International Journal of Multidisciplinary Research and Growth Evaluation.

Isolation of coliform bacteria from surface and drinking water in Gada-Shagari, Zango-Daji community, Lokoja, Nigeria and their characterization using antibiotic resistance profile

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Article Info

ISSN (online): 2582-7138
Volume: 03
Issue: 06
November-December 2022
Received: 26-09-2022;
Accepted: 16-10-2022
Page No: 114-122

Abstract

Adequate supply of safe and sanitised fresh water is an inevitable and distinct factor for human and economic development. However, in many parts of the developing countries like Nigeria, water pollution caused by fecal contamination is a serious problem due to the potential for contracting diseases from pathogens. The aim of this study was to isolate and identify coliform bacteria from various raw water sources as well as the drinking water distributions system in Gada-Shagari, Zango Area, Lokoja, Nigeria and to characterize their antibiotic resistance profiles. For the sole purpose of reference convenience, the entire community was divided into; Gada-North (GN), Gada-South (GS), Gada-East (GE), Gada-West and Gada-Central (GC). The sampled water were analysed for the presence of coliform indicator bacteria using standard microbiological assay for the detection and enumeration of coliforms and antibiotic susceptibility tests by agar well diffusion technique. Faecal and total coliforms were detected both during dry and rainy season in most of the water samples. Multi-drug resistance was found among E. coli, Citrobacter sp., Pseudomonas p. and Salmonella sp. All isolates were susceptible to kanamycin. The result from this work indicates that the main water supply for the community under study is grossly contaminated with bacteria pathogens which could be life threatening. In addition, some of the associated bacteria were resistant to some classes of antibiotics. Hence, adequate awareness of good hygiene practice, sanitary education as well as provision of basic water supply is urgently needed in the studied community because both animal and humans are at risk of various waterborne diseases.

Keywords: Antibiotic, Resistance, Coliforms, Sanitation, Contamination and Hygiene

Introduction

Background Information

Although various antibiotic applications are required in the treatment of both human and animal diseases, however, the high rates of antibiotic-resistant microorganisms are now a global health issue. Adequate supply of safe and sanitised fresh water is an inevitable and distinct factor for human and economic development. Waterborne infections are particularly threatening owing to the importance of water for daily activities yet there is no available clean portable water in many communities in Nigeria. Therefore, there is a growing concern for the burden of antimicrobial resistance microorganisms associated with community sources of water. In this research, we use the detection of coliforms as indicator or index of sanitary conditions of the water system in the study area.

Coliforms are divided into Total coliforms which include both soil intermediate forms and fecal forms while fecal coliforms are confined to those from fecal origins as they inhabit the intestine of warm-blooded animals and are therefore used as standard microbiological indicators of water quality in this research.

Despite the importance of water in the daily activities of man, it is often known to be associated with the propagation and dissemination of several infectious disease-causing bacteria. (Muhammad *et al*., 2022) [1]. Although naturally, water is expected to be clean and safe for drinking for every human, however, most body of water are not safe for drinking unless they are further purified. The presence and prevalence of contaminating opportunistic pathogenic bacteria from the environment have a lot of health implications. For any individual to function effectively, he needs to be in a complete state of good health which has to be maintained by protecting it from the adverse effects of harmful microorganisms. Therefore, water that is meant for consumption ought to be guided from being affected by environmental bacteria. In most rural areas, there is virtually no clean source of water rather they depend on run off water from open surfaces, dams, streams and rivers which are used directly without any form of treatment. All the water bodies open to contamination to varying degrees without adequate knowledge of the possible dangers by the consumers. Rain falls run-off faecal materials into the water system as well as from farm-treated organic manure mixed with sewage effluents thereby rendering the water unsafe for consumption. which render them unacceptable for human consumption (Englande *et al.*, 2015) [2].

In the monitoring of water sanitation and public health, the presence of certain bacteria such as faecal coliforms, *Aeromonas* and *Pseudomonas*, are used as indicators of faecal contamination in water. Their presence means that such water body is unfit for consumption because of possible health consequences (Nicole *et al*., 2016) [3]. Many parts of Nigeria experience very hot weather conditions at some points of the year. This results into people needing more water which also are scares because of high evaporation. The consequence is that the little source of water is recycled, reuse and some are used by both animals and man with the tendency that pathogenic bacteria are transmitted from animal to human with grave consequences including acquiring antibiotic-resistance bacteria. Antibiotics are used on daily bases for human and animal production without prior training by many rural inhabitants (Christy *et al*., 2018) [4]. This extensive use has resulted into the development and build-up of antibiotic-resistant bacteria with major public health concerns. The presence of these microorganisms with such resistance status call for education of the rural folks because the outbreak from the pathogenic bacteria is usually not confined to such rural areas.

