Antimicrobial sensitivity profile of bacterial isolated from stool samples In Federal Medical Centre, Nigeria

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ABSTRACT

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| **Aim:** to ascertain the antimicrobial Sensitivity profile of bacterial isolated from stool samples  **Study design:** A retrospective analytical cross-sectional study.  **Place and Duration of Study:** Federal Medical Center, Asaba, Delta State, Nigeria, between January 2019 and December 2022.  **Methodology:** Stool microscopy, culture and sensitivity results were collected from the archives of the Medical Laboratory Services over a period of 48 months. The stool samples collected were processed for bacteriological analysis where they were inoculated into MacConkey (MAC) O2, Selenite F broth, Xylose Lysine Deoxycholate agar (XLD), Hektoen, or Decoxycholate Agar (DCA), Sorbitol MacConkey (SMA) or Campylobacter Agar Microaerophilic by using sterile wire loop. The inoculum was incubated under aerobic condition at 370c for temperature between 24hours and 72hours. The Data that was collected was sorted into categories based on common features or attributes to enable analysis with SPSS® and the results presented with the aid of appropriate figures and diagrams or tables.  **Results:** A total of 15 records of microorganisms were reportedly isolated from 411 stool samples during the review period (1st of January 2019 to 31st December 2022). *Escherichia coli (E. coli)* was the most isolated organism, accounting for 51.3% of the isolates. Children (0–5 years) and older children (6-19years) had high *E. coli* prevalence (71.6%) and (74.5%) respectively which may reflect to early exposure through contaminated food or water and underdeveloped immune systems. Gender distribution for these microbes shows a general trend where females tend to have higher percentages, except for *S. paratyphi C* (9.4%), *P. vulgaris* (2.2%), *S. aureus* (1.1%), and *Pseudomonas spp* (0.6%) where males are higher. Resistance to Fluoroquinolones, Ciprofloxacin and Ofloxacin in *E. coli* is substantial (~47.2–55.2%). Similarly, *S. typhi* shows moderate resistance (20.1% to Ciprofloxacin). Resistance to Gentamicin is highest for *E. coli* (48.5%) and *S. typhi* (24%), though it retains some susceptibility in other pathogens. Particularly troubling resistance in *P. vulgaris* and *Shigella*, with *P. vulgaris* showing 100% resistance to several antibiotics, including cephalosporins and fluoroquinolones.  **Conclusion:** This study reveals *Escherichia coli* and *Salmonella species* being the most frequently identified, *E. coli* is associated with gastroenteritis and is responsible for infectious diarrhea among children. The prevalence of *Salmonella typhi* and *Salmonella paratyphi* observed in this study is consistent with other studies in West Africa, where *Salmonella species* are a major public health concern. Public health implications include improving sanitation, promoting vaccinations, antibiotic stewardship, and developing alternative therapies. |

*Keywords: Antimicrobial, bacteria Isolate, stool specimens, Federal Medical Centre, Asaba, Delta State, Nigeria.*

1. INTRODUCTION

Although antibiotics generally refer to antibacterial, antibiotic compounds are differentiated as antibacterial, antifungals and antivirals to reflect the group of microorganisms they antagonize [1]. Antibiotics have transformed the practice of medicine, making once lethal infections readily treatable and making other medical advances, like cancer chemotherapy and organ transplants, possible. Prompt initiation of antibiotics to treat infections reduces morbidity and save lives, for example, in cases of sepsis [2]. However, about 30% of all antibiotics prescribed in U.S. acute care hospitals are either unnecessary or suboptimal [3,4]. Like all medications, antibiotics have serious adverse effects, which occur in roughly 20% of hospitalized patients who receive them [5].

Patients who are unnecessarily exposed to antibiotics are placed at risk for these adverse events with no benefit. The misuse of antibiotics has also contributed to antibiotic resistance, a serious threat to public health [6].The misuse of antibiotics can adversely influence the health of antibiotics naïve patients through the spread of resistant organisms and *Clostridium difficile* (*C. difficile*) [7]. Both misuse and overuse of antibiotics have been a leading cause of the evolution of antibiotics resistance mechanism amongst pathogenic bacteria. Bacteria have developed different mechanisms to inhibit the effect of antibiotics [8]. The resistance to antimicrobial agents can be natural, acquired, genetic, phenotypic or biological [9]. Furthermore, resistance may be developed due to spontaneous mutation in genes, acquisition of plasmid or transposon, the physiological change in the state of bacterial cell or decreasing of the permeability of cell. Bacteria develop resistance in various ways such as enzymatic drug inactivation, drug target alteration and drug permeability [10].

