Prevalence, Profile and Antibiotic Susceptibility Pattern of Bacterial Isolates from Blood


In the present study, attempt was made to isolate bacterial pathogens in blood and determination of their antibiogram. A total of 448 blood samples were analyzed. Out of which 405 (92%) samples of aerobic blood culture and 43 (8%) samples of anaerobic blood culture. From aerobic culture 111 (27%) pathogens and from anaerobic culture 6 (13%) pathogens were identified. In aerobic culture Staphylococcus aureus 71 (64.54%) was the most common cause of bacteraemia followed by Listeria monocytogenes 17 (15.45%), Diplococcus sp. 7 (6.36%), Salmonella typhi 6 (5.45%), Streptococci sp. 4 (3.63%), Klebsiella pneumoniae 3 (2.72%) and Campylobacter sp., E. coli and Haemophilus influenzae (single isolates of each, respectively). From anaerobic culture Clostridium perfringens 6 (13%) were identified. The antibiotic sensitivity test was done by disc diffusion method. The antibiogram of these pathogens showed resistance to cefotaxime, cefadroxil, cefaclor, cefuroxime, ceftazidime, ceftriazone and sensitivity to meropenem, linezolid and amikacin. Thus study indicated that the bacterial blood pathogens are becoming resistant to commonly used antibiotics, which may be due to indiscriminate use of these antibiotics. So it is very much important to have culture and sensitivity test of concern pathogens.

Key words: Blood culture, pathogens, drug resistance, antibiotic susceptibility

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INTRODUCTION

Bacteraemia is an important and frequent condition with increasing mortality (Madsen et al., 1999). *Staphylococcus* is one of the most common bacterial isolates causing bacteraemia in hospital patients infections, which permits the organism to gain access to tissue with diverse clinical diseases and the other two pathogens being *E. coli* and *Streptococcus pneumoniae* (Phorde, 1970; Hryniewicz et al., 1993). The blood culture is fundamental investigation in infection. Illness is associated with bacteraemia ranges from self-limiting infection to life threatening sepsis that requires rapid and aggressive antimicrobial treatment, which is complicated by increasing worldwide antibiotic resistance (Reacher et al., 2000). The emergence of antimicrobial resistance globally has not been uniform for all agents and pathogens, or along the same lines. Even today's environment, there are disproportionate rates of resistance between countries, within countries and even within different geographical regions of the same countries, province or city (Blondeau and Vaughan, 2000). Antibiotic resistance pattern may vary locally and regionally, patterns can change rapidly and they need to be monitored closely because of their implications for public health and as an indicator of appropriate or inappropriate antibiotic usage by physicians in that area (Lalitha et al., 1997). Therefore, knowledge of the current drug resistance pattern of the common, local blood pathogenic bacteria in particular region is useful in clinical practice. Therefore, attempt was made to isolate and identify the common bacteria from blood culture and their antibiotic resistance pattern.

MATERIALS AND METHODS

A total of 448 blood samples from patients (270 male, 153 female and 25 children) were collected from hospitals. Out of these blood samples, 405 (92%) were aerobically and 43 (8%) anaerobic cultured. In aerobic culture, for adult 10 mL and for children 2-5 mL of blood were inoculated in 50 mL of Brain Heart Infusion broth. The bottles were vented by inserting a sterile cotton-wool plugged needle. For anaerobic blood culture, Hartley's Digest broth were used. These bottles were incubated at 37°C for 24 h. The inoculated broth medium (from day 2) was then sub-cultured every day on blood agar and MacConkey's agar subsequently for 3 days and incubated for another 24 h.

Identification of organism was based on gram reactions, morphology and biochemical characteristics (Forbes et al., 1988). Isolates were tested for antimicrobial susceptibility by Bauer et al. (1966) disc diffusion technique on Muller Hinton agar using the readymade antibiotics discs (Table 1).

### Table 1: Antibiotics disc use in study

<table>
<thead>
<tr>
<th>Antibiotics</th>
<th>Concentration (µm)</th>
<th>Antibiotics</th>
<th>Concentration (µm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cefazolin</td>
<td>5</td>
<td>Cefotaxime</td>
<td>5</td>
</tr>
<tr>
<td>Cefoxitin</td>
<td>10</td>
<td>Ceftriaxone</td>
<td>30</td>
</tr>
<tr>
<td>Meropenem</td>
<td>10</td>
<td>Cefazidime</td>
<td>30</td>
</tr>
<tr>
<td>Amikacin</td>
<td>30</td>
<td>Cefadroxil</td>
<td>30</td>
</tr>
<tr>
<td>Norfloxacil</td>
<td>10</td>
<td>Cefaclor</td>
<td>30</td>
</tr>
<tr>
<td>Ofloxacin</td>
<td>5</td>
<td>Linezolid</td>
<td>30</td>
</tr>
</tbody>
</table>

RESULTS AND DISCUSSION

A total of 448 blood samples (405 aerobically and 43 aerobically) were cultured, out of them, 111 (27%) pathogens from aerobic and 6 (5%) pathogens from anaerobic culture were isolated and identified. In aerobic culture, *Staphylococcus aureus* 71 (64.54%) was the most prominent pathogen followed by *Listeria monocytogenes* 17 (15.45%), *Diplococcus sp.* 7 (6.36%), *Salmonella typhi* 6 (5.45%), *Streptococci sp.* 4 (3.63%), *Klebsiella pneumoniae* 3 (2.72%) and one each strain of *Campylobacter sp.*, *E. coli* and *Haemophilus influenzae* were isolated. In anaerobic culture 6 samples were positive for *Clostridium perfringens* (Fig. 1). The frequency of bacteraemia was 53% in male, 35% in female and 12% in children.