The concern is usually that the bacteria carrying the resistance genes become monsters that can no longer be destroyed by the usual antibiotics meant to kill them. Although chlorination of water helps to kill many bacteria, not many people can afford the cost nor the requisite knowledge to be able to use them. Therefore, the building up of multi-drug resistant bacteria strains in the community become inevitable. Gada-Shagari is a settlement in the outskirt of Lokoja, along Abuja-Okene express way, Kogi state, Nigeria. Considering the fact that the public health of this community may be related to the quality of lives in the adjacent town, determination of their water quality and subsequent offering substantive education regarding the dangers associated with water usage in the area will go a long way in offering preventive measure against outbreak of waterborne diseases in the near future. Therefore, this study was undertaken to isolate some coliforms and non- coliform bacteria from surface and drinking water in the community and to further characterize the isolates using their antibiotic resistance profiles.

Materials and Methods

Study Area

For the sole purpose of reference convenience, the entire community was divided into; Gada-North (GN), Gada-South (GS), Gada-East (GE), Gada-West and Gada-Central (GC).

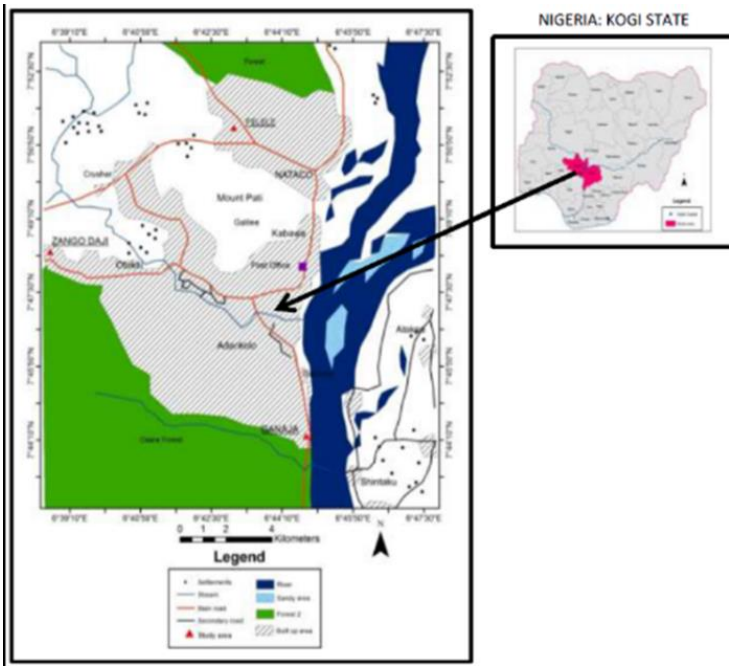

Fig 1: Lokraj: Study Area: Adopted and modified from Lokraj Topographic Map, Sheet 247, (2008)

Using sterile sample bottles, water was collected from six major sampling points around the community (Gada-Shagari) which included both water from the ground, stream and well. The choice of points of sampling was based purely on level of usage because the respective points are close by and are readily available for assessment. There is little or no treatment of the water before use. The small-scale farms are distributed around the water bodies such that surface run-off could get collected and temporary dams from where the villagers help themselves before the water finally evaporates before another rainfall. Also, patches of bushes are all around inside which both human and animals defaecates which often are washed into the nearby streams and water ways which are the major source of pathogenic bacteria of human and animal origins (João *et al*., 2010) [5].

Sampling

The water samples were collected between the months of November to June in order to cover dry and raining seasons. In 500ml capacity sterile bottles by directly dipping the bottles down from the surface of the water. Well water was collected by using their conventional fetcher after carefully drawing it up. The respective water samples were labeled properly and transported to the laboratory for analysis using standard microbiological procedures (Pramod *et al*., 2014) [6].

Isolation, Purification, and Characterization of Bacteria

The water samples (100ml) were respectively filtered through a 0.45 μm pore-sized filter (cellulose nitrate membranes, Whatman Laboratory Division, Maidstone, England) by using a water pump (model Sartorius 16824). These membranes were then placed carefully and aseptically on appropriate selective media ensuring that no air bubbles were trapped. The selective media used were prepared according to the manufacturer's instructions. Each sample was analysed in triplicate. Water samples from highly polluted sites were serially diluted and 1 ml of the 5-fold serial dilution was pread on the appropriate agar media and were incubated at 37^0C for 24 hours. Colonies were thereafter counted, studied and documented. The results were expressed as the number of faecal coliforms and total coliforms bacteria in 1 mL of water. Blue colonies from mFC agar (presumptive coliforms), metallic-sheen colonies from mEndo agar (presumptive total coliforms) selective media were picked for further studies and enumeration (Nicholson *et al*., 2017) [7].

Purification of Colonies

The discrete colonies obtained were purified by subculturing twice on sterile media from where the overnight cultures were used for Gram staining and the resulting Gram-negative Bacilli were further subjected to biochemical identification protocols (Ehsan *et al.*, 2015) [8].