The widespread microbial resistance has been blamed for the complexity of today's bacterial infection management and therapy. It also places a significant economic burden on any Nation. It is predicted that by 2050, microbial resistance will cost over $100 trillion and cause over 10 million fatalities compared to the present low estimate of ~700,000 persons [11]. Antibiotic resistance underpins major advances in the treatment and management of infectious diseases. Undoubtedly, the emergence and dissemination of resistant bacterial strains, which is today`s major global public health threat, jeopardizes the efforts gained over the years [12]. Indeed, antibiotic resistance has impacted all facets of mankind, causing immense human suffering, extended hospital admissions, expensive healthcare access, and a significant number of deaths (Department of Health, Public Health England, 2016). The aim of this study was therefore to ascertain the antimicrobial Sensitivity profile of bacterial isolated from stool samples

2. materialS and methods

**2.1 Study Design**

A retrospective study covering 48 months was carried out at the Federal Medical Centre, Asaba between 1st of January, 2019 and 31st December, 2022 (48 months). Patient variables were collected from the archives of the Medical Laboratory Services along with the results of their microscopy culture and sensitivity investigations. These were accessed from the registers kept at the microbiology department and corresponding relevant demographic and clinical information retrieved from the rapid MEDCHAT® or the SMART CLINIC®.

**2.2 Study Area**

This study took place at Federal Medical Centre, (FMC), Nnebisi Road, located within Asaba, the capital city of Delta State in the southern part of Nigeria. FMC Asaba was established on the 12 August 1998 in response to the felt need to provide tertiary and specialist healthcare services, training of various healthcare professionals and research in best medical practice for the people of Delta State and environs especially as there is no prior Federal Teaching Hospital in the state. In 1962, the then Regional Commissioner of Health, Mr. J. Adigun laid the foundation stone of a 30-bed cottage hospital of the defunct Mid-Western Region of Nigeria upgraded to Asaba Central Hospital when Delta State was created in 1991 to provide primary preventive and specialized care to the people of Asaba and its surroundings. This was the take off point for the Federal Medical Centre, Asaba which has grown to a 334-bed tertiary healthcare facility. It now offers primary, secondary, and tertiary services with the help of a plethora of different specialties in healthcare practice. The institution serves Asaba Metropolis and neighboring communities and as a referral center to parts of Edo, Kogi and Anambra States. It is accredited for residency training in various fields, internship training and provides hands-on experience to a host of other categories of both clinical and nonclinical professions related to medical practice.

**2.3 Study Population**

All the individuals tested stool microscopy, culture and sensitivity from 1st of January 2019 to 31st of December 2022. All eligible microscopy culture and sensitivity investigations within the study period were collected and the microbes isolated were analyzed for their prevalence and susceptibility as well as resistance to anti-microbial agents

**2.4 Sampling Size Determination**

Sample size (N) was calculated using the formular described by Cochran, [13]

N=Z2PQD2

N= Sample Size

Z= The confidence interval, usually set at 1.96

P= Expected prevalence using the prevalence rate of 12.3% in Abakaliki, South-Eastern, Nigeria [14]

Q= 1-P (1-0.123)

D= Desired level of significance, usually set at 0.05

Therefore

N= (1.96)2 x 0.123 x 0.877 x (0.05)2

N= 166

**2.5 Selection Criteria**

**2.5.1 Inclusion Criteria**

Any record which cannot be related to a patient was excluded. All the microscopy, culture and sensitivity investigations that were not completed were excluded from the study.

**2.5.2 Exclusion Criteria**

All Stool microscopy culture and sensitivity investigations done at microbiology department were collected. Results that were validly reported with identifiable patient records were selected.

**2.6 Analytical Methods**

All the stool microscopy, culture and sensitivity results for the years under review from the records of Medical Laboratory Services department of Federal Medical Centre Asaba were collected.

**2.6.1 Stool Sample Collection and Transport**

Freshly passed stool specimens were transported to the laboratory within 30 minutes of collection and processed within 2 hours. Anytime there was a delay in transport and/or processing, the specimen always transferred into a transport container with Cary-Blair medium. Any specimens that contain urine, tissue paper or any external contamination were rejected.

**2.6.2 Stool Examination**

The first physical examination was performed on the stool to know if it has pus, presence of worm, blood or mucus then also if it was a watery stool from diarrhea or not. After the physical examination, the stool samples were examined under microscopy by identifying the presence of parasitic larva, cyst, ova and trophozoite of some parasites.

**2.6.3 Culturing, Identification and Antimicrobial Susceptibility Testing**

Stool samples collected were processed for bacteriological analysis where they were inoculated into MacConkey (MAC), Selenite F broth, Xylose Lysine Deoxycholate Agar (XLD), Hektoen, or Deoxycholate Citrate Agar (DCA), Sorbitol MacConkey (SMA) or Campylobacter Agar Microaerophilic by using sterile wire loop. The inoculum was incubated under aerobic conditions at 37oC between 24 hours and 72 hours. The identification colony characteristics were performed where all the pathogens were isolated using biochemical tests. In vitro antimicrobial susceptibility tests were carried out on all the pathogens isolated. Antibiotic discs were placed on the surface of the inoculated agar. Local drug availability and Committee for Chemical Laboratory Standards (CCLS, 2000) protocols determined antibiotic disc selection. The selected drugs are Kamalox©. Ampiclox©, chloramphenicol, Zinacef, © gentamycin, ciprofloxacin, cefuroxime, cefixime, ceftazidine, ofloxacin, Augmentin©, clindamycin, erythromycin, ampicillin, levofloxacin, rifampicin, azithromycin, perfloxacin. Streptomycin, ceftriaxone, Septrin© and Tarivid©. After overnight incubation, the diameter of growth inhibition around the discs was measured and interpreted as sensitive, intermediate or resistant according to clinical and laboratory standards institute (CLSI, 2000).

