ORIGINAL ARTICLE

A Study of Trends in Bacteremia with their Antibiotic Susceptibility in Different Age Groups from a Tertiary Care Hospital of Pune

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Abstract:

Background: Bloodstream infections are globally a leading cause of morbidity and mortality in all age groups. *Aim and Objective*: To study the bacteriological profile among different age group patients along with the antibiotic resistance pattern from blood cultures. *Material and Methods:* This study was conducted on blood culture isolates and their antibiotic resistance from 2018-2019. Identification of organism and antibiotic sensitivity test was performed using standard guidelines. *Results:* During the two year study, 12,173 blood samples were processed and 1282(10.5%) were culture positive. Of these culture positive, 56.1% were Gram-positive bacteria and 43.9% were Gram-negative isolates. *K. pneumoniae* was the common isolate from neonates and Coagulase negative *Staphylococcus* species were the commonest isolates from other age groups. Maximum sensitivity was seen to Linezolid and Vancomycin while maximum resistance to Erythromycin and Ciprofloxacin in Gram positive organisms. Enterobacteriace members except *Salmonella spp* showed maximum sensitivity to Carbapenem and Chloramphenicol and maximum resistance to Ampicillin and Cephalosporins. *Acinetobacter spp* and *K. pneumoniae* showed increased resistance to most drugs over these two years. *Conclusion:* Early identification of causative agent and antimicrobial sensitivity improves the treatment outcome. Knowing the local changing trend of organism and antibiotic sensitivity pattern helps in rationalizing the use of antibiotics.

Keywords: Bacteremia, Antibiotic Resistance Trends, Blood Culture

Introduction:

Blood by its nature is a sterile body fluid. Presence of microorganisms in the blood may be benign transient bacteremia with no or few symptoms, but it can be a threat for the body in various situations with immediate serious consequences like Disseminated Intravascular Coagulation (DIC), multiple organ failure, septic shock, and death. The mortality rate in the case of bloodstream infections (bacteremia, fungemia) ranges from 20% to 50% [1]. Common bacteria known to cause bacteremia are species of *Staphylococcus*, *Streptococcus*, *Enterococcus*, *Escherichia, Klebsiella*, *Pseudomonas, Acinetobacter,* and *Enterobacter* [2-3]. Bloodstream infections are the most important cause of morbidity and mortality throughout the world. One of the reasons for potential adverse outcomes of Bloodstream Infections (BSIs) is longer processing required in comparison to other samples in performing and receiving results of blood culture and sensitivity. Treatment given till then is empirical. There is limited data available and published from developing countries. The use of empirical drugs for treatment are usually based on international guidelines and not always as per changing antibiotic trends of local emerging organism and hospitals based surveillance studies.

A global rise in antibiotic resistance is also one of the factors which increase chances of poor therapeutic outcomes. In developing countries, the

situation of antibiotics resistance is worsened due to less availability of well-equipped microbiology laboratories and clinical microbiologists for correct interpretation. The knowledge of the epidemiology of the organism, local antibiotic resistance pattern of emerging bacteria improves the chances of selecting effective empirical therapy and better outcomes. The present study was undertaken to assess the changing trend of bacteria and their antibiotic resistance from blood cultures of patients in a teaching hospital, Pune, India.

Material and Methods:

A two years (1st Jan 2018 to 31st Dec 2019) cross-sectional study was conducted in the Department of Microbiology of Dr. D. Y Patil Medical College, Hospital and Research Centre (Dr. D. Y Patil Vidyapeeth) a tertiary care, 2000 bedded hospital.

Sample Processing:

Blood sample from suspected bacteremia patients was collected with standard aseptic precautions in Brain heart infusion broth (1:5) and sent for culture and sensitivity to the microbiology laboratory. Received samples were incubated at 37°C aerobically. Subcultures were done on blood agar and MacConkey's agar plates for up to 7 days asper standard guidelines. Phenotypic bacterial identification in positive cultures was done by conventional methods [1]. For critical patients as per clinician requisition, automated culture methods including BacT/ALERT and Vitek-2 system were used for bacterial identification and MIC of antibiotics. Antimicrobial susceptibility testing was performed on Mueller-Hinton agar except for *Streptococcus* species where the test was done on blood agar by Kirby–Bauer disc diffusion method as per the Clinical and Laboratory Standards Institute (CLSI) guidelines. Cefoxitin disc diffusion was used to identify MRSA and Methicillin-resistant Coagulase Negative *Staphylococcus* (MRCoNS) [4].

