African Scientist Vol. 26, No. 1 March 31, 2025
Printed in Nigeria

1595-6881/2025 $80.00 + 0.00
© 2025 Society for Experimental Biology of Nigeria
https://africansciientistjournal.org

afs2024054/26103

Comparative Study on Water Quality Monitoring of Underground and Surface Water in Some Rural Agricultural Communities in Ogun State, South-Western Nigeria

Adesetan, Titilayo Oyeronke*[1], Adekunle, Oladunni Nimota[2], Owagboriaye, Folarin Ojo[2], Oladunjoye, Rasheed Yemi[2], Adeleke, Mistura Temitope[2], Banjo, Omowunmi Abosede[1] and Osibogun, Abdulwahab Adesanya[2]

[1]Department of Microbiology, Olabisi Onabanjo University, Ago-Iwoye, Nigeria
[2]Department of Zoology and Environmental Biology, Olabisi Onabanjo University, Ago-Iwoye, Nigeria

*Corresponding author email: titilayo.adesetan@oouagoiwoye.edu.ng; +234 (0) 805 546 9763

(Received December 20, 2024; Accepted in revised form February 21, 2025)

ABSTRACT: Portable water supply is crucial to the survival of the human race since water is life. Samples of water from 69 wells, 40 boreholes and 4 streams were collected and the isolation of microorganisms from the samples was carried out according to International Standard Organization (ISO) methods and bacteria recovered were characterized using standard biochemical tests. The susceptibility of the bacteria to antibiotics was ascertained using the Kirby-Bauer disc diffusion method. The highest viable, coliform, *Escherichia coli*, *Salmonella*, *Shigella*, *Pseudomonas* and fungal counts were 1683.33±416.67, 52.67±6.26, 6.50±1.50, 2.00±0.00, 1.50±0.0, 4.00±0.00, 10.00±2.35 from Ilaporu wells, Mamu wells, Mamu stream, Mamu stream and wells, Mamu stream, Mamu boreholes and Oru stream, respectively. The occurrence of the bacteria in descending order was *Klebsiella pneumoniae* (31.7%), *Enterobacter* spp (27.0%), *E. coli* (20.4%), *P. aeruginosa* (9.0%), *Salmonella* sp (8.4%), *Shigella* sp. (3.0%) and *Proteus mirabilis* (0.6%). Fungi such as *Penicillium*, *Aspergillus* and *Trichoderma* were recovered. The susceptibility of the bacteria to the different antibiotics showed 72.5% susceptibility to ciprofloxacin and 19.8% to chloramphenicol. The presence of *E. coli*, which is known as a faecal indicator of water quality in these water sources, calls for concern because consumption of this water may lead to waterborne diseases.

Keywords: Antibiotics resistance, Bacteria, Community, Fungi, Water

Introduction

Water is indispensable for the survival of all organisms. Without water, there is no life as plants depend on water for growth, while animals feeding on these plants also need water for digestion. Access to potable water is crucial to human survival; hence, the absence of potable drinking water can subject people to serious waterborne diseases such as typhoid, gastroenteritis, cholera, amoebiasis, hepatitis, scabies and worm infections. About 2 billion people globally lack access to clean and safe drinking water (Bayram, 2023). There is a gradual increase in the contamination of river waters by microorganisms which include bacteria, parasites, and fungi (Niyogi, 2005; Abraham *et al*., 2010) from humans and other animals. Also, water can be polluted by pathogens through the discharge of untreated sewage from wastewater plants (Donovan *et al.*, 2008; Musyoki *et al.*, 2013). Some of the pathogens include *Shigella*, *Escherichia coli*, *Salmonella*, *Vibrio*, *Norwalk* virus, *Entamoeba*, *Cryptosporidium* and *Giardia*.

The presence of fungi in surface or underground water has been reported by different authors, and the most frequently encountered genera are *Aspergillus*, *Penicillium* and *Acremonium* (Oliveria *et al.*, 2016; Nwankwo *et al.*, 2020; Ren *et al.*, 2023). Fungi are known for the production of odor and pigment in water as well as the blocking of water pipes (Hussain *et al.*, 2010). Among the yeasts, *Candida*, *Rhodotorula* and *Cryptococcus* have been reported (Pereira *et al.*, 2009; Ayanbimpe *et al.*, 2012).

