MULTIDRUG RESISTANT MICROORGANISMS FROM WATER SOURCES IN ALABATA COMMUNITY

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ABSTRACT

Alabata community is a remote community with no infrastructural accessibility such as electricity, good road and good water sources; this makes the quality of the water sources available in the three villages within Alabata community questionable. The aim of this study was to investigate the microbial quality of different water sources from three villages (Fami, Oojo and Afemo) in Alabata community in relation to seasonal change. Drinking water sources (rain, river, hand dug well and bore-hole) in the three villages were collected during rainy and dry season. Microbial isolates in the water samples were enumerated and identified using standard microbiological technique. Antibiotic susceptibility test was determined using disc diffusion method. Result showed that during the dry season, Fami stored rain water sample had the highest bacterial count of 58cfu/100 ml in January and lowest count of 2cfu/100 ml in March was recorded from Ojoo bore-hole sample. Fami river gave the highest fungal count of 14 cfu/100ml and Afemo rain recorded least count of 3 cfu/ 100 ml in the rainy season. Highest and least bacterial counts of 64cfu/100 ml and 5cfu/100 ml from Fami river in June and Afemo river in July was recorded during the dry season. The predominant genus are Bacillus, Micrococcus, Pseudomonas, Citrobacter, Klebsiella, Aspergillus and Penicillium. Highest resistance Gram positive and negative bacteria isolates are Streptococcus sp and Proteus vulgaris, respectively. Highest and lowest resistance ranged from 16.0mm to 1.24mm for Gram positive bacteria as well as 13.6mm to 2 mm for Gram negative bacteria. All the fungal isolates were highly resistant to fluconazole in all the concentrations except for Rhodotorula sp at 8 (µg/ml). Highest susceptibility was exhibited by Aspergillus flavus (19.0) mm while

***Penicillum notatum* gave the lowest sensitivity value of 1.3 mm. This study revealed that drinking water in Alabata Community contains antimicrobial resistance isolates and need adequate treatment.**

Keywords: Antibiotics; Pollution; Drinking water; Multiple antibiotic resistance; Water-borne diseases; Agar well diffusion; Alabata; *Bacillus; Pseudomonas; E.coli*

INTRODUCTION

Water is important for the survival of life and pleasant health (Owamah, 2020). The essence of water quality to human physiology and sustenance cannot be undermined (Onweluzo and Akuagbazie, 2010). Inadequate water and contamination of the available water sources are obvious in many areas of the developing nations (Muhammad *et al*., 2017). Goal 6 of the sustainable development goals (SDGs) is water supply and accessibility and seek at ensuring environmental sustainability (Edbert *et al*., 2017). In most African countries, e.g. Nigeria, provision of adequate water quality and quantity remains an essential public health requirement (Tilley et al., 2014) and according to the World Health Organization (WHO), about 1.1 billion human beings need good quality water and 2.4 billion lack access to adequate sanitation (Diakite *et al.,* 2018).

Inaddition, water is vulnerable to contamination by microorganisms and organic matter amidst other pollutants irrespective of the origin (Oludairo and Aiyedun, 2016; Anyamene and Ojiagu, 2014). Kuta et al. (2014) opined that water pollution is largely attributed to deficient personal hygiene, insufficient and ineffective water and wastes treatment facilities. The contamination of water remains a challenge of the world and contributes to high unhealthful and death due to the water and food borne diseases (Garba *et al.,* 2009). The prospect of water-borne diseases is high in several low and middle-income nations due to inadequate infrastructure, lack of appropriate public health practice, defaulted water treatment facilities, overflowing sanitary sewer systems, domestic and industrial sewage, surface run off, run off of animal faecal matters during storm, inadequate sanitation and delayed emergency action (Uprety *et al*., 2020, Egberongbe *et al*., 2012; Akinnibosun and Ayejuyoni 2015; Daramola *et al*., 2019)**.** Egberongbe *et al*. (2021) also documented that the degree of the reliance on surface water in the rural environments remains extremely high and could be exposed to contamination at point and non-point sources.

