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Assessment of Bacterial Profile and Antimicrobial Resistance Pattern of Bacterial Isolates from Blood Culture at Rims, Ranchi, Jharkhand

Manoj Kumar[1], Vidushi Topno[2*], Ashok Kumar Sharma [3], Amber Prasad [4], Kumari Seema[5]

[1]Professor and Head of Department, [2]Post Graduate, [3] Associate Professor, [4] Assistant Professor, [5]Assistant Professor
Department of Microbiology, RIMS, Ranchi, India

*Corresponding Author

Abstract: ***Blood stream infection is one of the most noxious complications that can be prevented in critical care units. Its consequences are prolonged period of hospital stay which is expensive for the individual and most of the times, there is loss of life. Main device for assessment of blood stream infection in clinically suspected bacteraemia or septicaemia is blood culture which gives guidance for proper antimicrobial management. Aim: To determine various organisms causing blood stream infection along with their antibiotic resistance pattern at Rajendra Institute of Medical sciences, Ranchi, Jharkhand. Material and methods: The study was conducted in Department of Microbiology, RIMS, Ranchi. The duration of study was of one year from June 2018 to May 2019 during which total of 248 blood samples were received. Identification of isolates was done by standard biochemical tests and antimicrobial resistance pattern by following CLSI guidelines 2018. Result: Out of 248 blood samples, 162 blood samples were positive (65.3%). Among gram positive organism Staphylococcus aureus was 32.7% followed by Coagulase Negative Staphylococcus Aureus 11.1% and Enterococcus 1.8%. Klebsiella spp. was found to be 11.7% which was highest among gram negative organisms followed by E.coli (4.3%) and Acinetobacter spp. 3.7% and candida isolated in 4.9% cases.***

Keywords: Blood Stream Infection, Antibiotic resistant

1. Introduction

Blood stream infection is defined as presence of viable bacteria or fungal pathogen in blood stream, giving inflammatory response with change in clinical laboratory and haemodynamic parameters.[1] The range of microorganisms causing blood stream infection differ with various geographical areas.[2] Cases like infective endocarditis, central venous catheter associated bloodstream infections, primary and secondary bacteremia are included in blood stream infections.[3] Important tool for clinically suspected bacteraemia and septicaemia is blood culture. Blood culture detects infections that are spreading through the blood stream. It is observed that resistance in blood stream pathogen is increasing.[4-6] Hence right choice of empric therapy is very important because blood stream infection is associated with high mortality and morbidity.[7]

The study was done to assess spectrum of organisms causing septicaemia and their antibiotic resistance pattern. This information will be useful in conducting empric antimicrobial therapy.

2. Material and Methods

In this study, a total of 248 blood samples were included which were clinically suspected as a case of bacteraemia. The study was done from month of June 2018 to May 2019. All samples were collected from indoor patients admitted at RIIMS, Ranchi. Processing of sample was done in Department of Microbiology at RIMS, Ranchi.

Blood was collected by strict aseptic precautions and inoculated immediately into BD BACTECTM plus Aerobic/F culture vials for adults and BD BACTECTM Peds PlusTM/F Culture Vials for paediatric patients. After blood collection in bottles they were immediately incubated in Automated Blood Culture System in BD BACTECTM FX. This is an automated blood culture system for detection of bacterial growth in blood culture. When positive growth occurred, automatically it gave an alert. In case of negative growth, results were followed upto 5 days and final report was given. Positive blood culture were subcultured in Blood agar and MacConkey agar and put for overnight incubation and bacterial identification was done by biochemical test.

After growth the colonies from Blood agar and MacConkey agar were used to make smear for gram staining. For further identification of species standard biochemical test were done. 0.5 McFarland suspension was prepared for Antibiotic susceptibility of bacterial isolate done by Kirby Bauer method as per the CLSI guidelines 2018.

3. Results and Discussion

Total 248 blood cultures were cultured over one year duration, 162(65.3%) blood cultures were positive. Among them 162 blood samples were positive and 86 cases were negative. All blood stream infection was due to single organism. Gram positive organisms were found more often than gram negative organisms. The common Gram positive organisms were Staphylococcus aureus 32.7% followed by CONS 11.1% and Enterococcus 1.8%. Klebsiella spp. was found to be 11.7% which was highest among gram negative organisms followed by E.coli (4.3%) and Acienetobacter spp. 3.7%.

