Journal of Public Health and Epidemiology Vol. 4(9), pp. 230-237, November 2012
Available online at http://www.academicjournals.org/JPHE
DOI: 10.5897/JPHE12.055
ISSN 2141-2316 ©2012 Academic Journals

*Full Length Research Paper*

# Incidence of *Staphylococcus aureus*, coliforms and antibiotic resistant strains of *Escherichia coli* in rural water supplies in Calabar South Local Government Area

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Accepted 17 August, 2012

**An investigation on the incidence of *Staphylococcus aureus*, coliforms and antibiotic resistant *Escherichia coli* strains in both treated and untreated rural water supplies was carried out in Calabar South Local Government Area of Cross River State, Nigeria. Analysis revealed significant differences between the different water sources, locations and the months of sampling, with the stream and well water showing higher bacterial contamination compared to the tap water source (P<0.05). The isolation of *S. aureus, Bacillus* species, *Pseudomonas aeruginosa* and other bacterial pathogens present enough evidence that water from these sources are unfit for human consumption and constitute significant public health implications except subjected to further treatment. High percentages of the *E. coli* strains isolated from the water sources showed multiple resistances to most of the antibiotics commonly used by humans. Strains recovered from the stream and well water sources were most resistant and showed significantly higher minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) (P < 0.05) than those from the tap water source. The results of this investigation therefore revealed that the bacteriological quality of both the treated tap and untreated well and stream water sources failed to meet the standards for drinking water.**

**Key words:** Incidence, *Staphylococcus aureus,* coliforms, *Escherichia coli*, antibiotic resistance, water supplies.

## INTRODUCTION

The illnesses resulting from consuming faecal contaminated water are mostly treated with antibiotics, but unfortunately, there has been recent development of antimicrobial resistance by many strains of microorganisms which is now making it difficult to treat some infectious diseases (Inyang, 2009). It has long been established, that multiple drug resistances could be transferred among members of the Enterobacteriaceae, especially *Escherichia coli*; many strains of *E. coli* carry resistance factors (R-factors or plasmids) which confer resistance to antibiotics and can be transmitted among themselves and to other bacteria (Oyedeji et al., 2011). The ability of environmental bacteria to transfer antibiotic resistance genes to human pathogens can have grave consequence for human health, most especially the children and the immunocompromised individuals who are more vulnerable to bacterial illnesses (Oyedeji et al., 2011), including limiting the number of drugs available for treatment of diseases leading to fewer treatment options for the sick (Oyedeji et al., 2011). This study therefore was designed to evaluate the incidence of *Staphylococcus aureus,* coliforms and antibiotic–resistant strains of *E. coli* in rural water supplies in Calabar South Local Government Area of Cross River State.

## MATERIALS AND METHODS

### Study areas

The study sites were rural communities randomly selected within Calabar South Local Government Area located between 4°57°N latitude and 8°19°E and covering an area of 264 $km^2$, with the

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**Table 1.** Description of the rural water samples collected from different sources at different locations from Calabar South Local Government Area.

| S/N | Location | No. of samples | Source of samples |
|---|---|---|---|
| 1 | Ekpo Abasi Street | 30 | Private tap water (treated) |
| 2 | New Airport/Jeb Street | 30 | Private tap water (treated) |
| 3 | Palace Road/Anantigha Street | 30 | Private tap water (treated) |
| 4 | Rev. Mbukpa Close | 30 | Well water (majority uncovered) |
| 5 | Creek Road/Ekpenyong Abasi Street | 30 | Well water (uncovered) |
| 6 | Jebs area | 30 | Stream water |
| 7 | Anantigha abattoir water | 30 | Stream water (polluted with faecal materials from the slaughter) |
| 8 | Anantigha phase 2 | 30 | Stream water |

population size of 191,630 (NPC, 2006). The area is surrounded by lots of rural communities whose inhabitants engage mainly in farming and trading activities.

**Sample sources and collection**

The main water sources in the rural communities were identified and sampled according to the methods described by Adejuwon et al. (2011) and Oyedeji et al. (2011). A total of 240 water samples comprising of 90 tap water samples from three locations, 60 well water samples from two locations, and 90 stream water samples from three locations were collected between the months of June to October, 2011 (Table 1). Samples from streams were collected at six different points where the communities fetch their water, thereby making direct contact with the water, while those from wells and taps were collected from six different wells and taps for each location.