Triple Sugar Iron (TSI) Test

Triple sugar iron (TSI) agar is a differential medium with the substrates glucose, sucrose, and lactose at sample concentrations of 0.1, 1.0, and 1.0%, respectively. It distinguishes between a number of Gram-negative enteric bacteria based on their physiological ability (or lack thereof) to metabolize lactose and/or sucrose, conduct fermentation to produce acid, produce gas during fermentation, and generate H_2S. The media were prepared according to the manufacturer's instructions. Aliquots were placed in test tubes and autoclaved. After autoclaving, the tubes were placed on a rack and clamped so that the tubes (with liquid medium in them) have a 3 cm slant with a 2 to 3 cm butt. After solidification, they were inoculated with a pure culture by streaking over the entire surface of the slant and then stabbing deep into the butt. They were incubated at 37°C for 24 hours. If only glucose is fermented, acid is produced in the butt and it will turn yellow. However, if either sucrose or lactose is fermented, sufficient fermentation products will be formed to turn both the butt and the slant yellow. If gas is formed during the fermentation, it will be shown in the butt either as bubbles or as cracking of the agar. If no fermentation occurs, the slant and butt will remain red. The medium also contains ferrous sulphate. If the bacterium forms H_2S, this chemical will react with the iron to form ferrous sulphide, which is seen as a black precipitate in the butt (a black butt) (Rajiv *et al*., 2012) [9].

Oxidase Test

Oxidase reagent (PL.390) from Mast Diagnostics (Nesto, Wirral, UK) in accordance with the manufacturer's published protocol was used for this test. Pure isolates were placed on a filter paper using a sterile wire loop. A drop of test oxidase reagent was added on it and mixed. After 30 seconds, the filter was observed for a colour change with oxidase positive isolates producing a purple colour. Oxidase negative colonies were colourless and were presumptively considered to be *E. Coli* (Sharon *et al*., 2012) [10].

Indole Test

Sterile test tubes containing 5ml of tryptophan broth were set on a test tube rack, the tubes were inoculated aseptically and the bacteria growth added into it. The tubes were incubated at 37^0C for 24 hours. After the 24 hours, 0.5ml of Kovac's reagent was added to the mixture and allowed to stand for 5minutes, formation of pink or red colour ring in the reagent layer on the medium (within 10 seconds) indicates positive result. Negative result shows no formation of pink or red colour ring (Darma *et al.*, 2016) [11].

Methyl Red Test

The isolates were grown in 5 ml of MR broth (glucose-phosphate peptone water) and incubated for 24 hours at 37^0C. Thereafter, 3 drops methyl red were added into each test tube. A reddish colour was observed on the addition of indicator showing positive result while a yellowish colour showed negative result (Arora and Arora, 2012) [12].

Citrate Test

Simon citrate agar was prepared and sterilized into a test tube and slanted. It was allowed to solidify before organism was inoculated on the surface of the solidified Simon citrate agar in the test tube. It was covered with cotton wool and incubated at room temperature for 24 hours. For positive result, there will be visible growth and the medium will be blue while the negative result showed no visible growth and no colour change (Adams and Moss, 1999) [13].

Catalase Test

Catalase test was done using a test tube. A clean test tube was placed on the rack, 1ml of hydrogen peroxide solution was poured into the test tube, using a sterile glass rod to remove bacteria growth and immerse it into the hydrogen peroxide solution. Presence of effervescence indicated catalase positive reaction whereas negative reaction showed no

effervescence (Adams and Moss, 1999) [13].

Sugar Fermentations

10ml of peptone water was introduced into 5 sterile test tubes respectively. Three (3) drops of methyl red was added with Durham's in an inverted position in each of the tubes and sealed with foil before sterilization in autoclave at 121^0C for 10 minutes. 1g of the respective carbohydrates, (glucose, lactose, fructose, sucrose and mannitol), were sterilized using membrane filter and added into each of the sterilized test tubes that contained the peptone water. Thereafter, the cultured organisms were inoculated into each of the tubes respectively. They were then incubated at 370c for 24 hours. Positive result indicates yellow colour while gas production was seen in the Durham's tubes (Upasana *et al*., 2020) [14].

Haemolysis on Blood Agar

Blood agar (Biolab, Merck, SA) supplemented with 5% (v/v) sheep blood was used for this test which was determined after the incubation of the plates at 37°C for 24 hours. Haemolysis is determined by streaking isolates on a blood agar plate. After incubation overnight, the medium is inspected for signs of alpha- or beta-haemolysis. If the medium is discoloured or darkened after growth, the organism has demonstrated alpha-haemolysis. If the medium develops clear halo under growth, the organism is beta-haemolytic. If there is no discernible change in the colour of the medium it is recorded for gamma haemolysis (Suma *et al*., 2014) [15].

Antimicrobial Susceptibility Testing

Cultures were sub-cultured on nutrient agar slants, plate and then incubated overnight for antibiotic susceptibility test and temporary storage. The antibiotic tests were performed using the standard Kirby-Bauer disk diffusion method () using the antibiotic discs (Mast Diagnostics, UK) at the final concentrations indicated: ampicillin (AP) −10 μg, cephalothin (KF) 5 μg, streptomycin (S) 10 μg, erythromycin (E) 15 μg, chloramphenicol (C) 30 μg, neomycin (NE) 30 μg, amoxycillin (A) 10 μg, ciprofloxacin (CIP) 5 μg, trimethoprim (TM) 25 μg, kanamycin (K) 30 μg, and oxytetracycline (OT) 30 μg. The choice of antibiotics was based on regular use for both human and animals. Few colonies resulting from each water sample were picked and transferred into 3 mL of sterile normal saline and used to prepare bacteria suspension. Aliquots of 100 μL from each suspension were spread-plated on Mueller-Hinton agar plates. Antibiotic discs were then applied carefully on to the plates using sterile needles and the plates were incubated at 37°C for 24 hours (). After incubation, the antibiotic inhibition zone diameters (IZD) were measured with caliper and the results obtained were used to classify isolates as being resistant, intermediate resistant, or susceptible to a particular antibiotic using standard reference values according to National Committee for Clinical Laboratory Standards (). Multiple antibiotic resistance (MAR) phenotypes were recorded for isolates that showed resistance to 3 or more antibiotics (Dumontet *et al*., 2000) [16].

