Evaluation of the Types of Bacteria in the Blood of HIV-1 Patients Attending ART Clinic at the FMC Owo, Nigeria and their Antiibiogram Profile

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Abstract

In this investigation, the types of bacteria present in the blood of HIV-1 positive individuals attending the Antiretroviral Therapy clinic at a tertiary healthcare centre in Southwest, Nigeria and their antiibiogram profile were assessed. A total number of Five Hundred confirmed HIV-1 Positive Patients were recruited for this study. Their blood was collected and subjected to standard microbiological techniques to isolate and identify the types of bacteria present and also determine the antiibiogram profile of the isolates. The bacterial species identified are Klebsiella pneumoniae, Pseudomonas aeruginosa, Pseudomonas fluorescens, Staphylococcus aureus, Staphylococcus lentus, Salmonella enterica serovar Typhimurium, Salmonella enterica serovar Typhi, Salmonella enterica serovar Enteritidis, Proteus mirabilis, Proteus vulgaris, Enterobacter aerogenes, Escherichia coli, O103:H2, Escherichia coli O26:H11, Shigella flexneri, Shigella dysenteriae, Shigella sonnei and Streptococcus pneumoniae. Escherichia coli and Salmonella typhimurium were isolated from the control group of apparently healthy individuals consisting of fifty respondents. Approximately, 4% of the patients were found to have more than one type of bacterial species in their blood. The antiibiogram profile of isolates revealed Ofloxacin as the most effective antibiotic against most isolated bacterial species. Only two isolates were resistant to each of Streptomycin and Chloramphenicol. Proteus mirabilis displayed the highest level of resistance while other bacterial isolates exhibited resistance to Cotrimoxazole, Augmentin, Amoxycillin, Cloxacillin and Erythromycin.

Keywords: HIV; Blood; Bacteria

Introduction

Human Immunodeficiency Virus (HIV) infection is still a serious problem globally. It is usually contracted through contact with HIV-infected blood and other body fluids via mucosal membranes or non-intact skin surfaces, sexual intercourse, intravenous drug use - infected blood and other body fluids via mucosal membranes or vertical transmission (mother to child transmission) [1-3].

The management of HIV infection is enhanced by early detection, prompt CD4 assessment and strict adherence to antiretroviral therapy. The scourge of HIV/AIDS is much felt in Africa, with much burden in the sub-Saharan and Southern Africa [4].

Bacteraemia is a major cause of morbidity and mortality in HIV Patients. This is because in addition to the pathological effects caused by these microorganisms, the immunological response elicited by the immune system of the host to these microorganisms in the bloodstream can lead to septic shock, which usually has high mortality rate [5].

Although infections caused by bacterial pathogens can be treated with antibiotics, however the issue of their resistance to most of the available antibiotics makes this difficult. Some of the bacterial species implicated in bloodstream infections are Klebsiella sp. and Escherichia coli [6]. This study therefore is to screen the blood of HIV-1 patients in the studied community for the types of bacterial pathogens present and to know the antiibiogram profile of these microorganisms.

Materials and Methods

Patients were recruited from the HIV Clinic of the Federal Medical Centre, Owo, Ondo State, Nigeria. The sampling and isolation processes with suitable bacteriological media were commenced in May, 2015.

A total of Five Hundred (500) serologically confirmed HIV-1 patients, who were previously identified through the national parallel algorithm for HIV testing provided by the United State Agency for International Development (USAID) were recruited for the study, consisting of 162 males and 338 females across all age groups, 452 patients under Antiretroviral Therapy and 48 Non - Antiretroviral Therapy Patients.

Retroviral screening is conducted using the the National serial algorithm for HIV testing. The algorithm consists of Determine - Unigold - Stat pak (tiebreaker).

The blood samples (non-repeat) were collected after approval by the ethical review committee of the healthcare institution.

Two milliliters (2 ml) of the collected blood was introduced into 5ml Brain-Heart infusion broth and were incubated at 37°C for 24hrs before culturing on suitable agar plates for bacterial growth [7]. The bacterial isolates from each plate were subcultured for pure colonies at 37°C for 18 - 24 hours. The isolates were identified by Gram staining, biochemical tests, sugar fermentation, motility test and molecular characterization techniques.

The antibiotics used were manufactured by Abtek Biologicals Limited, Liverpool, United Kingdom. They comprised both broad spectrum and narrow spectrum antibiotics engaged in the treatment
of both Gram positive and Gram negative bacterial infections. The antibiotics are Cotrimoxazole (25 μg), Cloxacillin (5 μg),ERYthromycin (5 μg), Gentamicin (10 μg), Augmentin (30 μg), Streptomycin (10 μg), Tetracycline (10 μg), Chloramphenicol (10 μg),Ofloxacin (5 μg), Nalidixic Acid (30 μg), Nitrofurantoin (200 μg), Amoxycillin (5 μg).