**2.7 Statistical Analysis**

The Data that was collected was sorted into categories based on common features or attributes to enable analysis with SPSS® and the results presented with the aid of appropriate figures and diagrams or tables. The data was analyzed using frequency tables, Chi square (X2) and t-test. The study will assume a probability value of <0.05 to be statistically significant for all inferences made.

3. results and discussion

A total of 15 records of microorganisms were reportedly isolated from 411 stool samples during the review period (1st of January, 2019 and 31st December, 2022).

Table 1: Association between age and isolates

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Isolates** | **0 - 5 Years  (Infants & Young Children)** | **6 - 19 Years  (Children & Adolescents)** | **20 - 39 Years  (Young Adults)** | **40 - 59 Years  (Middle-aged Adults)** | **60 Years and above  (Elderly)** | **Frequency (%)** | **X2** | **P-Value** | **Φc** |
| **N = 116 (%)** | **N = 137 (%)** | **N = 77 (%)** | **N = 49 (%)** | **N = 32 (%)** | **N = 411** |
| *E. coli* | 83 (71.60) | 102 (74.50) | 8 (10.40) | 6 (12.20) | 12 (37.50) | 211  (51.30) | 197.01 | > 0.001 | 0.343 |
| *Klebsiella spp* | 2 (1.70) | 2 (1.50) | 5 (6.50) | 1 (2.00) | 0 (0.00) | 10  (2.40) |
| *P. vulgaris* | 0 (0.00) | 0 (0.00) | 4 (5.20) | 2 (4.10) | 0 (0.00) | 6  (1.50) |
| *Proteus spp* | 0 (0.00) | 1 (0.70) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1  (0.20) |
| *Pseudomonas spp* | 0 (0.00) | 0 (0.00) | 1 (1.30) | 0 (0.00) | 0 (0.00) | 1  (0.20) |
| *S. aureus* | 1 (0.90) | 1 (0.70) | 0 (0.00) | 0 (0.00) | 1 (3.10) | 3  (0.70) |
| *S. dysenteriae* | 0 (0.00) | 0 (0.00) | 1 (1.30) | 0 (0.00) | 0 (0.00) | 1  (0.20) |
| *S. paratyphi A* | 8 (6.90) | 1 (0.70) | 5 (6.50) | 5 (10.20) | 2 (6.30) | 21  (5.10) |
| *S. paratyphi B* | 6 (5.20) | 6 (4.40) | 11 (14.30) | 6 (12.20) | 2 (6.30) | 831  (7.30) |
| *S. paratyphi B & C* | 0 (0.00) | 0 (0.00) | 1 (1.30) | 0 (0.00) | 0 (0.00) | 1  (0.20) |
| *S. paratyphi C* | 6 (5.20) | 4 (2.90) | 10 (13.00) | 7 (14.30) | 3 (9.40) | 30  (7.30) |
| *S. pneumoniae* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (3.10) | 1  (0.20) |
| *S. typhi* | 9 (7.80) | 18 (13.10) | 31 (40.30) | 19 (38.80) | 11 (34.40) | 8  (21.40) |
| *Shigella spp* | 1 (0.90) | 2 (1.50) | 0 (0.00) | 2 (4.10) | 0 (0.00) | 5  (1.20) |
| *Vibrio spp* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (2.00) | 0 (0.00) | 1  (0.20) |

Table 1 shows the profile of the microbes extracted from stool during the review period. The microbial pattern isolated from stool samples at the Federal Medical Centre (FMC), Asaba, reflects a diverse range of pathogens, with *Escherichia coli* and *Salmonella species* being the most frequently identified.

*Escherichia coli* (*E. coli*) was the most isolated organism, accounting for 51.3% of the isolates. The prevalence of *E. coli* in FMC, Asaba, aligns with findings in other parts of sub-Saharan Africa, where *E. coli* remains a dominant cause of gastroenteritis. For instance, studies in Nigeria, Kenya, and Ethiopia have reported similar findings, with *E. coli* constituting around 40-60% of stool isolates among patients presenting with diarrhea, emphasizing the burden of enteric pathogens in these areas [15, 16, 17, and 18]. *E. coli* strains cause various forms of diarrheal diseases, especially in children. They are associated with fecal contamination in water and food.

*Salmonella species* were the next most prevalent, with *Salmonella typhi* (21.4%) being the primary isolate, followed by *Salmonella paratyphi* A, B, and C (19.7%). This high frequency is notable because *Salmonella species* are a major cause of typhoid and paratyphoid fevers, diseases that are widespread in areas with poor sanitation. The prevalence of *Salmonella typhi* and *Salmonella paratyphi* observed in this study is consistent with other studies in West Africa, where *Salmonella species* are a major public health concern. Studies in Nigeria and other regions have similarly reported *Salmonella* as a leading pathogen in stool samples, often linked to poor sanitation and water contamination [19, 20, 21, 22].