Pollution of drinking water sources such as hand dug wells, rivers and streams can occur from the surface through the use of dirty buckets that contains pathogens, flood, accidental dropping of waste, below ground contamination of the aquifer itself through leaching of wastewater from landfills or nearby wastes (Mwevura *et al*., 2021). Contamination from above may be caused by unhygienic usage of wells without covers and unhygienic sanitary practices such as disposal of human excreta in open spaces close to water sources (Opisa *et al*., 2012). The level of water contamination depends on several factors such as the amount and contaminants velocity from outside sources into groundwater, type of vicinity soil, depth of water level and closeness of the origin (Mwevura *et al.,* 2012). Seasonal changes in stream flow, standing water and dispersion of infectious agent by surface runoff and flood waters also have negative effect on levels of pathogens in water resources (Bandyopadhyay *et al.,* 2015).

Significantly, microbial contaminants such as coliforms, *Escherichia coli, Clostridium perfringens, Salmonella*, *Cryptosporidium parvum* and *Giardia lamblia* in water compromise it's safety (Opara and Nnodim, 2014). The isolation of *Escherichia coli*, *Klebsiella* and *Enterobacter species* in water are indicators of the presence of pathogenic organisms (Anyamene and Ojiagu, 2014). Studies have shown that outbreaks of water-related diseases have both spatial and temporal variations (Clennon et al., 2020) while Memon *et al*. (2011) and Thliza *et al.* (2015) in their reports, documented that working and living acting lives by human may be hindered due to water related diseases such as, diarrhoea, giardiasis, dysentery and gastroenteritis etc. which are common among the rural dwellers of developing nations.

Microbial biomass and abundance of nutrients in polluted water bodies represent a favorable habitat for the survival of microorganisms (Bouki *et al*., 2013). Knapp *et al*. (2010); Bhullar *et al*. (2012) reported that increased antibiotics resistance microorganisms and the transfer of resistance materials is a recent phenomenon that have a strong link with anthropogenic activities. Direct or indirect contact with water (drinking or recreational use) contaminated by antibiotics resistant microorganisms could harm and infect the human population and cause a menace to public health (Jiang *et al*., 2013). Different kinds of antibiotic resistant microorga-nisms have now being frequently detected in various aquatic and terrestrial environs (Ayandiran *et al*., 2014).

Moreover, growth rates of many bacteria, protozoa, viruses and helminthes may be altered as a result of temperature changes and could increase the spread of contamination in water resources (Bandyopadhyay et al., 2015). Severity of water contamination appears to be seasonal and therefore elucidation of water quality in different seasons of the year is necessary. Accessibility to safe drinking water is still a challenge in most rural areas of many developing countries. The knowledge on the quality of water from different drinking water sources of the three villages in Alabata community is very scanty, thus, this study investigated the microbiological quality of drinking water at Alabata Community (Fami, Oojo and Afemo villages) in relation to season change. This will give a systematic microbiological data and a better understanding that can serve as a basis for designing an action plan to improve the water quality in Alabata area.

MATERIALS AND METHODS

COLLECTION OF SAMPLES

Water samples (rain, river, hand- dug well and borehole) were collected three times during rainy and dry season from three villages in Alabata Communities, Odeda Local Government of Ogun State. The water samples were collected using a sterile bottle and transported to the microbiology laboratory for analyses.

MICROBIOLOGICAL ANALYSIS OF WATER SAMPLES

This was performed by the Membrane Filtration Technique. One hundred millilitres of each water sample was filtered through a 47-mm, 0.45-µm pore size cellulose ester membrane filter (Miller) and placed aseptically on the following media in a sterile petri-plates: nutrient agar, macconkey agar, eosin methylene blue agar, plate count agar and sabouraud dextrose agar. The sterile petri-plates agar containing the different media were incubated at 37 °C for 24 h, 48 h and 196 h for bacterial and fungal isolates, respectively and the resultant colonies per 100ml of samples were recorded (Abubakar *et al*., 2018).

IDENTIFICATION OF MICROBIAL ISOLATES

Bacterial isolates were characterized on the basis of their morphological and biochemical characteristics. Gram staining, catalase, coagulase, motility, oxidase, citrate utilization, indole, voges-proskaeur, methyl red, urease and sugar (glucose, lactose and sucrose) fermentation tests were carried out as described by Onuorah *et al.* (2018). The fungi isolates were identified macroscopically and microscopically using lacto phenol cotton blue (Muhammad *et al.,* 2018).