**Enumeration techniques**

Total heterotrophic bacteria count was prepared on standard plate count agar (Biotech Lab Ltd, UK) using pour plating technique (Oyedeji et al., *2011*). Enumeration of total and faecal coliforms, *S. aureus* and *Streptococcus faecalis* were made on MacConkey agar (Biotech Lab Ltd., UK), mFC agar (Biotech Lab Ltd., UK), *S. aureus* M110 agar (Hardy Diagnostics, USA), and bile esculine agar (Biotech Lab Ltd., UK), respectively using the standard membrane filtration technique (Ojo et al., 2005; Mihdhdir, 2009; Oyedeji et al., 2011). Plates were incubated at 35°C for 24, except the faecal coliform agar that was incubated at 44.5°C and thereafter, characteristic colonies indicative of these organisms were counted and expressed as colony forming unit per 100 ml of water samples.

Pure bacterial isolates were characterized and identified by standard methods (Cheesebrough, 2002; Prescott et al., 2002). Biochemical tests such as catalase, coagulase, citrate utilization, indole, methyl red, Voges-Proskauer, motility, ornithin decarboxylase production, oxidase, sugar fermentation (glucose, sucrose and lactose), gas, and $H_2S$ production on triple sugar agar (TSI) tests were employed.

**Antibiotic sensitivity screening of *E. coli***

Antibiotic sensitivity screening was carried out using multi-disc (Maxicare Lab., Nigeria) diffusion method as described by Akinyemi et al. (2005), Oyetao et al. (2007) and Duru and Mbata (2010). Precisely, 0.1 ml of the prepared *E. coli* strains in nutrient broth were poured onto the surface of dried Mueller-Hinton (MH) agar plate spread using swab stick and allowed to dry for about 30 min at room temperature before placing the multi-disc antibiotics on the culture plates using sterile forceps. Plates were left at room temperature on the bench for 15 min to allow for diffusion of the antibiotics before incubation at 35°C for 18 to 24 h. Results were recorded by measuring the zones of inhibition and strains were recorded as resistant if the zone of inhibition was ≤ 10 mm wide around the disc, as intermediate if the zone of inhibition was ≤ 16 mm, and as sensitive if there was a clear zone of inhibition ≥ 17 mm surrounding the disc (CLSI, 2003). However, intermediate strains were considered resistant. Gram negative discs, such as ampicillin (30 µg), augmentin (30 µg), ceporex (10 µg), gentamycin (10 µg), ciprofloxacin (10 µg), nalidixic acid (30 µg), tarivid (10 µg), perflaxin (10 µg), streptomycin (30 µg), and septrin (30 µg) were used.

**Determination of minimum inhibitory and bactericidal concentration (MIC and MBC)**

Determination of MIC and MBC was carried out using broth dilution method as described by Akinyemi et al. (2005) and Duru and Mbata (2010). A two-fold serial dilutions of the antimicrobial agents was done in series in test tubes to obtained different concentrations of 0.05, 0.10, 0.19, 0.39, 0.78, 1.56, 3.12, 6.25, 12.5, 25, 50.0, 100, 200, and 400 mg/ml for each of the antibiotics. After the different concentrations were obtained, sterile pipettes were used to deliver 0.2 ml of the 24 h nutrient broth cultures of the *E. coli* into each tube and were incubated at 35°C for 18 to 24 h. The east concentrations of the antibiotics that resulted in complete inhibition of the test bacteria after incubation were recorded as the MIC using turbidity as index, while the least concentrations in the MIC test, of which no growth was observed after sub-culturing a loopful onto freshly prepared nutrient agar were recorded as the MBC.

