Original Research

Microbiological Profile and Antimicrobial Resistant Pattern among Isolates from Bloodstream Infection in a Tertiary Care Hospital

Sonali Waske, Pratibha Singh, Soumendra Mathy, Yogyata Maroyhi*

Background- Blood stream infection is a very important cause of morbidity and mortality worldwide, especially in resource limited countries. It ranges from transient bacteremia to life-threatening septic shock. Blood culture is a gold standard method of diagnosis of infectious agents present in the blood.

Method- This study was conducted From August 2021 to October 2021 at Ruxmaniben Deepchand Gardi medical and Ujjain Charitable trust Hospital, Ujjain (M.P.). All received blood samples were processed, isolates were identified, and antibiotic susceptibility testing was performed using the Vitek 2 Compact (Biomerieux) system in the Microbiology laboratory.

Results- A total of 74(17%) pathogens were isolated from 432 blood samples. Gram-positive bacteria 47(64%) were predominant organisms obtained, followed by gram-negative bacteria 25(34%) and non-albicans candida species 2(2.7%). The predominant pathogens were Staphylococcus aureus 40(54%), Klebsiella pneumoniae and Pseudomonas aeruginosa 6(24%) each. Among Staphylococcus aureus isolates 36 (90%) were methicillin-resistant Staphylococcus aureus (MRSA). And among gram-negative bacteria, all isolates of K. pneumoniae were extensively drug-resistant. Majority of drug-resistant organisms were isolated from neonatal intensive care unit (%).

Conclusion- Successful treatment of bloodstream infection depends on early diagnosis and appropriate use of antimicrobial agents.

Access this article online

Website:
www.cijmr.com

Keywords:
Blood stream infection, *Staphylococcus aureus Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *non-albicans candida*, Multidrug-resistant, Extensive drug-resistant

10.58999/cijmr.2022.132

Introduction

Bloodstream infection is one of the major causes of morbidity and mortality worldwide despite the availability of broad-spectrum and highly potent antimicrobial agents and major advances in diagnostic and treatment facilities. The condition can be life-threatening for the critically ill with prior antimicrobial exposure or with comorbidities.[1,2,3] Emergence of multi-drug resistant (MDR), extensive drug-resistant (XDR) and pandrug resistant (PDR) organisms are also fanning the flame in poor and developing countries. MDR was defined as acquired non-susceptibility to at least one agent in three or more antimicrobial categories. XDR was defined as non-susceptibility to at least one agent in all but two or fewer antimicrobial categories (i.e., bacterial isolates remain susceptible to only one or two antimicrobial categories). PDR was defined as non-susceptibility to all agents in all antimicrobial categories.[4] Rising rates of antimicrobial resistance (ABR) in India are a significant concern because of the high burden of bacterial diseases and the poor health system infrastructure, which relies on antibiotics and other public health measures.[5]

Blood stream infections (BSI) include infective endocarditis, central venous catheter-associated bloodstream infection, primary and secondary bacteremia due to focus of infection elsewhere in the body (abscesses, osteomyelitis, urinary tract infection, pneumonia etc.)

Department of Microbiology, Ruxmaniben Deepchand Gardi Medical College, Ujjain, Madhya Pradesh, India

Correspondence to: Sonali Waske, Department of Microbiology, Ruxmaniben Deepchand Gardi Medical College, Ujjain, Madhya Pradesh, India. E-mail: drsonalip@gmail.com

Submitted: 10/11/2022 Revision: 22/11/2022
Accepted: 03/12/2022 Published: 27/12/2022

How to cite this article: Waske S, Singh P, Mathy S, Maroyhi Y. Microbiological Profile and Antimicrobial Resistant Pattern among Isolates from Bloodstream Infection in a Tertiary Care Hospital. Central India Journal of Medical Research. 2022;1(3):7-10.

Infectious pathogens enter the bloodstream by direct invasion, via lymphatic invasion or through vascular devices such as intra vascular devices.

We conducted this study to evaluate the microbial flora from blood culture and study their AMR pattern contributing to better management to these patients

Material and Method

Present study was a hospital based study conducted in the Microbiology Department of Tertiary care centre. All admitted patients suspected of bloodstream infection from C R Gardi, Ujjain Charitable Trust and Avanti hospital unit of R.D.Gardi Medical College from August 2021 to October 2021 were included in this study. The blood samples of these patients were collected, taking all aseptic precautions and sent to the Microbiology laboratory. Approximately 5 mL of blood from adult and 0.5 to 4.5 mL from pediatric patients was collected in the automated blood culture bottles and incubated in the BacT/Alert (biomerieux) blood culture system. On positive signal, it was sub cultured on blood agar and macConkeys agar and incubated for 24 hours aerobically. Blood culture bottles that showed no signs of bacterial growth were reported negative after 5 days of incubation. Isolates were identified by Vitek 2 Compact (Biomerieux) using gram-negative, gram-positive and yeast identification and AST cards for sensitivity. Antibiotic sensitivity results were interpreted as per CLSI guidelines.[6] In our study MDR, XDR, and PDR strains were detected as per criteria described by European Centre for Disease Prevention and Control (ECDC) and Centers for Disease Control and Prevention (CDC).[4]

Ethical approval: The study was conducted after getting ethical approval from the ethical committee of the institution.

