Bacteriological profile and drug resistance patterns of blood culture Isolates: A five year audit from tertiary care hospital.

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ABSTRACT

Objective: To identify the bacteriological profile of bloodstream infections and their antibiotic susceptibility pattern. **Study Design:** Descriptive observational study (Retrospective study).

Place and Duration: Microbiology section, Dow University of Health Sciences from 2nd January, 2010 to 3rd January, 2015.

Methodology: Blood culture reports were screened for the presence of bacterial growth. Then Frequency of different bacterial isolates along with their antibiotic resistance pattern was noted and analyzed.

Results: During the study period, 13544 blood cultures were analyzed of which 18% were positive for growth. Among those 97% were bacterial isolates and only 2% were candida species. Among the Gram positive isolates, Coagulase negative Staphylococcus (20%) and Staphylococcus aureus (14%) were the commonest. Among the Gram-negative isolates, Salmonella species (18%) followed by Klebsiella species (15.7%) and E.coli (12.9%) and Pseudomonas species (7%). Staphylococcus aureus was found highly resistant to penicillin (95%), followed by erythromycin (68%), Co-trimoxazole (56%), Fusidic acid (54%) and Oxacillin (48%).Resistance was found to be on lower side against ciprofloxacin (38%), gentamicin (21%), chloramphenicol (13%) and Amikacin (6%).All isolates were sensitive to Linezolid. Salmonella species was resistant to ampicillin (54%) followed by Ciprofloxacin (44%), Co-trimoxazole (44%) and Chloramphenicol (44%).

Conclusion: Both Gram positive and Gram negative bacteria were responsible for blood stream infection. Piperacillin/Tazobactam, Meropenem and Amikacin were the most effective antibiotics against Gram negative bacteria while vancomycin and linezolid was most sensitive antibiotic against Gram positive bacteria.

Keywords: Bloodstream, Infections, Bacteriological profile, Gram positive bacteria, Gram negative bacteria, Antibiotic susceptibility, Drug resistance.

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INTRODUCTION

Presence of bacteria in blood is called bacteremia, and bacterial colonization is usually not a life threatening condition¹. The transient bacteremia can be due to many physiological reasons without any apparent clinical condition. But bacteremia in an individual can lead to life threatening septicemia. Globally, blood stream infections are one of important cause of increased morbidity and mortality². Usual presentation of septicemia is presence of fever, chills, malaise, tachycardia hyperventilation, toxicities, prostration and hypertension³. Major complications are development of disseminated intra vascular coagulation and acute renal failure that results in poor outcome. In patient with suspected sepsis, blood culture provides essential information related to several disease, including endocarditic, pyrexia of unknown origin and pneumonia⁴.

In the last twenty to thirty years, there have been a big revolution in the epidemiology of bloodstream infections and change in the causation. Although both Escherichia coli and Staphylococcus aureus persistently to be the most common causal agents. Also, one important finding is the emergence of coagulase negative Staphylococcus (CoNS). A Study conducted in western world showed increased number of Staphylococus epidermidis isolates from blood stream infection followed by S. aureus⁵. Moreover, microbial pathogen causing nosocomial and community acquired infection showing increasing frequency of antimicrobial resistance. This is because of the selective pressure of antimicrobial application leading to antimicrobial resistance and as a result several antimicrobial agents lose their effectiveness^{4,5}. The close observation on pathogen causing blood stream infections in hospital is vital in monitoring the range of microorganism that invades the bloodstream and the types of organisms linked with a particular clinical outcome⁶.

For that reason, it is essential from time to time to document blood culture analyses. Moreover, it assists clinicians to make the right decision on the treatment rather than waiting the blood culture results. We conducted this study with an objective to find out the bacteriological profile of bloodstream infections and their antibiotic susceptibility pattern from patients attending the Microbiology section Dow University of Health Sciences.

METHODOLOGY

This retrospective descriptive observational study was carried out in the Department of Microbiology, Dow University Research and Referral Laboratory. After approval blood culture Reports from 2nd January, 2010 to 3rd January, 2015 were obtained from laboratory data software (PASCLink). This data was then transferred to Microsoft excel and final analysis was performed to find out the isolated bacterial pathogen in blood, their frequency and antibiotic susceptibility pattern. A total number of 13544(N) blood cultures samples were included in this study. Twenty two antimicrobials were included in the study for antimicrobial susceptibility pattern. All patient blood culture samples were included. Blood culture samples from patient on antibiotic were excluded.