Less frequently isolated pathogens included *Klebsiella species* (2.4%), *Proteus vulgaris* (1.5%), *Shigella species* (1.2%), *Staphylococcus aureus* (0.7%), *Pseudomonas species* (0.2%), *S. pneumoniae* (0.2%), *S. dysenteriae* (0.2%), *Proteus species* (0.2%), *S. paratyphi* B&C (0.2%) and Vibrio species (0.2%). These organisms, though isolated in smaller proportions, are important as they can cause a range of gastrointestinal and extra-intestinal infections. For example, *Shigella* is a known cause of dysentery, while *Vibrio species* are associated with cholera, a disease with significant epidemic potential. *Klebsiella species* has 10 (2.4%) out of 411 stool samples when compared the study done at General surgical wards of Sree Balaji Medical College and Hospital where total of 189 (19.8%) were isolated [24]

Table 1 shows the microbial distribution according to the age of those whose stool samples were tested, and the data shows a moderate association between age and isolated microbes. The distribution of microbes across age groups highlights the role of age-related physiological and environmental factors. Children (0–5 years) and older children (6-19years) had high *E. coli* prevalence (71.6%) and (74.5%) respectively which may reflect to early exposure through contaminated food or water and underdeveloped immune systems. Though the young adults and elderly people recorded low levels of multiple pathogen *E. coli* suggest increased exposure to diverse environments (e.g., schools). While the young adults (19-39years) had increased prevalence of *S. paratyphi* B and C pathogens separately with 14.3% and 13.0% respectively among other age groups. The young adults also have increase in opportunistic infections such as *Klebsiella* and *P. vulgaris* that could reflect occupational, lifestyle, and health factors (e.g., weakened immunity, chronic disease).

The younger populations seem at higher risk of *E. coli* infection, possibly due to their less developed gut microbiota and poor hygiene behaviors and this aligns with research among children in daycare where *E. coli* was the highest isolate [16]. This association was also found to be significant.

Higher *S. typhi* and *S. paratyphi* prevalence in adults signals the need for targeted interventions (e.g., vaccination campaigns, hygiene improvements) in environments where typhoidal fevers are endemic. Opportunistic pathogens (Klebsiella and Pseudomonas) in older age groups may require hospital-based infection control practices.

Table 2: Association between gender and isolates

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Isolates** | **Male** | **Female** | **X2** | **P-Value** |
| **N = 180** | **N = 231** |
| *E. coli* | 88 (48.90) | 123 (53.20) | 11.756 | 0.626 |
| *Klebsiella spp* | 3 (1.70) | 7 (3.00) |
| *P. vulgaris* | 4 (2.20) | 2 (0.90) |
| *Proteus spp* | 0 (0.00) | 1 (0.40) |
| *Pseudomonas spp* | 1 (0.60) | 0 (0.00) |
| *S. aureus* | 2 (1.10) | 1 (0.40) |
| *S. dysenteriae* | 0 (0.00) | 1 (0.40) |
| *S. paratyphi A* | 10 (5.60) | 11 (4.80) |
| *S. paratyphi B* | 12 (6.70) | 19 (8.20) |
| *S. paratyphi B & C* | 1 (0.60) | 0 (0.00) |
| *S. paratyphi C* | 17 (9.40) | 13 (5.60) |
| *S. pneumoniae* | 1 (0.60) | 0 (0.00) |
| *S. typhi* | 39 (21.70) | 49 (21.20) |
| *Shigella spp* | 2 (1.10) | 3 (1.30) |
| *Vibrio spp* | 0 (0.00) | 1 (0.40) |

In Table 2, the isolated microbes were distributed according to the gender of those whose samples were tested. Gender distribution for these microbes shows a general trend where females tend to have higher percentages, except for *S. paratyphi* C (9.4%), *P. vulgaris* (2.2%), *S*. aureus (1.1%), *S. paratyphi B & C* (0.6%), *S. pneumonia* (0.6%) and *Pseudomonas spp* (0.6%) where males are higher. Most of the pathogens, like *E. coli*, show a common trend of higher occurrence in females, which may reflect biological or behavioural factors.

Some pathogens like *pseudomonas spp* were seen exclusively in males, while *Proteus species*, *S. dysenteriae* and Vibrio spp were seen exclusively in females. This finding may be due to the smaller samples sizes, or they could warrant investigation into environmental or healthcare exposure differences.

However, despite a notable count difference, the p-value indicates no significant gender difference in microbial presence. Other studies also reported gender as a non- significantly associated factor with the microorganism isolated from patient stool [19, 23].

