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Prevalence of *Staphylococcus aureus* and Multiple Antibiotic-Resistant Strains of Coliforms in Rural Water Supplies in Odukpani LGA

P. L. Manji*, S.P. Antai and I.O. Jacob

Department of Microbiology, Faculty of Science University of Calabar, P.M.B 1115, Calabar, Nigeria.

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A study to determine the prevalence of *Staphylococcus aureus* and multiple antibiotic - resistant strains of coliforms in rural water supplies in Odukpani Local Government Area of Cross River State, Nigeria was carried out using standard microbiological methods. Samples were collected from different sources including taps, wells and streams at different locations in the LGA between the months of June to October, 201. The results of the analyses revealed that the bacteriological quality of both the treated tap and untreated well and stream water sources failed to meet the maximum permissible standards for drinking water, although significant differences were observed between the different sources, with the stream and well water sources significantly ($P<0.05$) showing higher bacterial contamination compared to the tap water sources. The isolation of potential bacterial pathogens shows that water from these sources may constitute significant public health hazards, such as water-borne diseases except subjected to treatment. This situation may be complicated by the fact that high percentages of the coliforms isolated from such water sources showed multiple resistance to most of the commonly used antibiotics. Strains recovered from the stream and well water sources were most resistant and showed significantly higher MIC and MBC than those from the tap water.

Key words: Prevalence, *Staphylococcus aureus,* Coliforms, Antibiotic Resistance, Water supplies.

Antibiotic resistance in bacteria is a serious problem facing the society and is as a results of several factors, among which include overuse of antibiotics by humans (Antai, 1986; Oyedeji *et al.,* 2011). The sources of water contamination also contribute significantly in determining the extent of antimicrobial resistance (Oyedeji *et al.,* 2011). The presence of antibiotic – resistant coliform bacteria in water sources used by humans may pose a serious threat to human health because of their potentials for the transfer of antibiotic resistance genes to pathogens and the environment (Oyedeji *et al.,* 2011). Many strains of coliform bacteria carry genes called resistance - factors (R-factors) or plasmids which confer resistance to antibiotics and can be transmitted readily among themselves and to other bacterial pathogenes (Antai, 1987).

Many researchers has reported resistance to multiple antibiotics among coliforms and other bacterial strains in rural water supplies in other parts of Nigeria (Antai, 1987; Olaoluwa *et al*., 2010; Oyedeji *et al*., 2011), but none has been reported in the area investigated in this study. This study was therefore undertaken to determine the prevalence of Staphylococcus aureus and multiple

* To whom all correspondence should be addressed.
E-mail: donliberty11@yahoo.com

antibiotic resistance among strains of coliforms in the rural water supplies in Odukpani LGA of Cross River State, Nigeria.

MATERIALS AND METHODS

Study areas

The study sites were rural communities randomly selected within Odukpani Local Government Areas which is located between $4^0 55^0$N latitude and $4^0 42^0$E longitude, covering an area of 361km^2, with a population size of 231,630 (NPC, 2006). The area is surrounded by lots of rural communities whose inhabitants engage mainly in farming and trading activities. The supply of municipal water is completely lacking in the areas, and as such inhabitants rely on the use of wells, streams and a few private taps as the only available sources of water for drinking and other purposes. The area is characterized by high annual rainfall in the range of 350-400mm and run-off estimated to reach 90% and as such, probability of contamination of the water sources from waste water contaminations from urban and rural run-off and agricultural activities is therefore high especially during the rainy season.

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 was 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 bacterial count was prepared on standard plate count agar (Biotech Lab Ltd, UK) using pour plating technique (Antai, 1987; Oyedeji *et al., 2011*). Enumeration of total and faecal coliforms, *Staphylococcus aureus* and *Streptococcus faecalis* were made on MacConkey agar (Biotech Lab Ltd., UK), mFC agar (Biotech Lab Ltd., UK), *Staphylococcus 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 35^0C for 24 h except the faecal coliform agar that was incubated at 44.5^0C 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 and Prescott *et al*., 2002). Biochemical tests such as catalase, coagulase, citrate utilization, indole, methyl red, Voges- Proskauer, motility, ornithine decarbozylase production, oxidase, sugar fermentation (glucose, sucrose and lactose), gas and H_2S production on triple sugar agar (TSI) tests were employed.