Results

Occurrence of Coliform Bacteria

The aim of this study was to determine the levels of coliform and faecal coliforms bacteria from source and drinking water from Gada-Shagari in Zango-Daji community, Lokoja, Kogi State Nigeria and the available raw water sources were analysed for the presence of the bacteria concerned. Table 1 shows the various species of different bacteria isolated from the various sites during Raining and dry season. Both coliforms and faecal coliform bacteria were isolated from all the sampling sites. Total coliforms were the most prevalent during the dry season.

Table 1: Identified Bacteria Isolates from the various Sources of Water in the Community Using Biochemical tests

Site	Bacteria Isolate
GN	*Aeromonas sp.*
	E. coli
	Pseudomonas sp
	Serratia liquifaciens
	Proteus vulgaris
	Citrobacter sp.
GS	*Serratia liquifaciens*
	Proteus vulgaris
	E. coli
	Providencia sp
	Pseudomonas oleovorans
	Serratia sp.
GE	*Proteus vulgaris*
	Providencia sp
	Pseudomonas oleovorans
	Serratia sp.
	E. coli
GW	*Aeromonas sp.*
	E. coli
	Pseudomonas sp
GC	*Proteus vulgaris*
	Providencia sp.
	Pseudomonas oleovorans
	Serratia sp.
	Salmonella sp
	E. coli

Gada-North (GN), Gada-South (GS), Gada-East (GE), Gada-West and Gada-Central (GC)

Total coliform, fecal coliform and *E. coli* were detected in all the sites in the community studied but E. coli was low (Table 2). Gada-North has the highest number during the rainy season, 72 while Gada-South, dry season, Gada-West rainy season and Gada-Central rainy season recorded no bacteria isolate respectively.

Table 2: Occurrence and Distribution of Isolate in the Community Studied

Site	Season	Total coliform	Fecal coliform	*E. coli*	Total
GN	Dry	63	12	02	77
	Rain	72	18	07	87
GS	Dry	26	21	00	47
	Rain	31	27	06	64
GE	Dry	35	27	03	65
	Rain	39	33	08	80
GW	Dry	17	11	04	32
	Rain	24	15	00	39
GC	Dry	35	22	02	59
	Rain	17	05	00	22

Gada-North (GN), Gada-South (GS), Gada-East (GE), Gada-West and Gada-Central (GC).

Table 3 shows the occurrence of isolated bacteria based on the type of water available to the community. That is stream, Well, Borehole or Aquifer. The highest form of contamination was the stream while borehole recorded the lowest. No *E.coli* (coliforms) was observed in GC during rainy season, GW during rainy season and GS during dry season respectively.

Table 3: Occurrence of Bacteria Based on the Source of Water in the Studied Community

Site	Source of water			
	Stream	Well	Borehole	Aquifer
GN	53	21	03	08
GS	41	14	06	18
GE	32	24	16	19
GW	43	23	17	12
GC	31	18	12	25

Gada-North (GN), Gada-South (GS), Gada-East (GE), Gada-West (GW) and Gada-Central (GC).

Figure 1 shows the proportion of the bacteria isolates during the dry season while figure 2 shows similar distribution during the rainy season of the year.

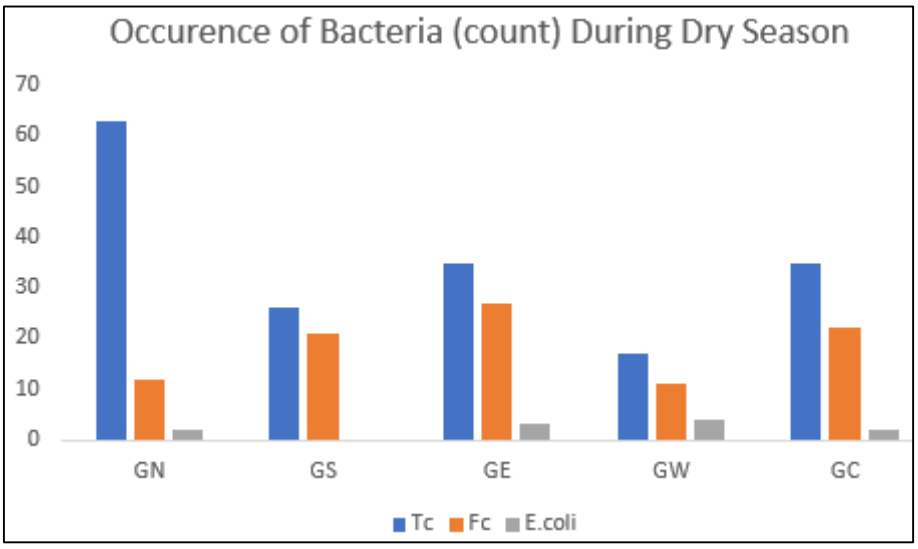

Fig 2: Occurrence of Bacteria Count during the dry season

Gada-North (GN), Gada-South (GS), Gada-East (GE), Gada-West and Gada-Central (GC).
Tc = Total coliform; Fc= Fecal coliform