Results

Among 432 blood culture samples processed, 74(17%) were culture positive. Maximum 47(64%) were gram-positive bacteria followed by 25(34%) gram-negative bacteria and 2(2.7%) were non-albicans Candida species. Among these, 51(69%) isolates belonged to male and 23(31%) female patients. The age distribution showed that, 61(82.4%) were from pediatric patients, out of them 36(49%) were neonates and 25(71.4%) were males. Among gram-positive bacteria, *Staphylococcus aureus* 40(54%), Coagulase-negative *Staphylococcus* (CONS) 5(11%) and *Enterococcus species* 2(4.3%) were isolated. CONS isolated were, *S. epidermidis* 3(60%), *S. hominis* 1(20%) *and S. hemolyticus* 1(20%). Their repeat isolation from blood culture confirmed the pathogenic role of CONS and candida species. Among gram-negative bacteria, *K. pneumoniae* and *P. aeruginosa* 6(24%) each, *E. coli, E. aerogens, Serratia marcescens, Acinetobacter baumanii complex* 2 (3%) each and 3 *Burkholderia cepacia complexes* (4%) were isolated. Among fungi, non-albicans Candida species 2(3%) were isolated (Table 1).

Table 1: The causative agents of bloodstream infection (n=74)

Name of Organisms	*No. 74 (%)*
MRSA	36 (49)
MSSA	4 (5.4)
CONS	5 (6.8)
Enterococcus species	2 (3)
Klebsiella pneumonia	6 (8.1)
Escherichia coli	2 (3)
Enterobacter aerogens	2 (3)
Serratia marcescens	2 (3)
Acinetobacter baumanii complex	2 (3)
Burkholderia cepacia complex	3 (4)
Pseudomonas aeruginosa	6 (8.1)
Candida species	2 (3)

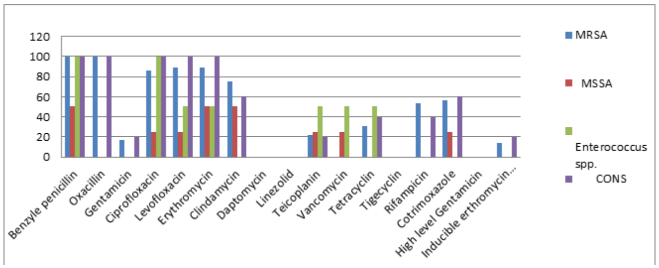

Figure 1: Antimicrobial resistance pattern among gram-positive Bacteria (n=47)

The resistance trend in gram-positive bacteria (n = 47) is shown in Figure 1. Among *S. aureus*, 36(90%) were methicillin-resistant (MRSA). Sensitivity to linezolid, daptomycin and tigecycline of all isolated gram-positive bacteria was 100%. Among MRSA, 95% MRSA were recovered from the neonatal intensive care unit (NICU). Among *S. aureus*, 18(45%) were positive for hetero Vancomycin Intermediate *S. aureus* (HVISA) and 6(15%) were positive for VISA screening test by Vitek-2. Among CONS, 4(80%) were methicillin-resistant and 100% resistant to ciprofloxacin, levofloxacin and erythromycin and all isolates were positive for modification of PBP mec A gene screening test. Both isolates of *Enterococcus species* (4.3%) were resistant to penicillin, ciprofloxacin and MDR.

Among gram-negative bacteria, all *K. pneumoniae* isolates from neonates were resistant to third-

Table 2: Antimicrobial resistance pattern among gram-negative bacteria (n=25)

