Antibiotic resistance pattern of bacteria isolated from various clinical specimens in a tertiary care hospital

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Abstract

Background: Antibiotic resistance is a common phenomenon in bacteria, and it is a significant threat all over the world. With this a study was conducted to find the antibiotic resistance pattern of various bacterial isolates. Methods: This is a hospital-based study involving both in and outpatients. Patients with various infections were included, clinical specimens were collected accordingly. The pathogenic bacteria were isolated and identified. Antibiotic sensitivity testing was done by Kirby Bauer disc diffusion method. Results: The male female ratio was 1.23; 30% isolates were gram positive cocci and 70% were gram negative bacilli; Klebsiella spp (30.5%) was the predominant isolate followed by Staphylococcus aureus (25%); statistically the difference was not significant. Samples wise, predominant isolates were from urine followed by respiratory samples and skin samples; significant drug resistance was detected. Conclusion: A Significant rise of antibiotic resistance to various antibiotics in different classes of bacteria has been observed. Always there should be proper communication between the clinician and microbiologists is essential to get the best result while treating patient.

Keywords: Antibiotic resistance, Bacteria, Patients, Infections

Introduction

Antibiotic resistance of bacteria is significant threat all over the world. But the developing countries like India this is an even greater public health problem because India is one of the highest bacterial disease like urinary tract infections (UTI), respiratory tract infections (RTI), skin& soft tissue infections (STI). With this, antibiotics have a significant role in mortality and morbidity [1, 2].

UTIs are important medical problem, usually caused by the microbial invasion of the urinary tract that extends from the renal cortex. The most common bacterial infection accounting for 35% of total hospital acquired infections (HAIa) [3,4].

RTI pose serious problems owing to their great prevalence with associated high mortality rates and economic status [5]. STI are common infections of the skin, subcutaneous tissue and muscle which may be minor, self-limiting may lead to life threatening diseases requiring; these may be complicated and uncomplicated infections [6].

India is one of the highest consumers of antibiotics in the world [7] and the drug resistance (DR) bacteria have increased in the last decade. Uncontrolled and inappropriate use of antibiotics is the main cause for DR. Among these, multi drug resistance (MDR), extremely drug resistance (XDR) TB, methicillin resistance Staphylococcus aureus (MRSA), penicillinase producing Neisseria gonorrhoea (PPNG), VA resistance Enterococci (VRE) are some important DR bacteria [8]. Surveillance studies are mandatory so that we every hospital can revise their antibiotic policies. With this a study was conducted to find the DR pattern of various bacterial isolates.

Methods

Study period: Study was conducted in the department of Microbiology, GSL Medical College from March to May 2019. Study protocol was approved by the institutional ethical committee.

Inclusion criteria: Individuals aged ≥ 18 years, with various UTI, RTI, STIs attending inpatient and outpatients’ departments were included in the study.
Exclusion criteria: Patients on antibiotic treatment for the last three months, known foreign bodies implants, mechanical heart valves were excluded from the study.

Study design: The patients were explained about the study protocol in detail and informed written consent was taken either from the participants or their representatives. Various clinical samples such as urine, sputum, BAL, pleural fluid, tracheal aspirate, bronchial wash, endotracheal tip, throat swabs, pus swabs, blood, IV catheter tips, body fluids (CSF, ascitic fluid, synovial fluid) were collected based on the site of infection. Specimen was transported to microbiology laboratory immediately. Direct microscopic examination such as gram stain, wet mount and culture sensitivity was done as per the standards [9, 10, 11, 12, 13]. After overnight incubation, growth was classified by gram stain to gram positive cocci (GPC) and gram-negative bacilli (GNB). All the isolates were identified based on Gram staining and by using various biochemical reactions [13]. After identifying the bacteria, antibiotic sensitivity of isolates was done on Muller-Hinton agar (MHA) by the disk diffusion method [13], *Escherichia coli* ATCC 25922 was used as the control.