Table 3: Antibiotic susceptibility profiles

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Isolates** | **CFD** | | | **CRX** | | | **CXM** | | | **CAZ** | | | **CFT** | | |
| Resistance | Intermediate | Susceptible | Resistance | Intermediate | Susceptible | Resistance | Intermediate | Susceptible | Resistance | Intermediate | Susceptible | Resistance | Intermediate | Susceptible |
| N = 29 (%) | N = 88 (%) | N = 93 (%) | N = 224 (%) | N = 26 (%) | N = 8 (%) | N = 265 (%) | N = 41 (%) | N = 11 (%) | N = 263 (%) | N = 54 (%) | N = 38 (%) | N = 119 (%) | N = 16 (%) | N = 14 (%) |
| *E. coli* | 16 (55.20) | 50 (56.80) | 42 (45.20) | 112 (50.00) | 14 (53.80) | 5 (62.50) | 136 (51.30) | 23 (56.10) | 6 (54.50) | 132 (50.20) | 29 (53.70) | 22 (57.90) | 55 (46.20) | 7 (43.80) | 8 (57.10) |
| *Klebsiella spp* | 0 (0.00) | 2 (2.30) | 2 (2.20) | 7 (3.10) | 0 (0.00) | 0 (0.00) | 7 (2.60) | 1 (2.40) | 0 (0.00) | 6 (2.30) | 0 (0.00) | 1 (2.60) | 2 (1.70) | 0 (0.00) | 0 (0.00) |
| *P. vulgaris* | 2 (6.90) | 0 (0.00) | 3 (3.20) | 4 (1.80) | 0 (0.00) | 0 (0.00) | 5 (1.90) | 1 (2.40) | 0 (0.00) | 4 (1.50) | 1 (1.90) | 0 (0.00) | 0 (0.00) | 1 (6.30) | 0 (0.00) |
| *Proteus spp* | 0 (0.00) | 1 (1.10) | 0 (0.00) | 1 (0.40) | 0 (0.00) | 0 (0.00) | 1 (0.40) | 0 (0.00) | 0 (0.00) | 1 (0.40) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) |
| *Pseudomonas spp* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (0.40) | 0 (0.00) | 0 (0.00) | 1 (0.40) | 0 (0.00) | 0 (0.00) | 1 (0.40) | 0 (0.00) | 0 (0.00) | 1 (0.80) | 0 (0.00) | 0 (0.00) |
| *S. aureus* | 0 (0.00) | 0 (0.00) | 2 (2.20) | 1 (0.40) | 1 (3.80) | 0 (0.00) | 0 (0.00) | 2 (4.90) | 1 (9.10) | 0 (0.00) | 1 (1.90) | 2 (5.30) | 1 (0.80) | 0 (0.00) | 0 (0.00) |
| *S. dysenteriae* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (0.40) | 0 (0.00) | 0 (0.00) | 1 (0.40) | 0 (0.00) | 0 (0.00) | 1 (0.80) | 0 (0.00) | 0 (0.00) |
| *S. paratyphi A* | 2 (6.90) | 3 (3.40) | 2 (2.20) | 10 (4.50) | 0 (0.00) | 1 (12.50) | 10 (3.80) | 0 (0.00) | 1 (9.10) | 12 (4.60) | 1 (1.90) | 0 (0.00) | 6 (5.00) | 2 (12.50) | 2 (14.30) |
| *S. paratyphi B* | 1 (3.40) | 9 (10.20) | 6 (6.50) | 15 (6.70) | 2 (7.70) | 0 (0.00) | 24 (9.10) | 2 (4.90) | 0 (0.00) | 22 (8.40) | 4 (7.40) | 3 (7.90) | 14 (11.80) | 1 (6.30) | 0 (0.00) |
| *S. paratyphi B & C* | 0 (0.00) | 0 (0.00) | 1 (1.10) | 1 (0.40) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (0.40) | 0 (0.00) | 0 (0.00) | 1 (0.80) | 0 (0.00) | 0 (0.00) |
| *S. paratyphi C* | 0 (0.00) | 6 (6.80) | 8 (8.60) | 21 (9.40) | 0 (0.00) | 0 (0.00) | 25 (9.40) | 2 (4.90) | 0 (0.00) | 25 (9.50) | 2 (3.70) | 1 (2.60) | 9 (7.60) | 1 (6.30) | 0 (0.00) |
| *S. pneumoniae* | 0 (0.00) | 1 (1.10) | 0 (0.00) | 1 (0.40) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (0.40) | 0 (0.00) | 0 (0.00) | 1 (0.80) | 0 (0.00) | 0 (0.00) |
| *S. typhi* | 7 (24.10) | 16 (18.20) | 25 (26.90) | 46 (20.50) | 9 (34.60) | 2 (25.00) | 51 (19.20) | 9 (22.00) | 3 (27.30) | 53 (20.20) | 15 (27.80) | 8 (21.10) | 26 (21.80) | 4 (25.00) | 3 (21.40) |
| *Shigella spp* | 1 (3.40) | 0 (0.00) | 2 (2.20) | 3 (1.30) | 0 (0.00) | 0 (0.00) | 3 (1.10) | 1 (2.40) | 0 (0.00) | 3 (1.10) | 1 (1.90) | 1 (2.60) | 2 (1.70) | 0 (0.00) | 1 (7.10) |
| *Vibrio spp* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (0.40) | 0 (0.00) | 0 (0.00) | 1 (0.40) | 0 (0.00) | 0 (0.00) | 1 (0.40) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) |