Antibiotic sensitivity screening

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 0.1ml of the prepared strains of isolates 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 minutes 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 minutes to allow for diffusion of the antibiotics before incubation at 35^0C for 18 – 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), nalixadic acid (30 µg), tarivid (10 µg), Perflaxin (10 µg), streptomycin (30 µg), 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); Duru and

Mbata, (2010). A twofold serial dilution of the antimicrobial agents was carried out to obtain 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. MIC was determined as the least concentrations of the antibiotics that resulted in complete inhibition of the test bacteria after incubation using turbidity as index, while the least concentrations in the MIC test which no growth was observed after sub - culturing a loopful onto freshly prepared nutrient agar were recorded as the MBC.

RESULTS

Bacterial Counts

All the samples collected from tap, wells and the streams gave a total heterotrophic bacterial count, total and faecal coliform counts, *Staphylococcus aureus* and *Streptococcus faecalis* counts. Table 2 shows the mean counts of total heterotrophic bacteria which ranged from $2.6 \pm 1.24 \times 10^2$ cfu/ml (location 1 in September) to $3.5 \pm 4.10 \times 10^2$ cfu/ml (location 2 in July), $3.2 \pm 2.56 \times 10^3$ cfu/ml (location 5 in October) to $4.3 \pm 1.61 \times 10^3$ cfu/ml (location 4 in August), and $4.1 \pm 2.01 \times 10^4$ cfu/ml (location 6 in September) to $5.4 \pm 0.91 \times 10^4$ cfu/ml (location 7 in July) for the tap, well and stream water samples respectively.

The mean total and faecal coliform counts (Table 3) ranged from 18 ± 0.89 cfu/100 ml (location 1 in June) to 30 ± 2.31 cfu/100 ml (location 2 in July) and 9 ± 3.04 cfu/100 ml (location 1 in June) to 20 ± 2.31 cfu/100 ml (location 2 in July) respectively for the tap water samples, 30 ± 42.1 cfu/100 ml (location 5 in June) to 45 ± 2.31 cfu/100 ml (location 5 in July) and 20 ± 1.54 cfu/100 ml (location 5 in June) to 28 ± 1.98 cfu/100 ml (location 4 in October) respectively for the well water samples, and 31 ± 0.34 cfu/100 ml (location 7 in August) to 50 ± 4. 31 cfu/100 ml (location 8 in October) and 17 ± 0.01 cfu/100 ml (location 7 in September) to 33 ± 0.84 cfu/100 ml (location 8 in September) respectively for the stream water samples.

The mean counts of *Staphylococcus aureus and Streptococcus faecalis* (Table 4) ranged from 6 ± 1.88 cfu/100 ml (location 3 in August) to 15 ± 1.50 cfu/100 ml (location 3 in July) and 7 ± 1.10 cfu/100 ml (location 2 in September) to 14 ± 1.2 cfu/100 ml (location 1 in June) respectively for the tap water samples, 10 ± 2.0 cfu/100 ml (location 5 in October) to 16 ± 1.81 cfu/100 ml (location 5 in August) and 10 ± 2.41 cfu/100 ml (location 4 in October) to 24 ± 0.31 cfu/100 ml (location 4 in July) respectively for the well water samples, and 10 ±

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

S. No.	Location Name	No. of samples	Source of sample
1	Okut Ikang	30	Tap water
2	Creek Town1	30	Tap water
3	Council area	30	Tap water
4	Creek Town2	30	Well water
5	Okonyong	30	Well water
6	Pamol area	30	Stream water
7	Adiabo area 1	30	Stream water
8	Adiabo area 2	30	Stream water

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

Month	*Sample Sources/Locations							
	Tap water			Well water		Stream water		
sample	1	2	3	4	5	6	7	8
June	3.0±2.10	3.3±1.24	2.7±3.24	3.0±2.10	3.3±1.24	4.6±1.61	5.2±3.10	4.8±2.1
July	3.4±0.94	3.5±4.10	3.0±3.25	3.4±0.94	3.5±4.10	4.4±0.94	5.4±0.91	4.7±1.0
August	2.9±1.24	3.0±1.61	3.4±1.98	2.9±1.24	3.0±1.61	4.2±3.11	5.1±2.10	5.0±0.9
September	2.6±1.24	2.8±1.57	2.8±4.57	2.6±1.24	2.8±1.57	4.1±2.01	5.3±1.11	4.9±2.2
October	2.6±3.11	2.9±2.77	2.7±1.77	2.6±3.11	2.9±2.77	5.0±2.31	5.0±2.31	4.6±0.3

Data are expressed as mean ± SE of triplicate trials.
*1-3 = tap water locations, 4-5 = well water locations, 6 - 8 = stream water locations

1.83 cfu/100 ml (location 6 in August) to 23 ± 1.14 cfu/100 ml (location 7 in September) and 15 ± 0.34 cfu/100 ml (location 7 in June) to 23 ± 1.34 cfu/100 ml (location 5 in July) respectively for the stream water samples.