Detection of Extended-Spectrum Beta-Lactamase (ESBL), Metallo-Beta-Lactamase (MBL), AmpC and Inducible AmpC producers: Tests were performed on Mueller–Hinton agar plates. Ceftazidime resistant isolates were screened for ESBL by the double-disc approximation test using the Ceftazidime, Ceftazidime-Clavulanic and Ceftazidime-Tazobactam discs. An impression of a figure of eight was considered positive for ESBL production [5]. Isolates resistant to Imipenem were tested for MBL Production using Imipenem and Imipenem-EDTA disc, increase in Zone of inhibition in the imipenem-EDTA disc in comparison to Imipenem $\geqslant$ 7mm considered positive for MBL production [6]. Cefoxitin (30µg) resistance isolates were tested for AmpC enzyme with Cefoxitin and Cefoxitin-Cloxacillin (30/200 µg) disc. Zone of inhibition $\geqslant$ 4mm of Cefoxitin-Cloxacillin minus the Cefoxitin disc considered positive. Cefotaxime (30µg) and Cefoxitin (30µg) discs were placed 20mm apart from center to center on the plate. Blunting of a zone of inhibition of disc Cefotaxime was considered positive for producing inducible AmpC β-lactamase [7-8]. Multidrug-Resistant (MDR) isolates were defined as those showing non-susceptibility to at least one agent in three or more antimicrobial categories [9].

Results:

A total of 12,173 blood samples of patients received in the Department of Microbiology were included in the study. Of these, 1282(10.5%)were culture positive. Of these, 56.1% (719/1282) were Gram-positive bacteria and 43.9% (563/1282) were Gram-negative isolates. The year wise

distribution of organisms isolated is shown in (Tables 1, 2). Catalase positive Gram positive organisms were common isolates 676/1282 (52.7%) followed by Enterobacteriaceae family members 412/1282 (32.1%). Nonfermenters were 151/1282 (11.9%) and Catalase negative Gram

Table 1: Distribution of Gram Positive Bacterial Isolates from Blood over the Two Years

2018 Prevalent group of isolates	2018 Isolates	Number of isolates (%)	2019 Prevalent group of isolates	2019 Isolates	Number of isolates (%)
Catalase positive Gram positive organisms 382 (57.0%)	CoNS	351 (52.4%)	Catalase positive Gram positive organisms 294(48.0%)	CoNS	247 (40.4%)
	S. aureus	27 (4.02%)		*S. aureus*	42 (6.9%)
	Others	4 (0.6%)		Others	5 (0.8%)
Catalase negative Gram positive organisms 10 (1.5%)	*Enterococcus sps*	6 (0.9%)	Catalase negative Gram positive organisms 33 (5.4%)	*Enterococcus sps*	25 (4.1%)
	Streptococcus sps	4 (0.6%)		*Streptococcus sps*	8 (1.3%)
Total isolates including Gram positive and Gram negative		**670**	**Total isolates including Gram positive and Gram negative**		**612**

Table 2: Distribution of Gram Negative Bacterial Isolates from Blood over the Two Years

2018 prevalent group of isolates	2018 Isolates	Number of isolates (%)	2019 prevalent group of isolates	2019 Isolates	Number of isolates (%)
Enterobactericeae 220(32.8%)	*K. pneumoniae*	98 (14.6%)	Enterobactericeae 192(31.4%)	*K. pneumoniae*	102 (16.7%)
	Citrobacter sps	54 (8.8%)		*Citrobacter sps*	14 (2.3%)
	E. coli	31 (4.6%)			
	Salmonella sp	26 (3.9%)		*Salmonella sps.*	15 (2.5%)
	Enterobacter sps	2 (0.3%)		*Enterobacter sps*	5 (0.8%)
	Proteus sps	1 (0.1%)		*Proteus sps*	2 (0.3%)
	Serratia marsecens	4 (0.6%)			
	Others	4 (0.6%)			
Non-fermenters 58(8.7%)	*Pseudomonas aeruginosa*	29 (4.3%)	Non-fermenters 93(15.2%)	*Pseudomonas aeruginosa*	47 (7.7%)
		19 (2.8%)		*Acinetobacter sps*	43 (7.0%)
	Others	10 (1.5%)		Others	3 (0.5%)
Total isolates including Gram positive and Gram negative		**670**	**Total isolates including Gram positive and Gram negative**		**612**

positive cocci were 43/1282 (3.4%). Nonfermenters and Catalase negative Gram positive organisms showed an increasing trend over the two years.