The antibiogram pattern of *S. aureus* showed high resistance to cefotaxime (90%), cefadroxil (93%), cefaclor (95%) and cefazidime (93.10%) and high sensitivity to meropenem (70%), linezolid (74.8%) while *Diplococci sp.* showed high resistance to cefuroxime (91.42%) and cefazidime (91.50%) and sensitivity to amikacin (100%), linzolid (70%) and meropenem (71.43%). The *Listeria monocytogenes* showed high resistance against cefuroxime (95%) and cefazidime (93.63%) and high sensitivity to meropenem (100%), linezolid (85.72%) and amikacin (87.5%).

The blood isolate, *Salmonella typhi* was highly resistant to cefotaxime (91.10%) and cefazidime (97.5%) and sensitive to meropenem (83.34%), linezolid (74.9%) and amikacin (77.15%), while *Streptococci sp.* was resistant to cefotaxime, cefuroxime, ciprofloxacin and pefloxacin (100% each) and sensitive to amikacin, meropenem and linezolid (100% each). The *Klebsiella pneumoniae* showing highest (100%) resistance to cefaclor, cefuroxime, cefazidime and ceftriazone.

In present study, the single isolate *Campylobacter* showed 100% resistance to cefotaxime, cefadroxil, cefaclor, cefuroxime, cefazidime, ceftriazone, norfloxacain, ofloxacin, pefloxacin, cefazolin and 100% sensitivity to
meropenem, amikacin, linzolid and ciprofloxacin, while the single isolate *Escherichia coli* showed resistance to cefotaxime, cefadroxil, meropenem, cefaclor, cefuroxime, ceftazidime, amikacin, ciprofloxacin, ceftiraxone, norfloxacin, cefazolin and sensitive to linzolid, ofloxacin and pefloxacin. *Haemophilus influenzae* showed high resistance to cefotaxime, cefadroxil, cefaclor, cefuroxime, ceftazidime, norfloxacin, ofloxacin, pefloxacin, ceftazidime and sensitivity to meropenem, linzolid, amikacin, ciprofloxacin and ceftiraxone. In anaerobically isolated *Clostridium perfringens* was highly resistant to ceftaxime and sensitivity to norfloxacin (Table 2).

All the pathogens isolated from blood showed high resistance to cefuroxime (96%) and ceftazidime (95%), cefotaxime (91%) and highly sensitivity to meropenem (74%), linezolid (83%) and amikacin (77%) (Fig. 2).

Meremikmu *et al.* (2005) also recorded the prominent presence of *Staphylococcus aureus* (65%) in bacteremia. The frequency of occurrence of *Streptococcus* sp. in blood was 3.63%, which was similarly reported by Sobhani *et al.* (2004). The frequency of occurrence of *Diplococcus* sp. (6.36%), *Salmonella typhi* (5.45%), *Streptococcus* sp. (3.63%) and *Klebsiella pneumoniae* (2.72%) in present study was similarly reported by Gholam and Kashanian (2005). Rosemarie *et al.* (1994) also reported the presence of *Haemophilus influenzae* in blood culture.

Fig. 2: The antibiotic resistance pattern of the bacterial pathogens isolated from blood

Sobhani *et al.* (2004), Zakaria El-Astal (2004) and Gholam and Kashanian (2005) also reported the presence of highly sensitive blood bacterial pathogens to amikacin and ciprofloxacin and Huang *et al.* (2002) reported highly resistance pathogens to ceftazidime.

The present study showed the increasing antibiotic resistance against the common bacterial isolates. Resistant bacteria could be mutant form of wild bacteria due to over-use or misuse of broad-spectrum antibiotics.

Ideally blood culture and antibiotic susceptibility should be performed for the proper management of microbial infections. It is not possible to delay initiation of treatment until laboratory reports are available. In such instances and without culture facilities, knowledge of local antimicrobial resistance pattern from accurate bacteriological records of culture reports may provide guidance towards an empirical therapy before sensitivity pattern are available.

In present study all the pathogens isolated from blood showed high resistance to cefuroxime, ceftazidime,
cefotaxime and highly sensitivity to meropenem, linzolid and amikacin. The study indicated the common antibiotics pattern in this region, which helps in prescribing the proper antibiotics against bacteraemia and avoid the misuse or overuse of unwanted or resistant antibiotics for proper treatment to patients. The increasing resistance of organisms indicates that periodic monitoring and possibly modification of empirical therapy are required.

REFERENCES