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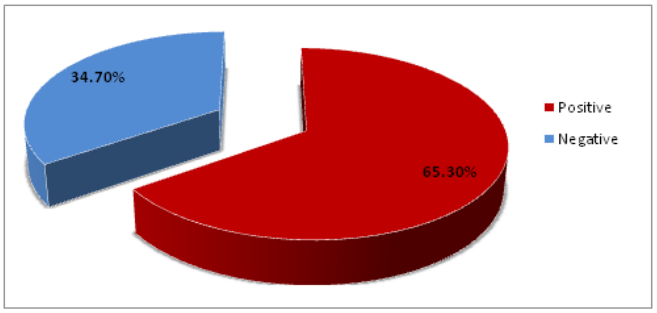
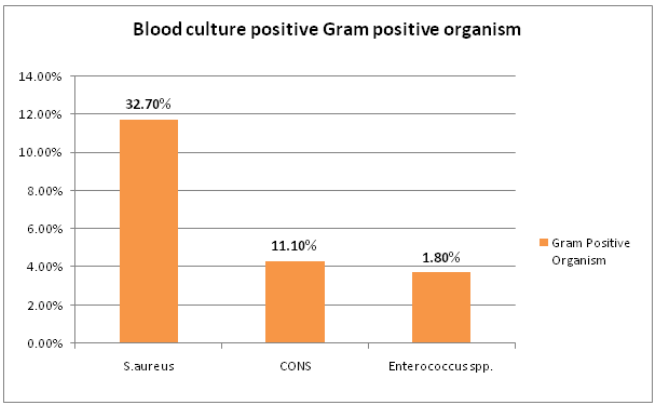
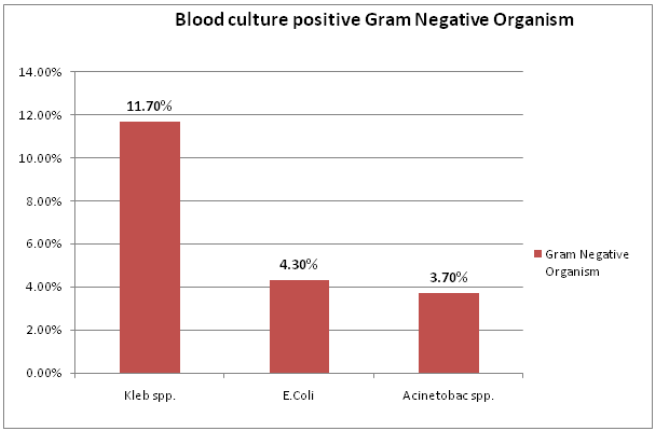
S.aureus strain showed resistance to Ampicillin followed by ciprofloxacin and gentamycin, 43.9%, 26.4%, and 22.6% respectively. 100% sensitivity was seen in Vancomycin and Linezolid for all isolates. Among Gram negative organisms Amikacin was noted as highest resistant drug i.e. 68.4% followed by Amoxicillin (47.4%). In current study fungal infection caused by Candida infection was 4.9%.

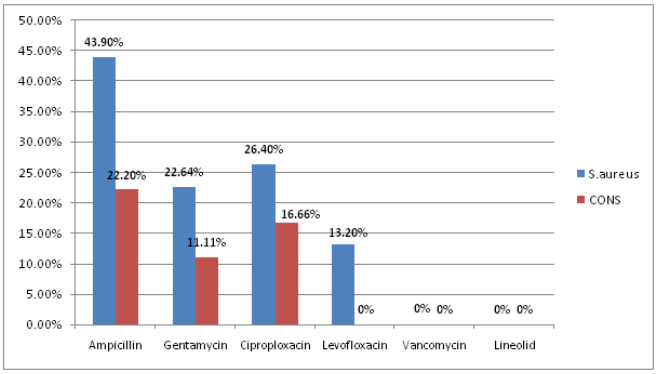
Overall Positivity of Blood Culture Organisms



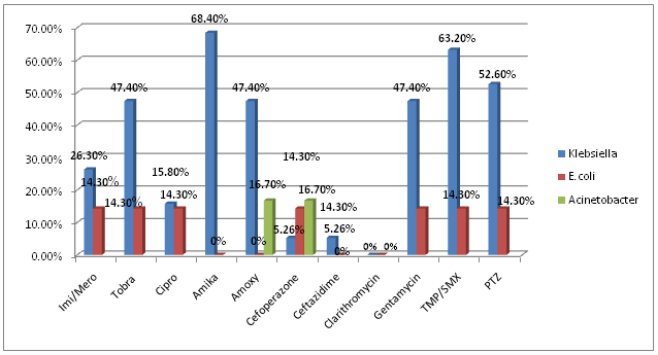




Showing Antibiotic Resistant Pattern of S.aureus, CONS and Enterococci



Showing Antibiotic Resistant Pattern of Klebsiella, E.coli, Acinetobacter



This study provided us important information on the prevalence of antimicrobial resistance among pathogens causing blood stream infection. Our result seems to be helpful in providing useful guidelines for choosing an effective antibiotic against blood stream infection and also a useful guide for clinicians initiating an empiric anti – microbial therapy.

In our paper overall incidences of Gram-positive organisms were 72/162 (45.7%) and gram negative organisms were 33/162 (20.4%). It was similar with the studies of Kamga et al.[8], Karlowsky et al. [9], China and Gupta [10], and Anbumani et al.[11] who reported similar incidences in accordance with the present study. But in most of the studies Gram negative organisms were predominant over Gram-positive organisms as in Barati et al. [12], Ayobola et al. [13], Mehta et al. [14], Mehdinejad et al. [15].

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