Statistical analysis: Statistical analysis was done by using SPSS version 21. Chi square test was to find statistical analysis, P<0.05 was considered as statistically significant.

Results

During the study period the culture positivity was 302 (100%); 30% were GPC and 70% GNB. The male female ratio was 1.23. Isolate wise, *Klebsiella spp* was the predominant among GNB and *Staphylococcus aureus* among GPC (Figure 1); statistically the difference was not significant.

Table-I: Number of isolates, clinical specimen wise; n (%)

<table>
<thead>
<tr>
<th>Specimen</th>
<th>GPC (92)</th>
<th>GNB (210)</th>
<th>Total (302)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Urine</td>
<td>8 (9.3)</td>
<td>78 (90.6)</td>
<td>86 (28.3)</td>
</tr>
<tr>
<td>Respiratory</td>
<td>47 (46)</td>
<td>55 (53.9)</td>
<td>102 (33.6)</td>
</tr>
<tr>
<td>Skin &amp; Soft tissue</td>
<td>37 (32.4)</td>
<td>77 (67.5)</td>
<td>114 (37.7)</td>
</tr>
</tbody>
</table>

GPC: Gram positive cocci; GNB: Gram negative bacilli

Table-2: Antibiotic susceptibility pattern of the isolates in percentage.

| Isolate      | P & CON GEN ERS | 2nd Gen CPS | 3rd Gen CPS | 4th Gen CPS | FQ | AG | M | GP | TE | LZ | COT | NIT | PIT | AMC | IMP | MRP |
|--------------|-----------------|-------------|-------------|-------------|----|----|---|----|----|----|-----|-----|-----|-----|-----|-----|-----|
|              | P& A MP | CX | CTR | CTX | CAZ | CIP | NX | AK | GEN | E | AZ | VA | TEI |     |     |     |     |     |     |     |     |     |     |     |     |     |
| S. aureus    | S94   | S03 | S07 | S08 | S31 | S82 | S89 | S100 | S08 | S100 | S24 | S89 | S100 | S100 | S100 | S100 | S100 | S100 |
|              | R06   | R97 | R93 | R92 | R69 | R18 | R11 | R0 | R92 | R0 | R76 | R11 | R11 | R0 | R0 | R0 | R0 | R0 |
| Streptococcus| S100  | S24 | S22 | S12 | S54 | S100 | S89 | S100 | S55 | S100 | S100 | S100 | S100 | S100 | S100 | S100 | S100 |
|              | R0    | R76 | R78 | R88 | R44 | R0 | R11 | R0 | R45 | R0 | R0 | R0 | R0 | R0 | R0 | R0 | R0 | R0 |
| Enterococcus | S100  | S23 | S08 | S06 | S0 | S0 | S10 | S0 | S0 | S0 | S89 | S0 | S0 | S0 | S0 | S0 | S0 | S0 |
|              | R0    | R77 | R92 | R94 | R100 | R100 | R50 | R100 | R100 | R100 | R100 | R100 | R100 | R100 | R100 | R100 | R100 |
| E.coli       | S97   | S25 | S10 | S08 | S71 | S14 | S24 | S92 | S8 | S18 | S0 | S0 | S0 | S0 | S0 | S0 | S0 | S0 |
|              | R03   | R75 | R90 | R92 | R69 | R86 | R76 | R0 | R86 | R100 | R82 | R100 | R100 | R100 | R100 | R100 | R100 | R100 |
| Klebsiella   | S100  | S46 | S22 | S14 | S22 | S22 | S12 | S81 | S04 | S22 | S0 | S0 | S0 | S0 | S0 | S0 | S0 | S0 |
|              | R0    | R54 | R78 | R86 | R78 | R76 | R78 | R19 | R0 | R66 | R78 | R100 | R100 | R100 | R100 | R100 | R100 | R100 |
| Pseudomonas  | S100  | S66 | S50 | S50 | S42 | S22 | S21 | S77 | S04 | S28 | S0 | S0 | S0 | S0 | S0 | S0 | S0 | S0 |
|              | R0    | R36 | R50 | R50 | R58 | R78 | R79 | R23 | R96 | R72 | R100 | R100 | R100 | R100 | R100 | R100 | R100 | R100 |
| Proteus      | S100  | S24 | S08 | S08 | S22 | S22 | S11 | S89 | S0 | S12 | S0 | S0 | S0 | S0 | S0 | S0 | S0 | S0 |
|              | R0    | R76 | R92 | R92 | R78 | R78 | R89 | R11 | R100 | R88 | R100 | R100 | R100 | R100 | R100 | R100 | R100 | R100 |