The distributions of isolates reveal Coagulase negative *Staphylococcus* species followed by *K. pneumoniae* were the commonly isolated bacteria in the two years. The trend over the two years revealed an increase rate of CoNS, *Citrobacter spp* in 2018 and considerable increase in number of *Enterococcus spp*, *Acinetobacter spp*, and *E. coli* in 2019 (Tables 1, 2).

Table 3 shows age wise distribution of isolates. While analyzing age wise distribution, we found *K. pneumonie,* 70(36.8%) commonest isolate in neonates followed by CoNS(33.2%) and *Citrobacter spp* (10.5%). Maximum isolation of *Citrobacter spp* were seen in paediatric patients in comparison to adults. Except neonates in other age groups CoNS isolation rate was maximum followed by *K. pneumoniae.* Distribution of CoNS in various wards and ICUs shows the maximum isolation from paediatric ward and the various ICUs (Fig.1).

Table 3: Bacterial Isolates in Different Age Groups

Age → Isolates ↓	0-1 mn (n/%)	1 mn-1 yr (n/%)	1 yr-15 yrs (n/%)	15 yrs-65 yrs (n/%)	>65 yrs (n/%)
CoNS	63/33.2	61/59.2	131/48.9	289/47.8	54/46.6
S. aureus	8 /4.2	3/2.9	15/5.6	36/6	7/6
Enterococcus sps	3 /1.6	4/3.9	2/0.7	15/2.5	7/6
Streptococcus sps	1 /0.5	1/1%	3/1.1	7/1.2	-
Other Gram positive organisms	1 /0.5	1/1%	2/0.7	3/0.5	2/1.7
K. pneumoniae	70/36.8	13/12.6	31/11.6	70/11.6	16/13.8
Citrobacter species	20/10.5	3/2.9	14 /5.2	30/5	1/0.9
E. coli	8 /4.2	3/2.9	13/4.9	46/7.6	15/12.9
Salmonella sps	-	4/3.6	25/9.3	12/2	-
Enterobacter sps	-	-	2/0.7	5/0.8	-
Proteussps	1/0.5	-	-	2/0.3	-
Acinetobacter sps	3 /1.6	4/3.9	13/4.9	35/5.8	7/6
Pseudomonas aeruginosa	4 /2.1	6/5.8	17 /6.3	45/7.4	4/3.4
Other Gram negative organisms	8 /4.2	-	-	10/1.7	3/2.6
Total	190	103	268	605	116

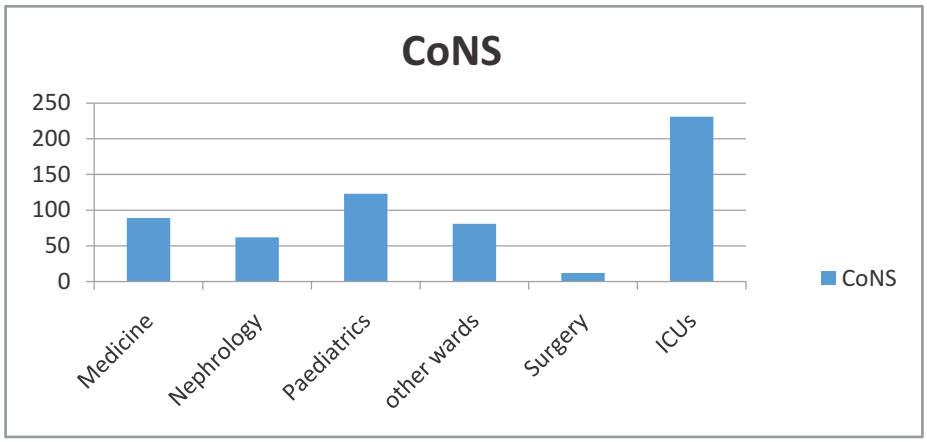

Fig. 1: Distribution of CoNS in Various Wards and ICUs

Antibiotic resistance pattern in Gram positive isolates is represented in (Table 4). Data showed Linezolid and Vancomycin had high susceptibility in all Gram positive organisms. Gentamicin was sensitive drug after Linezolid and Vancomycin in *Staphylococcus* species. Three CoNS isolates showed resistance to Linezolid and/or Vancomycin. Methicillin Resistant CoNS (MRCoNS) were seen in 52% of isolates. In CoNS after Methicillin, Erythromycin was most resistant drug followed by Ciprofloxacin, Cotrimoxazole and Clindamycin. Out of 69, *S.aureus*, 33(47.8%) were MRSA and increased number was observed in 2019 as compared to 2018. In *S. aureus* (MRSA and MSSA), Ciprofloxacin appeared to be the most resistant drug followed by Erythromycin,

