Antibiotic Resistance of Isolated Gram Negative Bacilli from Different Clinical Sample in a Central Teaching Hospital of Pediatric in Baghdad

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Abstract

The number of infections caused by microorganisms is increasing significantly over the last few years. A total of 140 patients admitted to the central teaching hospital of pediatrics from the 1st of Jun 2017 to 31 October 2017. The Clinical samples was processed from culture and sensitivity testing. Antibiotic discs used for gram negative isolates. The most prevalent gram negative isolates included Escherichia coli 63 (45.0 %), Pseudomonas spp. 21 (15.0 %), Klebsiella spp. 19 (13.6 %) predominantly. Escherichia coli were the most prevalent isolates from urine 45 (71.4 %), Klebsiella spp. 11 (57.9 %) and Enterobacter spp. 11 (68.8 %) followed by Escherichia coli 10 (15.9 %) predominant from blood. 68 (48.6 %) of specimens were urine, 47 (33.6 %) were blood and 25 (17.8 %) were from other origins. Resistance to CTR was 42 (51.2 %) in Escherichia coli, 15 (18.3 %) in Pseudomonas spp. 9 (11.0 %) in Klebsiella spp. and similarly AMC showed 41 (62.1) resistance among Escherichia coli, 8 (12.1 %) among Pseudomonas spp. and Klebsiella spp. and also GEN showed 27 (57.4 %) resistance among Escherichia coli, 7 (14.9 %) among Pseudomonas spp. and 6 (12.8 %) in Klebsiella spp.

Keywords: Antimicrobial Resistance, Gram Negative bacilli, Patient Pediatric, Hospital.

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INTRODUCTION

Number of infections caused by microorganisms is increasing significantly over the last few years; one of the reasons for this increase is development of microbial resistance to drugs used to treat these infections. The infection due to gram negative bacteria increasing problem in recent years. Most common reasons responsible for these infections are multidrug resistant gram negative bacilli particularly members of the family Enterobacteriaceae and non-fermenting gram negative rods. Enterobacteriaceae family had shown high rates of antibiotic resistance. Resistance gram negative bacteria are a serious global public health concern especially in developing countries. Gram negative bacilli are common cause of intra-abdominal infections, urinary tract infections, nosocomial pneumonia and bacteremia. Most infections may be related to unbalanced microbiota and host defenses mechanisms but undoubtedly hospital environments are great source of potentially pathogenic microorganisms. A number of factors have been reported that were related to infection with resistant microorganisms, including previous use of antibiotics, corticosteroid therapy, mechanical ventilation, length of hospital stay and use of invasive device such as catheters. The prevalence of resistant gram negative bacteria can vary at local, regional, national and international levels. The mortality is increasing every day because of global changing of antimicrobial resistance patterns.

MATERIALS AND METHODS

A total of 140 children admitted to the central teaching hospital of pediatrics from the 1st of Jun 2017 to 31 October 2017. Gram-negative isolates from clinical samples were included in the study. The Clinical samples included urine, blood, wound secretions, pus, ear, endotracheal, doubluma, peritoneal. The sample was processed from culture and sensitivity testing. Antimicrobial susceptibility was evaluated by the Kirby-Bauer disk diffusion method in guide lines of clinical and laboratory standards Institute. Antibiotic discs used for gram negative isolates [Ampicillin (AMP), Augmentin (AMC), Cefotaxime (CTX), Ceftriaxone (CTR), Cefipime (CFP), Cefixime (CFM), Cephalothin (CLT), Gentamycin (GEN), Amikacin (AK), Nitrofurantin (NIT)].

Statistical Analysis

The suitable statistical methods were used in order to analyze and assess the results, they include the followings:

- Descriptive statistics: Statistical tables including observed frequencies with their percentages.
- Inferential statistics: These were used to accept or reject the statistical hypotheses, Persons Chi-Square test ($\chi^2$) at level of significance 0.05. P value < 0.05 level of significance was considered statistically significant.

RESULTS

In a total of 140 different clinical samples which were processed. The most prevalent gram negative isolates included Escherichia coli 63 (45.0 %), Pseudomonas spp. 21 (15.0 %), Klebsiella spp 19 (13.6 %) predominantly. Escherichia coli were the most prevalent isolates from urine 45 (71.4 %), Klebsiella spp 11 (57.9 %) followed by Escherichia coli 10 (15.9 %) predominant from blood. 68 (48.6 %) of specimens were urine, 47 (33.6 %) were blood and 25 (17.8 %) were from other origins. Resistance to CTR were examined after 24 hours and organisms identified by their colonial morphology, Gram staining and API 20 E kits biochemical tests using standard techniques.
was 42 (51.2 %) in *Escherichia coli*, 15 (18.3 %) in *Pseudomonas* spp, 9 (11.0 %) in *Klebsiella* spp and similarly AMC showed 41 (62.1) resistance among *Escherichia coli*, 7 (12.1 %) among *Pseudomonas* spp and *Klebsiella* spp and also GEN showed 27 (57.4 %) resistance among *Escherichia coli*, 7 (14.9 %) among *Pseudomonas* spp and 6 (12.8 %) in *Klebsiella* spp.