**Table 3: Antibiotic susceptibility profiles (contd.)**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Isolates** | **ERC** | | **AZI** | **CLN** |
| Resistance | Intermediate | Resistance | Resistance |
| N = 27 (%) | N = 2 (%) | N = 3 (%) | N = 21 (%) |
| *E. coli* | 8 (29.00) | 1 (50.00) | 0 (0.00) | 5 (23.80) |
| *Klebsiella spp* | 1 (3.70) | 0 (0.00) | 2 (66.70) | 0 (0.00) |
| *Pseudomonas spp* | 1 (3.70) | 0 (0.00) | 0 (0.00) | 0 (0.00) |
| *S. paratyphi A* | 2 (7.40) | 0 (0.00) | 1 (33.30) | 2 (9.50) |
| *S. paratyphi B* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (4.80) |
| *S. paratyphi C* | 2 (7.40) | 1 (50.00) | 0 (0.00) | 2 (9.50) |
| *S. pneumoniae* | 1 (3.70) | 0 (0.00) | 0 (0.00) | 1 (4.80) |
| *S. typhi* | 11 (40.70) | 0 (0.00) | 0 (0.00) | 9 (42.90) |
| *Shigella spp* | 1 (3.70) | 0 (0.00) | 0 (0.00) | 1 (4.80) |

Table 3: Antibiotic susceptibility profiles (contd.)

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Isolates** | **CIP** | | | **OFL** | | | **LEV** | | | **PEF** | | |
| Resistance | Intermediate | Susceptible | Resistance | Intermediate | Susceptible | Resistance | Intermediate | Susceptible | Resistance | Intermediate | Susceptible |
| N = 174 (%) | N = 91 (%) | N = 105 | N = 106 (%) | N = 201 (%) | N = 68 (%) | N = 3 (%) | N = 3 (%) | N = 11 (%) | N = 8 (%) | N = 3 (%) | N = 9 (%) |
| *E. coli* | 96 (55.20) | 37 (40.70) | 58 (55.20) | 50 (47.20) | 106 (52.70) | 36 (52.90) | 0 (0.00) | 2 (66.70) | 6 (54.50) | 4 (50.00) | 2 (66.70) | 5 (55.60) |
| *Klebsiella spp* | 5 (2.90) | 1 (1.10) | 4 (3.80) | 0 (0.00) | 4 (2.00) | 3 (4.40) | 1 (33.30) | 0 (0.00) | 1 (9.10) | 0 (0.00) | 0 (0.00) | 0 (0.00) |
| *P. vulgaris* | 4 (2.30) | 1 (1.10) | 1 (1.00) | 1 (0.90) | 5 (2.50) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) |
| *Proteus spp* | 1 (0.60) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (0.50) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) |
| *Pseudomonas spp* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (0.90) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) |
| *S. aureus* | 0 (0.00) | 2 (2.20) | 1 (1.00) | 2 (1.90) | 1 (0.50) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) |
| *S. dysenteriae* | 1 (0.60) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (0.50) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) |
| *S. paratyphi A* | 10 (5.70) | 3 (3.30) | 6 (5.70) | 2 (1.90) | 9 (4.50) | 6 (8.80) | 1 (33.30) | 0 (0.00) | 1 (9.10) | 1 (12.50) | 1 (33.30) | 1 (11.10) |
| *S. paratyphi B* | 11 (6.30) | 9 (9.90) | 10 (9.50) | 8 (7.50) | 18 (9.00) | 5 (7.40) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) |
| *S. paratyphi B & C* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (0.50) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) |
| *S. paratyphi C* | 7 (4.00) | 14 (15.40) | 7 (6.70) | 16 (15.10) | 9 (4.50) | 4 (5.90) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (12.50) | 0 (0.00) | 0 (0.00) |
| *S. pneumoniae* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (0.50) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) |
| *S. typhi* | 35 (20.10) | 23 (25.30) | 18 (17.10) | 23 (21.70) | 42 (20.90) | 14 (20.60) | 1 (33.30) | 1 (33.30) | 3 (27.30) | 2 (25.00) | 0 (0.00) | 3 (33.30) |
| *Shigella spp* | 3 (1.70) | 1 (1.10) | 0 (0.00) | 3 (2.80) | 2 (1.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) |
| *Vibrio spp* | 1 (0.60) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (0.50) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) |

**Table 3: Antibiotic susceptibility profiles (contd.)**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Isolates** | **CHL** | | | **NIT** | | | **RIF** | **SPN** | | |
| Resistance | Intermediate | Susceptible | Resistance | Intermediate | Susceptible | Intermediate | Resistance | Intermediate | Susceptible |
| N = 11 (%) | N = 1 (%) | N = 5 (%) | N = 38 (%) | N = 32 (%) | N = 12 (%) | N = 1 (%) | N = 16 (%) | N = 1 (%) | N = 3 (%) |
| *E. coli* | 5 (45.50) | 1 (100.00) | 2 (40.00) | 13 (34.20) | 22 (68.80) | 10 (83.30) | 1 (100) | 9 (56.30) | 1 (100) | 1 (33.30) |
| *Klebsiella spp* | 1 (9.10) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (33.30) |
| *S. aureus* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 2 (16.70) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) |
| *S. paratyphi A* | 2 (18.20) | 0 (0.00) | 0 (0.00) | 1 (2.60) | 3 (9.40) | 0 (0.00) | 0 (0.00) | 3 (18.80) | 0 (0.00) | 0 (0.00) |
| *S. paratyphi B* | 1 (9.10) | 0 (0.00) | 0 (0.00) | 7 (18.40) | 2 (6.30) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) |
| *S. paratyphi C* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 3 (7.90) | 2 (6.30) | 0 (0.00) | 0 (0.00) | 1 (6.30) | 0 (0.00) | 0 (0.00) |
| *S. typhi* | 2 (18.20) | 0 (0.00) | 3 (60.00) | 14 (36.80) | 3 (9.40) | 0 (0.00) | 0 (0.00) | 3 (18.80) | 0 (0.00) | 1 (33.30) |

