characteristics, epidemiology and clinical importance of emerging strains of Gram-negative bacilliproducing extended spectrum of beta lactumses. Res Microbiol 2004 Jul-Aug;155(6):409-421.
13. Collee, JG.; Duguid, JP.; Fraser, AG.; Marmion, BP.; Simmion, BP.; Simmons, A., editors. Laboratory strategies in the diagnosis of infective syndromes. Mackie and MacCartney practical medical microbiology. 14th ed. New Delhi, India: Elsevier; 2006. p. 55-57.
14. Cheesbrough, M. District laboratory practice in Tropical Countries. Part II. Cambridge: Cambridge University Press; 2006. p. 63.
15. Clinical and Laboratory Standards Institute. Performance standards for antimicrobial susceptibility Testing: 16th International Supplement (CLSI document M100-S16). Wayne (PA): CLSI; 2006.
16. Mehta M, Dutta P, Gupta V. Antimicrobial susceptibility pattern of blood isolates from a teaching hospital in North India. Jpn J Infect Dis 2005 Jun;58(3):174-176.
17. Qureshi M, Aziz F. Prevalence of microbial isolates in blood culture and their antimicrobial susceptibility profile. Biomedica 2011 Jul-Dec;27(6):136-139.
18. Devi AV, Sahoo B, Damrolien S, Praveen SH, Lungran P, Devi Ksh M. A study on the bacterial profile of bloodstream infections in Rims Hospital. IOSR J Dental Med Sci 2015 Jan; 1(1):18-23.
19. Irenge LM, Kabego L, Kinunu FB, Itongwa M, Mitangala PN, Gala JL, Chirimwami RB. Antimicrobial resistance of bacteria isolated from patients with blood stream infections at a tertiary care hospital in the Democratic Republic of the Congo. S Afr Med J 2015 Sep;105(9):752-755.
20. Aboud S, Sabaya S, Masangi V. Bacteria isolated from blood culture specimens at Muhimbili National Hospital in Dar es Salaam. Tanzania from 1995 – 2004. Tanzania Med J 2005; 20(2):22-26.
21. Ahmed SH, Daef EA, Badary MS, Mahmoud MA, Abd-Elsayed AA. Nosocomial blood stream infection in intensive care units at Assiut University Hospitals Upper Egypt with special reference to extended spectrum β-lactamase producing organisms. BMC Res Notes 2009 May;2:76.

22. Reddy EA, Shaw AV, Crump JA. Community-acquired blood stream infections in Africa. A systemic review and meta-analysis. Lancet Infect Dis 2010 Jun;10(6):417-432.
23. Murdoch DR. Microbiological pattern in sepsis: What happened in last 20 years? Int J Antimicrob Agents 2009;34 (Suppl 4):S5-S8.
24. Jombo GT, Akpan S, Epoke J, Akaa PD, Eyong KI, Gyuse AN, Amefule EN, Uket OO. Microbial isolates from clinical specimens of blood culture and antimicrobial susceptibility profiles: Findings from an analysis of 3255 blood culture specimens at a University teaching hospitals in southern Nigeria. Int J Biol Med Res 2010;1(3):66-70.
25. Newton O, English M. Young infant sepsis: aetiology, antibiotic susceptibility and clinical signs. Trop Med Hyg 2007 Oct;101(10):959-966.
26. Warren DK, Zack JE, Elward AM, Cox MJ, Fraser VJ. Nosocomial primary blood stream infections in intensive care unit patients in a nonteaching community medical centre: a 21-month prospective study. Clin Infect Dis 2001 Oct;33(8):1329-1335.
27. Jombo GT, Ayilara AO, Bello K, Gadzama GB, Mbaawuaga EM. Microbial isolates from surgical sites infection at a Federal Medical Centre in North Eastern Nigeria. Mary Slessor J Med 2006; 6(2):59-66.
28. Zarnayeva M, Slebor E, Pechinot A, Duez JM, Bujdakova H, Labia R, Neuwirth C. Survey of Enterobacteriaceae producing extended spectrum beta-lactamase in a Slovak hospital: dominance of SIV-2a and characterization of TEM-132. Antimicrob Agents Chemother 2005 Jul;49(7):3066-3069.
29. Baraniak A, Flett J, Sulikowska A, Hryniewiez W, Gniadkowski M. Countrywide spread of CTX M-3 extended spectrum beta-lactamase producing microorganisms of the family Enterobacteriaceae in Poland. Antimicrob Agents Chemother 2002 Jan;45(1):151-159.
30. Bonnet R, Sampalo JLM, Labia R, De Champs C, Sirot D, Chanal C, Sirot J. A novel CTX-M beta-lactamases (CTX-M-8) in cefotaxime-resistant Enterobacteriaceae isolated in Brazil. Antimicrob Agents Chemother 2000 Jul;44(7):1936-1942.
31. Cao V, Lambert T, Nhu DQ, Loan HK, Hoang NK, Ariet G, Corvalin R. Distribution of extended spectrum beta-lactamase in clinical isolates of Enterobacteriaceae in Vietnam. Antimicrob Agents Chemother 2002 Dec;46(12):3739-3743.
32. Pitout JDD, Thompson KS, Hanson ND, Ehrhardt AF, McSanders ES. Beta-lactamase responsible for resistance to expanded spectrum cephalosporins in *Klebsiella pneumoniae*, *Escherichia coli* and *Proteus mirabilis* isolates recovered in South Africa. Antimicrob Agents Chemother 1998 Jun;42(6): 1350-1354.
33. Bell JM, Turidge JD; Sentry APAC Participants. High prevalence of oxacillin-resistant *Staphylococcus aureus* isolates from hospitalized patients in Asia Pacific and South Africa: results from SENTRY surveillance programme, 1998-1999. Antimicrob Agents Chemother 2002 Mar;46(3):879-881.
34. Von Eiff C, Reinert RR, Kresken M, Bravers J, Hafner D, Peters G. Nationalwide German multicentre study on prevalence of antibiotic resistance in staphylococcal bloodstream isolates and comparative in vivo activities of quinupristin-dalfopristin. J Clin Microbiol 2000 Aug;38(8):2819-2823.
35. Nko-Nai AK, Ikem IC, Aziba A, Ajayi AA, Onipede OA. Bacteriological examination of chronic osteomyelitis cases in lIe Ife, Southwestern Nigeria. Afr J Clin Exp Microbiol 2003; 4(2):41-51.