Data Analysis: Statistical analyses of the result were done by SPSS version 16. The results were interpreted as frequencies and percentages of isolated organism and their antibiotic susceptibility pattern.

RESULTS

During the study period, 13544(N) blood cultures were analyzed of which 2455(18%) were positive for growth. Out of which 2407 (97%) were bacterial isolates and 49(2%) were candida species. Among the Gram positive isolates, the predominant isolate was Coagulase negative Staphylococcus (n=481, 20%), Staphylococcus aureus (n=336, 14%) and Streptococci (n=103, 4.3%) and Streptococcus pneumonia (n=2, 0.1%), Enterococci (19, 0.8%). Among the Gram-negative isolates, the predominant isolates were Salmonella specie (n=432, 18%) followed by Klebsiella species (n=377, 15.7%) and E. coli (n=310, 12.9%) and Pseudomonas species (n=168, 7%) respectively as highlighted in Figure-1.

Table-I shows resistance patterns of gram positive organisms: Staphylococcus aureus was found highly resistant to penicillin (n=319,95%), followed by erythromycin (n=228,68%), cotrimoxazole (n=188,56%), Fusidic acid (n=181,54%) and Oxacillin (n=161,48%). Resistance was found to be on lower side against ciprofloxacin (n=127,38%), gentamicin (n=70,21%), chloramphenicol (n=43,13%) and Amikacin (n=20,6%).

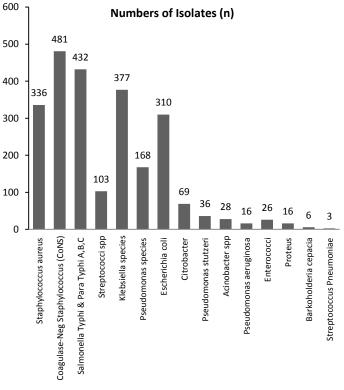


Figure-1: Frequency of different bacterial isolates from blood culture samples (N= 2407)

Table-I:	Antibiotic	Resistance	pattern	of	Gram	Positive
Organism	n isolated fr	om blood sa	mples (N:	=949))	

Antibiotics tested	S. aureus	Staphylococcus	Enterococci n=19(%)	
Antibiotics tested	n=336 (%)	spp. n=481(%)		
Pencillin	319(95%)	428(89%)	11(62%)	
Ampicillin	NT	NT	6(31%)	
Oxacillin	161(48%)	173(36%)	NT	
Amikacin	20(6%)	24(5%)	NT	
Gentamycin	70(21%)	101(21%)	NT	
Tetracyclin	137(41%)	245(51%)	NT	
Erythromycin	228(68%)	351(73%)	13(69%)	
Clindamycin	70(21%)	101(21%)	NT	
Ciprofloxacin	127(38%)	202(42%)	10(54%)	
Chloramphenicol	43(13%)	62(13%)	2(15%)	
Co-Trimoxazole	188(56%)	278(58%)	NT	
Fusidic Acid	181(54%)	NT	NT	
Vancomycin	0	0	1(5%)	
Linezolid	0	0	0	

NT – not tested

All isolates were sensitive to Linezolid. Staphylococcus species exhibit high resistance to penicillin (n=428, 89%), Erythromycin (n=351, 73%), and Co-trimoxazole (n=278, 58%) and least

resistant to Amikacin (n=24,5%), all isolates were sensitive to vancomycin and Linezolid. Enterococcus was found highly resistant to Erythromycin (n=13,69%), followed by penicillin (n=11,62%), and ciprofloxacin (n=10,54%) ampicillin (n=6,31%).Penicillin and Erythromycin were found to be the highly resistant antibiotics among gram positive organisms.