Table 4: Drug Resistance Pattern of Gram Positive Organisms

Isolates → Antibiotics ↓	CoNS n=598 (%)	MRSA n=33(%)	MSSA n=36(%)	Enterococcus sps n=31(%)
E	468.6	60.6	47.2	83.9
CD	36.6	42.4	19.4	NT
CX	52.0	100	0	NT
COT	38.0	12.1	11.1	NT
GEN	23.9	9.1	2.8	64.5
CIP	40.0	90.9	61.1	74.2
LZ	0.3	0	0	9.7
VA	0.3	0	0	6.5
AMP	NT	NT	NT	38.7
P	NT	NT	NT	44.4

E-Erythromycin, CD-Clindamycin, CX-Cefoxitin, COT-Cotrimoxazole, GEN-Gentamicin, CIP-Ciprofloxacin, LZ-Linezolid, VA-Vancomycin, AMP-Ampicillin, P-Penicillin, NT-Not tested

Clindamycin, and Cotrimoxazole. *Enterococccus spp* showed maximum resistance to Erythromycin followed by Ciprofloxacin, Gentamicin, Penicillin and Ampicillin. Out of 31 strains, 2(6.5%) were Vancomycin resistant *Enterococcus* (VRE).

Table 5 shows Antibiotic resistance pattern in Enterobacteriaceae. All isolates in the table except *Salmonella spp* showed high degree of resistance to Ampicillin, Cephalosporins, Ciprofloxacin and Gentamicin. Drugs showed maximum Sensitivity to Carbapenem, Chloramphenicol, Amikacin, Piperacillin-Tazobactam and Cotrimoxazole. Drug resistance to most drugs in *K. pneumoniae* was higher in 2019 as compared to 2018. For *Salmonella spp*, Ampicillin, Cotrimoxazole, Chloramphenicol, Cefotaxime showed 100% sensitivity. In Gram negative organisms from Non-Enterobacteriaceae family, *Acinetobacter* was resistant to most drugs with maximum resistance to Ampicillin and Cephalosporins. Drug resistance to all drugs except Piperacillin-Tazobactam was higher in 2019 as compared to 2018.

Carbapenems were most sensitive drug. In *P. aeruginosa,* maximum resistance was observed to Cephalosporins and Amikacin was the most sensitive drug followed by Carbapenem, Gentamicin, Ciprofloxacin and Carbenicillin. Data revealed most drugs showed decrease resistance trend in *Pseudomonas* except Carbapenem. Although Carbapenem was the most sensitive drug in both the organisms increasing resistance trend was seen (Table 6).

Table 5: Drug Resistance Pattern of Gram Negative Organisms from Enterobacteriaceae Family

Isolates	***K. pneumoniae***		***Citrobacter sps***		***E. coli***		***Enterobacter sps***		***Salmonella sps***	
Year → Antibiotics ↓	**2018 n=98 (%)**	**2019 n=102 (%)**	**2018 n=54** (%)	**2019 n=14 (%)**	**2018 n=31 (%)**	**2019 n=54 (%)**	**2018 n=2 (%)**	**2019 n=5 (%)**	**2018 n=26 (%)**	**2019 n=15 (%)**
AMP	96.9	96.4	61.1	71.4	87.1	79.6	100	80	**0**	**0**
CIP	38.8	53.9	27.8	20	56.8	59.2	50	0	26.9	6.6
AK	21.4	30.4	27.8	7.1	12.9	14.8	100	0	NT	NT
GEN	57.1	44.1	29.6	14.3	32.3	20.4	100	0	NT	NT
COT	38.8	54.0	20.4	14.3	41.9	44.4	50	0	**0**	**0**
C	18.4	23.5	16.7	7.1	0	7.4	0	0	**0**	**0**
CX	71.4	71.6	90.7	57.1	64.5	42.6	100	100	19.2	13.3
CTX	89.8	82.4	57.4	57.1	67.7	70.4	100	60	**0**	**0**
CAZ	82.7	71.6	46.3	28.6	67.7	44.4	100	20	3.8	**0**
CTR	NT	70.2	NT	14.3	NT	64.3	NT	60	NT	0
IPM/MRP	11.2	28.4	11.1	7.1	25.8	13	50	20	NT	NT
PIT	57.5	43.1	NT	7.1	40	14.8	NT	20	NT	NT