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.

Antibiotic – resistant coliforms

Isolates were most frequently resistant to ampicillin, augmentin, ceporex, gentamycin, nalixadic acid, tarivid, and perflaxin (Table 6). Isolates that exhibited resistance to at least three antibiotics were recorded as multiple antibiotic – resistant strains (Table 7). The result shows that 2 (6.1 %), 16 (67.6 %), and 36 (44.4 %) of *E. coli* strains from tap, well and stream water samples respectively, 8 (44.4 %), 10 (35.7 %), and 12 (38.7

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

Microbial	Month	*Sample Sources/Locations							
		Tap water			Well water		Stream water		
count	sample	1	2	3	4	5	6	7	8
	June	18±0.89	25±0.24	28±0.94	35±4.51	30±2.41	41±3.12	40±3.12	33±2.41
TCBC	July	26±1.41	30±3.12	30±2.69	38±3.24	45±2.31	49±0.94	43±2.34	37±2.31
(cfu/100ml)	August	24±0.82	26±4.41	26±0.47	28±3.12	32±4.31	40±0.64	31±0.34	39±1.01
	September	25±3.81	22±0.64	25±1.73	32±0.94	35±0.63	35±1.41	36±1.45	45±1.01
	October	26±1.34	28±3.51	26±1.49	38±1.02	35±1.34	40±0.24	44±1.84	50±4.31
	June	9±3.04	15±0.61	10±3.29	21±4.10	20±1.54	26±1.15	28±1.12	24±1.31
FCBC	July	10±3.9	20±2.31	18±4.46	25±2.31	23±1.11	24±2.11	25±1.12	32±1.81
(cfu/100ml)	August	10±0.5	14±3.10	11±1.61	22±1.33	25±1.84	23±1.84	18±2.21	23±1.42
	September	12±0.6	12±2.02	15±1.37	23±2.38	21±0.61	20±1.26	17±0.01	22±0.34
	October	11±0.9	10±1.21	17±1.21	28±1.98	21±1.21	24±1.68	25±1.25	33±0.84

Data are expressed as mean ± SE of triplicate trials. *1-3 = tap water locations, 4-5 = well water locations, 6 - 8 = stream water locations, TCBC = total coliform bacteria counts, FCBC faecal coliform bacteria counts

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

Microbial	Month	*Sample Sources/Locations							
		Tap water			Well water		Stream water		
count	sample	1	2	3	4	5	6	7	8
	June	13±1.28	12±1.25	8±1.29	11±1.31	14±1.88	11±1.21	13±1.11	12±1.24
SAC	July	8±0.51	10±1.81	15±1.50	12±0.61	13±1.11	8±1.11	15±1.25	13±0.66
(cfu/100ml)	August	11±1.2	11±2.11	6±1.88	15±1.18	16±1.81	10±1.83	15±0.34	18±2.11
	September	10±2.1	12±1.20	9±3.71	11±2.50	10±2.10	15±1.84	23±1.14	16±0.41
	October	10±0.5	13±0.68	10±2.74	12±0.74	10±2.10	18±2.10	19±0.18	18±0.68
	June	14±1.2	8±2.81	7±2.73	19±1.81	23±1.94	21±1.21	20±1.81	19±2.13
SFC	July	10±1.3	13±1.25	10±2.60	13±0.34	24±0.31	23±1.34	15±0.34	20±1.18
(cfu/100ml)	August	8±1.11	9±1.82	8±1.88	15±1.25	22±1.81	21±1.34	20±1.11	19±1.54
	September	10±0.8	7±1.10	10±2.42	15±1.38	20±1.11	20±0.18	23±0.81	21±3.18
	October	11±1.0	11±1.83	7±2.26	10±2.41	21±2.41	20±2.10	16±2.18	20±1.81

Data are expressed as mean ± SE of triplicate trials. *1-3 = tap water location, 4-5 = well water location, 6 - 8 = stream water location, SAC = *Staphylococcus aureus* count, SFC = *Streptococcu faecali* counts