The antibiotic sensitivity testing of isolates was done employing the Kirby Bauer's method, Mueller Hinton agar was prepared according to manufacturer's specification and about 15 ml was poured into sterile Petri dishes at about 45°C. Fresh cultures of about 18 hours of each isolate was then used to seed the agar, after obtaining a broth culture compared with 0.5 Mcfarland's standard solution. The antibiotic discs for testing were then placed on the surface of each seeded agar medium. These were incubated for 24 hours at 37°C. Sensitivity was recorded for any isolate that had a clear zone of inhibition of up to 17 mm diameter or more for each disc [8].

The DNA extraction, amplification and gel electrophoresis of amplicons were conducted by adopting the method of Barraquio et al. [9].

The DNA from bacterial isolates were extracted and purified using the Qiagen Extraction Kit, samples from, an aliquot portion of a previously 24-hrs broth culture made from each isolate was aseptically transferred into each kit and vortexed for about 15 minutes. The cells broke up, liberating the DNA of each bacterial isolate.

The DNA extracted from the bacterial cells were amplified with the aid of the thermocycler (PCR machine), using the primers
\[ 3'-GACGGCGTGTA\, 1101F \]
\[ 5'-AACGAGCGACC – 3' \]

with the aid of the thermocycler (PCR machine), using the primers is isolate.

The stages in the amplification included initial denaturation (94°C for 5 minutes), cycling, denaturation 94°C for 1 minute, annealing (52°C for 30 secs), extension (72°C for 8 minutes) and holding (4°C for 20 minutes). The DNA polymerase was used was Taq polymerase.

A total of 5 μL of the DNA isolate were mixed with 3 μL violet buffer on paper film, and then the mixture was electrophoresed at 5 v cm using 1.5% agarose gel in Tris-acetate EDTA (TAE) buffer. Then the purity of the DNA isolated was visualized under UV light, after staining for 30 min with 0.2 mg mL ethidium bromide adopting the method of Barraquio et al. [9].

The amplicons were sequenced, the nucleotide sequences were compared with the standard reference sequences for alignment using the Basic Local Alignment Search tool (BLAST) from the National Centre for Biotechnology Information (NCBI).

Data analysis and interpretation of results
Statistical Package for Social Sciences Version 17.0 (SPSS Inc., Chicago, IL) was used for all analyses. Descriptive statistics were used in the computing of the results in order to give lucid representations of the data analysed. The Chi-square (X²) test was used to determine significant differences and effects.

Results
Types of bacteria isolated
A total of ten (10) bacterial species were isolated from the blood of HIV-1 Patients. These bacterial isolates are Escherichia coli,

<table>
<thead>
<tr>
<th>S/No</th>
<th>Probable Organism</th>
<th>Frequency (%)</th>
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</thead>
<tbody>
<tr>
<td>1</td>
<td>Staphylococcus aureus</td>
<td>10(45%)</td>
</tr>
<tr>
<td>2</td>
<td>Klebsiella pneumoniae.</td>
<td>2(9%)</td>
</tr>
<tr>
<td>3</td>
<td>Escherichia coli / Salmonella typhimurium</td>
<td>5(23%)</td>
</tr>
<tr>
<td>4</td>
<td>Proteus mirabilis / Salmonella typhimurium</td>
<td>5(23%)</td>
</tr>
<tr>
<td>Total</td>
<td></td>
<td>22(100%)</td>
</tr>
</tbody>
</table>

Table 2: Frequency of occurrence of mixed bacterial pathogens in the blood samples of HIV-1 patients examined.

Klebsiella pneumoniae, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Streptococcus pneumoniae, Pseudomonas aeruginosa, Shigella dysenteriae, Proteus mirabilis and Enterobacter sp. (Table 1). The frequency of occurrence of these bacterial species from this investigation can be seen in (Table 1). More than one bacterial species were isolated in 22 of the patients sampled as seen in Table 2.

Using the 16 subunit ribosomal DNA technique [9], the following bacterial species were sequenced, Klebsiella pneumoniae, Pseudomonas aeruginosa, Pseudomonas fluorescens, Staphylococcus aureus, Staphylococcus lentus, Salmonella enterica serovar Typhimurium, Salmonella enterica serovar Typhi, Salmonella enterica serovar Enteritidis, Proteus mirabilis, Proteus vulgaris, Enterobacter aerogenes, Escherichia coli, O103:H2, Escherichia coli, O26:H11, Shigella flexneri, Shigella dysenteriae and Shigella sonnei.

Seventy-Eight (78%) percent of cases were by sexual transmission, 19.8 percent were by vertical transmission, 2.2 percent of cases were from contact with blood other than sexual transmission (parenteral route).

The overall evaluation of the CD4 counts of HIV-1 Patients studied revealed that more of the female patients had their CD4 counts within the normal CD4 range than their male counterparts.
were the control group, the bacterial isolates implicated in the respondents patients studied (Figure 1). This suggests better immune reconstitution in the group of female pattern towards tested antibiotics while displayed Proteus mirabilis and Erythromycin (Table 3).