**RESULTS**

**Bacterial count**

All the samples collected from tap, wells, and the streams gave total heterotrophic bacterial count, total and faecal coliform counts, *S. aureus* and *S. faecalis* counts. Table 2 shows the mean counts of total heterotrophic bacteria ranged from $2.7 \pm 4.1 \times 10^2$ cfu/ml (location 1 in June) to $4.5 \pm 0.9 \times 10^2$ cfu/ml (location 3 in August), $3.2 \pm 1.2 \times 10^3$ cfu/ml (location 5 in June) to $4.8 \pm 5.2 \times 10^3$ cfu/ml (location 4 in July) and $3.3 \pm 2.0 \times 10^4$ cfu/ml (location 7 in August) to $5.6 \pm 1.6 \times 10^4$ cfu/ml (location 8 in June) for the tap, well and stream water samples, respectively.

The mean total and faecal coliform counts (Table 3) ranged from $11 \pm 2.8$ cfu/100 ml (location 1 in July) to $29 \pm 3.9$ cfu/100 ml

**Table 2.** Mean total heterotrophic bacterial counts for the water sources collected between the months June to October.

| Month sample | *Sampling sources/Location | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | Tap water | | | Well water | | | Stream water | |
| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 |
| June | 2.7 ± 4.11 | 2.7 ± 3.08 | 3.3 ± 1.61 | 3.6 ± 3.25 | 3.2 ± 1.21 | 3.7 ± 2.05 | 4.6 ± 2.89 | 5.6 ± 1.61 |
| July | 2.9 ± 2.75 | 3.0 ± 4.04 | 3.6 ± 2.084 | 4.8 ± 5.18 | 3.7 ± 5.69 | 4.0 ± 3.42 | 5.0 ± 3.85 | 3.7 ± 2.10 |
| August | 3.5 ± 3.25 | 3.1 ± 3.44 | 5 ± 0.94 | 4.5 ± 1.95 | 3.8 ± 4.76 | 4.5 ± 2.49 | 3.3 ± 2.0 | 3.3 ± 2.89 |
| September | 3.3 ± 3.13 | 3.4 ± 2.13 | 3.5 ± 3.0 | 4.4 ± 2.56 | 3.9 ± 3.68 | 4.9 ± 1.79 | 3.6 ± 3.10 | 4.0 ± 1.57 |
| October | 2.9 ± 1.97 | 3.5 ± 1.77 | 3.7 ± 1.57 | 4.1 ± 4.39 | 3.8 ± 2.31 | 4.6 ± 2.38 | 5.2 ± 4.28 | 4.6 ± 2.31 |

Data are expressed as mean ± standard error (SE) of triplicate trials. Values with different superscript across each row are significant ($P < 0.05$). *1-3 = tap water location, 4-5 = well water location, 6 – 8 = stream water location.

**Table 3.** Mean total and faecal coliform bacterial counts for the water sources collected between the months June to October.

| Microbial count | Month sample | *Sampling sources/Location | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | Tap water | | | Well water | | | Stream water | |
| | | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 |
| TCBC (cfu/100 ml) | June | 15 ± 3.02 | 26 ± 2.83 | 19 ± 3.55 | 26 ± 4.82 | 35 ± 2.36 | 35 ± 2.14 | 45 ± 3.13 | 49 ± 4.61 |
| | July | 11 ± 2.80 | 20 ± 4.93 | 29 ± 3.98 | 33 ± 4.96 | 38 ± 3.50 | 36 ± 2.67 | 51 ± 5.98 | 37 ± 2.12 |
| | August | 23 ± 3.85 | 28 ± 5.06 | 25 ± 1.53 | 29 ± 4.07 | 35 ± 2.16 | 32 ± 3.86 | 40 ± 5.59 | 40 ± 3.03 |
| | September | 18 ± 5.46 | 23 ± 2.75 | 23 ± 2.91 | 34 ± 1.34 | 32 ± 2.36 | 33 ± 3.99 | 57 ± 4.4 | 52 ± 2.50 |
| | October | 15 ± 3.40 | 16 ± 2.45 | 20 ± 2.92 | 30 ± 1.89 | 31 ± 3.98 | 35 ± 5.06 | 41 ± 4.64 | 45 ± 1.54 |
| FCBC (cfu/100 ml) | June | 6 ± 3.04 | 16 ± 3.79 | 11 ± 3.09 | 15 ± 2.75 | 19 ± 2.99 | 21 ± 4.92 | 29 ± 6.39 | 28 ± 2.31 |
| | July | 10 ± 3.90 | 13 ± 1.86 | 13 ± 1.59 | 21 ± 3.55 | 22 ± 2.54 | 27 ± 2.54 | 35 ± 3.12 | 26 ± 1.24 |
| | August | 13 ± 3.62 | 15 ± 2.52 | 18 ± 3.14 | 15 ± 2.77 | 20 ± 3.07 | 23 ± 4.19 | 28 ± 3.68 | 20 ± 1.13 |
| | September | 11 ± 2.29 | 7 ± 3.54 | 17 ± 3.13 | 24 ± 4.26 | 21 ± 2.29 | 20 ± 6.74 | 24 ± 3.19 | 28 ± 1.03 |
| | October | 9 ± 3.70 | 11 ± 2.94 | 15 ± 5.21 | 21 ± 2.89 | 22 ± 2.56 | 20 ± 2.51 | 36 ± 4.57 | 27 ± 1.41 |