**Table 3: Antibiotic susceptibility profiles (contd.)**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Isolates** | **AMX** | | | **AUG** | | | **AMP** | |
| Resistance | Intermediate | Susceptible | Resistance | Intermediate | Susceptible | Resistance | Susceptible |
| N = 17 (%) | N = 2 (%) | N = 2 (%) | N = 354 (%) | N = 11 (%) | N = 3 (%) | N = 16 (%) | N = 2 (%) |
| *E. coli* | 10 (58.80) | 2 (100) | 0 (0.00) | 180 (50.80) | 7 (63.60) | 2 (66.70) | 8 (50.00) | 2 (100) |
| *Klebsiella spp* | 1 (5.90) | 0 (0.00) | 0 (0.00) | 8 (2.300 | 0 (0.00) | 0 (0.00) | 1 (6.30) | 0 (0.00) |
| *P. vulgaris* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 6 (1.70) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) |
| *Proteus spp* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (0.30) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) |
| *Pseudomonas spp* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (0.30) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) |
| *S. aureus* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 3 (0.80) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) |
| *S. dysenteriae* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (0.30) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) |
| *S. paratyphi A* | 3 (17.60) | 0 (0.00) | 0 (0.00) | 16 (4.50) | 0 (0.00) | 0 (0.00) | 2 (12.50) | 0 (0.00) |
| *S. paratyphi B* | 0 (0.00) | 0 (0.00) | 1 (50.00) | 30 (8.50) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) |
| *S. paratyphi B & C* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (0.30) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) |
| *S. paratyphi C* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 29 (8.20) | 0 (0.00) | 1 (33.30) | 0 (0.00) | 0 (0.00) |
| *S. pneumoniae* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (0.30) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) |
| *S. typhi* | 3 (17.60) | 0 (0.00) | 1 (50.00) | 71 (20.10) | 4 (36.40) | 0 (0.00) | 5 (31.30) | 0 (0.00) |
| *Shigella spp* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 5 (1.40) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) |
| *Vibrio spp* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (0.30) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) |

**Table 3: Antibiotic susceptibility profiles (contd.)**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Isolates** | **STY** | | | **GEN** | | |
| Resistance | Intermediate | Susceptible | Resistance | Intermediate | Susceptible |
| N = 25 (%) | N = 3 (%) | N = 9 (%) | N = 229 (%) | N = 122 (%) | N = 43 (%) |
| *E. coli* | 11 (44.00) | 1 (33.30) | 7 (77.80) | 111 (48.50) | 68 (55.70) | 21 (48.80) |
| *Klebsiella spp* | 1 (4.00) | 0 (0.00) | 1 (11.10) | 5 (2.20) | 2 (1.60) | 3 (7.00) |
| *P. vulgaris* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 2 (0.90) | 1 (0.80) | 0 (0.00) |
| *Proteus spp* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (0.40) | 0 (0.00) | 0 (0.00) |
| *Pseudomonas spp* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (0.40) | 0 (0.00) | 0 (0.00) |
| *S. aureus* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (0.40) | 1 (0.80) | 1 (2.30) |
| *S. dysenteriae* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (0.80) | 0 (0.00) |
| *S. paratyphi A* | 5 (20.00) | 0 (0.00) | 0 (0.00) | 14 (6.10) | 3 (2.50) | 4 (9.30) |
| *S. paratyphi B* | 1 (4.00) | 0 (0.00) | 0 (0.00) | 16 (7.00) | 11 (9.00) | 4 (9.30) |
| *S. paratyphi B & C* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (0.80) | 0 (0.00) |
| *S. paratyphi C* | 1 (4.00) | 0 (0.00) | 0 (0.00) | 19 (8.30) | 6 (4.90) | 3 (7.00) |
| *S. pneumoniae* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (0.80) | 0 (0.00) |
| *S. typhi* | 6 (24.00) | 2 (66.70) | 1 (11.10) | 55 (24.00) | 25 (20.50) | 7 (16.30) |
| *Shigella spp* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 3 (1.30) | 2 (1.60) | 0 (0.00) |
| *Vibrio spp* | 0 (0.00) | 0 (0.00) | 0 (0.00) | 1 (0.40) | 0 (0.00) | 0 (0.00) |

Key note: CFD (Cefpodoxime), AMX (Ampiclox), CHL (Chloramphenicol),GEN (Gentamycin),CIP (Ciprofloxacin), CRX (Cefuroxime), CXM (Cefixime), CAZ (Ceftazidine),OFL (Ofloxacin),AUG (Augmentin),CLN (Clindamycin),ERC (Erythromycin),AMP (Ampicillin),LEV (Levofloxacin),NIT (Nitrofurantoin), RIF (Rifampicin), AZI (Azithromycin), CFT (Ceftriaxone), SPN (Septrin), PEF (Pefloxacin), STY ( Streptomycin)

Table 3 illustrates the antibiotic susceptibility pattern of the isolated microorganisms. According to the antimicrobial susceptibility pattern in this study, there is high resistance across multiple antibiotics. Universally Augmentin (Amoxicillin-Clavulanate) had high resistance rates across all organisms, including *E. coli* (50.8%), *S. typhi* (21.5%) and *S. typhi* (20.1%). This suggests that Augmentin is largely ineffective for treating infections caused by these bacteria.