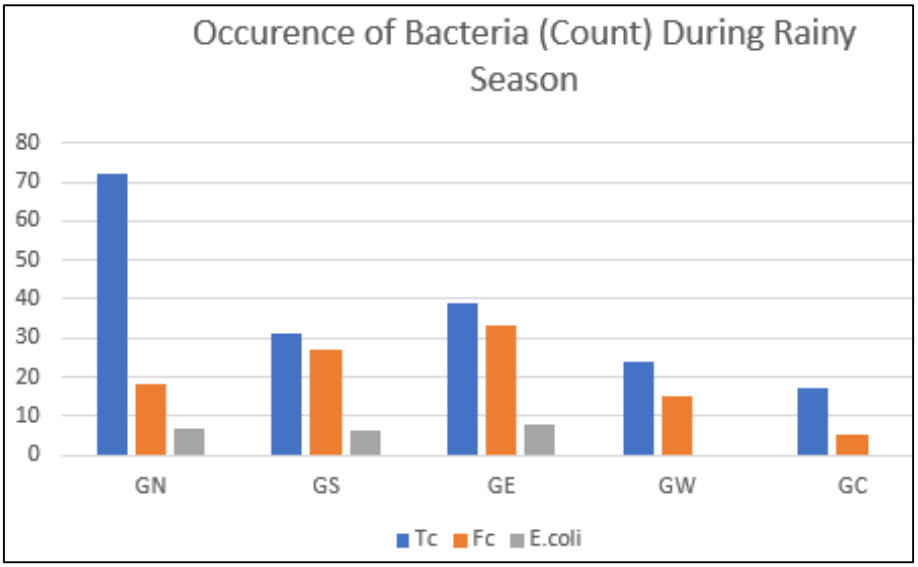

Fig. 3: Occurrence of Bacteria Count during the rainy season

Gada-North (GN), Gada-South (GS), Gada-East (GE), Gada-West and Gada-Central (GC).
Tc = Total coliform; Fc= Fecal coliform

Table 4 presents the antibiogram profile of the susceptibility of the isolated bacteria to the common antibiotics viz; ampicillin (AP) −10 μg, cephalothin (KF) 5 μg, streptomycin (S) 10 μg, erythromycin (E) 15 μg, chloramphenicol (C) 30 μg, neomycin (NE) 30 μg, amoxycillin (A) 10 μg, ciprofloxacin (CIP) 5 μg, trimethoprim (TM) 25 μg, kanamycin (K) 30 μg, and oxytetracycline (OT) 30 μg.

Table 4: Antibiotic Susceptibility Profile of Coliform Bacteria Isolated from the Study Site

Isolate	Antibiotic and the Susceptibility Pattern										
	AP	**KF**	**S**	**E**	**C**	**NE**	**A**	**CIP**	**TM**	**K**	**OT**
Aeromonas sp.	R	S	S	S	S	S	S	S	S	S	S
E. coli	R	R	S	S	R	R	R	R	S	S	S
Pseudomonas sp	R	S	S	S	S	S	S	S	S	S	S
Serratia liquifaciens	S	S	S	S	S	S	S	S	S	S	S
Proteus vulgaris	S	S	S	S	S	S	S	S	S	S	S
Citrobacter sp.	R	S	R	S	R	R	S	S	S	S	S
Providencia sp	S	S	S	S	S	S	S	S	S	S	S
Pseudomonas oleovorans	R	S	R	S	S	R	R	S	S	S	S
Serratia sp.	S	S	S	S	S	S	S	S	S	S	S
Salmonella sp	R	S	S	R	R	S	S	R	R	S	R

Ampicillin (AP), cephalothin (KF), streptomycin (S), erythromycin (E), chloramphenicol (C), neomycin (NE) 30, amoxycillin (A), ciprofloxacin (CIP), trimethoprim (TM), kanamycin (K), and oxytetracycline (OT); R=Resistant, S=Susceptible.

Serratia liquifaciens, *Proteus vulgaris*, *Providencia sp* and *Serratia sp.* were susceptible to all the antibiotic tested, *Aeromonas sp.*, *Pseudomonas sp.* and *Aeromonas sp.* were resistant to only Ampicillin but susceptible to all other antibiotics tested. However, multi-drug resistance was reported for *Salmonella spp.*, *Pseudomonas oleovorans*, *Citrobacter sp.* and *E. coli*. While resistance occurred in one drug or the other, none of the bacteria showed resistance to kanamycin making it the only drug that did not resistance in this study (Table 4).

Discussion

Our results of biochemical test confirmed the presence of bacteria listed on Table 1. Difference species of bacteria were isolated from the various sources of water that serves Gada-Shagari community during both dry and raining seasons. The diversity of bacteria isolates could be understood on the bases of differences in the water sources (Lei *et al*., 2020) [17]. While well and borehole are underground water source that might not be too exposed to contaminating agents, the stream is open to various degrees of contaminations. *E. coli* were isolated from all the sites.