Antibiotics are life savers, but recently microorganisms have become resistant to these antibiotics at an alarming rate. Antimicrobial Resistance (AMR) is identified as one of the threats to global health as bacteria resistant to antimicrobials will be the leading cause of death globally by 2050 (O'Neill, 2014). Human can be exposed to Environmental AMR bacteria through contaminated water and food which can result in infections. Most people living in agricultural settlements do not have access to clean and safe drinking water, rather, they get their water from unsafe sources such as streams. Some of these settlers defecate directly into the water bodies and still use the same water for domestic purposes. Unsafe drinking water transmits waterborne diseases to the population. Therefore, this research aims to compare the microbial load and identify the different microorganisms in the water samples to observe the quality of underground and surface water in rural agricultural settlements.

Materials and methods

Sampling: This cross-sectional study involved 69 hands dug wells, 40 boreholes and 4 streams across the study communities. The study communities are: Ago-Iwoye, Ilaporu, Oru, Awa, Ijebu-Igbo, Mamu and Abeokuta. Early morning visits were made to the communities and the Global Positioning System (GPS) coordinates of all the different sources of water were taken. Three (3) litres of water were collected from each source into polyethylene water containers. All the collected water samples were labelled, preserved in ice boxes at a temperature between 4 – 10 °C to avoid any contamination, and transported to the Microbiology Laboratory of the Department of Microbiology, Olabisi Onabanjo University, Ago - Iwoye for microbial analysis within the first 12 h.

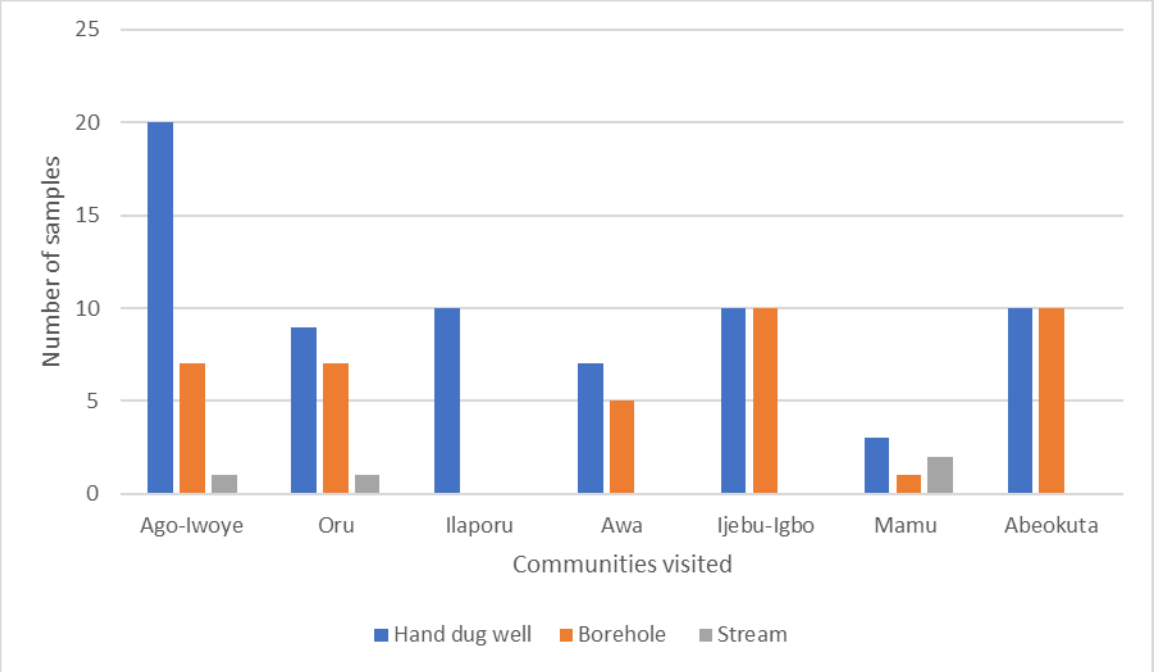

Figure 1: Distribution of water samples and their sources among the communities visited within the study area

Isolation of microorganisms: Total viable count (TVC) (by the use of the spread plate method), total coliform count (TCC) and *Escherichia coli* count were carried out according to ISO (2000). The *P. aeruginosa* parameter was tested using the membrane filtration technique according to the standard method ISO 16266:2006 (ISO, 2006). Deoxycholate Citrate Agar (DCA) plates were streaked with the water samples and the plates were incubated at 37 °C for 24 h. For the detection of *Shigella* and *Salmonella*, the water samples were cultured on S*almonella-Shigella* Agar.

For fungi detection, 0.1 ml of each water sample was streaked on Malt agar and Potato Dextrose Agar (PDA) plates, and the plates containing were incubated at 25 - 30 ºC. After 24 – 72 h, the number of mold and yeast colonies was counted using the colony counter (Rompre *et al.*, 2002).