ANTIBIOTICS SUSCEPTIBILITY ASSAY

Antibiotic sensitivity of bacterial isolates

Antibiotics sensitivity patterns of the isolates were determined using the disc diffusion method. The discs were placed on Muller-Hinton agar plates that was streaked with the test cultures. The plates were inverted and left on the work bench for 30 min to allow for diffusion of antibiotics into the agar, this was followed by incubation at 37 °C for 24 h to 48hr, after which zones of inhibition were examined and interpreted using standard charts (Imarhiagbe *et al*., 2016)

Antibiotic sensitivity of fungal isolates

This was carried out using agar well diffusion method as described by Mulamattathil *et al*. (2013).

Concentrations of 0.25µg/ml, 0.5µg/ml, 1.00µg/ml, 2µg/ml, 4µg/ml and 8µg/ml of antibiotics (fluconazole, ketoconazole and iatraconazole) each was prepared. Sterile Mueller-Hinton agar plates were seeded with each of the test fungal isolates. Wells were made using a sterile cork-borer (6 mm) on the seeded plates. Different concentrations of the antibiotics were introduced into each wells and incubated at 37°C for 72 h. The diameter of inhibition zones was measured and the mean values ± SD were recorded.

RESULTS

Bacterial and fungal isolates were recovered from all the drinking water sources in Alabata Community. The bacterial and fungal counts of the different water sources investigated are shown in fig 1 to fig 4. Microbial counts were higher during the rainy season. In the dry season, Fami stored rain water and Ojoo borehole had the highest and lowest bacterial counts of 58 cfu/100ml and 2 cfu/100ml, respectively. During the rainy season, Fami river gave the highest bacterial count of 64 cfu/100 ml and Afemo rain exhibited the lowest bacterial count of 5 cfu/100 ml.

The highest and lowest fungal counts during the rainy season were 14 cfu/ 100ml (Fami river) and 2 cfu/ 100 ml (Afemo rain), respectively. Fungal counts of 3 cfu/ 100 ml (Ojoo borehole) and 10 cfu/ 100 ml (Afemo river) was also recorded during the dry season. Table 1 shows the distribution of the microbial isolates in different water sources. The predominant bacterial isolates are *Bacillus, Micrococcus, Pseudomonas, Citrobacter and Klebsiella* species while the predominant fungal isolates are *Aspergillus* and *Penicillium* species.

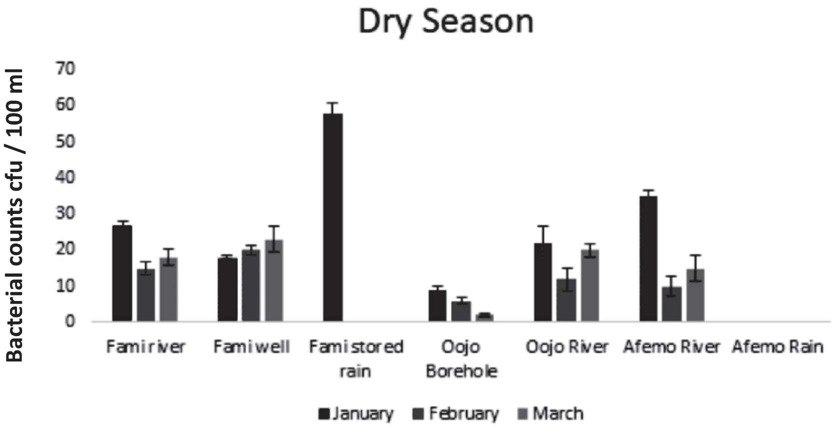

Fig 1: Total heterotrophic bacterial count of different drinking water sources in Alabata Community during dry season