Stream has the highest coliform bacteria population (53 Cfu/100ml water sample) while the lowest was found in borehole water source (03 Cfu/100ml water sample). This agrees with work of Patrick *et al*., 2019 [18] in the work on Bacterial contamination of drinking water sources in rural villages of Mohale Basin, Lesotho: exposures through neighbourhood sanitation and hygiene practices.

From the study, the contamination levels of household point-of-use (POU) water samples were very high when compared with those of Akeem *et al*., 2022 [19] where a total of 500 samples were tested, and 72.5% were found contaminated with faecal coliforms and 13.4% with *E. Coli*. Other studies also showed that POU water(s) are highly contaminated than those of their sources. It is well established that faecal coliforms can survive in water for longer periods than *E. coli*, this leads to the assumption that that the sources that are contaminated with faecal coliforms and not with *E. coli* might

not be contaminated recently (Zahid *et al*., 2019) [20]. The presence of *E. coli* is considered as the indicator of recent faecal contamination, and selection of *E. coli* is common because it is economical to detect and often present where faecal contamination is a problem such as Gada-Shagari study area where inappropriate disposal of fecal materials poses challenge as reported also in the review by Jang *et al*., 2017 [21] titled Environmental *Escherichia coli*: ecology and public health implications.

The detection of salmonella sp. in the community water source also indicate some potential sanitary and health dangers. This was in accord with the investigation carried out by Akinyem *et al*., 2011 [22] on prevalence of *Salmonella enterica* in water from taps, wells, channels and reservoirs, fish, and lettuce grown in Ouagadougou, Burkina Faso where they found that *Salmonella* contamination was rare in drinking water but common in the samples from the other sources (15-50 % prevalence). And in another study in Lagos, Nigeria, *Salmonella* was isolated from 18.5 % of drinking water samples, 23 % of the surface water samples (channels and reservoirs). This frequency is lower than in the survey conducted in Yaoundé, Cameroon, where *Salmonella* was isolated in 49.4 % of the surface water samples according to Ateba *et al*., 2012 [23].

This means that the water supplies in the locality may harbour potential pathogens and the presence of the pathogenic organisms that can pose severe health risks to the populace in general and immunocompromised individuals in particular. This agrees with the work of Wright (1989) [24] whch reported that the microbiologically contaminated water is a potential source of human enteric infections and indicates poor maintenance of hygiene-related infrastructure and problems in implementation of control measures especially in developing countries. And that, discharge of inadequately treated sewage, run-off storm water and leakage of animal waste into the environment can lead to deterioration of quality of water sources. Similar to our report in the present study, *Salmonella* has been found to survive in tropical fresh waters, such as rivers, streams and wells in Sierra Leone, for several days (Oumar *et al*., 2015) [25]. Reduction in the number of bacteria in the well, borehole and aquifer water sources could be due to the fact that they are underground sourced and are generally less proned to contamination. The presence of bacteria in such sources as recorded in this work are usually due to point-of-fetch or after fetch handlings. This agrees with work of Reed & Rasnake, 2016. However, occurrence of bacteria in the water after fetching could also harbour potential pathogens and the health risk caused by these should be taken into consideration when water has to be transported far from the source. This is of particular importance where the drinking water abstraction and purification facility are not available such as in the study area.

As shown on Table 4, the isolates were subjected to an antibiotic susceptibility test from which their antibiotic resistance profiles and multiple antibiotic resistance phenotypes were compiled. The results obtained are depicted. It can be deduced from the studied community that the issue of community bacteria resistance requires urgent attention. The presence of E. coli isolates resistant to important antibiotics such as ampicillin, Streptomycin and Chloramphenicol call for attention because these are antibiotic with high effectiveness in use against the pathogen. This is supported by the work of Dagmar *et al.*, 2014 [27] where they reported that the seriousness of the problem of bacterial resistance was confirmed by the number of deaths associated with drug-resistant bacterial infections. That only in the EU it affected 25,000 people a year. They also recalled that, with the discovery of multi-resistant strains in the broader community, public health officials have begun to realize the potential danger of the spread of these antibiotic resistant bacteria.

The results also revealed that a large proportion of the environmental isolates were susceptible to most of the antibiotic tested. None of the isolates were resistant to Kanamycin and only few isolates were resistant to oxytetracycline which are important veterinary antibiotics in common use. Multiple antibiotic-resistant (MAR - 4 to 6 antibiotics) bacteria were recorded among the isolates.

Different types of multiple antibiotic resistance patterns were observed amongst few of the the bacterial groups isolated from the various sites. The predominant antibiotic-resistant phenotypes that were obtained for the groups from different sites as depicted in Table4 occurred among *Salmonella sp., Citrobacter sp., E. coli and Pseudomonas*. Similar types of MAR phenotypes were observed in the research carried out by Jennifer *et al*., 2021 [28] in their investigation into the antimicrobial resistance among *Enterobacteriaceae*, *Staphylococcus aureus*, and *Pseudomonas* spp. isolates from clinical specimens from a hospital in Nairobi, Kenya.