For the Cephalosporin, Ceftazidime has the highest resistance to *E. coli* with 50.20% and with 20.20% for *S.typhi*. Cefixime and Cefuroxime show even higher resistance in *E. coli* (51.3%, 50%) and *S. typhi* (19.2%, 20.5%). These third-generation cephalosporins are crucial in empirical therapy, and their reduced efficacy reflects the widespread presence of extended-spectrum beta-lactamase (ESBL)-producing strains.

Resistance to Fluoroquinolones, Ciprofloxacin and Ofloxacin in *E. coli* is substantial (~47.2–55.2%). Similarly, *S. typhi* shows moderate resistance (20.1% to Ciprofloxacin). Resistance to Gentamicin is (48.5%) for *E. coli* and *S. typhi* (24%), though it retains some susceptibility in other pathogens. Particularly troubling resistance in *P. vulgaris* and *Shigella*, with *P. vulgaris* showing almost 100% resistance to several antibiotics, including cephalosporins and fluoroquinolones. A study was conducted at kenya which also discovered high resistance rate of the isolates was noted on quinolones [25].

Mbuthia and Ny’ayo [12] reported similar antibiotic resistance spectrum in their antibiotic sensitivity profiling of bacterial isolates from stool samples among children below five years in Murang'a County, Kenya. In their study, all the *E. coli* subtypes, *Salmonella*, *Klebsiella*, Shigella, and other bacteria were found to be resistant ampicillin, amoxicillin, chloramphenicol, ciprofloxacin, ceftriaxone, and kanamycin antibiotics.

The resistant pattern by the *Salmonella* *spp* in this study is like the findings from a systematic review of 86 articles on *Salmonella* enterica serovars in Nigeria (1999-2018) which found that Ampicillin, cotrimoxazole, amoxicillin-clavulanate and tetracycline had the highest frequency of antimicrobial resistance by Salmonella isolates [19].

These findings highlight a critical public health threat. Resistance to frontline antibiotics like Augmentin, fluoroquinolones, and third-generation cephalosporins compromises the ability to treat common bacterial infections effectively. The rising AMR increases morbidity, mortality, and healthcare costs, requiring more expensive or toxic antibiotics and longer hospital stays. High resistance rates also limit the use of commonly prescribed antibiotics, particularly for Gram-negative pathogens like *E. coli* and *Klebsiella*, thus reducing the effectiveness of empirical treatment strategies, leading to potential treatment failures.

To reduce these occurrences, antibiotic stewardship programs are critical to limit the unnecessary use of broad-spectrum antibiotics. Physicians must rely on local antibiograms for informed prescription choices. Enhancing hygiene and sanitation is also a cost-effective strategy to reduce antibiotic usage by preventing infection, likewise the use of vaccines *S. typhi* and other relevant pathogens can reduce disease burden and subsequent antibiotics usage. There is also the need for public education on the importance of proper antibiotic usage and hygiene practices to prevent infections and more investment in developing new antibiotics and alternative therapies (e.g., phage therapy, monoclonal antibodies) for effective therapy.

4. Conclusion

This study reveals Escherichia coli and Salmonella species being the most frequently identified, *E. coli* is associated with gastroenteritis and is responsible for infectious diarrhoea among children. The prevalence of *Salmonella typhi* and *Salmonella paratyphi* observed in this study is consistent with other studies in West Africa, where *Salmonella species* are a major public health concern. The isolated microorganism distributed across the gender more microbes such as *S. paratyphi* C, *P. vulgaris*, *S. aureus* and *Pseudomonas spp* shown in male while *E. coli* shown more in female which maybe because of biological and behavioral factors. The distribution of microbes according to age like *E. coli* was higher in young children and adolescents. This may be due to source of drinking water supply, sanitation and hygiene practice differences. Due to immunological or life style differences, typhoid pathogen and opportunistic infections such as *Klebsiella* and *P. vulgaris* have higher prevalence in young adult (20-39years). These findings highlight a critical public health threat. Resistance to frontline antibiotics like Augmentin, fluoroquinolones, and third-generation cephalosporins compromises the ability to treat common bacterial infections effectively which will eventually increase morbidity and mortality rate. Therefore, the misuse of antibiotics for the treatment of diarrhoea needs to be avoided.

Consent

All authors declare that written informed consent was obtained from the patient (or other approved parties) for publication of this case report and accompanying images.

Ethical approval

Ethical approval was obtained from the Federal Medical Centre ethics and research committee, Asaba. Authorization was be obtained from Microbiology Laboratory Department and Medical Record Departments of Federal Medical Centre, Asaba for ease access to patients’ folders and laboratory investigation results. All the information was kept confidential during and after the study and protected the safety, privacy and confidentiality of the patients whose results were used in the study.

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