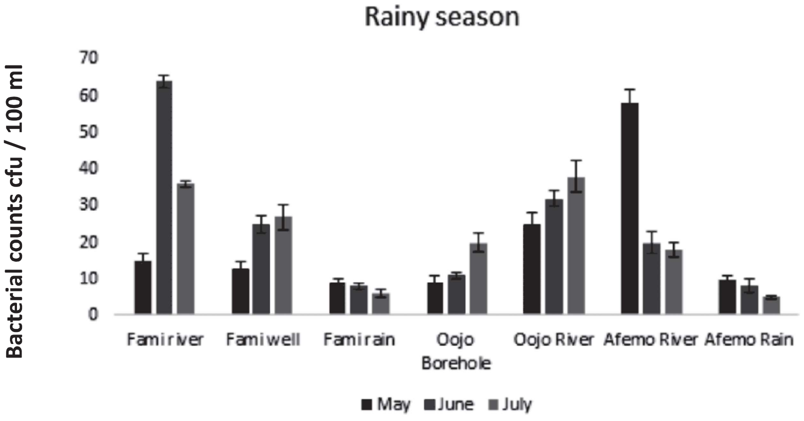

Fig 2: Total heterotrophic bacterial count of different drinking water sources in Alabata Community during rainy season

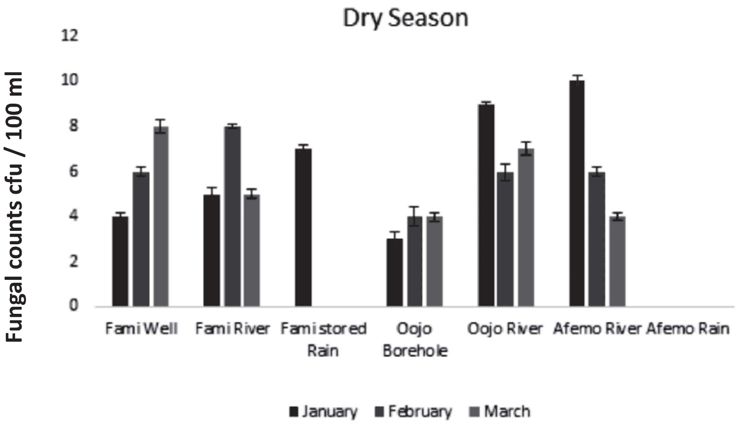

Fig 3: Total heterotrophic fungal count of different drinking water sources in Alabata Community during dry season

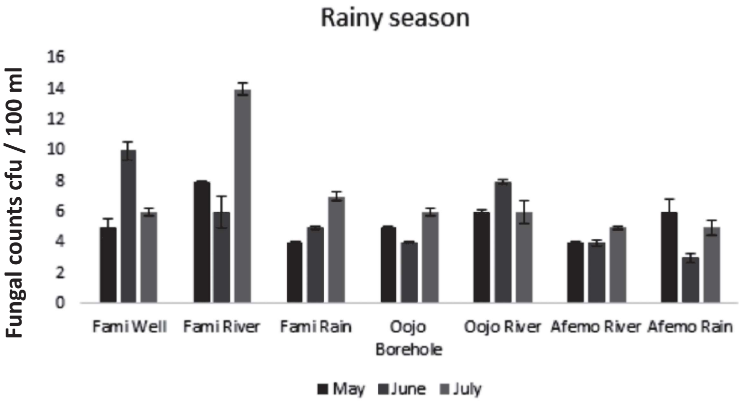

Fig 4: Total heterotrophic fungal count of different drinking water sources in Alabata Community during rainy season

Table 1: Microbial isolates from different water sources in Fami, Afemo and Ojoo villages

S/N	WATER SOURCES	BACTERIAL ISOLATES IN DRY SEASON	BACTERIAL ISOLATES IN RAINY SEASON	FUNGAL ISOLATES IN DRY SEASON	FUNGAL ISOLATES IN RAINY SEASON
1	Fami well	*Bacillus, Enterobacter and Klebsiella pneumonia*	*E. coli, Enterococcus faecalis, Micrococcus luteus, Klebsiella pneumonia, Bacillus sp, Streptococcus sp, Staph. aureus* and *Citrobacter sp,*	*Rhodotorula, Penicillium sp, Mucor sp.* and *A. niger*	*Rhodotorula, Penicillium sp, Alternaria, A. oryzae, Candida sp, Mucor sp.* and *A. niger,*
2	Fami River	*Bacillus subtilis, Citrobacter* sp, *E. coli , Enterococcus faecalis, Klebsiella pneumonia and Micrococcus sp.*	*P. aeruginosa, Serratia sp, Rhodococcus* sp., *Proteus vulgaris, Bacillus sp, Salmonella sp, Enterobacter sp,, Shigella, Klebsiella sp., Citrobacter and S. aureus*	*A. oryzae, A. flavus and Penicillium sp*	*Trichoderma spp, A. nidulans, Penicillium sp, Fusarium sp. and A. flavus*