Table 5. Morphological and biochemical characteristics of isolates

Isolate No.	Gram's Reaction	Shape	Catalase	Coagulase	Citrate	Motility	Indole	Ornithin	MR	VP	Oxidase	Glucose	Lactose	Sucrose	Gas	H_2S	Probable Organism
1	-	Short rods	NT	NT	-	+	+	+	+	-	-	+	+	+	+	+	*Escherichia coli*
2	+	Cocci in cluster	+	+	+	-	-	+	+	-	-	+	-	+	-	-	*Staphylococcus aureus*
3	+	Cocci in chains	-	-	+	-	-	+	+	-	-	+	-	-	+	-	*Streptococcus faecalis*
4	-	Short rods	NT	NT	+	+	-	+	+	-	+	-	+	+	+	-	*Enterobacter aerugenes*
5	-	Short rods	NT	NT	+	-	-	-	-	+	-	+	+	+	+	-	*Klebsiella* sp
6	-	Short rods	NT	NT	+	+	-	+	+	-	-	+	+	+	+	+	*Salmonella typhi*
7	-	Short rods	NT	NT	+	+	+	-	-	+	+	+	-	-	+	-	*Pseudomonas aeruginosa*
8	-	Short rods	NT	NT	+	+	-	+	-	+	-	+	-	+	+	-	*Seratia marcescens*
9	-	Short rods	NT	NT	-	+	+	-	+	-	-	+	-	+	+	+	*Proteus* sp
10	-	Short rods	NT	NT	-	-	-	+	+	-	-	+	+	-	+	-	*Shigella* sp
11	+	Long rods	+	NT	+	+	-	-	+	-	-	+	+	-	+	-	*Bacillus* sp
12	-	Short rods	NT	NT	+	+	-	-	+	-	+	+	-	-	-	+	*Chromobacterium violeceum*
13	-	Short rods	NT	NT	+	+	-	+	+	-	-	+	+	+	+	+	*Citrobacter* sp
14	+	Cocci (singly)	+	-	+	-	-	+	+	-	-	+	-	-	+	-	*Micrococcus* sp

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

Table 6. Frequency percentage of resistance of Coliforms isolated from rural water sources to test antibiotics

*Antibiotic	*Escherichia coli*			*Enterobacter aerugenes*			*Klebsiella* sp		
(µg/disc)	TW (33)	WW (31)	SW (81)	TW (18)	WW (28)	SW (31)	TW (12)	WW (21)	SW (27)
AMP (30)	22 (66.7)	13 (41.9)	42 (51.9)	10 (55.6)	19 (67.9)	15 (48.4)	8 (66.7)	20 (95.2)	15 (55.6)
AUG (30)	13 (39.3)	6 (19.4)	31 (38.3)	5 (27.8)	13 (46.4)	18 (58.1)	2 (16.7)	18 (85.7)	23 (85.2)
CEP (10)	15 (45.5)	14 (45.2)	29 (35.8)	8 (44.4)	10 (35.7)	18 (58.1)	10 (83.3)	15 (71.4)	18 (66.7)
CN (10)	13 (39.5)	13 (41.9)	29 (35.8)	5 (27.8)	8 (28.6)	14 (45.2)	3 (25.0)	18 (85.7)	15 (55.6)
CPX (10)	0 (0.0)	3 (9.7)	8 (9.9)	2 (11.1)	8 (28.6)	18 (58.1)	3 (25.0)	11 (52.4)	21 (77.8)
NA (30)	12 (36.4)	14 (45.2)	25 (30.9)	9 (50.0)	13 (46.4)	11 (35.5)	8 (66.7)	15 (71.4)	18 (66.7)
OFX (10)	0 (0.0)	11(35.5)	23 (28.4)	5 (27.8)	11 (39.3)	8 (25.8)	5 (41.7)	3 (14.3)	13 (48.1)
PEF (10)	11 (33.4)	11(35.5)	26 (32.1)	8 (44.4)	10 (35.7)	15 (48.4)	3 (25.0)	8 (38.1)	18 (66.7)
S (30)	0 (0.0)	2 (6.5)	4 (4.9)	0 (0.0)	3 (10.7)	11 (35.5)	6 (50)	10 (47.1)	5 (18.5)
SXT (30)	0 (0.0)	2 (6.5)	4 (4.9)	0 (0.0)	0 (0.0)	9 (29)	2 (16.)	1 (4.8)	3 (11)