Antibiotic resistance as observed among the isolates in this work could be attributed to the overuse of antibiotics in the clinical and veterinary setting. This is supported by previous studies which obtained similar results of Chattaway *et al*., 2016 [29]. Multiple antibiotic resistance (MAR) in *E. coli* and *Pseudomonas* spp. isolated from environmental samples and hospitalized patients had previously been reported. These studies support the findings of the present study. Antibiotic resistance patterns were generally similar in all the different sites. However, the largest numbers of isolates that were resistant to the largest numbers of antibiotics was were from the stream water supply in the community.

Conclusion

Although global distribution of antibiotic-resistant bacteria in surface and ground waters has been reported in several previous studies Zahid *et al*., 2019 [20], this appear to be the first recorded study from the community in particular. There is therefore the concern about the the incidence of MAR in organisms from various sources of their water supplies. Bacteria contamination with resistant strains could be attributed to heavy contamination from open fecal surface runoff, agricultural activities, wild life, and so forth which are obvious in the study area. Considering the high level of poverty in the area, the importance of such findings cannot be overemphasized to avoid the incidence of outbreak which might not be easy to contained. The results of this study on coliform bacterial presence and their resistance profiles should be used to educate the community about the danger of compromising sanitary standards as prevention is far better than cure.

Recommendations

Based on our findings, the following recommendations are drawn; Since the community (Gada-Shagari) supports small scale farming close to and around the streams, livestock graze leading to faeces wash-off around the water sources should cautioned;

Overhead tanks should be constructed for the available wells so that the wells could be closed with access being from the pumped water freserved in the tanks;

The respective local government authority should establish simple water closet and sewage treatment system to deter the populace from open defecation to prevent contaminations;

There is need to study the correlation between the resistant isolates and the trend of available antibiotics in and aroud the community. This would provide information about the health risks associated with the consumption of contaminated water and the common antibiotics around.

Our findings showed that almost all of the water samples collected directly from the well, borehole and aquifer were free from faecal contamination. This means that most of the underground aquifers are safe and could be assumed that contaminations are mainly secondary after the water were collected. Post collection contamination is mainly due to inadequate knowledge and lack of personal and domestic hygienic practices which needs to be communicated to the populace. Therefore, necessary measures should be taken to build up awareness programs about proper hygienic practices in the study area and other places and they should be trained on basic treatment of contaminated household water by a suitable method to provide safe water.

Conflict of Interest

The authors declare that there is no conflict of interests regarding the publication of this paper.