3	Fami stored Rain	*Bacillus subtilis, Citrobacter sp, Klebsiella sp. and Enterobacter aerogenes*	*Streptococcus sp, Micrococcus spp Enterococcus faecalis*	*A. niger, Mucor sp and Penicillium sp*	*Asp flavus, Mucor sp. , A.oryzae and Penicillium sp*
4	Oojo Borehole	*P.aeruginosa, Micrococcus sp and Proteus vulgaris*	*Bacillus sp, Klebsiella variicola, P. aeruginosa, Enterococcus faecalis, Micrococcus, S. aureus and Enterobacter aerogene*	*Mucor*	*Rhodotorula and Penicillium*
5	Oojo River	*Enterococcus faecalis, Micrococcus* sp *Citrobacter sp, Bacillus subtilis, P.aeruginosa, S. aureus and Klebsiella sp.*	*Enterococcus faecalis, E.coli, Bacillus sp, Staph aureus, S. epidermidis, Citrobacter, Enterobacter sp*	*Penicillium sp and A. niger*	*Penicillium sp, A. niger, Trichoderma sp, Asp flavus*
6	Afemo River	*E. coli¸ Micrococcus sp. and P.aeruginosa.*	*Enterococcus faecalis, E.coli, Bacillus sp, Citrobacter, Micrococcus* sp *Enterobacter, S. aureus, Streptococcus sp.*		*Pen sp, Asp flavus, mucor, S.cerevisae,*
7	Afemo Rain	-	*S. epidermidis, Micrococcus* sp and *Bacillus subtilis*	-	*Asp niger* and *Penicillium sp*

Highest resistance Gram positive and negative bacteria isolates are *Streptococcus sp* and *Proteus vulgaris*, respectively. *Streptococcus sp* of Afemo river had the highest resistance to antibiotics and Citrobacter sp exhibited the least resistance to the antibiotics (Table 2). Among the Gram positive isolate, *Streptococcus sp* was susceptible to only Zinnacef. Highest and lowest resistance ranged from 16.0mm to 1.24mm for Gram positive bacteria. Gram negative bacteria showed the highest resistance value of 13.6mm by *Pseudomonas aeruginosa* and lowest of 2 mm by *Klebsiella* sp (Table 3). All the fungal isolates were highly resistant to fluconazole in all the concentrations except for *Rhodotorula sp* at 8 (µg/ml). Highest susceptibility was exhibited by *Aspergillus flavus* of 19.0 mm and *Penicillum notatum* had the lowest sensitivity value of 1.3 mm. It was observed that the fungal isolates were resistant to the antifungal drugs at lower concentrations of 0.25 to 1.0 (µg/ml). All the fungal isolates are sensitive to itraconazole at higher concentrations. *Saccharomyces cerevisiae* and *Aspergillus fumigatus* were sensitive to all the concentrations of ketoconazole except for fluconazole (Table 4).

Table 2: Antibiotic Susceptibility Pattern of Bacterial Isolates against Gram Positive Antibiotics