Table-II shows resistant pattern of gram negative organism. Among the gram negative bacteria isolated, E. coli was highly resistant to ampicillin (n=288,93%), followed by Cefixime (n=182, 59%), ceftriaxone (n=182,59%) and ciprofloxacin (n=176,57%). Resistance was found to be on lower side against piperacillin + tazobactam (n=49,16%), Meropenem (n=37,7%). Klebsiella species was highly resistant to Ampicillin (n=377,100%) followed by cefuroxime (n=211,56%), cefixime (n=203,54%) and ceftriaxone (n=203,54%). The resistance pattern of Pseudomonas aeruginosa was Aztreonam (n=15,43%) followed by Ceftazidime, (n=13,38%), Ciprofloxacin (n=12,35%) Amikacin (n=7, 20%) and Piperacillin-Tazobactam (n=5,13%).Salmonella species was resistant to ampicillin (n=233,54%) followed by Ciprofloxacin (n=207,48%), Cotrimoxazole (n=207,48%) and Chloramphenicol (n=207,48%). Resistance was found to be on lower side against cefixime (n=26; 6%).Acinetobacter spp was highly resistant to ceftazidime (n₌15, 52%) followed by Meropenem (n=12,43%).Many of the gram negative organisms were resistant to ampicillin and cephalosporin as shown in Table-II.

DISCUSSION

The current study was conducted to determine the pattern and frequency of blood stream infection causing bacteria and their antibiotic sensitivity pattern. Susceptibility to antimicrobials and the bacteriological profile is constantly evolving. This plays a vital role in the effective management of bloodstream infections. All over the globe, several studies have been conducted to find out the frequency of blood stream infections and their antimicrobial susceptibility pattern. The results differ among different countries as well as in different setups .In our setup, the rate of positive blood culture was found to be 18%. This finding is comparable to studies conducted by Qureshi et al¹ and Mamta et al⁷ respectively. However, slight higher rate 27.9% was reported by Latif et al⁸. Such differences in prevalence of blood stream infections could be due to difference in blood culture system, geographical location, and difference in infection control policies.

In the present analysis gram negative bacteria account for 60.5% while 39.4% isolates were gram positive bacteria. It is in accordance with the study conducted by Qureshi et al in which isolation rate of gram negative were higher (60%) as compared to gram positive (40%)¹. In contrast, study conducted by Abdullah et al find the predominance of gram positive bacteria⁹. Another study from Iran documented increased number of Gram Positive Isolates with the predominance of CoNs (65%) followed by Gram negative Escheria coli(42%) as most common pathogen¹⁰. The reason for differences in the pattern of bacterial isolates is because of variation in the geographical location, study plan, disparity of the etiological agents ,seasonal variations and different in blood culture setup.

Coagulase negative staphylococcus aureus (CoNS) followed by S. aureus was found to be the most common etiological agent amongst the gram positive bacteria. Other surveillance studies also had similar findings related to CoNS^{11,12} Over the past two decades, CoNS, the usual skin commensals are increasingly being considered bloodstream pathogens in select settings. Improper methods of blood collection and the presence of long-standing intravascular catheters are recognized as possible modes of spread of BSI by CoNS. In fact, two studies reported CoNS as the most common isolate causing BSIs in ICU patients^{13,14}.

Antibiotics	E.coli	Klebsiella Species	Citrobacter	Acinetobacter spp	Salmonella Typhi &Para A,B &C	Pseudomonas species
tested	n= 310 (%)	n=377 (%)	n= 69 (%)	n= 28 (%)	n= 432 (%)	n=36 (%)
AMP	288(93%)	377(100%)	47(69%)	NT	233(54%)	NT
AMC	158(51%)	241(64%)	37(54%)	NT	NT	NT
TZP	49(16%)	105(28%)	18(27%)	7(28%)	NT	5(13%)
CXM	186(60%)	211(56%)	37(55%)	NT	NT	NT
CFM	182(59%)	203(54%)	37(54%)	NT	26(6%)	NT
CAZ	NT	NT	NT	15(52%)	NT	13(38%)
CRO	182(59%)	203(54%)	37(54%)	NT	NT	NT
ATM	167(54%)	196(52%)	30(44%)	NT	NT	15(43%)
MEM	37(7%)	75(20%)	9(13%)	12(43%)	NT	8(22%)
AK	37(12%)	90(24%)	16(24%)	10(37%)	NT	7(20%)
CIP	176(57%)	282(75%)	16(23%)	NT	207(48%)	12(35%)
SXT	183(59%)	218(58%)	23(34%)	13(48%)	207(48%)	NT
С	NT	NT	NT	NT	207(48%)	NT

NT: not tested AMP-Ampicillin, AMC-Amoxil/Calvulanicacid, TZP-Piperacillin-Tazobactam, CXM-Cefuroxime, CFM-Cefixime, CAZ-Ceftazidime, CRO-Cefiaxone, ATM-Aztreonam, MEM-Meropenem, AK-Amikacin, CIPCiprofolxacin, SXT-Co-trimoxazole, C-Chroramphenicol.

