

Original Research Article

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Bacteriological Profile of the Organisms Causing Septicaemia and their Antibiotic Resistance Patterns

V. Deepali and R. Shyamala*

Department of Microbiology, MRMCW, Hyderabad, India

*Corresponding author

ABSTRACT

Blood stream infections are mainly caused by multi drug resistant organisms which more likely prolong the hospital stay and leads to increased health care costs. Hence, early diagnosis and treatment with appropriate antibiotics is the only way to treat bacteraemia. To study the bacteriological profile of the organisms causing septicaemia and their antibiotic resistance patterns to guide the clinicians to initiate the empirical therapy. Blood samples were collected aseptically from patients before taking any antibiotics. Samples were inoculated into Brain heart infusion broth and incubated at 37 degree for 24 hours. Blind subculture was done on to fresh 5% sheep blood agar and MacConkey agar. A negative result was followed up by examining the broth daily and doing a final subculture at the end of 7th day organisms identified by colony morphology and standard biochemical tests. A total of 273 blood samples were analysed, out of which 50 yielded growths (18.3%). Among this, 49 (98%) yielded bacterial isolates and 1 (2%) was *Candida* species. Out of 49 bacterial isolates, 28 (56%) were Gram positive organisms and 21 (42%) were Gram negative organisms. Among Gram positive isolates Coagulase negative *Staphylococci* (36%) were the predominant isolates. Among the Gram negative organisms, *Escherichia coli* (22%) were the predominant isolate. The incidence of blood stream infection was 18.3%. Majority were bacterial isolates. Gram positive were more than gram negative. Among Gram positive isolates. Coagulase negative *Staphylococci* (36%) were the predominant isolates. Among the Gram negative organisms, *Escherichia coli* (22%) was the predominant isolate

Keywords

Bacteriological profile, Organisms, septicaemia, Antibiotic resistance patterns, Therapy

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Introduction

In the hospital patients, deaths and morbidities are most commonly caused by septicemias. There are many diseases that are associated with the infections of the origin of the health care. But among them all, septicemias are the most common infections. These infections can be sometimes mild and they are self-limiting. But sometimes they are life threatening and require immediate attention and appropriate treatment. The treatment must be rapid. Septicemia can be caused by a variety of

microorganisms. The causative organisms depend upon the area to area. The case fatality rate can reach up to 100% if the patient is not treated properly (Atul et al., 2007). Broadly organisms causing health care associated septicemias can be classified as gram positive and gram negative. Death rate of infections caused by gram negative organisms is more compared to death rate of infections caused by gram positive organisms. Septicemia problem is compounded by increasing resistance to antibiotics commonly used in the hospital practice. It leads to increased morbidity and

mortality and patient needs to stay for prolonged periods of time in the hospital. This leads to increased costs of the health care (Gangoue *et al.*, 2006).

In some cases, it becomes very difficult to achieve the cure rates due to infection caused by resistance of the causative organisms added with colonization. The therapeutic options are reduced in such cases. This leads to difficulty in treatment of the cases (Collignon, 2002).

A variety of reasons are listed for the above mentioned problems. The most common reason is the increasing use of the antibiotics followed by improper use not only in human beings but also in animals and other places. Improper control of the infection, overcrowding etc can also be treated as the reasons for this. In patients with septicemia, as there are increased chances of the deaths and diseases, it is a common strategy that the patient is treated as per the clinical decision with antibiotics i.e. empirical treatment. The blood is sent for culture and sensitivity. Once the results come, the patient is treated as per it (Kholly *et al.*, 2009).

The empirical treatment is based on the certain factors like pattern of the resistance to the antibiotics locally based on previous experiences of the local area. This has to be done before the availability of the reports which becomes available after the culture and sensitivity. Septicemia is caused by a variety of the microorganisms and their sensitivity pattern also varies. But the diagnosis must be very prompt and aggressive treatment has to be given to save the life of the patient (Adejuyigbe *et al.*, 2001).