Identification of bacteria isolates: Pure culture of positive colonies from all the media used were further identified using colonial, microscopic and biochemical tests. Catalase, indole, urease, citrate, oxidase, methyl red, triple sugar iron agar and sugar fermentation tests are the biochemical tests carried out as described by Cheesbrough (2006).

Fungal identification: Fungal colonies on PDA plates were subcultured several times, to get a pure culture of each isolate. Identification of fungi was done by observing the morphology under the microscope. The hyphae were stained with cotton blue in lactophenol, viewed under the x 40 objective lens and further identified with standard reference (Barnett and Hunter, 1987).

Antimicrobial susceptibility test: Antimicrobial susceptibility tests for the bacteria isolates recovered from the water samples were carried out using the Kirby-Bauer disc diffusion method (Bauer *et al*.,1966). The pure culture of the isolates was introduced into normal saline water and standardized to 0.5 McFarland solution. A sterile swab stick was used to seed the bacteria on Muller Hinton plates and the antibiotic discs: aztreonam (30 µg), ciprofloxacin (5 µg), ceftazidime (30 µg) and chloramphenicol (30 µg) were placed on the plates aseptically. The plates were incubated invertedly at 35 ºC overnight. The zones of inhibition of the antibiotic discs were read to the nearest millimeter (mm).

Results

Microbial loads in water sample: The frequency of occurrence of bacteria in wells, boreholes and stream water from the study area collection sites is presented in Fig 1. Most of the bacteria recovered from the water samples were from Ago-Iwoye, followed by Abeokuta while Ilaporu had the least bacterial isolates.

The microbial load of the microorganisms in the water samples is presented in Tables 1a and 1b. The highest total viable count was from the Ilaporu well, followed by Oru stream; for the total coliform count, the Mamu well and borehole have the highest count of 52.67 ± 6.26^{a} and 35.00 ± 0.00^{b} respectively. The highest fungal load was from the Ago-Iwoye borehole, followed by water sourced from boreholes in Abeokuta and the least were from wells from Oru. Yeast and mould were not recovered from Oru and Awa boreholes and wells.

Identification of microorganisms: The colonial morphology of the bacteria isolates on the different media is presented in Table 2. One hundred and sixty-seven (167) Gram-negative bacteria were recovered from the water samples after carrying out Gram staining and biochemical tests, which comprised six genera of bacteria. The bacteria identified with their percentage occurrence were *Klebsiella pneumoniae* (31.7%), *Enterobacter* spp (27.0%), *E. coli* (20.4%), *P. aeruginosa* (9.0%), *Salmonella* sp (8.4%), *Shigella* sp. (3.0%) and *Proteus mirabilis* (0.6%) (Figure 3) while *Penicillium*, *Aspergillus*, *Trichoderma* and *Candida* were the fungi identified in the water.

Antimicrobial susceptibility test: The result of the antimicrobial susceptibility test is presented in Table 4. The susceptibility of the bacterial isolates in descending order to the tested antibiotics was 72.5%, 64.7%, 23.9% and 19.8% respectively for chloramphenicol, ceftazidime, aztreonam and ciprofloxacin. *Klebsiella* was the most sensitive to all the tested antibiotics.

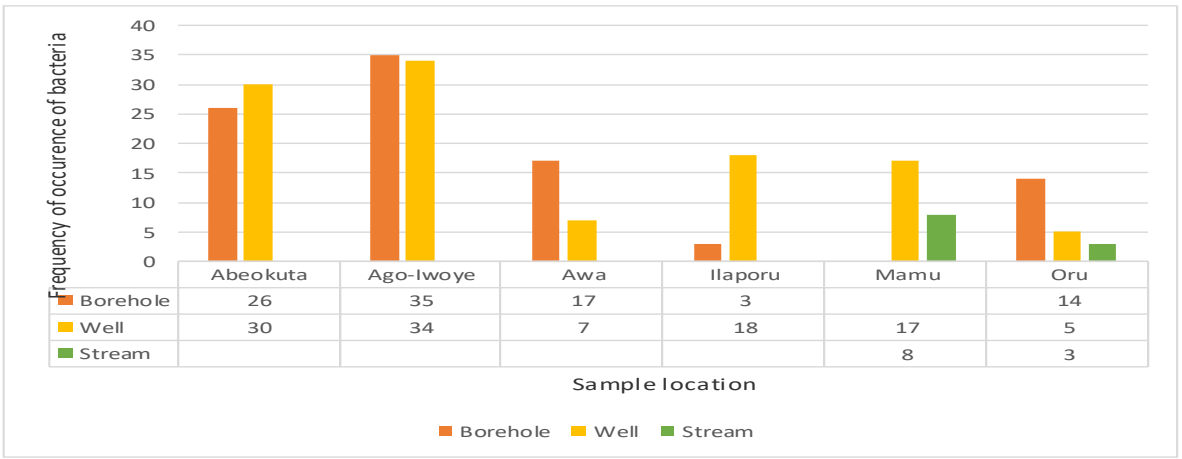

Figure 2: Frequency of occurrence of bacteria in water sources in relation to the study area