The most common Gram negative organism isolated in the present study was Salmonella species especially in children (18%). Similar finding was observed by others, Abdullah et al in Karachi 2008 and Kaur A and Sigh V et al in 2014^{9,15.} The higher rate of infection by Salmonella spp might have occurred due to unhygienic practices, unavailability of safe drinking water, and consumption of contaminated food particles. In adults most common bacteria found was Klebsiella species (15.7%).Which also been reported in the study conducted Tarig et al⁶. In contrast, E.coli followed by Klebsiella spp was found to be most common among gram negative bacteria by Fayyaz et al and Nvasdeva et al^{16,17}. According to the results of antibiotic sensitivity testing E.coli and Klebsiella species showed moderate to high level of resistance against Ampicillin, amoxicillin-calvulanic acid, cefuroxime, cefixime, ceftrizone and ciprofloxacin. The most sensitive antibiotics was found to be Meropenem, Amikacin and piperacillin -Tazobactam. Theses finding are consistant with the study conducted by Tariq et al in 2014⁶. Similarly, Higher resistant against cephalosporins was documented by Naveeed et al in 201818. The increased in antimicrobial resistance may have resulted from the frequent use of these specific groups of antibiotics in our hospital over the years leading towards increased resistance.

Resistance of Acinetobacter species to Carbepenem was found to be high in the current study. Similarly, higher Carbepenem resistance in Acinetobacter from different hospitals of Pakistan was reported^{19,20}. The emerging pattern of resistance against Carbepenem suggesting the cautious use of antibiotic should be promoted as resistance to this may evoke a great challenge for physician as the treatment options for resistant strains are limited.

In this study, Staphylococcus aureus showed high resistance to ampicillin which corresponds with other studies⁶. Penicillin resistant S. aureus are usually treated with cloxacillin or nafcillin, but the upsetting reality is the emergence of MRSA. In this study, the rate of MRSA strains was 48%. The occurrence of MRSA is more common because of indiscriminate use of superior antibiotics as an emergency empirical therapy. However, it remained highly sensitive to vancomycin and linezolid as reported by other authors^{16,17}. This suggests that guideline should be made for the wise use of these antibiotics, in an attempt to prevent the spread of resistant strains. Among the gram positive bacteria vancomycin and linezolid were the most sensitive antibiotic .The results were consistent with the studies done by Fayyaz et al in 2013, Vasudeva et al in 2014^{16,17}.

Early commencement of appropriate antimicrobial treatment plays a vital role in reducing morbidity and mortality in blood stream infections. This early empirical treatment is based on the information about the likely pathogen and its antibiotic resistance pattern. Present study provided much needed information on the prevalence of bacterial pathogens in blood stream infections and their antibiotic sensitivity patterns. The analysis of drug resistance will help in formulating antibiotic policy and to decide the vacation period for any antibiotic in particular if required. The data will also help in limiting the indiscriminate use of antibiotics.

CONCLUSION

The present study display that both gram positive and gram negative bacteria were responsible for blood stream infection.Piperacillin/Tazobactam, Meropenem and Amikacin were the most effective antibiotics against Gram negative bacteria while vancomycin and linezolid were most sensitive antibiotic against Gram positive bacteria.

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AUTHOR'S CONTRIBUTION

Fasih F: Manuscript writing, Data analysis and, Literature review

Baig S: Data compilation, Data analysis, Data interpretation

Zameer S: Data collection and compilation, Manuscript drafting

Naseem S: Conception and design of study, Final critical review of manuscript.