S- Sensitive; R- Resistance; β lactam group (Penicillin: P, Ampicillin: AMP); 2nd generation Cephalosporins (Cefoxitin: CX); 3rd generation Cephalosporins (Ceftaxone: CTR, Cefotaxime: CTX, Cefazidime: CAZ), 4th generation Cephalosporins (Cefepime: CPM); Fluoroquinolones (Ciprofloxacin: CIP, Norfloxacin: NX); Aminoglycosides (Amikacin: AK, Gentamycin: GEN); Macrolides (Erythromycin: E, Azithromycin: AZ); Glycopeptides (Vancomycin: VA, Teicoplanin: TEI); Tetracyclines: TET; Linezolid: LZ; Cotrimoxazole: COT; Nitrofurantoin: NIT; β lactum + β lactamase inhibitors (Piperacillin tazobactam: PIT, Amoxycillin clavulanic acid: AMC); Carbapenems (Meropenem: MRP, Imipenem: IMP).
Samples wise, predominant isolates were from urine followed by respiratory samples and skin samples (Table 1); significant DR was detected (Table 2).

**Discussion**

In this study, an attempt was made to find the prevalence of various bacteria as well as the drug susceptibility to various anti microbial agents. DR is the main concern for the treating specialists to choose the antibiotics especially for the hospitalized patients [14, 15] and also for pediatric group [16, 17]. For developing countries such as India, DR is a significant threat [18] because DR was reported to be one of the main causes of morbidity and mortality in India. This is mainly because of indiscriminate usage of antibiotics [19, 20].

Among GPC, *Staph. aureus* (75) is the prevalent pathogen isolated followed by *streptococcus pneumoniae* (16) and *Enterococcus spp.* (1); among GNB, the rate of isolation was Klebsiella species 92(30.4%), *Escherichia coli* 63 (20.8%), *Pseudomonas aeruginosa* 50 (16.5%) and Proteus species 05 (1.6%); DR was observed to almost all the pathogens.

*Staph. aureus*, commonest GPC showed 100% sensitivity to LZ, V, IMP; 82% sensitivity to GEN. Azimi Taher et al., reported that highest resistance rate to LZ (R=50%) and VA was reported to be an effective antibiotic [21]. Similar results were reported in the literature [22, 23, 24]. However, the results of these studies were not consistent with our findings and they had reported high resistance to VA.

However, this study had certain limitation. Short duration, small sample size, no IP and OP categorization, no categorization of infections such as UTI, RTI and no species level identification.

**Conclusion**

A significant rise of antibiotic resistance to various antibiotics in different classes of bacteria has been observed. Always there should be proper communication between the clinician and microbiologists is essential to get the best result while treating patient.

**What the study adds to the existing knowledge?**
The present study provides an epidemiological status of the significant rise of antibiotic resistance which is vital while designing the treatment plan.

**Author’s contribution**

Dr. B. S. G Sailaja: Concept, study design and conduct of study.

Dr. P.D. Prasad P.D: Data analysis and manuscript preparation.

**Findings:** Nil; **Conflict of Interest:** None initiated

**Permission from IRB:** Yes

**References**


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