Table 1a: Microbial evaluation of drinking water collected from the rural communities of Ijebu-North, Southwestern Nigeria

	Ilaporu Well	Awa Well	Borehole	Ago-Iwoye Well	Borehole	Ijebu-Igbo Well	Borehole
	Microbial load in cfu/ml						
Total viable count, cfu/ml	1683.33±416.67^{a}	116.00±36.03^{c}	325.83±110.80^{b}	168.12±58.78^{b}	94.29±24.19^{b}	286.00±92.44^{b}	86.75±14.74^{d}
Total coliform count	5.33±3.53^{b}	0.00±0.00^{c}	4.83±3.17^{b}	3.83±1.71^{b}	2.00±0.86^{b}	3.40±0.93^{b}	0.00±0.00^{c}
E. coli cfu/100ml	0.33±0.33^{b}	0.00±0.00^{c}	1.50±1.12^{b}	1.00±0.44^{b}	0.00±0.00^{b}	0.80±0.37^{b}	0.00±0.00^{c}
Salmonella count	0.00±0.00^{c}	0.00±0.00^{c}	0.33±0.33^{b}	0.58±0.42^{b}	0.00±0.00^{b}	0.20±0.20^{b}	0.00±0.00^{c}
Shigella count	0.00±0.00^{c}	0.00±0.00^{c}	0.17±0.17^{b}	0.25±0.18^{b}	0.00±0.00^{b}	0.00±0.00^{c}	0.00±0.00^{c}
P. aeruginosa count	1.33±0.67^{a}	0.00±0.00^{c}	0.67±0.49^{b}	0.67±0.33^{b}	0.83±0.65^{b}	0.40±0.24^{b}	0.00±0.00^{c}
Yeast & mould count	6.67±4.41^{a}	0.00±0.00^{b}	0.00±0.00^{b}	8.91±2.35^{a}	4.33±3.20^{b}	0.50±0.50^{b}	0.50±0.29^{c}

^{abcd}Mean values (±Standard deviation) in the same row having similar superscripts are not significantly different ($p > 0.05$)

Table 1b: Microbial evaluation of drinking water collected from Mamu, Oru and Abeokuta, Ogun State Nigeria

	Mamu Stream	Well	Borehole	Oru Stream	Well	Borehole	Abeokuta Well	Borehole
	Microbial load in cfu/ml							
Total viable count	350.00±130.00^{a}	96.25±54.74^{b}	410.00±0.00^{a}	2100.00±0.0^{a}	148.8±25.18^{c}	52.75±19.94^{d}	134.45±34.0^{c}	383.3±87.24^{b}
Total coliform count	25.00±10.00^{c}	52.67±6.26^{a}	35.00±0.00^{b}	22.00±0.00^{a}	1.25±0.48^{c}	0.00±0.00^{d}	3.60±1.45^{c}	14.50±1.86^{b}
E. coli cfu/100ml	6.50±1.50^{a}	5.33±2.40^{a}	5.00±0.00^{a}	5.00±0.00^{a}	0.00±0.00^{b}	0.00±0.00^{b}	0.80±0.49^{b}	4.20±0.66^{a}
Salmonella count	2.00±0.00^{a}	2.00±0.00^{a}	1.00±0.00^{a}	4.00±0.00^{a}	0.00±0.00^{b}	0.00±0.00^{b}	0.60±0.43^{b}	1.60±0.40^{b}
Shigella count	1.50±0.50^{a}	1.00±0.00^{a}	0.00±0.00^{b}	0.00±0.00^{b}	0.00±0.00^{b}	0.00±0.00^{b}	0.20±0.13^{b}	1.00±0.26^{a}
P. aeruginosa	2.50±0.50^{b}	2.33±1.33^{b}	4.00±0.00^{a}	4.00±0.00^{a}	0.00±0.00^{c}	0.00±0.00^{c}	0.40±0.27^{c}	1.10±0.41^{b}
Yeast & mould count	7.00±3.00^{a}	4.67±2.91^{a}	5.00±0.00^{a}	10.00±0.00^{a}	0.25±0.25^{c}	0.00±0.00^{c}	4.60±3.01^{b}	7.70±1.42^{a}

^{abcd}Mean values (±Standard deviation) in the same row having similar superscripts are not significantly different ($p > 0.05$)