In most cases of suspected septicemia antimicrobial therapy is always initiated empirically because bacteriological culture results take about a week to be available (Adejuyigbe *et al.*, 2001).

The present study was undertaken to study the bacteriological profile of the organisms causing septicaemia and their antibiotic resistance patterns to guide the clinicians to initiate the empirical therapy.

Materials and Methods

Study design

Hospital based retrospective study

Place of the study

Present study was carried out in the department of Microbiology, Malla Reddy Medical College for Women, Hyderabad

Study period

Present study was carried out from November 2018 to April 2019.

Sample size

A total of 273 blood samples from clinically suspected cases of bacteraemia were studied.

A total of 273 blood samples from clinically suspected cases of bacteraemia were studied.

This study is a retrospective observational study conducted in the department of microbiology laboratory for a period of 6 months from November 2018 to April 2019.

Blood samples were collected aseptically from patients before taking any antibiotics. Samples were inoculated into Brain heart infusion broth and incubated at 37 degree for 24 hours. Blind subculture was done on to fresh 5% sheep blood agar and MacConkey agar. A negative result was followed up by examining the broth daily and doing a final subculture at the end of 7th day organisms identified by colony morphology and standard biochemical tests.

Antibiotic susceptibility testing was performed by Kirby Bauer’s disc diffusion method according to CLSI guidelines.

Statistical analysis

The data was entered in the Microsoft Excel worksheet and was analyzed using proportions.

Results and Discussion

A total of 273 blood samples were analysed, out of which 50 yielded growths (Table 1).

Among 50 positive blood culture samples, 49(98%) yielded bacterial isolates and 1(2%) was *Candida* species. Out of 49 bacterial isolates, 28 (56%) were Gram positive organisms and 21(42%) were Gram negative organisms. Among Gram positive isolates Coagulase negative staphylococci (36%) were the predominant isolates followed by *Staphylococcus aureus* (14%) and *Enterococcus* species (4%) (Figure 1).

Among the total *S. aureus* isolates MRSA was found to be in 14.3% whereas MRCONS was found in 21.4% of total CONS isolates.

Among the Gram negative organisms, *Escherichia coli* (22%) was the predominant isolate followed by *Klebsiella* sp (14%) (Figure 2).

During the study period we did not observe any Polymicrobial growth.

The present study shows the sensitivity pattern of Gram positive isolates towards various antibiotics. Among the Gram positive isolates, most of the isolates showed resistance to penicillin, erythromycin, and clindamycin, azithromycin followed by cotrimoxazole, doxycycline and ciprofloxacin. None of the isolates exhibited resistance to Vancomycin, Teicoplanin and linezolid. Among the Gram negative isolates, majority of the isolates were resistant to Beta lactam antibiotics, followed by Amoxyclav, cotrimoxazole, fluoroquinolones and amino glycosides. Majority of the isolates showed least resistance to Carbapenems and Tigecycline. Enterobacteriaceae showed high sensitivity to cefoperazone/sulbactam combination (90.4%). None of the isolates showed resistance to colistin and polymyxin (Table 2).

In the present study, a total of 273 blood samples were analysed, out of which 50 yielded growths (18.3%). Among this, 49 (98%) yielded bacterial isolates and 1 (2%) was *Candida* species. Out of 49 bacterial isolates, 28 (56%) were Gram positive organisms and 21 (42%) were Gram negative organisms. Among Gram positive isolates Coagulase negative staphylococci (36%) were the predominant isolates. Among the Gram negative organisms, *Escherichia Coli* (22%) were the predominant isolate.