Antimicrobial agents	*K. pneumoniae No. (%)*	*P. aeruginosa No. (%)*	*E. coli No. (%)*	*E. aerogens No. (%)*	*S. marcescens No. (%)*	*baumanii complex No. (%)*	*B. cepacia complex No. (%)*
Amoxicillin-clavulanic acid	6 (100)	-	2 (100)	2 (100)	-	-	-
Piperacillin-Tazobactam	6 (100)	1 (17)	00 (0)	2 (100)	-	1 (50)	3 (100)
Ceftazidime	-	00 (0)	00 (0)	-	-	2 (100)	00 (0)
Cefuroxime	6 (100)	-	00 (0)	2 (100)	-	-	-
Cefuroxime- axetil	6(100)	-	00 (0)	2 (100)	-	-	-
Ceftriaxone	6 (100)	-	00 (0)	2 (100)	-	-	-
Cefoperazone-sulbactam	6 (100)	00 (0)	00 (0)	2 (100)	00 (0)	00 (0)	2 (67)
Cefepime	6 (100)	00 (0)	00 (0)	2 (100)	00 (0)	50	3 (100)
Imipenem	6 (100)	1 (17)	00 (0)	2 (100)	00 (0)	00 (0)	3 (100)
Meropenem	6 (100)	1 (17)	00 (0)	2 (100)	00 (0)	00 (0)	1 (33.3)
Ertapenem	6 (100)	-	00 (0)	1 (50)	00 (0)	-	-
Doripenem	-	1 (17)	00 (0)	-	00 (0)	1(50)	-
Ciprofloxacin	6 (100)	00 (0)	00 (0)	2 (100)	00 (0)	1(50)	3 (100)
Levofloxacin	-	00 (0)	00 (0)	2 (100)	00 (0)	00 (0)	00 (0)
Amikacin	5 (83.3)	00 (0)	00 (0)	2 (100)	00 (0)	-	3(100)
Gentamicin	5 (83.3)	00 (0)	00 (0)	2 (100)	00 (0)	00 (0)	3(100)
Tigecycline	00 (0)	6 (100)	00 (0)	00 (0)	00 (0)	00 (0)	00 (0)
Colistin	00(0)	3 (50)	00 (0)	00 (0)	2 (100)	1 (50)	2 (67)
Aztreonam	-	-	00 (0)	-	00 (0)	100	2 (67)
Minocycline	-	-	00 (0)	-	00 (0)	00 (0)	00 (0)
Ticarcillin-clavulanate	-	1 (17)	-	-	00 (0)	1 (50)	00 (0)
Cotrimoxazole	4 (67)	-	00 (0) 0	2 (100)	00 (0)	00 (0)	00 (0)
ESBL	3 (50)	-	1	0	0	-	1
Total	6 (8.1%)	6 (8.1%)	2 (3%)	2 (3%)	2 (3%)	2 (3%)	3 (4%)

generation cephalosporin (cefotaxime, ceftriaxone etc), aminoglycosides (amikacin and gentamicin) and carbapenem group (imipenem, meropenem) and all sensitive to colistin and tigecycline. All isolates were XDR and half were positive for ESBL screening test based on Vitek-2 reports. Four isolates of *P. aeruginosa* were recovered from pediatric patients. Out of it, 50% were resistant to colistin, while resistance to imipenem, meropenem and doripenem was 17% each and all strains were MDR. Good susceptibility pattern was seen in *E.coli*, all strains were sensitive to all antimicrobial groups except amoxicillin-clavulanic acid (Table 2). All isolates of non-albicans Candida species were sensitive for voriconazole and fluconazole.

Discussion

As per WHO, antibiotic resistance is rising dangerously in all parts of the world.[7] Antibiotic resistance leads to a financial burden to the patients, prolonged hospital stays, and increased mortality. The emergence and spread of resistance is made worse by using antimicrobials without prescription, without standard guidelines and non following of antibiotic policies. This study analyzed the various pathogenic organisms and their antimicrobial resistance pattern among bloodstream infection cases. The etiological agents of bloodstream infection were changing over the last few years. In the present study, maximum isolates 64% were gram-positive bacteria and 34% were gram-negative bacteria, which was comparable to other studies from India and abroad.[8,9] Another study by Ezaz *et al.* reported similar isolation rate.[10] *S. aureus* is the commonest pathogen isolated, as approximately 20% of the human population are long term carrier and can cause infections in hospitals and communities, thus become the leading pathogen in hospitals worldwide.[11] On contrast, many other parts of India reported GNB as the commonest pathogen.[12] Wattal *et al.* also reported gram-negative organisms as major causative agents of BSI among pediatric patients.[13]

Among GNBs, the commonest pathogens were *K. pneumoniae* and *P. aeruginosa* 24% each. This study was concordance with study from North India.[13] In neonatal sepsis cases *K. pneumoniae* was the commonest isolate, that is similar with many studies from India and abroad**.**[14,15] Maximum drug resistance was seen among isolates recovered from NICU. All *K. pneumoniae* isolates were XDR, only sensitive to colistin and tigecycline. In this study, all isolates of *P. aeruginosa, Enterobacter aerogens, Burkholderia cepacia complex* and *A. baumanii complex* were MDR. This is matching with result reported by Laxmi *et al*. and Sophae' *et al*. in their studies.[14,15]

The Indian scenario of BSI is very complicated. Etiology ranges from gram positive, gram negative spectrum of bacteria to candida species and shows varying drug resistance patterns that need intense study and research. This might be responsible for higher rate of mortality in ICUs. Advanced diagnostic modalities are required to detect and prevent transmission of MDR organisms by religiously following infection control practices, antimicrobial surveillance, and stewardship. The combined efforts of infection control practitioners, microbiologists, and public health professionals are needed to limit the spread of drug resistance organisms.