Table 2: Colonial Morphology of Gram-negative bacteria isolated from the different water samples

No of isolates	Nutrient Agar	MacConkey Agar	Eosin Methylene Blue	Salmonella-Shigella Agar	Deoxycholate Agar
34	Large, thick, moist opaque, greyish white colony	Circular, convex, smooth, surface, pink, opaque	Circular, convex, smooth surface, green metallic sheen, opaque		
53	Large, mucoid, whitish colony	Large, mucoid, pink to red colonies	Large mucoid pink to purple colonies	Red coloured colonies	
15	Large, flat, opaque colonies with a greenish colour	Pink, mucoid small colonies	Pink colour colonies with a dark center		
45		Round, flat and colourless colonies	Raised and mucoid with colourless colonies		
5	Grey, white, moist, smooth colonies		Colourless colonies	Smooth, colourless colonies with a black center	Colourless, smooth, and shiny colonies with black centers
14	Off-white colonies with smooth surface		Colourless colonies	Colourless colonies	Colourless, smooth, shiny colonies
1	Small, and glistening colony				

Table 3: Gram staining and biochemical characteristics of Gram-negative bacteria recovered from borehole, well and stream water samples

No of Isolates	Gram staining	Catalase	Oxidase	Citrate	Urease	Methyl red	VP	Motility	Indole	Gas	H_2S	Gelatin hydrolysis	Starch	Sucrose	Glucose	Lactose	Arabinose	Mannitol	Maltose	Probable Identity
34	- R	+	-	-	-	+	-	+	+	+	-	-	-	-	+	+	+	+	-	*E. coli*
53	- R	+	-	+	+	-	+	-	-	+	-	-	-	+	+	+	+	+	+	*Klebsiella pneumoniae*
45	- R	+	-	+	-	-	+	+	-	+	-	-	-	+	+	+	+	+	+	*Enterobacter aerogenes*
15	- R	+	+	+	-	-	-	+	-	+	-	+	-	-	-	-	-	+	-	*Pseudomonas aeruginosa*
14	- R	+	-	-	-	+	-	+	-	-	+	-	nd	-	+	-	-	+	+	*Salmonella typhi*
5	- R	+	-	-	-	+	-	-	-	-	-	-	nd	-	+	-	-	+		*Shigella flexneri*
1	- R	+	-	+	+	+	-	+	-	+	+	+	-	-	+	-	-	-	-	*Proteus mirabilis*

Key: nd - not done, H_2S - Hydrogen Sulphide, VP - Voges Proskauer, R - rods, - : negative, +: positive

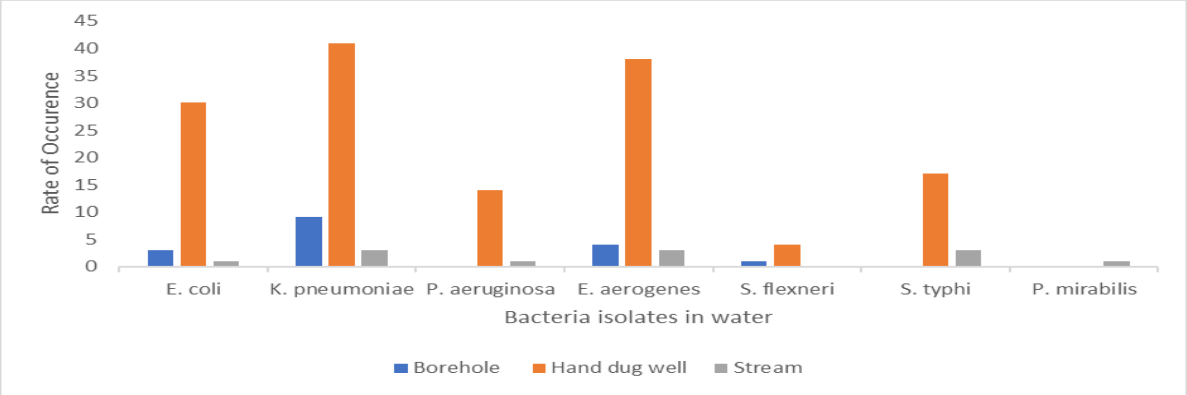

Figure 3: Rate of occurrence of Gram-negative bacteria in water samples

Table 4: Classification of the bacterial isolates into susceptibility class

Isolate code	No of Isolates	Aztreonam			Chloramphenicol			Ceftazidime			Ciprofloxacin		
		R	I	S	R	I	S	R	I	S	R	I	S
KL	53	12	39	2	17	31	5	5	15	33	9	7	37
EA	45	10	20	15	9	29	7	5	11	29	9	6	30
EC	34	4	10	20	4	17	13	5	1	28	3	3	28
PA	15	6	8	1	2	5	8	4	4	7	4	0	11
ST	14	7	6	1	1	13	0	1	7	6	0	4	10
SF	5	0	5	0	0	5	0	0	1	4	0	1	4
PM	1	0	0	1	0	1	0	0	0	1	0	0	1
% total	167	39	88	40	33	101	33	20	39	108	25	21	121