**DISCUSSION**

The Microbial Pathogens as well as their antibiotic sensitivity patterns may change from place to place and from time to time. In present study show in Table (1) the most common microorganisms isolated were *Escherichia coli* 63 (45.0 %), *Pseudomonas* spp 21 (15.0 %), *Klebsiella* spp 19 (13.6 %). *Escherichia coli* found to be the

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**Table 2. Distribution of Organisms Isolated from various Clinical sample**

<table>
<thead>
<tr>
<th>Clinical Sample</th>
<th><em>Escherichia coli</em> spp</th>
<th><em>Klebsiella</em> spp</th>
<th><em>Proteus</em> spp</th>
<th><em>Enterobacter</em> spp</th>
<th><em>Serretia</em> spp</th>
<th><em>Acinetobacter</em> spp</th>
<th><em>Pseudomonas</em> spp</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Urine</td>
<td>45 (71.4)</td>
<td>6 (31.6)</td>
<td>3 (50.0)</td>
<td>2 (12.5)</td>
<td>2 (66.7)</td>
<td>1 (8.3)</td>
<td>9 (42.9)</td>
<td>68 (48.6)*</td>
</tr>
<tr>
<td>Blood</td>
<td>10 (15.9)</td>
<td>11 (57.9)</td>
<td>2 (33.3)</td>
<td>11 (68.8)</td>
<td>1 (33.3)</td>
<td>8 (66.7)</td>
<td>4 (19.0)</td>
<td>47 (33.6)*</td>
</tr>
<tr>
<td>Wound</td>
<td>4 (6.3)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>5 (23.8)</td>
<td>9 (6.4)</td>
</tr>
<tr>
<td>Pus</td>
<td>0 (0.0)</td>
<td>2 (10.5)</td>
<td>1 (16.7)</td>
<td>1 (6.2)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>1 (4.8)</td>
<td>5 (3.6)</td>
</tr>
<tr>
<td>Ear</td>
<td>2 (3.2)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>1 (4.8)</td>
<td>3 (2.1)</td>
</tr>
<tr>
<td>Endotracheal</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>2 (16.7)</td>
<td>0 (0.0)</td>
<td>2 (1.4)</td>
</tr>
<tr>
<td>Doubluma</td>
<td>1 (1.6)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>2 (12.5)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>1 (4.8)</td>
<td>4 (2.9)</td>
</tr>
<tr>
<td>Peritoneal</td>
<td>1 (1.6)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>1 (8.3)</td>
<td>0 (0.0)</td>
<td>2 (1.4)</td>
</tr>
<tr>
<td>Total</td>
<td>63 (45.0)*</td>
<td>19 (13.6)*</td>
<td>6 (4.3)</td>
<td>16 (11.4)</td>
<td>3 (2.1)</td>
<td>12 (8.6)</td>
<td>21 (15.0)*</td>
<td>140 (100.0)</td>
</tr>
</tbody>
</table>

(P < 0.05).