References

1. Muhammad Junaid, Junaid Ali Siddiqui, Mamona Sadaf, Shulin Liu, Jun Wang. Enrichment and dissemination of bacterial pathogens by microplastics in the aquatic environment; Science of The Total Environment. 2022; 830:154720.
2. AJ Englande, Jr Peter Krenkel, J Shamas. Wastewater Treatment &Water Reclamation; Reference Module in Earth Systems and Environmental Sciences. 2015; B978-0-12-409548-9.09508-7.
3. Nicole H Martin, Aljoša Trmčić, Tsung-Han Hsieh, Kathryn J Boor, Martin Wiedmann. The Evolving Role of Coliforms As Indicators of Unhygienic Processing Conditions in Dairy Foods; Microbial food safety along the dairy chain; Front. Microbiol. 30 September 2016 Sec. Food Microbiology, 2016.
4. Christy Manyi-Loh, Sampson Mamphweli, Edson Meyer, Anthony Okoh. Antibiotic Use in Agriculture and Its Consequential Resistance in Environmental Sources: Potential Public Health Implications; Molecules, 2018, 23(4):795.
5. João PSC. Water Microbiology. Bacterial Pathogens and Water; Int J Environ Res Public Health. 2010; 7(10):3657-3703.
6. Pramod K Pandey, Philip H Kass, Michelle L Soupir, Sagor Biswas, Vijay P Singh. Contamination of water resources by pathogenic bacteria; AMB Express. 2014; 4:51.
7. Nicholson KN, Neumann K, Dowling C, Sharma SE. *E. coli* and coliform bacteria as indicators for drinking water quality and handling of drinking water in the Sagarmatha National Park, Nepal. Environ Manag Sustain Dev. 2017; 6:411-28.
8. Ehsan Humayun, Aqsa Bibi, Atif Ur Rehman, Sajjad Ahmad, Nodia Shujaat. Isolation and Identification of Coliform Bacteria from Drinking Water Sources of Hazara Division, Pakistan; IOSR Journal Of Pharmacy. 2015, 5(4):36-40.
9. Rajiv P, Salam HS, Kamaraj M, Sivaraj R, Balaji R. Comparative physicochemical and microbial analysis of various pond waters in Coimbatore District, Tamil Nadu, India. Ann Biol Res. 2012; 3:3533-40.
10. Sharon L, Abbott JA, Lidgard WKW, Cheung MN, Obeso ZL, Berrada J, *et al*. Expression of ESBL-like activity in infrequently encountered members of the FamilyEnterobacteriaceae. Cur Microbiol. 2012; 64:222-225.
11. Darma AI, Sani I, 1Anisa IA. Isolation and Identification of Coliform Bacteria Escherichia Coli And Staphylococcus Aureus In Some Commercially Sold Yoghurts Within Kano Metropolis; International Journal of Pure and Applied Zoology. 2016; 4(1):8-11. 2320-9577.
12. Arora DR, Arora B. Textbook of Microbiology, 3rd edition. CBS Publishers, New Delhi, 2012.
13. Adams MR, Moss MO. Food Microbiology low priced edition. The Royal Society for Chemistry Thomas Graham House, Science Park Cambridge CB 4 OWF, 1999, 103.
14. Upasana Bhumbla, Shipra Majumdar, Sarita Jain, AS Dalal. A study of isolation and identification of bacteria from lake water in and around Udaipur, Rajasthan; J Family Med Prim Care. 2020; 9(2):751-754.
15. Suma George Mulamattathil, Carlos Bezuidenhout, Moses Mbewe, Collins Njie Ateba. Isolation of Environmental Bacteria from Surface and Drinking Water in Mafikeng, South Africa, and Characterization Using Their Antibiotic Resistance Profiles; J Pathog. 2014; 2014:371208.
16. Dumontet S, Krovacek K, Svenson SB, Pasquale V, Baloda SB, Figliuolo G. Prevalence and diversity of *Aeromonas* and *Vibrio* spp. in coastal waters of Southern Italy. Comparative Immunology, Microbiology and Infectious Diseases. 2000; 23(1):53-72.
17. Lei Zhang, Yanan Cai, Miao Jiang, Jing Dai, Xiyao Guo, Wei Li, *et al*. The levels of microbial diversity in different water layers of saline Chagan Lake, China; Journal of Oceanology and Limnology. 2020; 38:395–407.
18. Patrick Gwimbi, Maeti George, Motena Ramphalile. Bacterial contamination of drinking water sources in rural villages of Mohale Basin, Lesotho: exposures through neighbourhood sanitation and hygiene practices; Environmental Health and Preventive Medicine. 2019; 24:33.
19. Akeem Ganiyu Rabiu, Olutayo Israel Falodun, Obasola Ezekiel Fagade, Rotimi Ayodeji Dada, Iruka N Okeke. Potentially pathogenic *Escherichia coli* from household water in peri-urban Ibadan, Nigeria; J Water Health jwh2022117, 2022.
20. Zahid Hayat Mahmud, Md Shafiqul Islam, Khan Mohammad Imran, Syed Adnan Ibna Hakim, Martin Worth, *et al*. Occurrence of *Escherichia coli* and faecal coliforms in drinking water at source and household point-of-use in Rohingya camps, Bangladesh; Gut Pathogens. 2019; 11:52.
21. J Jang, HG Hur, MJ Sadowsky, MN Byappanahalli, T Yan, S Ishii. Environmental *Escherichia coli*: ecology and public health implications-a review. 2017;

123(3):570-581.
22. Akinyemi KO, Iwalokun BA, Foli F, Oshodi K, Coker AO. Prevalence of multiple drug resistance and screening of enterotoxin (stn) gene in *Salmonella enterica* serovars from water sources in Lagos, Nigeria. Public Health. 2011; 125:65-71.
23. Ateba BH, Nougang ME, Noah EO, Tamatcho KB, Tawedi RE, Mbilongo J. Occurrence of *Salmonella* spp in surface waters of Yaoundé, Cameroon. J Environ Sci Water Resource. 2012; 1:243-50.
24. Wright R. The survival patterns of selected faecal bacteria in tropical fresh waters. Epidemiol Infect. 1989; 103:603-11.
25. Oumar Traoré, Outi Nyholm, Anja Siitonen, Isidore Juste O Bonkoungou, Alfred S Traoré, Nicolas Barro, *et al*. Prevalence and diversity of *Salmonella enterica* in water, fish and lettuce in Ouagadougou, Burkina Faso; BMC Microbiology. 2015; 15:151.
26. Reed BC, Rasnake MS. An Assessment of Coliform Bacteria in Water Sources Near Appalachian Trail Shelters Within the Great Smoky Mountains National Park; Wilderness & Environmental Medicine. 2016; 27(1):107-110.
27. Dagmar Chudobova, Simona Dostalova, Iva Blazkova, Petr Michalek, Branislav Ruttkay-Nedecky, Matej Sklenar, *et al*. Effect of Ampicillin, Streptomycin, Penicillin and Tetracycline on Metal Resistant and Non-Resistant *Staphylococcus aureus;* Int J Environ Res Public Health. 2014; 11(3):3233-3255.
28. Jennifer Lord, Anthony Gikonyo, Amos Miwa, Agricola Odoi. Antimicrobial resistance among Enterobacteriaceae, Staphylococcus aureus, and Pseudomonas spp. isolates from clinical specimens from a hospital in Nairobi, Kenya; Peer J. 2021; 9:e11958.
29. Chattaway MA, Aboderin AO, Fashae K, Okoro CK, Opintan JA, Okeke IN. Fluoroquinolone-resistant enteric bacteria in sub-saharan Africa: clones, implications and research needs. Frontiers in Microbiology. 2016; 7:558.