Key: KL - *Klebsiella pneumonie*, EA - *Enterobacter aerogenes*, EC - *Escherichia coli*, PA - *Pseudomonas aeruginosa*, ST - *Salmonella typhi*, SF - *Shigella flexneri*, PM - *Proteus mirabilis*, S - Susceptible, R - Resistant, I - Intermediate Resistant.

Discussion

The total viable count of stream water in Oru is greater than the well and borehole while the microbial load for Mamu stream is lesser than the borehole but greater than the microbial load in the well. This conforms with the work of Shahina *et al.* (2020) who stated that the MPN indicator of the surface water obtained was higher when compared with groundwater. The total viable count was high in well water from Ilaporu and stream water from Oru while the highest total coliform count was recorded in Mamu well, closely followed by the borehole. WHO permissible limit for heterotrophic count in water is < 500 cfu/ml. Stream water from Oru and well water from Ilaporu exceeded this limit, therefore they are not fit for drinking. The presence of coliform in well water and underground water has been reported, such as Shahina *et al.* (2020) who reported the presence of a large number of coliforms in both surface and underground water. Coliform was detected in almost all the water samples except the Oru borehole and Awa well. The mean coliform count in the water samples analyzed is greater than the permissible limit of WHO which says no *E. coli* must be detected in a 100 mL sample of drinking water (WHO, 2018), which means that all the drinking water samples containing coliform are not good for consumption.

The contamination of stream and well water from this area may be because of flood water entering into the stream while that of well water may be due to openness and shallowness of the groundwater that allows easy entrance of particles from the surrounding. It may also be a result of poor hygienic conditions (Adesakin *et al.*, 2020) of people using the well. This is further corroborated by the findings of Oyedele *et al.* (2019) who stated that the shallowness of the well makes it susceptible to unfitting disposal and penetration of effluent from solid waste, biological wastes, septic tanks and latrines into the groundwater. It is estimated that 842,000 deaths per year are as a result of inadequate water supply, sanitation and hygiene, mostly in low- and middle-income countries (Murray *et al.*, 2012).

Six bacteria species were identified in this study, which differs from the findings of Shahina *et al*. (2020) who reported 13 species of bacteria from both surface and underground water. The six bacteria species recovered in our study were also reported in their findings. Adesakin *et al*. (2020) did not detect any *S. aureus* in the borehole and tap water analyzed. However, they reported an abundance of *Proteus* spp. in tap and reservoir water than other bacteria while *Enterobacter* spp. were recovered mostly in river water. Agwaranze *et al*. (2017) reported *Staphylococcus aureus* as having the highest occurrence followed by *E. coli* (46.67%). *S. aureus* was not recovered from any of the water sources in the current study, meanwhile *E. coli* occurred more than any of the isolates. Shahina *et al*. (2020) reported that *E. coli*, *K. pneumoniae* and *E. aerogenes* occurred more in both underground and surface water than any of the other bacteria recovered. *Pseudomonas* was reported as the most prevalent in surface and drinking water in Mafikeng, South Africa (Mulamattathil *et al.*, 2014).

Many people living in rural areas lack proper hygiene and septic due to space limitations, crowding and a lack of a proper drainage network; thus the septic pit system is extensively used in this area, and seepage from these underground pits into the nearby wells might have contaminated the well water sources (Mukhopadhyay *et al.*, 2012). The presence of *E. coli* in water may be because of contamination from sewage or animal waste (EPA, 2001). It has been used as an indicator of water quality. WHO guidelines demand the absence of coliform of faecal origin in municipal drinking water supplies as reported by Javaid *et al.* (2022). According to the EPA, the presence of *E. coli* shows fresh sewage or animal waste contamination. Digging of pit latrines or septic tanks very close to boreholes and wells may result in the seepage of bacteria into these water sources. Also, the dumping of refuse inside water bodies can lead to an increase in bacteria load in the water which is corroborated by Lukubye and Andamaery's (2017) findings. *P. mirabilis* is predominantly a commensal of the gastrointestinal tract of humans and animals (Armbuster and Mobley, 2012) along with *E. coli* and *Klebsiella*, and causes serious infection.