**Table 3. Antibiotic Resistance in Gram Negative Bacilli**

<table>
<thead>
<tr>
<th>Antibiotic Used</th>
<th><em>Escherichia coli</em> spp</th>
<th><em>Klebsiella</em> spp</th>
<th><em>Proteus</em> spp</th>
<th><em>Enterobacter</em> spp</th>
<th><em>Serretia</em> spp</th>
<th><em>Acinetobacter</em> spp</th>
<th><em>Pseudomonas</em> spp</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>AMP</td>
<td>19 (43.2)</td>
<td>4 (9.1)</td>
<td>3 (6.8)</td>
<td>7 (15.9)</td>
<td>2 (4.5)</td>
<td>6 (13.6)</td>
<td>3 (6.8)</td>
<td>44 (12.5)</td>
</tr>
<tr>
<td>AMC</td>
<td>41 (62.1)</td>
<td>8 (12.1)</td>
<td>1 (1.5)</td>
<td>2 (3.0)</td>
<td>1 (1.5)</td>
<td>5 (7.6)</td>
<td>8 (12.1)</td>
<td>66 (18.7)</td>
</tr>
<tr>
<td>CTX</td>
<td>8 (34.8)</td>
<td>4 (17.4)</td>
<td>3 (13.0)</td>
<td>2 (8.7)</td>
<td>2 (8.7)</td>
<td>2 (8.7)</td>
<td>2 (8.7)</td>
<td>23 (6.5)</td>
</tr>
<tr>
<td>CTR</td>
<td>42 (51.2)</td>
<td>9 (11.0)</td>
<td>4 (4.9)</td>
<td>4 (4.9)</td>
<td>3 (3.7)</td>
<td>5 (6.1)</td>
<td>15 (18.3)</td>
<td>82 (23.2)*</td>
</tr>
<tr>
<td>CFP</td>
<td>15 (38.5)</td>
<td>2 (5.1)</td>
<td>4 (10.3)</td>
<td>6 (15.4)</td>
<td>0 (0.0)</td>
<td>1 (2.6)</td>
<td>11 (28.2)</td>
<td>39 (11.0)</td>
</tr>
<tr>
<td>CFM</td>
<td>27 (57.4)</td>
<td>6 (12.6)</td>
<td>4 (8.5)</td>
<td>3 (6.4)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>7 (14.9)</td>
<td>47 (13.3)</td>
</tr>
<tr>
<td>CLT</td>
<td>2 (18.2)</td>
<td>2 (18.2)</td>
<td>0 (0.0)</td>
<td>1 (9.1)</td>
<td>0 (0.0)</td>
<td>4 (36.4)</td>
<td>2 (18.2)</td>
<td>11 (3.1)</td>
</tr>
<tr>
<td>GEN</td>
<td>3 (20.0)</td>
<td>6 (40.0)</td>
<td>0 (0.0)</td>
<td>3 (20.0)</td>
<td>0 (0.0)</td>
<td>1 (6.7)</td>
<td>2 (13.3)</td>
<td>15 (4.2)</td>
</tr>
<tr>
<td>AK</td>
<td>5 (35.7)</td>
<td>7 (50.0)</td>
<td>0 (0.0)</td>
<td>1 (7.1)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>1 (7.1)</td>
<td>14 (4.0)</td>
</tr>
<tr>
<td>NIT</td>
<td>6 (50.0)</td>
<td>1 (8.3)</td>
<td>0 (0.0)</td>
<td>3 (25.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>2 (16.7)</td>
<td>12 (3.4)</td>
</tr>
<tr>
<td>Total</td>
<td>168 (47.6)*</td>
<td>49 (13.9)*</td>
<td>19 (5.4)</td>
<td>32 (9.1)</td>
<td>8 (2.3)</td>
<td>24 (6.8)</td>
<td>53 (15.0)*</td>
<td>353 (100.0)</td>
</tr>
</tbody>
</table>

(P < 0.05).

[Ampicillin (AMP), Augmentin (AMC), Cefotaxime (CTX), Ceftriaxone (CTR), Cefpime (CFP), Cefixime (CFM), Cephalothin (CLT), Gentamycin (GEN), Amikacin (AK), Nitrofurantin (NIT)].
Fig. 1. Distribution of Organisms Isolated from various Clinical sample

Fig. 2. Antibiotic Resistance in Gram Negative Bacilli
most common in study which was isolated from urine and this agree with Javeed et al.\textsuperscript{19}, Saravanan et al.\textsuperscript{20} and Vipin et al.\textsuperscript{21}. Showed significant differences (P < 0.05) in Table (2). Urine samples were 68 (48.6 %) and blood samples were 47 (33.6 %) this agreement with Sharif et al.\textsuperscript{22}. Showed significant differences (P < 0.05) in Table (3). Resistance emerges from over utilization of antibiotics trying to sterilize the environment and also the inappropriate use of the antibiotics for treatment, uncontrolled antibiotics resistance surveillance\textsuperscript{23}. There was 168 (47.6 %) resistance rate of \textit{Escherichia coli} to [CTR 42 (51.2 %), AMC 41 (62.1 %), CFM 27 (57.4 %), AMP 19 (43.2 %)] which is the most resistance and there was 53 (15.0 %) resistance rate \textit{Pseudomonas} spp to [CTR 15 (18.3 %), CFP 11 (28.2 %), AMC 8 (12.1 %), CFM 7 (14.9 %)] also 49 (13.9 %) resistance rate to [CTR 15 (18.3 %), CFP 11 (28.2 %), AMC 8 (12.1 %), AK 7 (50.0 %), CFM 6 (12.8 %), GEN 6 (40.0 %), this result show in Table (3) with significant differences (P < 0.05).

**CONCLUSION**

In this study, the most common microorganisms isolated was \textit{Escherichia coli} isolated from urine samples most resistance rate to Ceftriaxone 42 (51.2 %), Augmentin 41 (62.1 %), Cefixime 27 (57.4 %), Ampicillin19 (43.2 %).

**ACKNOWLEDGMENTS**

None

**CONFLICT OF INTEREST**

The author declares that there are no conflict of interest.

**REFERENCES**

17. Clinical and Laboratory Standards Institutes Performance Standards for antimicrobial susceptibility