Sharafat S: Conceived idea, Designed research methodology, Manuscript final reading and approval

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REFERENCES

- 1. Qureshi M, Aziz F. Prevalence of microbial isolates in blood cultures and their antimicrobial susceptibility profiles. Biomedica. 2011;27(6):136-139.
- 2. Reinhart K, Bauer M, Riedemann NC, Hartog CS. New approaches to sepsis: molecular diagnostics and biomarkers. Clin Microbiol Rev. 2012;25(4):609-634.
- 3. Smart OC. Septicaemic Patients in Uyo, Nigeria. J Res Med Sci. 2013;7(2):35-39.
- Khan HA, Baig FK, Mehboob R. Nosocomial infections: Epidemiology, prevention, control and surveillance. Asian Pac F Trop Biomed. 2017;7(5):478-482.
- 5. Becker K, Heilmann C, Peters G. Coagulase-negative staphylococci. Clin Microbiol Rev. 2014;27(4):870-926.
- Tariq TM. Bacteriologic profile and antibiogram of blood culture isolates from a children's hospital in Kabul. J Coll Phys Surg Pak. 2014;24(6):396-399.
- Sarwariya M, Sadawarte K, Rukadikar AR, Prabhu T. Aerobic bacterial profile of blood stream infections and its antimicrobial sensitivity pattern in tertiary care hospital. Indian J Microbiol Res 2017;4(4):363-366.
- Latif S, Anwar MS, Ahmad I. Bacterial pathogens responsible for blood stream infection (BSI) and pattern of drug resistance in a tertiary care hospital of Lahore. Biomedica. 2009;25(2):101-5.
- 9. Abdullah F, Yasmeen T, Shaheen S. Current pattern of bloodstream infections in a tertiary care hospital of

Karachi and clinical significance of positive blood cultures. J Dow Uni Health Sci 2010;4(1):25-30.

- Kalantar E, Motlagh M, Lordnejad H, Beiranvand S. The prevalence of bacteria isolated from blood cultures of iranian children and study of their antimicrobial susceptibilities. Jundishapur J Nat Pharm Prod. 2008;3(1):1-7.
- 11. Jain A, Agarwal J, Bansal S. Prevalence of methicillinresistant, coagulase-negative staphylococci in neonatal intensive care units: findings from a tertiary care hospital in India.J Med Microbiol. 2004;53(9):941-944.
- 12. Hebeisen UP, Atkinson A, Marschall J, Buetti N. Catheterrelated bloodstream infections with coagulase-negative staphylococci: are antibiotics necessary if the catheter is removed? Antimicrob Resist Infect Control 2019;8(1):21-28.
- Valencia-Rey P, Weinberg J, Miller NS, Barlam TF. Coagulase-negative staphylococcal bloodstream infections: Does vancomycin remain appropriate empiric therapy? J Infect. 2015;71(1):53-60.
- 14. Wattal C, Raveendran R, Goel N, Oberoi JK, Rao BK. Ecology of blood stream infection and antibiotic resistance in intensive care unit at a tertiary care hospital in North India. Braz J Infect Dis. 2014;18(3):245-251.

- 15. Kaur A, Singh VA. Bacterial isolates and their antibiotic sensitivity pattern in clinically suspected cases of fever of unknown origin. JK Science. 2014;16(3):105-109.
- Fayyaz M, Mirza IA, Ikram A, Hussain A, Ghafoor T, Shujat U. Pathogens causing blood stream infections and their drug susceptibility profile in immunocompromised patients. J Coll Phys Surg Pak. 2013;23(12):848-851.
- 17. Vasudeva N, Nirwan PS, Shrivastava P. Bloodstream infections and antimicrobial sensitivity patterns in a tertiary care hospital of India. Ther Adv Infect Dis. 2016;3(5):119-127.
- Naveed S, Zafar A, Javed H, Atif M, Abosalif KO, Ejaz H. Bacterial Spectrum and Antimicrobial Susceptibility Pattern in Septic Paediatric Patients. Pak J Med Health Sci. 2018 1;12(2):845-848.
- 19. Shamim S, Abbas M, Qazi MH. Prevalence of Multidrug Resistant Acinetobacter baumannii in Hospitalized Patients in Lahore, Pakistan. Pakistan J Mol Med. 2015;2(1):23-28.
- 20. Hasan B, Perveen K, Olsen B, Zahra R. Emergence of carbapenem-resistant Acinetobacter baumannii in hospitals in Pakistan. J Med Microbiol. 2014; 63(1):50-55.