Table.1 Overall adult and paediatrics blood culture results

| Result | Adults (%) | Paediatrics (%) | Total (%) |
|-----------|------------|-----------------|-----------|
| Growth | 42 | 8 | 50 |
| No growth | 190 | 33 | 223 |
| Total | 232 | 41 | 273 |

Table.2 Antibiotic sensitivity patterns of Gram negative bacilli

| Antibiotics | E. Coli and <i>Klebsiella</i> | Other GNB |
|---------------------------|-------------------------------|-----------|
| Ampicillin | 2(18.2) | 2(66.6%) |
| Amoxyclav | 0 | 0 |
| Cefepime | 10(55.5%) | 3(100%) |
| Ceftazidime | 7(39%) | 3(100%) |
| Cefuroxime | 7(39%) | 2(66.6%) |
| Piperacillin - tazobactam | 16(82%) | 3(100%) |
| Cefoperazone-sulbactam | 18(100) | 3(100%) |
| Gentamicin | 10(55.5%) | 2(66.6%) |
| Amikacin | 10(55.5%) | 2(66.6%) |
| Imipenem | 10(94.4%) | 3(100%) |
| Meropenem | 17(94.4%) | 3(100%) |
| Ciprofloxacin | 15(83.3%) | 2((66.7) |
| Polymyxin | 18(100) | 3(100%) |
| Colistin | 18(100) | 3(100%) |
| Tigecycline | 18(100) | 3(100%) |

Fig.1 Distribution of Gram positive cocci

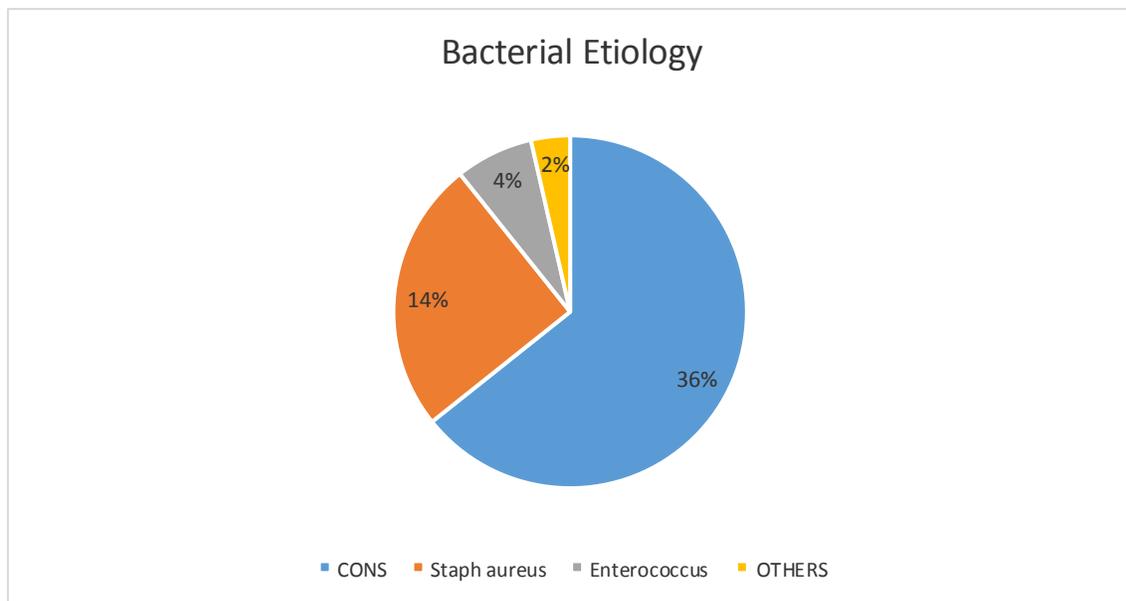
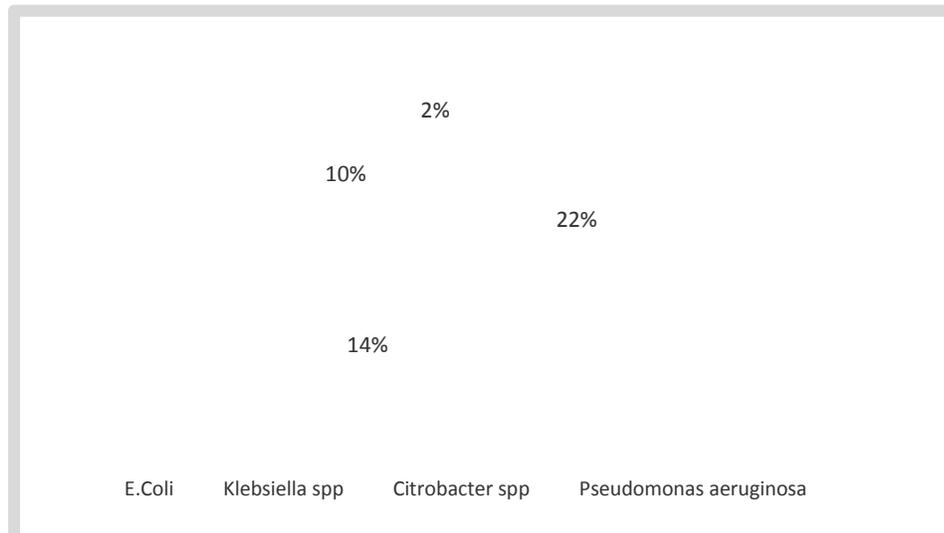