Data are expressed as mean ± standard error (SE) of triplicate trials. Values with different superscript across each row are significant ($P < 0.05$). *1-3 = tap water location, 4-5 = well water location, 6 – 8 = stream water location, TCBC = total coliform bacterial counts, FCBC = faecal coliform bacterial counts.

(location 3 in July) and 6 ± 3.0 cfu/100 ml (location 1 in July) to 18 ± 3.1 cfu/100 ml (location 3 in August), respectively for the tap water samples, 26 ± 4.8 cfu/100 ml (location 4 in June) to 38 ± 3.5 cfu/100 ml (location 5 in July) and 15 ± 2.8 cfu/100 ml (location 4 in June) to 24 ± 4.3 cfu/100 ml (location 4 in September), respectively for the well water samples, and 32 ± 3.9 cfu/100 ml (location 6 in August) to 57 ± 4.4 cfu/100 ml (location 7 in September) and 20 ± 2.5 cfu/100 ml (location 6 in October) to 36 ± 4.6 cfu/100 ml (location 7 in October), respectively for the stream water samples.

The mean counts of *S. aureus and S. faecalis* (Table 4) ranged from 3 ± 0.7 cfu/100 ml (location 1 in August) to 10 ± 4.5 cfu/100ml (location 2 in October) and 5 ± 2.7 cfu/100 ml (location in October) to 12 ± 1.5 cfu/100 ml (location 3 in July), respectively for the tap water samples, 9 ± 1.9 cfu/100 ml (location 1 in August) to 18 ± 2.5 cfu/100 ml (location 1 in July) and 10 ± 1.7 cfu/100 ml (location 1 in June) to 25 ± 2.3 cfu/100 ml (location 2 in July), respectively for the well water samples, and 11 ± 2.9 cfu/100 ml (location 1 in October) to 26 ± 1.3 cfu/100 ml (location 2 in September) and 10 ± 2.6 cfu/100 ml (location 1 in August) to 28 ± 2.5 cfu/100 ml (location 2 in October) for the stream water samples.

**Table 4.** Mean *S. aureus* and *S. faecalis* counts for the water sources collected between the months June to October.