Bacterial isolates	Mean diameter of inhibition zone (mm)									
	Amoxacillin (30µg)	Ampiclox (30µg)	Gentamycin (10µg)	Ciprofloxacin (10µg)	Erythromycin (10µg)	Pefloxacin (10µg)	Rocephin (25µg)	Streptomycin (30µg)	Septrin (30µg)	Zinnacef (20µg)
Bacillus subtilis	2.13±0.7	4.00±1.33	9.13±2.02	0.0±0.0	0.0±0.0	13.75±1.97	14.88±0.85	2.0±0.5	0.0±0.0	1.36±1.12
Micrococcus luteus	0.0±0.00	5.66±1.3	7.88±1.9	0.0±0.00	0.0±0.0	0.0±0.0	11.23±0.9	0.0±0.00	0.0±0.00	2.83±1.2
Rhodococcus sp	6.3±1.2	4.00±0.5	5.00±1.1	16.0±3.8	0.0±0.0	0.0±0.00	9.0±2.0	15.0±4.2	5.25±1.9	1.29±0.8
Citrobacter sp	8.26±0.8	6.10±1.7	8.89±1.5	14.8±3.1	9.0±3.5	14.75±1.1	15.88±0.9	15.92±1.6	11.23±2.83	2.3±1.0
Streptococcus sp	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	1.5±0.03	0.0±0.00
Staphylococcus aureus	0.0±0.0	3.92±0.57	0.0±0.0	15.13±0.42	0.0±0.0	0.0±0.0	10.96±0.89	0.0±0.00	10.71±0.7	1.24±0.3
Enterococcus faecalis	0.0±0.0	0.0±0.00	0.0±0.00	11.25±.2.6	7.62±2.8	0.0±0.00	0.0±0.00	10.13±1.1	0.0±0.0	1.70±0.4
S. epidermidis	6.92±2.48	0.00±0.00	8.35±2.1	9.76±3.4	9.37±3.9	10.24±1.6	13.65±2.3	13.74±3.6	0.0±0.0	4.3±1.0

Table 3: Antibiotic Susceptibility Pattern of Bacterial Isolates against Gram Negative Antibiotics

Organisms	Mean diameter of inhibition zone (mm)									
	Amoxacillin (30µg)	Augmentin (30µg)	Chloranphenicol (10µg)	Gentamycin (10µg)	Ciprofloxacin (10µg)	Tarivid (10 µg)	Pefloxacin (30µg)	Streptomycin (30µg)	Sparfloxacin (10 µg)	Septrin (30µg)
Pseudomonas aeruginosa	0.00±0.0	0.00±0.0	9.6±0.5	7.5±0.3	9.33±3.18	13.60±1.72	0.00±0.00	9.00±1.6	8.13±5.17	5.67±5.17
Klebsiella sp	0.00±0.0	3.60±0.4	0.00±0.0	8.00±1.45	6.80±2.96	0.00±0.0	0.00±0.0	0.00±0.0	0.00±0.0	2.00±0.7
Salmonella sp	7.40±1.1	5.90±0.3	0.00±0.0	2.50±0.8	0.00±0.00	0.00±0.00	7.00±0.00	5.00±0.9	0.00±0.00	3.0±0.5
Escherichia coli	5.1±1.6	0.00±0.0	11.2±5.33	0.00±0.0	10.82±3.6	0.00±0.0	13.33±2.73	0.00±0.0	0.00±0.0	0.00±0.0
Shigella sp	4.18±1.3	5.23±1.9	7.11±1.9	8.63±1.4	9.4±1.8	10.46±3.5	11.25±0.7	0.00±0.0	0.00±0.0	0.00±0.0
Proteus vulgaris	9.2±2.7	3.5±1.6	0.00±0.0	0.00±0.0	0.00±0.0	0.00±0.0	6.1±0.9	0.00±0.0	0.00±0.0	0.00±0.0
Serratia	9.40±1.58	7.81±3.0	10.12±1.9	0.00±0.00	0.00±0.00	8.46±2.1	5.81±1.1	9.53±1.8	0.00±0.0	2.48±1.6
Enterobacter aerogenes	0.00±0.0	2.40±0.5	0.00±0.0	0.00±0.0	9.80±2.1	0.00±0.0	9.33±0.8	4.0±0.5	9.79±1.6	0.00±0.0