Table 3. The highest level of resistance to antibiotics tested as presented in

**Discussion**

The bulk of microbial isolates from this study are members of the Enterobacteriaceae family, which is the largest and most heterogenous group of medically significant gram-negative helix-shaped bacteria. They are most frequently isolated in clinical samples. The infections include diarrhoea, dysentery, Salmonellosis, Haemolytic-uremic syndrome (HUS), necrotizing enterocolitis and various nosocomial infections. Pathogenicity of Enterobacteriaceae as a family of gram negative bacteria is associated with the Lipopolysaccharide (LPS) situated in the outer membrane of the bacterial cell wall which is usually responsible for endotoxin production in Gram negative bacteria – a cause of septicemia. Infections from enterobacteriaceae are regarded as one of the two leading killers of children in developing countries. This goes in agreement with the submission of Frey and Sherk [10].

Shigella species were the most commonly encountered isolates in the research, this could be due to negligence of patients in ensuring proper hygiene with regards to food preparation, handling, their choices of food vendors and/or ineffective feeding habits (malnutrition). This is also an indicator to the increasing rate of Shigella bacteraemia. According to the findings of Trevett et al. [11], the presence of Shigella bacteraemia occurs usually in adults with underlying disease conditions, such as leukaemia, diabetes, sickle cell anaemia, cirrhosis and HIV. Kotloff et al. [12] also submitted that HIV infected individuals are at high risk of recurrent, severe and fatal occurrences of Shigella bacteremia.

The most frequent occurrence of mixed bacterial populations in the samples was found to occur between Staphylococcus aureus and Klebsiella pneumoniae category. Both of these bacteria commonly colonise the upper respiratory tract, which is a part of the body notable for significance in pathogenesis of infections and epidemiology. This is in line with a report from Bodenstein and Du Toit [13] on the evaluation of the susceptibility of these microorganisms to selected classes of flavonoids.

Ofl oxacin, which is a member of the Quinolone antibiotics displayed the highest antimicrobial effect of all the antibiotics used in the antimicrobial susceptibility testing, this outcome agrees with a report from Prajna et al. [14] on the bacteriologic and clinical efficacy of Ofl oxacin and Ciprofl oxacin Ophthalmic solutions in the treatment of Bacterial Keratitis, stating that the antibiotics are effective and safe in the treatment of patients with culture positive bacterial keratitis. However, Multzum [15] reported major side effects on ofloxa in are onset of pseudomembranous colitis during or after treatment, seizures, diarrhea, easy bruising or bleeding, pale skin, severe skin reactions and fever. Proteus mirabilis was the most resistant microorganism to antimicrobial testing. This is likely due to the mutation rate of the particular species of Proteus, that confers antibiotic resistance to it. This agrees with the report of Foglio et al. [16], that Proteus spp. is resistant to Ampicillin, Cotrimoxazole, Tetracycline and Chloramphenicol. A report from Newmann et al. [17] further buttresses this phenomenon.

**Conclusion**

This study has been able to show that Shigella dysenteriae is the most frequently encountered bacterial species in the blood of HIV-1 patients in the community sampled while the least encountered

**Antibiotic sensitivity profile of the bacterial isolates from HIV-1 Patients sampled**

Ofl oxacin and Gentamicin were found with the highest antimicrobial activities while Cloxacillin was found to have the least antibacterial effect on the bacterial isolates. Nalidixic acid, Nitrofurantoin, Tetracycline, Streptomycin and Chloramphenicol had intermediate antimicrobial actions on most bacterial isolates, while bacterial isolates exhibited resistance to the following antibiotics; Cotrimoxazole, Amoxy cillin, Augmentin, Cloxacillin and Erythromycin (Table 3).

**Klebsiella pneumoniae** displayed the highest susceptibility pattern towards tested antibiotics while **Proteus mirabilis** displayed
<table>
<thead>
<tr>
<th>Bacterial Isolates</th>
<th>GEN</th>
<th>NAL</th>
<th>NIT</th>
<th>COT</th>
<th>AMX</th>
<th>TET</th>
<th>AUG</th>
<th>OFL</th>
<th>CXC</th>
<th>STR</th>
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<tr>
<td>1. Escherichia coli</td>
<td>14</td>
<td>37</td>
<td>37</td>
<td>86</td>
<td>96</td>
<td>27</td>
<td>100</td>
<td>12</td>
<td>100</td>
<td>0</td>
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<td>2. Klebsiella pneumoniae</td>
<td>5</td>
<td>10</td>
<td>6</td>
<td>56</td>
<td>65</td>
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<td>7</td>
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<td>4. Salmonella typhimurium</td>
<td>14</td>
<td>29</td>
<td>33</td>
<td>83</td>
<td>81</td>
<td>36</td>
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<td>14</td>
<td>100</td>
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<td>5. Staphylococcus aureus</td>
<td>14</td>
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<td>20</td>
<td>76</td>
<td>60</td>
<td>8</td>
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<td>100</td>
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<td>7. Pseudomonas aeruginosa</td>
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<td>9. Proteus mirabilis</td>
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Table 3: The Resistance Pattern of Bacterial isolates to antibiotics (%).


Pathogen was *Proteus mirabilis*. All the bacterial species isolated are resistant to Cloxacin, Cottrimoxazole, Ampoxycillin, Augmentin and Erythromycin but sensitive to Ofloxacin [18-24].

References