| Microbial count | Month sample | *Sampling Sources/Location | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | Tap water | | | Well water | | Stream water | | |
| | | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 |
| | June | 6 ± 1.21 | 9 ± 2.54 | 5 ± 2.08 | 15 ± 2.08 | 12 ± 2.49 | 15 ± 1.64 | 25 ± 1.63 | 14 ± 1.01 |
| | July | 8 ± 2.13 | 11 ± 1.38 | 4 ± 0.81 | 18 ± 2.54 | 15 ± 2.08 | 20 ± 1.37 | 28 ± 1.67 | 15 ± 1.81 |
| SAC | August | 3 ± 0.68 | 3 ± 1.34 | 6 ± 3.21 | 9 ± 1.86 | 12 ± 2.21 | 12 ± 2.92 | 13 ± 2.92 | 18 ± 0.54 |
| (cfu/100 ml) | September | 5 ± 1.95 | 7 ± 3.44 | 9 ± 3.84 | 15 ± 3.21 | 13 ± 1.82 | 15 ± 1.80 | 16 ± 1.25 | 15 ± 0.05 |
| | October | 6 ± 1.77 | 10 ± 4.49 | 6 ± 3.84 | 13 ± 2.74 | 11 ± 1.38 | 11 ± 2.96 | 14 ± 2.96 | 15 ± 2.10 |
| | June | 6 ± 3.48 | 6 ± 2.49 | 8 ± 1.57 | 10 ± 1.73 | 13 ± 3.30 | 13 ± 1.41 | 27 ± 3.13 | 26 ± 2.11 |
| | July | 8 ± 2.14 | 7 ± 2.36 | 12 ± 1.52 | 13 ± 3.73 | 25 ± 2.33 | 16 ± 1.59 | 25 ± 1.97 | 18 ± 1.25 |
| SFC | August | 10 ± 2.33 | 8 ± 3.09 | 6 ± 2.47 | 21 ± 1.79 | 12 ± 2.09 | 10 ± 2.06 | 25 ± 2.56 | 24 ± 1.10 |
| (cfu/100 ml) | September | 6 ± 3.01 | 5 ± 2.93 | 7 ± 2.73 | 13 ± 2.23 | 24 ± 2.06 | 13 ± 3.43 | 21 ± 2.05 | 23 ± 0.0 |
| | October | 5 ± 2.73 | 8 ± 3.18 | 5 ± 2.23 | 23 ± 2.30 | 15 ± 1.89 | 13 ± 2.06 | 28 ± 2.51 | 24 ± 1.24 |

Data are expressed as mean ± SE of triplicate trials. Values with different superscript across each row are significant ($P < 0.05$). *1-3 = tap water location, 4-5 = well water location, 6-8 = stream water location, SAC = *Staphylococcus aureus* count, SFC = *Streptococcus faecalis* counts.

Table 5 presents a summary of the morphological and biochemical characteristics of the bacteria isolated from the rural water samples from the different sources between the months of June to October.

### Incidence of antibiotic–resistant *E. coli*

The overall resistance observed was most frequently observed to ampicillin, augmentin, ceporex, gentamycin, nalidixic acid, tarivid, and perflaxin (Table 6). Isolates that exhibited resistance to at least three antibiotics were regarded as multiple antibiotic–resistant strains (Table 7). The result shows that 6 (15.4%), 19 (37.3%), and 39 (53.4%) strains from tap, well, and stream water samples, respectively were resistant to three or more antibiotics. Strains isolated from stream and well water samples gave highest MIC and MBC as compared to the tap water samples (Table 8 and 9).

## DISCUSSION

The results of the investigation revealed that the bacteriological quality of both the treated tap water samples and the untreated well and stream water samples collected from the different locations failed to meet the standard for drinking water, although significant ($P < 0.05$) differences existed between the water sources, with the stream and well water samples consistently showing higher bacterial contamination as compared to the tap water samples. The values were higher than the recommended standard for total heterotrophic bacterial counts in drinking water. Other studies had earlier reported such high bacterial loads in treated and untreated water supplies (Inyang, 2009; Oyedeji et al., 2011).

The presence of coliform in a high proportion of water samples is a good indicator of water contamination. Water meant for human consumption should be free of coliform (NIS, 2007; WHO, 2007). A high proportion of the rural water samples analysed in this study were positive for total and faecal coliforms. Stream and well water samples showed significantly ($P < 0.05$) higher total and faecal coliforms as compared to the tap water samples. The World Health Organisation (2007) recommends zero counts of faecal coliform bacteria in any 100 ml of drinking water.