The detection of moulds such as *Penicillium*, *Aspergillus* and *Trichoderma* is in line with the findings of Oliveria *et al*. (2016) and Ren *et al*. (2023) who reported the presence of these fungi in groundwater. Fungal pollution of water can lead to mycotoxin production, food contamination, odour and turbidity (Ren *et al*., 2023). The presence of these fungi in water may be from the soil, crops, plant debris and organic matter (Hageskal *et al*., 2009). Ayanbimpe *et al.* (2012) also reported the presence of *Candida* and *Rhodotorula* in water used for domestic purposes.

Shahina *et al*. (2020) reported that the Gram-negative bacteria recovered from water samples were 100% resistant to ceftazidime/clavulanic acid, amoxyclav followed by gentamicin, ceftriaxone and ceftazidime whereas they were susceptible to amikacin and ciprofloxacin. The isolates in this study also displayed a high resistance to ceftazidime and chloramphenicol. Mulamattathil *et al.* (2014) reported that coliforms from surface and drinking water are 100% susceptible to ciprofloxacin. Resistance to these antibiotics may be because of the production of enzymes capable of introducing chemical changes to the antibiotics (Wilson, 2014). Amarasiri *et al.* (2020) reported that the aquatic environment is one of the key routes for the spread of antimicrobial resistance. Pathogenic bacteria of human and animal origin that are released with wastewater into the water body harbour antibiotic-resistance genes and can spread among water and soil organisms (Alonso *et al*., 2001).

In conclusion. this study has revealed the presence of pathogenic bacteria of human and animal origin. Some of these pathogens are responsible for water-borne diseases if taken directly and may likely cause food-borne diseases if this water is used in preparing foods without taking the necessary precautions. These bacteria are also resistant to some common antibiotics which called for concern. Also, the presence of toxin-producing fungi is of great health implications for humans and livestock. The government should endeavor to provide open lectures to the inhabitants of these rural dwellings on the possible aftermath of defecating in water bodies. Consumers of the water should also ensure they practice good hygiene in terms of boiling and filtering the water before drinking.

Acknowledgments

We wish to appreciate household members across the study communities who gave their consent to allow us to take water from their water sources.

References

Abraham WR: Megacities as sources for pathogenic bacteria in rivers and their fate downstream. Int J Microbiol, 2011: 798292. 2010.

Adesakin TA, Oyewale AT, Bayero U, Mohammed AN, Aduwo IA, Ahmed PZ, Abubakar ND. Barje IB: Assessment of bacteriological quality and physico-chemical parameters of domestic water sources in Samaru community, Zaria, Northwest Nigeria. Heliyon, 6: e04773. 2020.

Agwaranze DI, Ogodo AC, Nwaneri CB: Bacteriological examination of well water in Wukari, Nigeria. Int J Environ Sci, 5(2): 0042-0046. 2017.

Alonso A, Sanchez P, Martinez JL: Environmental selection of antibiotic resistance genes. Environ Microbiol, 3:1-9. 2001.

Amarasiri M, Sano D, Suzuki, S: Understanding human health risks caused by antibiotic resistant bacteria (ARB) and antibiotic resistance genes (ARG) in water environment. current knowledge and questions to be answered. Crit Rev Environ Sci Technol, 50: 2016 - 2059. 2020.

Armbruster CE, Mobley HLT: Merging mythology and morphology: the multifaceted lifestyle of *Proteus mirabilis*. Nat Rev Microbiol, 10: 743 -754. 2012.

Ayanbimpe GM, Abbah VE, Ior CA: Yeasts and yeast-like fungal contaminants of water used for domestic purposes in Jos, Nigeria. Microbiol Res, 3(e24): 99 - 102. 2012.

Barnett HL, Hunter BB: Illiustrated Genera of Imperfect Fungi. 4th Edn. McMillian, New York. 218p. 1987.

Bayram S: Billions of people lack access to clean drinking water, U.N. report finds. Available at www.npr.org. Accessed on 2nd August 2023.

Bauer AW, Kirby WM, Sherris JC, Turck M: Antibiotic susceptibility testing by a standardized single disk method. Am J Clin Pathol, 45(4): 493-496. 1966.

Cheesbrough M: District Laboratory Practice in Tropical Countries. 2nd Edition, Cambridge University Press, New York. pp. 45-70. 2006.

Donovan E, Unice K, Roberts JD, Harris M, Finley B: Risk of gastrointestinal disease associated with exposure to pathogens in the water of the Lower Passaic River. Appl Environ Microbiol, 74(4): 994-1003. 2008.

EPA: Environment Public Authority Decision No. 210/2001 pertaining to the executive by-law of the law of environment public authority. Kuwait. pp. 47. 2001.