CX- Cefoxitin, AMP- Ampicillin, CIP- Ciprofloxacin, GEN- Gentamicin, COT- Cotrimoxazole, AK-Amikacin, C-Chloramphenicol, CTX-Cefotaxime, CAZ-Ceftazidime, IPM-Imipenem, MRP-Meropenem, PIT-Piperacillin/Tazobactam, CB-Carbenicillin, NT- Not tested

Table 6: Drug Sensitivity Pattern of Gram Negative Organisms from Non-Enterobacteriaceae Family

Isolates	*Acinetobacter sps*		*Pseudomonas sps*	
Year → Antibiotics ↓	2018 n=19 (%)	2019 n=43 (%)	2018 n=29 (%)	2019 n=47(%)
AMP	89.5	81.4	NT	NT
CIP	36.8	53.5	17.2	12.8
AK	31.6	55.8	6.9	6.4
GEN	47.3	53.5	13.8	12.8
COT	42.1	67.4	NT	NT
C	52.6	60.5	NT	NT
CX	78.9	86.0	96.6	59.6
CTX	84.2	79.1	93.1	44.7
CAZ	63.2	69.8	41.4	23.4
PI	NT	NT	24.1	14.9
PIT	71.4	46.5	NT	8.5
CB	NT	NT	24.1	21.3
CTR	NT	55.6	NT	28.9

CX- Cefoxitin, AMP- Ampicillin, CIP- Ciprofloxacin, GEN- Gentamicin, COT- Cotrimoxazole, AK-Amikacin, C-Chloramphenicol, CTX-Cefotaxime, CAZ-Ceftazidime, IPM-Imipenem, MRP-Meropenem, PIT-Piperacillin/Tazobactam, CB-Carbenicillin, NT- Not tested

Table 7: ESBL, MBL and AmpC, MDR Bacterial Isolates

Bacterial isolates ↓	ESBLs	MBLs	AmpC	Inducible AmpC	MDR isolates
K. pneumoniae	86/154 (55.8%)	21/40 (52.5%)	29/143 (20.3%)	3	144/200 (72%)
E. coli	31/45 (68.9%)	8/15 (53.3%)	16/43 (37.2%)	0	57/85 (67.1%)
Citrobacter sps	16/29 (55.2%)	5/7 (71.4%)	23/57 (40.4%)	6	21/68 (30.9%)
Pseudomonas aeruginosa	12/23 (52.2%)	4/7 (57.1%)	4/28 (14.3%)	20	14/76 (18.4%)
Acinetobacter sps	17/42 (40.5%)	15/24 (62.5%)	13/52 (25%)	-	40/62 (64.5%)
Salmonella sps	1/1 (100%)	-	3/5 (60%)	-	0/41 (0%)
Enterobacter sps	1/3 (33.3%)	0/2 (0%)	4/7 (57.1%)	1	3/7 (42.9%)

Percentage distribution of ESBL,MBL, AmpC producer and MDR organisms is in Table 7. In *Salmonella spp*, one organism was Ceftazidime resistant was ESBL producer. It was observed that maximum ESBL producers were *E. coli* isolates, *Citrobacter spp* were maximum MBL producers and *Enterobacter spp* were maximum AmpC producers. *Pseudomonas aeruginosa* were maximum AmpC inducible producers. In MDR isolates *K. pneumoniae* (72%) most prevalent followed by *E.coli* (67.1%), *Acinetobacter spp* (64.5%), *Enterobacter spp* (42.9%), *Citrobacter spp* (30.9%) and *Pseudomonas aeruginosa* (18.4%).

Discussion:

In this study, the prevalence of culture positivity was 10.5% of the suspected blood culture samples received in the Department of Microbiology. In a study conducted by Banik *et al.* (2018), from the hospital of Port Blair India, culture positivity was 14.24%, while in a study of Vasudeva *et al.* (2016), Jaipur culture positivity was seen in 31.2% [10-11]. Variation in positivity depends upon several factors like host factors, the virulence of microorganisms, epidemiological variation of microorganisms, on hospital infection control practices, antibiotic stewardship programme, and index of suspicion of a clinician.