The high counts obtained therefore suggest the unsuitability of these water sources for consumption purposes. The high faecal coliform bacteria counts obtained in the stream water samples could be attributed to the faecal materials consistently disposed into the stream from the abattoir house. The differences in the levels of contamination of the well water studied reflect the usually washed before used. In a similar study, Oyedeji et al. (2011) reported that the

**Table 5.** Morphological and biochemical characteristics of isolates.

| Microscopy | | | Catalase | Coagulase | Citrate | Motility | Indole | Ornithin | MR | VP | Oxidase | Glucose | Lactose | Sucrose | Gas | $H_2S$ | Probable organism |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Isolate No. | Gram's reaction | Shape | | | | | | | | | | | | | | | |
| 1 | - | Short rods | NT | NT | - | + | + | + | + | - | - | + | + | + | + | + | *E. coli* |
| 2 | + | Cocci in chister | + | + | + | - | - | + | + | - | - | + | - | + | - | - | *S. aureus* |
| 3 | + | Cocci in chains | - | - | + | - | - | + | + | - | - | + | - | - | + | - | *S. faecalis* |
| 4 | - | Short rods | NT | NT | + | + | - | + | + | - | + | - | + | + | + | - | *Enterobacter aerogenes* |
| 5 | - | Short rods | NT | NT | + | - | - | - | - | + | - | + | + | + | + | - | *Klebsiella* spp. |
| 6 | - | Short rods | NT | NT | + | + | - | + | + | - | - | + | + | + | + | + | *Salmonella typhi* |
| 7 | - | Short rods | NT | NT | + | + | + | - | - | + | + | + | - | - | + | - | *Pseudomonas aeruginosa* |
| 8 | - | Short rods | NT | NT | + | + | - | + | - | + | - | + | - | + | + | - | *Serratia marcescens* |
| 9 | - | Short rods | NT | NT | - | + | + | - | + | - | - | + | - | + | + | + | *Proteus* species |
| 10 | - | Short rods | NT | NT | - | - | - | + | + | - | - | + | + | - | + | - | *Shigella* species |
| 11 | + | Long rods | + | NT | + | + | - | - | + | - | - | + | + | - | + | - | *Bacillus* species |
| 12 | - | Short rods | NT | NT | + | + | - | - | + | - | + | + | - | - | - | + | *Chromobacterium violaceum* |
| 13 | - | Short rods | NT | NT | + | + | - | + | + | - | - | + | + | + | + | + | *Citrobacter* species |
| 14 | + | Cocci (singly) | + | - | + | - | - | + | + | - | - | + | - | - | + | - | *Micrococcus* species |

NT = Not tested, MR = Methyl red, VP = Voges-Proskauer, + = Positive test, - = Negative test.

**Table 6.** Frequency and percentage resistance of *E. coli* strains isolated in the rural water sources to test antibiotics.

| *Antibiotic (µg/disc) | Tap water (n = 39) | | Well water (n = 51) | | Stream water (n = 73) | |
|---|---|---|---|---|---|---|
| | Frequency | Percentage | Frequency | Percentage | Frequency | Percentage |
| AMP (30) | 8 | 20.5 | 17 | 33.3 | 58 | 79.5 |
| AUG (30) | 1 | 2.6 | 6 | 11.8 | 40 | 55.0 |
| CEP (10) | 6 | 15.4 | 16 | 31.4 | 35 | 47.9 |
| CN (10) | 7 | 17.9 | 16 | 31.4 | 31 | 42.4 |
| CPX (10) | 0 | 0.00 | 0 | 0.00 | 0 | 0.00 |
| NA (30) | 4 | 10.3 | 14 | 27.5 | 43 | 59.0 |
| OFX (10) | 4 | 10.3 | 9 | 17.7 | 28 | 38.4 |
| PEF (10) | 4 | 10.3 | 15 | 29.4 | 25 | 34.2 |
| S (30) | 0 | 0.00 | 0 | 0.00 | 13 | 4.0 |
| SXT (30) | 0 | 0.00 | 0 | 0.00 | 0 | 0.00 |

*AMP = Ampicillin, AUG = Augmentin, CEP = Ceporex, CN = Gentamycin, CPX = Ciprofloxacin, NA = Nalidixic acid, OFX = Tarivid, PEF = Perflaxin, S = Streptomycin, SXT = Septrin.

indiscriminate use of buckets for other purposesapart from drawing of water from wells alone could also be a potential source of contamination as these may have had contact with human faecal matter. They also reported that rain water can also pick harmful bacteria and other pollutants on the land surface and if this water pools are nearsanitary and hygienic qualities of the locations which they are sited