Table 4: Antifungal Susceptibility Pattern of Fungal Isolates

Isolates	**Antifungal**	**Concentration (µg/ml)**					
		0.25	**0.50**	**1.00**	**2.00**	**4.00**	**8.00**
		Zone of inhibition (mm)					
Aspergillus flavus	Itraconazole	0.0±0.0	3.5±0.4	5.2±1.3	9.6±2.0	16.4±0.8	19.0±1.2
	Ketoconazole	0.0±0.0	0.00±0.	0.00±0.0	2.7±1.0	10.0±0.8	14.1±1.3
	Fluconazole	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0
Penicillum notatum	Itraconazole	0.0±0.0	0.00±0	5.2±2.5	17.1±4.9	10.9±2.1	15.6±1.2
	Ketoconazole	0.0±0.0	3.9±0.8	5.3±1.3	7.5±2.1	14.3±1.5	16.9±3.1
	Fluconazole	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0
Aspergillus fumigatus	Itraconazole	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0
	Ketoconazole	0.0±0.0	0.0±0.0	0.0±0.0	12.6±0.9	16.7±2.9	17.4±3.3
	Fluconazole	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0
Fusarium oxysporum	Itraconazole	0.0±0.0	0.0±0.0	0.0±0.00	0.0±0.0	0.0±0.0	0.0±0.0
	Ketoconazole	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	8.5±1.1	12.0±1.9
	Fluconazole	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0
Aspergillus niger	Itraconazole	0.0±0.0	6.1±1.4	10.3±0.8	11.8±1.3	13.2±4.6	16.8±2.5
	Ketoconazole	0.0±0.0	5.3±0.9	9.4±1.6	10.0±4.8	11.0±1.7	15.8±3.6
	Fluconazole	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0
Aspergillus fumigatus	Itraconazole	1.8±0.5	3.2±2.8	5.1±0.2	7.7±2.1	10.7±2.5	15.2±1.3
	Ketoconazole	2.7±1.2	2.8±0.3	5.7±1.2	9.2±0.7	13.0±0.5	17.9±2.6
	Fluconazole	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0
Saccharomyces cerevisiae	Itraconazole	3.2±1.9	5.3±0.8	6.4±0.5	7.3±0.9	9.8±0.4	10.2±1.1
	Ketoconazole	2.6±1.4	4.9±1.3	5.1±2.7	9.4±0.6	16.9±1.8	17.1±3.5
	Fluconazole	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0
Mucor sp	Itraconazole	8.2±1.2	8.5±1.1	9.3±0.8	12.6±1.4	16.5±2.6	17.5±3.8
	Ketoconazole	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0
	Fluconazole	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0

Trichoderma sp	Itraconazole	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	5.46±0.9	7.0±1.3
	Ketoconazole	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	4.3±1.0
	Fluconazole	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0
Rhodotorula sp	Itraconazole	2.4±0.4	6.8±1.6	10.1±0.6	15.1±2.5	17.2±3.0	18.4±2.7
	Ketoconazole	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	5.30±0.9	8.1±0.6
	Fluconazole	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	6.1±1.8

DISCUSSION

The contamination of water bodies is majorly from either an identifiable point or a non-point source which is a major threat to ground water pollution. Contaminated water affect people who use the water for drinking, bathing or watering fruits and vegetable (Bouwer *et al*., 1999). Various studies on groundwater as well as surface water pollutants have been linked to aquifer run off, air and soil, leaching and direct faecal deposition into the water bodies via several livestock production activities like confined animal feedlot, free range system including solid and liquid wastes (Garba, *et al.,* 2009). Pathogenic microbes especially *Escherichia coli*, from water sources is the causative agent of gastroenteritis in humans and has been attributed to contamination by material of human and animal origin. The impacts of contaminated water depends on the individual's immune status and quantity of the water (Mazari-hiriart *et al*., 2005).

The growth of microbial isolates in the different water sources showed that the water is of poor microbiological quality, hence strict measures should be taken into consideration. Stored rain water exhibited the highest bacterial count during the dry season. Dust, particles and aerosols from the atmosphere could be washed directly into the rain water and this could be the reason why highest bacterial count was recorded from the stored rain water. Bacterial counts obtained in this study did not corroborate with the study of Oryue *et al.* (2018) where higher values of 156.6 cfu/ 100 ml and 159.1 cfu/ 100 ml was recorded during the dry and rainy season. Similarly, the fungal counts recorded was lower compared to the higher fungi counts of 207 cfu/ 100 ml recorded by Oliveira *et al*. (2016). The disparity in the microbial counts could be due to the different environmental factors as well as the human and animal activities. The identified bacterial isolates have been previously reported by several researchers. This result is in agreement with the work of Onuorah *et al*. (2018) who isolated *Klebsiella oxytoca*, *Proteus vulgaris* and *Pseudomonas aeruginosa.* Abdullahi *et al*. (2013) also isolated *E.coli*, *Klebsiella* and *Salmonella*; Ngele *et al*. (2014) isolated *Escherichia coli*, *Proteus sp*, *Pseudomonas aeruginosa* and *Enterobacter aerogenes* and Josiah *et al*. (2016) isolated *Staphylococcus aureus*, *Salmonella sp*, *Escherichia coli* and *Pseudomonas aeruginosa* from drinking water while *Aspergillus, Penicillium, Trichoderma* and *Fusarium* spp have also been reported by Siqueira *et al*. (2011) from water sources.