Fig.2 Distribution of Gram negative bacilli



Sravan Reddy *et al.*, (2018) found that the incidence of blood stream infection was seen in 22 out of 75 patients studied (Sravan Reddy *et al.*, 2018). Most commonly affected age group was 31-45 years. Gram positive isolates were more than gram negative isolates and this finding was similar to the finding of the present study. Among the gram-positive bacteria, majority isolated were *S. epidermidis*; followed by *S. aureus*, but we found that Among Gram positive isolates Coagulase negative staphylococci (36%) were the predominant isolates.

Anjum *et al.*, (2019) noted that the incidence of the blood stream infection was 36.6% which was double than that observed in the present study (Anjum *et al.*, 2019). Gram positive isolates were more than gram negative isolates and this finding was similar to the finding of the present study. Among gram-positive bacteria, predominant isolates were Coagulase Negative *Staphylococcus* (41%) and this finding was similar to the finding of the present study. Among gram-negative isolates, 14% were *Pseudomonas sp.* but we found that Among the Gram

negative organisms, *Escherichia coli* (22%) were the predominant isolate.

Garg *et al.*, (2007) observed that the incidence of the blood stream infection was 20.5% and this finding was similar to the finding of the present study (Garg *et al.*, 2007). They found that gram negative bacteria incidence was more than that of the gram positive bacteria but we found that Gram positive isolates were more than gram negative isolates. *Pseudomonas spp.* (16%) was common in the gram negative but we found that Among the Gram negative organisms, *Escherichia coli* (22%) were the predominant isolate. *Staphylococcus aureus* (8.3%) was the predominant isolate in gram positive cases, and this finding was similar to the finding of the present study.

Pandey *et al.*, (2017) found that the incidence of blood stream infection was 30.6% which was almost double than that observed in the present study (Pandey *et al.*, 2017). They found that gram negative bacteria incidence was more than that of the gram positive bacteria but we found that Gram positive

isolates were more than gram negative isolates. *Klebsiella* sp (23%) was common in gram negative cases but we found that Among the Gram negative organisms, *Escherichia coli* (22%) were the predominant isolate. *Enterococci* (20%) were the predominant isolate in gram positive cases but we found that Among Gram positive isolates Coagulase negative *Staphylococci* (36%) were the predominant isolates.

Kamga *et al.*, (2011) found that the incidence of blood stream infection was 28.3% which was more than that observed in the present study (Kamga *et al.*, 2011). They observed that the children were the most commonly affected but we found that age group of 31-40 years was the most commonly affected in the present study. Gram positive isolates were more than gram negative isolates and this finding was similar to the finding of the present study. Among the gram-positive bacteria, 52 (82.5%) were *Staphylococci* and this finding was similar to the finding of the present study.

The incidence of blood stream infection was 18.3%. Majority were bacterial isolates. Gram positive were more than gram negative. Among Gram positive isolates. Coagulase negative *staphylococci* (36%) were the predominant isolates. Among the Gram negative organisms, *Escherichia coli* (22%) was the predominant isolate

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