**Table 7.** Frequency and percentages of multiple-antibiotic resistance among *E. coli* strains.

| *Number of antibiotic | Tap water (n = 39) | | Well water (n = 51) | | Stream water (n = 73) | |
|---|---|---|---|---|---|---|
| | Frequency | Percentage | Frequency | Percentage | Frequency | Percentage |
| 1 | 9 | 23.1 | 8 | 15.7 | 25 | 34.2 |
| 2 | 3 | 7.7 | 6 | 11.8 | 4 | 5.5 |
| 3 | 5 | 12.8 | 8 | 15.7 | 12 | 16.4 |
| 4 | 1 | 2.6 | 8 | 15.7 | 14 | 19.1 |
| 5 | 0 | 0.00 | 1 | 1.9 | 7 | 10.0 |
| 6 | 0 | 0.00 | 2 | 3.9 | 2 | 3.0 |
| 7 | 0 | 0.00 | 0 | 0.00 | 4 | 5.4 |
| % not resistant: | 21 | 53.8 | 18 | 35.3 | 5 | 7.1 |
| % resistant: | 18 | 46.2 | 33 | 64.7 | 68 | 93.2 |
| % resistant to ≥1: | 12 | 30.8 | 14 | 27.5 | 29 | 40.0 |
| % resistant to ≥3: | 6 | 15.4 | 19 | 37.3 | 39 | 53.4 |

*No of antibiotics resistant.

**Table 8.** Antibiotic resistance patterns among the *E. coli* strains.

| [a]Number of antibiotic | [b]Resistance pattern |
|---|---|
| 1 | AMP; AUG; CEP; CN; NA; OFX; PEF |
| 2 | AMP/CEP; AMP/PEF; CN/NA; AMP/CN; CN/OFX; NA/CEP |
| 3 | AMP/CN/CEP; AMP/CE/PEF; AMP/CN/OFX; CN/NA/CEP; CN/NA/OFX; AUG/CN/OF; AMP/CN/PEF; CN/NA/PEF; AMP/OFX/CEP; AMP/AUG/NA; AMP/NA/CEP |
| 4 | AMP/CN/OFX/PEF; AMP/OFX/CEP/PEF; AMP/CN/NA/PEF; AMP/AUG/NA/PEF; AMP/NA/CEP/PEF; AMP/CN/OFX/CEP; AUG/CN/OFX/PEF; CN/NA/CEP/PEF; AMP/NA/OFX/CEP |
| 5 | AMP/CN/NA/CEP/PEF; AMP/AUG/OFX/CEP/PEF; AMP/CN/NA/OFX/PEF; AMP/AUG/CN/S/NA |
| 6 | AMP/AUG/NA/OFX/CEP/PEF; AMP/AUG/CN/NA/OFX/PEF; AMP/AUG/CN/OFX/CEP/PEF |
| 7 | AMP/AUG/CN/NA/OFX/CEP/PEF |

[a]No of antibiotics resistant to. [b]Resistance pattern constructed from the antibiogram; antibiotic codes as defined under methodology. AMP = Ampicillin, AUG = Augmentin, CEP = Ceporex, CPX = Ciprofloxacin, OFX = Tarivid, PEF = Perflaxin, S = Streptomycin, SXT = Septrin, CN = Gentamycin, NA = Nalidixic acid.

(Oyedeji et al., 2011). Majority of the well water studied were without protective covers and buckets used in taking water from all the wells from all locations were left carelessly on the ground after fetching water and were not the wells they can seeps down and pose potential health problems to those using the water from the wells.

The high total and faecal coliform bacteria obtained in the treated tap water samples in this destruction, in addition to providing functional study are not surprising and may be a reflection of several factors. It has been reported that coliform can be found both in chlorinated and unchlorinated water and that their total elimination from water would require the knowledge of their population in such water and determining the quantity of chlorine needed for their complete chlorinators (Inyang, 2009). However, tap water are usually stored in storage devices such as tanks and reservoirs after harvesting and therefore, having unsanitary storage devices is