The dominant microbial isolates are *Bacillus, Klebsiella, Micrococcus, Pseudomonas, Aspergillus* and *Penicillium* species. The abundance of these isolates could be attributed to the prevailing environmental conditions of the area which must have been more favorable to the selected isolates. Highest microbial contamination was recorded at Fami river, followed by Afemo river in the rainy season. This could be due to the deposition of pollutants into the river or flood that contain huge organic and inorganic matters that entered into the river during heavy rain. *Pseudomonas aeruginosa* and *Escherichia coli* were the predominant bacteria isolated by Onuorah *et al*., (2018) and Uhuo *et al*., (2014). The variation in the microbial isolates could likely be due to the presence of certain available nutrients and environmental conditions that favours the predominant organisms over others in the sampling area. In general, total microbial counts significantly increased from dry season to wet season. This increase is likely to be attributed to the flood and seepage of runoff (Mwevura *et al.,* 2021).

Gram positive bacteria was more susceptible to the antibiotics than the Gram negative isolates. *Streptococcus* sp was the highest resistant Gram positive isolate while *Citrobacter* sp had the highest sensitivity to antibiotics. *Proteus vulgaris* was the highest resistant Gram negative isolate and the highest sensitive Gram negative isolate was *Pseudomonas aeruginosa*. Similar multiple antibiotics resistant isolate was reported by Ayandiran *et al*. (2014). Fluconazole was the highest resistant antifungal agent followed by Ketoconazole while itraconazole was the most susceptible drug. Most of the fungal isolates were sensitive to the antibiotics at high doses of 2-8 (µg/ml). *A. niger and Penicillium sp* are the most sensitive fungi isolates. Higher resistant fungi are *A. fumigatus* and *Fusarium oxysporum*. Antibiotic resistance cells could persist and constitute an environmental reservoir. It has been reported that bacteria can obtain resistance by horizon gene transfer between microorganisms occurring autonomous in nature and that the total utilization of antibiotic affects the choice of available resistance processes (Stokes and Gillings, 2011). Koesak *et al*. (2012) have documented bacterial resistance against Ampicillin, Gentamycin, Erythromycin, Tetracycline and Ciprofloxacin at different times. Multiple antibiotic resistances by microorganisms may be coded on several hereditary materials such as plasmids, transposons or mutational events (Ayandiran *et al*., 2014).

Results showed that all isolates in this study are resistant to more than one antibiotics (multiple drug resistances) except for *Citrobacter* sp. This could be due to their long term exposure to pollutants in their different locations. Puah *et al.* (2013) had also documented multidrug resistance (two or more antibiotics) in 93% of the tested isolates. The relatively high resistance of isolates to antibiotics in this study agrees with the findings of Rakic-Martinez *et al*. (2011) who reported high prevalence of multi-drug resistant bacteria in wastewater. The observed high frequency of microorganisms and their resistance from river samples may not only result in the death of the river fauna population, but also endanger the health of the people who are at risk of infection with pathogens from these animals including the likelihood of plasmid transfer of resistance to human pathogenic bacteria (Ayandiran *et al.,* 2014).

Conclusion

This study has revealed the presence of pathogenic microbes as well as antimicrobial resistance microorganisms in drinking water sources from Fami, Afemo and Ojoo villages at Alabata Community. Microbial resistance to multiple antibiotics is of great threat to life forms and could lead to the occurrences of newly emerging resistant cells which may be transmitted to consumers and cause infections that are difficult to treat. Also, rain water and stored rain water should be discouraged as source of drinking water. Public awareness of the public health risk associated with drinking contaminated water and need to develop effective disinfection methods for making water safe for drinking is recommended.

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