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Ecology of blood stream infection and antibiotic resistance in intensive care unit at a tertiary care hospital in North India

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ABSTRACT

Objective: To analyse the prevalent microorganisms and their antimicrobial resistance among intensive care unit patients in a tertiary care centre in New Delhi.

Methods: A retrospective study of all consecutive blood cultures from various intensive care unit patients in the hospital during four years (January 2008 to December 2011). Antibiotic consumption data in the intensive care units were also analysed during the same period.

Results: Out of the total 22,491 blood cultures processed, 2846 samples were positive and 3771 microorganisms were isolated. The blood culture positivity was estimated as 12.7% of which 67.5% were monomicrobial and 32.5% polymicrobial infections. Gram negative bacilli, Gram positive cocci, and fungi were isolated in 49%, 33%, and 18% cases, respectively. Coagulase negative staphylococcus was the commonest single isolate followed by *Candida* spp. A drastic shift in the distribution of *Candida* spp. towards nonalbicans along with high resistance to azole group of antifungals suggest echinocandins for the empiric therapy of candidemia. High penicillin resistance in Gram positive isolates suggest vancomycin, linezolid and tigecycline as the options for empiric therapy, whereas tigecycline and colistin are the only options remaining for highly resistant Gram negative isolates. Aminoglycosides were observed to have better sensitivity and reduced usage when compared with cephalosporins and β -lactam + β -lactam inhibitor combinations.

Conclusions: High frequencies of multidrug resistant organisms were observed in intensive care units which is a warning as to use the only few effective antimicrobials wisely to reduce selective pressure on sensitive strains.

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Introduction

Infections caused by multidrug resistant bacteria constitute a serious problem for intensive care patients throughout

the world. Prevalent pathogens and their antimicrobial resistance pattern may vary in different intensive care units (ICUs) depending upon the antibiotic pressure in that health care facility. This information could be beneficial in choosing the

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appropriate antimicrobials, which in turn can reduce the length of stay as well as the morbidity and mortality in ICU patients.¹

The paradox remains where the antibiotics are needed the most (ICU), there the highest resistance, is observed due to multiple reasons. Random use of high-end antimicrobials has the risk of eventually selecting out mutants that are multidrug resistant. Every hospital must recognize the epidemiology of its microorganisms to recommend initial appropriate presumptive antimicrobial therapy. The application of hospital-wide antibiograms to guide clinicians in the initial choice of antimicrobials is the usual approach adopted. If more resistant organisms are isolated from ICU patients, this important information would be masked by the use of hospital-wide antibiogram.

Here we have made an attempt to analyse the prevalent microorganisms causing blood stream infection (BSI) and their antimicrobial resistance as seen among the ICU patients in a tertiary care centre in New Delhi.

Materials and methods

Patients

This retrospective study was conducted for a period of four years (January 2008 to December 2011) in a 650-bed tertiary care centre in New Delhi. A total of 22,491 blood samples were analysed from the patients admitted in various ICUs in the hospital, which include general adult ICU, coronary care unit (CCU), surgical ICU, and the liver, kidney and bone marrow transplant ICUs.

Sample collection and processing

Five to 10 mL of blood sample was collected and were inoculated immediately into BacT/ALERT culture bottles (bioMerieux, Durham, North Carolina, USA) under complete aseptic conditions and were processed as per the manufacturer's specifications.

Identification and susceptibility testing of isolates

Positive blood culture isolates were identified using VITEK 2 automated system (bioMerieux, Durham, North Carolina). MIC was confirmed using E-test (bioMerieux, France) in case of VRE. In case of any discrepancy E-test result was taken as final. Susceptibility testing was performed by Kirby Bauer method for tigecycline (15 µg, Oxoid Ltd., Basingstoke, Hampshire, England), and colistin (10 µg, HiMedia Laboratories, Mumbai) and results interpreted as per Clinical Laboratory Standards Institute (CLSI) guidelines² and British society for Antimicrobial Chemotherapy (BSAC) guidelines where ever CLSI guidelines were not available.³ Daptomycin MIC was determined for *Staphylococcus aureus* and *Enterococcus* spp. using E-test during the period of 2010 and 2011. Antibiotic resistance data were extracted from the hospital information system (Intersystems, Cambridge, MA, USA) using a software Speedminer (Petaling Jaya, Malaysia) and analysed using a customized software, Wattal-Protech, Delhi, India.

Screening for carbapenem resistance

Because of the observation of high carbapenem resistance among Enterobacteriaceae at our facility, we tried to assess the magnitude of different mechanisms of carbapenem resistance. All consecutive isolates of Enterobacteriaceae were screened for carbapenem resistance by modified Hodge test (MHT) during the period of December 2010 to April 2011. All MHT positive isolates were further tested for metallo-β-lactamase (MBL) by MBL E-test strips (bioMerieux, France). Further confirmation of all MBL positive isolates for New Delhi Metallo-beta-lactamases (NDM-1) was done using a real time polymerase chain reaction (PCR) assay for the detection of the bla_{NDM-1} using Taq Man probes.⁴

Antifungal susceptibility testing

Antifungal susceptibility testing was performed against amphotericin B, 5-flucytosine, fluconazole, itraconazole, and voriconazole by broth microdilution using API system (ATB FUNGUS 3, bioMerieux, France), during 2008. For isolates wherein API system was not recommended by the manufacturer, sensitivity was done using E-test for amphotericin B, fluconazole, and voriconazole. During 2009–2011, antifungal susceptibility testing was done using VITEK 2 automated system except for caspofungin, which was done using E-test. Results were interpreted as per the CLSI guidelines.⁵

Antimicrobial consumption data

Four years antimicrobial consumption data were evaluated from the antibiotic dispensing data from the hospital information system. Customized software Speedminer was used to extract the data from the hospital information system. The amount of antimicrobial drug in grams was converted into the number of defined daily doses (DDDs)/100 bed-days using ABC calc.⁶

Ethical considerations

The study was approved by the hospital ethics committee (reference number EC/09/12/414 and approval letter dated 31/01/2013). Consent was waived since this was an anonymised study with retrospective evaluation.

Results

A total of 2846 samples were positive from 22,491 blood cultures received from the study group. The blood culture positivity rate in our ICUs was estimated to be 12.7%. A total of 3771 microorganisms were isolated from 2846 episodes of BSIs. 67.5% (1921/2846) of infections were monomicrobial, while 32.5% (925/2846) were polymicrobial (Fig. 1).

Analysis of these isolates showed that the commonest single isolate among our ICU patients was coagulase negative staphylococcus (CoNS) (20.3%) followed by *Candida* spp. (17.5%). Gram negative bacilli (GNB), Gram positive cocci (GPC), and fungi were isolated in 49%, 33%, and 18% cases, respectively. Among GNB, *Klebsiella* spp. was the commonest

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