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

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

*Antibiotic	*Escherichia coli*			*Enterobacter aerugenes*			*Klebsiella* sp		
(µg/disc)	TW (33)	WW (31)	SW (81)	TW (18)	WW (28)	SW (31)	TW (12)	WW (21)	SW (27)
	TW (33)	WW (31)	SW (81)	TW (18)	WW (28)	SW (31)	TW (12)	WW (21)	SW (27)
1	19 (57.6)	3 (9.7)	6 (7.4)	8 (44.4)	11 (39.3)	14 (45.2)	3 (25.0)	8 (38.1)	5 (18.5)
2	6 (18.2)	8 (25.8)	4 (4.0)	2 (11.1)	4 (14.3)	2 (6.5)	1 (8.3)	2 (9.5)	4 (14.8)
3	2 (6.1)	4 (12.9)	2 (2.5)	1 (5.6)	3 (10.7)	2 (6.5)	1 (8.3)	4 (19.0)	4 (14.8)
4	0 (0.0)	6 (19.4)	7 (8.6)	3 (16.7)	1 (3.6)	6 (19.4)	3 (25.0)	1 (4.8)	3 (11.1)
5	0 (0.0)	2 (6.5)	6 (7.4)	4 (22.2)	3 (10.7)	1 (3.2)	1 (8.3)	3 (14.3)	3 (11.1)
6	0 (0.0)	3 (9.7)	6 (7.4)	0 (0.0)	1 (3.6)	1 (3.2)	2 (16.7)	1 (4.8)	2 (7.4)
7	0 (0.0)	1 (3.2)	15 (18.5)	0 (0.0)	2 (7.1)	2 (6.6)	1 (8.3)	2 (9.5)	4 (14.8)
% Not Resistant	6 (18.2)	4 (12.9)	35 (43.2)	0 (0.0)	3 (10.7)	3 (9.7)	0 (0.0)	0 (0.0)	2 (7.4)
% Resistant	27 (81.8)	27 (87.1)	46 (56.8)	18 (100)	25 (89.3)	28 (90.3)	12 (100)	21 (100)	25 (92.6)
% Resistant ≥ 1	25 (75.8)	11 (35.5)	10 (12.3)	10 (55.6)	15 (53.6)	16 (51.6)	4 (33.3)	10 (47.6)	9 (33.3)
% Resistant ≥ 3	2 (61.1)	16 (56.6)	36 (44.4)	8 (44.4)	10 (35.7)	12 (38.7)	8 (66.7)	11 (52.4)	16 (59.3)

*No of antibiotics resistant to. TW = Tap water, WW = Well water, SW = Stream water

%) of *Enterobacter aerogenes* strains from tap, well, and stream samples respectively and 8 (66.7 %), 11 (52.4 %), and 16 (59.3 %) of *Klebsiella* sp from tap, well, and stream samples respectively were resistant to three or more antibiotics (Table 7). The strains demonstrate 38 antibiotic resistant patterns (Table 8). Strains isolated from stream and well water samples gave highest MIC and MBC compared to the tap water samples (Table 9).

DISCUSSION

The results of the investigation revealed that all the samples collected from tap, wells and the streams contained total heterotrophic bacteria, total and faecal coliform, *Staphylococcus aureus* and *Streptococcus faecalis*. The presence of coliforms in the water samples is a good indicator of water contamination. Water meant for human consumption should be free of coliform (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 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 differences in the levels of contamination of the wells studied reflect the sanitary and hygienic qualities of the environment which they are sited (Oyedeji *et al.,* 2011). Majority of the wells studied were without protective covers and buckets used in taking water from the wells in all locations were left carelessly on the ground after fetching water and were not usually washed before used. In a similar study, Oyedeji *et al.,* (2011) reported that the indiscriminate use of buckets for other purposes apart 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 near the wells seeps through, it could pose potential health problems.

The high total and faecal coliform bacteria count obtained in the treated tap water samples in this 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 knowledge of their population in such water and determining the quantity of chlorine needed for their complete destruction, in addition to providing functional 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 known to contribute to substantial reduction in water quality (Welch *et al.,* 2000).

Members of the genus Staphylococci, mostly *Staphylococcus 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 *Staphylococcus aureus* and *Streptococcus 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 *Staphylococcus aureus* is present in drinking water supplies; *Staphylococcus aureus* is a pathogen and survives longer than coliforms in water (Antai, 1987) and are implicated in waterborne diseases. The high bacteria counts obtained in this study were also recorded by other workers (Oyedeji *et al.,* 2011; Popoola *et al.,* 2007; Mihdhdir, 2009). High incidence of coliform strains resistant to commonly used antibiotics by humans was recorded for the different water sources. 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 (Oyedeji *et al.* 2011). The results obtained in this study agree with that reported by Antai, (1987) in the rural water supplies in Port Harcourt. Stream water strains exhibited highest MIC and MBC, followed by the well water strains than the strains isolated from the tap water samples.

CONCLUSION

Based on the results of this investigation, the bacteriological quality of the water sources failed to meet the standard for drinking water. Greater proportion of the coliforms were resistant to multiple antibiotics, constituting serious health hazard to the rural inhabitants and therefore called for urgent provision of potable drinking water supplies in the area. Further studies on this subject to include other rural water sources and communities are suggested.

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