In this study, Gram-positive organisms were the most common isolates (>50%) in both years over Gram-negative isolates (>40%). Jegan *et al.* (2019), from Tamilnadu, India, also reported Gram-positive isolates as the predominant cause of infection [12]. In the present study, among Gram-positive organisms, catalase positive cocci and CoNS (46.6%) were the predominant isolates. Banik *et al.*(2018), also showed the same findings with CoNS as the second most common isolate [10]. Agarwal *et al.* (2018), from a tertiary hospital of Uttar Pradesh reported CoNS (33%) the most common isolate followed by *S. aureus* (25%) among all causative agents and Deku *et al*. (2019), conducted a study from 2009 to 2017 and they observed a changing trend of etiological agent, from 2009-2014. *S. aureus* was the leading cause of bacteremia but CoNS (50.5%) became the predominant agent from 2015-2017 followed by *S. aureus* (17.6%) and *Klebsiella spp* (10.7%) [13-14].

In the present study, maximum CoNS isolation was from the pediatric ward and various ICUs. In a study of Gill *et al.* (2016), 34.5% of CoNS isolates were from ICUs [15]. Various studies show the high isolation of CoNS in pediatric patients [16-17]. As CoNS is the commensal flora of the skin, an increase in the use of catheters, indwelling prosthetic devices, breaches in the integrity of underdeveloped epidermis of neonates may be a route of entry of organism. Earlier dismissed as a contaminant, this pathogen has now established its role in various infections as an opportunistic pathogen. Therefore these findings after surveillance have implications in infection control practices and treatment of patients.

Catalase negative Gram-positive cocci isolates identified were *Streptococcus spp* (0.9%) and *Enterococcus spp* (2.4%), in a study of Gupta *et al.,* 4.8% isolates were *Enterococcus spp* [18]. Among Gram-negative organisms in this study, Enterobacteriaceae members accounted for most cases of bacteremia with a predominance of *K. pneumoniae* (15.6%). The present study found *K. pneumonie,* 70(36.8%) commonest isolate in neonates followed by CoNS (33.2%) and

Citrobacter spp (10.5%). In a study done by Nazir (2019), study done in Srinagar, CoNS (30.27%) was the most common isolate in neonates followed by *Acinetobacter spp* (15.1%), and *Klebsiella spp* (5.4%) [19]. These types of surveillance analysis are always helpful to know a change in the trend of organisms which help to change the policies of a hospital for patient treatment. While comparing the trends of two years, it was observed among catalase positive Gram-positive organisms the number of CoNS decreased, in Enterobacteriaceae isolates except for *E.coli*, the number did not differ significantly. Among Gram-positive catalase negative and nonfermenter organisms, *Enterococcus spp*, *Acinetobacter spp* and *P. aeruginosa* showed an increase in trend over these two years. Banik *et al*. (2018), study from 2015-2017 isolated *Acinetobacter* predominant pathogen [10]. An increase in nonfermenters is a matter of concern because of their multidrug resistance.

In this study, observation of antibiotic sensitivity pattern revealed Erythromycin was the most resistant drug in CoNS and *Enterococcus spp* similarly reported by Banik *et al.* (2018), for *Enterococcus* but for CoNS, Penicillin showed maximum resistance followed by Erythromycin [10]. In the present study, 6.5% strains were VRE that varies in different studies [20-21]. In the present study for *S. aureus,* Ciprofloxacin was most resistant drug and Gentamicin found sensitive drug after the Vancomycin and linezolid in both CoNS and *S. aureus*. Banik *et al*. (2018), observed sensitivity to Ciprofloxacin 79.41%, 84.48%, 41.86%, and Gentamicin 93.10%, 97.7%, and 92.1% for CoNS, MSSA and MRSA respectively [10]. In this study, we found 47.8% of MRSA in two years with an increased percentage in 2019.Gupta and Kashyap (2016) in a study observed 26.5% of MRSA [18]. In this study, three CoNS isolate showed resistance to Linezolid andVancomycin. The emergence of these strains has been reported in different studies [22-23]. These types of surveillance are useful to know the changing trend of susceptibility patterns of organism.