Conclusion

Being a tertiary care reference centre highly drug-resistant both gram-positive and gram-negative organisms, including MDR pathogens were isolated from bloodstream infections in the present study. MDR was observed among gram-positive isolates from NICU. The development of effective antimicrobial resistance surveillance and reporting should be prioritized to sustain empirical antimicrobial recommendations in our setup.

References

1. Chan MC, Chiu SK, Hsueh PR, Wang NC, Wang CC, Fang CT. Risk factors for healthcare-associated extensively drug-resistant Acinetobacter baumannii infections: a case-control study. PLOS One 2014; 9:e85973.
2. Ben-David D, Kordevani R, Keller N, *et al.* Outcome of carbapenem resistant Klebsiella pneumoniae bloodstream infections. Clin Microbiol Infect 2012; 18:54–60.
3. Sunenshine RH, Wright MO, Maragakis LL, *et al.* Multidrug-resistant Acinetobacter infection mortality rate and length of hospitalization. Emerg Infect Dis 2007; 13:97–103.
4. A.-P. Magiorakos, A. Srinivasan, R. B. Carey *et al*., "Multidrugresistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance," Clinical Microbiology and Infection, vol. 18, no. 3, pp. 268–281, 2012
5. Sumanth Gandra a , Nestor Mojica a , Eili Y. Klein b,c , Ashvin Ashok b , Vidya Nerurkar d , Mamta Kumari d , Uma Ramesh d , Sunanda Dey d , Viral Vadwai d , Bibhu R. Das d , Ramanan Laxminarayan a,Trends in antibiotic resistance among major bacterial pathogens isolated from blood cultures tested at a large private laboratory network in India, 2008–2014International Journal of Infectious Diseases 50 (2016) 75–82.
6. CLSI. Performance Standards for Antimicrobial Susceptibility Testing; 32nd ed. CLSI supplement M100. Clinical and Laboratory Standards Institute; 2022.
7. World Health Organization. Antibiotic Resistance [Internet]. Geneva (CH). 2020 Jul 31. [cited 2020 Dec 16].
8. Manmeet Kaur Gill,*, Sarabjeet Sharma Bacteriological profile and antibiotic resistance pattern in blood stream infection in critical care units of a tertiary care hospital in North India. Indian J Microbiol Res 2016;3(3):270-274
9. Wasihun, A.G., Wlekidan, L.N., Gebremariam, S.A., *et al.* (2015) Bacteriological Profile and Antimicrobial Susceptibility Patterns of Blood Culture Isolates among Febrile Patients in Mekelle Hospital, Northern Ethiopia. Springer Plus,4,314.
10. Ejaz A, Khawaja A, Arshad F, Tauseef A, Ullah R, Ahmad I. Etiological Profile and Antimicrobial Patterns in Blood Culture Specimens in a Tertiary Care Setting. Cureus. 2020 Oct 17;12(10):e11000. doi: 10.7759/cureus.11000. PMID: 33209556; PMCID: PMC7669249.
11. Edwards, A. M., and Massey, R. C. (2011). How does Staphylococcus aureus escape the bloodstream? Trends Microbiol. 19, 184–190 doi: 10.1016/j.tim.2010.12.005
12. Singh AK, Venkatesh V, Singh RP, Singh M, Bacterial and antimicrobial resistance profile of bloodstream infections: A hospital based study. CHRISMED Journal of Health and Research 2014;1(3);140-144.
13. Wattal C, Goel N. Pediatric Blood Cultures and Antibiotic Resistance: An Overview. Indian J Pediatr. 2020 Feb;87(2):125-131. doi: 10.1007/s12098-019-03123-y. Epub 2019 Dec 21. Erratum in: Indian J Pediatr. 2020 Jun;87(6):486. PMID: 31863394; PMCID: PMC6974494.
14. Lakshmi KS, Jayashree M, Singhi S, Ray P. Study of nosocomial primary bloodstream infections in a pediatric intensive care unit. J Trop Pediatr. 2007 Apr;53(2):87-92. doi: 10.1093/tropej/fml073. Epub 2006 Dec 6. PMID: 17151083.
15. Wen SCH, Ezure Y, Rolley L, Spurling G, Lau CL, Riaz S, Paterson DL, Irwin AD. Gram-negative neonatal sepsis in low- and lower-middle-income countries and WHO empirical antibiotic recommendations: A systematic review and meta-analysis. PLoS Med. 2021 Sep 28;18(9):e1003787. doi: 10.1371/journal.pmed.1003787. PMID: 34582466; PMCID: PMC8478175.