**Table 9.** MIC and MBC of the different antibiotic against strains of *E. coli* isolated from well water samples.

| Antibiotic | Concentration (mg/ml) | | | | | | | | | | | | MIC range (mg/ml) | MBC range (mg/ml) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | 400 | 200 | 100 | 50.0 | 25.0 | 12.5 | 6.25 | 3.13 | 1.56 | 0.78 | 0.39 | 0.10 | | |
| AMP | - | - | - | $\beta_1$ | $\beta_2$ | $\beta_3$ | $\beta_4$ | + | + | + | + | + | 6.25 - 50 | 25 - 100 |
| AUG | - | - | - | $\beta_1$ | $\beta_2$ | $\beta_3$ | + | + | + | + | + | + | 12.5 - 50 | 25 - 100 |
| CEP | - | - | $\beta_1$ | $\beta_2$ | $\beta_3$ | $\beta_4$ | + | + | + | + | + | + | 12.5 - 100 | 50 - 200 |
| CPX | - | - | - | - | $\beta_1$ | $\beta_2$ | $B_3$ | + | + | + | + | + | 6.25 - 50 | 25 - 100 |
| OFX | - | - | $\beta_1$ | $\beta_2$ | $\beta_3$ | $\beta_4$ | + | + | + | + | + | + | 12.5 - 100 | 50 - 200 |
| PEF | - | - | $\beta_1$ | $\beta_2$ | $\beta_3$ | $\beta_4$ | + | + | + | + | + | + | 12.5 - 100 | 25 - 200 |
| S | - | - | - | $\beta_1$ | $\beta_2$ | $\beta_3$ | $\beta_4$ | $\beta_5$ | + | + | + | + | 3.13 - 50 | 12.5 - 100 |
| SXT | - | - | - | + | $\beta_1$ | $\beta_2$ | $\beta_3$ | $\beta_4$ | + | + | + | + | 3.13 - 50 | 12.5 - 50 |

AMP = Ampicillin, AUG = Augmentin, CEP = Ceporex, CPX = Ciprofloxacin, OFX = Tarivid, PEF = Perflaxin, S = Streptomycin, SXT = Septrin. β with different subscripts indicate MICs of each drug against test bacteria (many strains shared the same MIC and MBC). - = No turbidity, + = visible turbidity

known to contribute to substantial reduction in water quality (Welch et al., 2000).

Members of the genus *Staphylococci,* mostly *S. aureus* is considered as an indicator of hygienic status employed in the field of production or distribution of drinking water (Mihdhdir, 2009). Majority of the water samples from all the sources were positive for *S. aureus* and *S. faecalis,* with significantly higher counts in the stream water samples, followed by the well water samples than the tap water samples. There are many reasons for potential concern when *S. aureus* is present in drinking water supplies; *S. aureus* is a pathogen and survives longer than coliforms in water (Antai, 1987) and are implicated in waterborne diseases. The high bacterial counts obtained in this study were also recorded by other workers (Fong et al., 2007; Popoola et al., 2007; Mihdhdir, 2009; Oyedeji et al., 2011).

The presence of enteric bacterial pathogens in water sources may spell health hazards, such as diarrhoeal diseases, which accounts for a substantial degree of morbidity and mortality in adults and children (Obi *et* al., 2004). The situation is further complicated if these etiologic agents are antibiotic resistant strains (Olaoluwa et al., 2010). In this study, high incidence of *E. coli* strains resistant to commonly used antibiotics by humans is recorded. Higher incidence of multi-resistant strains were recorded in the stream and well water sources than the tap water source. Antibiotic resistance in bacteria is a serious problem facing our society today and one of the reasons responsible for this is overuse of antibiotics by humans (Oyedeji et al., 2011).

## Conclusion

The results of this investigation revealed that the bacteriological quality of both the treated tap water samples and the untreated well and stream water sources failed to meet the standard for drinking water. Strains of *E. coli* isolated from the stream and well water sources showed greater multiple antibiotic resistance as compared to the tap water source. It is therefore recommended that water from these sources be treated either by boiling or chlorinating before drinking, while the concern governmental agencies should channel effort towards improving or providing safe drinking water supplies to the areas. Thirdly, the indiscriminate use of antibiotics in therapy should be avoided to prevent the development of more antibiotic resistant bacterial strains. Further studies on this subject to include other rural water sources and communities are suggested.

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