Antibiotic resistance in this study for the Enterobacteriaceae family except for *Salmonella spp* showed the maximum resistance to Ampicillin followed by Cephalosporins, Gentamicin and Ciprofloxacin. Maximum Sensitivity was seen to drugs Carbapenem, Amikacin, and Piperacillin-Tazobactum, almost the same results found by Wattal *et al.* (2014) in their study [21]. In Rani *et al.* (2017), in a study both *Escherichia coli* (83.60%) and *Klebsiella* (61.53%) showed the highest activity to Amikacin, and Imipenem sensitivity was seen in 65.57% and 53.84% respectively [24]. This study also showed increased drug resistance in *K. pneumoniae* isolates over the two years to most drugs similar to Wattal *et al*. (2014).

In the present study, susceptibility pattern of *Acinetobacter* isolates showed considerably and increased resistance over the two years to all the antibiotics tested which is concordant with other studies [25-26]. Increased drug resistance for *Klebsiella* and *Acinetobacter* is a matter of concern for the treatment of such patients in future and a target to reduce the spread of such organisms for Hospital Infection Control Committee (HICC) in a hospital. The study also observed decreased drug resistance of *P. aeruginosa* to all antibiotics tested except Carbapenem. This may be related to the increased use of Imipenem. Decreased drug resistance to some drugs including Carbapenem

was also noted by some authors. [26-27].

Among β-lactamase producers, this study detected, maximum isolates of *E. coli* were ESBL producers, *Citrobacter spp* were MBL producers followed by *Acinetobacter spp* and *Salmonella spp* followed by *Enterobacter spp* were found to be maximum AmpC producers. *P. aeruginosa* were maximum AmpC inducible isolates. In Oberoi *et al*., (2013), study also *E. coli* were maximum ESBL producers, MBL producers in that study were *Klebsiella* followed by *Pseudomonas, E. coli*, *Citrobacter* and *Acinetobacter spp* in decreasing order [28]. In the study by Akinyemi *et al.* (2017), 5% isolates of *Salmonella spp* were AmpC producers [29]. In a study of Mohamudha *et al*. (2010), 42.8% of *P. aeruginosa* was inducible AmpC [30]. This percentage varied in different studies.

The present study found maximum MDR isolates were *K. pneumoniae* (72%) followed by *E. coli* (67.1%), *Acinetobacter* (64.5%), *Enterobacter spp* (42.9%), *Citrobacter spp* (30.9%) and *Pseudomonas aeruginosa* (18.4%). In Rani *et al*. (2017) study, 41.02% of *K. pneumoniae* were MDR. *Pseudomonas* and *Acinetobacter* MDR isolates were 13.60% and 18.18% respectively [24]. In a study of Beyene *et al.* (2019), 99.3% of *E. coli* were MDR, 90.3% of *K. pneumoniae* were MDR, 83.3% of *C. freundii,* and 75% of *E. cloacae.* [31]. In Gajul *et al.* study (2019), 93% of *K. pneumoniae* isolates were resistant to ampicillin and some Cephalosporins, 86% to other cephalosporin and aztreonam. Resistance to ciprofloxacin (73%) and co-trimoxazole (66%) was more among other antibiotics [32].

Conclusion:

K. pneumoniae, E. coli, Acinetobacter isolates had a high level of multi-drug resistance. A majority of *E. coli* isolates were ESBL producers. Isolation of MRSA showed an increasing trend. Therefore, the choice of empirical antibiotic treatment based on this information of local bacterial profile and antimicrobial sensitivity patterns is amikacin and ciprofloxacin with acinetobacter infections. Chloramphenicol, amikacin and imipenem with enterobacteriaceae infections and vancomycin, linezolid for Gram positive cocci infections. These types of surveillance data from various geographical locations will aid in the formulation of antibiotic policies and preventive measures. Knowledge of local organism epidemiology, commonest and emerging pathogen causing bloodstream infection helps in better clinical management, reservoir eradication for effective control of spread of multidrug-resistant bugs.

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How to cite this article:

Gupta N, Gandham N, Vyawahare C, Mirza SB, Misra RN. A Study of Trends in Bacteremia with their Antibiotic Susceptibility in Different Age Groups from a Tertiary Care Hospital of Pune. *J Krishna Inst Med Sci Univ* 2021; 10(1):52-63

Submitted: *25-Sept-2020* ***Accepted:*** *10-Dec-2020* ***Published:*** *01-Jan-2021*