Hageskal G, Lima N, Skaar I: The study of fungi in drinking water. Mycol Res, 113:165-172. 2009.

Hussain T, Ishtiaq CM, Hussain A, Mahmood T, Sultana K, Ashraf M: Incidence of fungi in water springs of Samahni Valley, District Bhiimber, Azad Kashmir, Pakistan. Int J Biol, 2:94- 101. 2010.

ISO: Water quality – Detection and enumeration of *Escherichia coli* and coliform bacteria – Part
1: Membrane Filtration method (ISO 9308 -1:2000). Available at www.iso.org/obp/ui/#iso:std:iso:9308:-1:ed-2:v1:en. 2000.

ISO: Water quality - Detection and enumeration of *Pseudomonas aeruginosa* - Method by membrane filtration (ISO 16266:2006). 12 pp. Available at www.iso.org/standard/39272.html. 2006.

Javaid M, Qasim H, Zia HC, Bashir MA, Hameed AQ, Samiullah K, Hashem M, Morsy K, Dajem SB, Muhammad T, Shaheen M, Ali MF, Saeed M, Alasmari A, Alshehri MA: Bacteriological composition of groundwater and its role in human health. J King Saud Uni Sci, 34: 102128. 2022.

Lukubye B, Andama M: Bacterial analysis of selected drinking water sources in Mbarara Municipality, Uganda. J Water Resour Prot, 9:999 – 1013. 2017.

Mukhopadhyay C, Vishwanath S, Eshwara VK, Shankaranarayana SA, Sagir A: Microbial quality of well water from rural and urban households in Karnataka cross-sectional study. J Infect Public Health, 5: 257-262. 2012.

Murray CJ, Vos T, Lozano R, Naghavi M, Flaxman AD, Michaud C, *et al*: Disability-adjusted life years (DALY) for 291 diseases and injuries in 21 regions,1990 - 2010: a systemic analysis for the global burden of disease study 2010. Lancet, 380(9859): 2197 - 2233. 2012.

Mulamattathil SM, Bezuidenhout C, Mbewe M, Ateba, CN: Isolation of environmental bacteria from surface and drinking water in Mafikeng, South Africa, and characterization using their antibiotic resistance profiles. J Pathog, 2014: 371208. 2014.

Musyoki AM, Abednego M, Suleiman MA., Mbithi JN, Maingi JM: Water-borne bacterial pathogens in surface waters of Nairobi River and health implication to communities downstream Athi river. Int J Life Sci Pharm Res, 3(1): 4-10. 2013.

Niyogi SK: Shigellosis. J Microbiol 43(2): 133-143. 2005.

Nwankwo CEI, Barika PN, Akani NP, Amadi ON: Physicochemical and mycological examination of groundwater (well water) in Rumuosi Community, Rivers State, Nigeria. Res J Microbiol, 15: 82-89. 2020.

Oliveira HMB, Santos C, Paterson RRM, Gusmao NB, Lima N: Fungi from a groundwater-fed drinking water supply system in Brazil. Int J Environ Res Public Health, 13(3): 304. 2016.

O'Neil J: Antimicrobial Resistance: Tackling a Crisis for the Health and Wealth of Nations. Review on Antimicrobial Resistance. Available at https://wellcomecollection.org/works/rdpck35v. 2014.

Pereira VJ, Basílio MC, Fernandes D, Domingues M, Paiva JM, Benoliel MJ, Crespo MT, San Romão MV: Occurrence of filamentous fungi and yeasts in three different drinking water sources. Water Res, 43, 3813–3819. 2009.

Oyedele AA, Ayodele OS, Olabode OF: Groundwater quality assessment and characterization of shallow basement aquifers in parts of ado Ekiti metropolis, Southwestern, Nigeria. SN Appl Sci, 1:669. 2019.

Ren W, Huang T, Wen G: Quantity, species, and origin of fungi in a groundwater-derived water source. Water, 15:1161. 2023.

Rompre A, Servais P, Baudart J, de-Roubin MR, Laurent, P. Detection and enumeration of coliforms in drinking water: current methods and emerging approaches. J Microbiol Methods, 49(1): 31 – 54. 2002.

Shahina SK, Sandhiya D, Rafiq S: Bacteriological quality assessment of groundwater and surface water in Chennai. Nat Environ Pollut Technol, 19: 349-353. 2020.

Wilson DN: Ribosome-targeting antibiotics and mechanisms of bacterial resistance. Nat Rev Microbiol, 12(1): 35 - 48. 2014.

WHO: WHO guideline values for drinking-water quality: bacteria. Available from: https://www.ncbi.nlm.nih.gov/books/NBK535301/table/ch8.tab3/. World Health Organisation, Geneva. 2018.