GVU-J.SHT *GVU Journal of Science, Health and Technology*

GVU-J. SHT 2025,**10**; **1**, 87–91, doi:10.5281/zenodo.15357155

Physicochemical and Microbial Quality of the Asa River, Ilorin, Southwestern Nigeria

Ogidi, T. J.[1*], Sanni, B. M.[2], Bewaji, S.[3], Olabode, J. A.[4]

[1]*Department of Science Laboratory Technology, Newland Polytechnics, Ilorin, Nigeria*
[2]*Department of Microbiology, Kwara State University, Malete, Nigeria*
[3]*Department of Geological Sciences, Achievers University, Owo, Nigeria*
[4]*School of Nursing Sciences, Achievers University, Akure, Nigeria*

Received: *15 December 2024 []* ***Published:*** *03 May 2025*

This study assessed the physicochemical and microbiological quality of water samples from a segment of the Asa River in Ilorin, Nigeria, over an eight-week period. Water samples were analysed using the multiple tube fermentation technique and spread plate method, with microbial identification performed via standard microbiological procedures. Physicochemical parameters included pH (7.47–8.95), temperature (22.9–28.2°C), biological oxygen demand (BOD) (6.40–9.10 mg/L), total suspended solids, total dissolved solids, dissolved oxygen, and total solids. Microbial analysis revealed total heterotrophic counts ranging from 2.70–7.25 $\times$ 10^4 cfu/mL, total coliform counts from 1.45–6.05 $\times$ 10^4 cfu/mL, and faecal coliform counts from 1.45–3.40 $\times$ 10^4 cfu/mL. Identified bacterial species included *Streptococcus* sp., *Escherichia coli*, *Shigella* sp., *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, and *Vibrio cholerae*. Antibiotic susceptibility tests against eight common antibiotics showed multiple resistance, particularly in *Klebsiella pneumoniae*. Fungal isolates included *Aspergillus niger*, *Rhizopus stolonifer*, *Aspergillus fumigatus*, and *Penicillium* sp. The presence of antibiotic-resistant microorganisms indicates significant contamination of the Asa River, posing a public health risk if used for domestic purposes.

Keywords: Asa River, Microbiological quality, Total coliform count, Faecal coliform count, Isolates

Introduction

Water is the most abundant and vital substance provided by nature (Foppen, 2018). Despite its abundance, access to potable water remains a critical challenge, with over one billion people lacking safe drinking water (Onuorah and Odibo, 2019; WHO, 2022). Ensuring access to safe and sufficient water for families in Ilorin, Kwara State, Nigeria, could significantly reduce mortality rates. Safe and reliable water is essential for agricultural, domestic, and industrial activities in the region (Igbinosa and Aisien, 2020; Oyediran et al., 2018). The lack of potable water, coupled with inadequate sanitation and poor hygiene, contributes to 9.1% of global infections and 6.3% of all deaths worldwide (WHO, 2022; Igbinosa, 2020). Microbial pollution affects various water sources, including surface water and piped water supplies (Alotaibi, 2009; Bekuretsion et al., 2018). Annually, 37.7 million people are affected by waterborne diseases, with 1.5 million children succumbing to diarrhea (WHO, 2022). Factors such as urbanisation, economic challenges, and climatic changes exacerbate the inaccessibility of safe drinking water (Hussain et al., 2013; Protor and Hammes, 2015).

Microbial pathogens from human and animal wastes contaminate various water bodies (Habtu and Zewdu, 2019; Hassan et al., 2018). These pathogens include bacteria, viruses, and parasites (Caggiano et al., 2020). Common waterborne infections include diarrhea caused by *Escherichia coli*, salmonellosis caused by *Salmonella*, and shigellosis caused by *Shigella* (Luyt et al., 2012).

The Asa River, located in the heart of Ilorin Metropolis, is a critical resource of economic, agricultural, and environmental significance. However, it is heavily impacted by pollutants such as lead, cadmium, and chromium, alongside human activities that degrade its quality (Oyediran et al., 2018). Industrial effluents, agricultural waste, and runoff containing pollutants are discharged directly into the river, making them primary sources of pollution (Adekunle and Eniola, 2008). Additionally, high levels of eutrophication, driven by organic matter from pig faeces and soap residues from laundry activities, further compromise the river's quality (Eletta et al., 2005). This study aims to characterise the microbial contaminants and evaluate the water quality of the Asa River.

Materials and Methods

Study Site

Ilorin, the capital city of Kwara State in North Central Nigeria, has a population of approximately 1,099,959. The Asa

River, a significant water body in Ilorin, is located at coordinates 8.4875°N and 4.5588°E. The river supports fishing and irrigation for vegetable farming. Approximately 4.5% of the population relies on piped water, while the majority depend on wells, boreholes, and streams. Water samples were collected from the Station Segment of the Asa River, specifically at points with heavy commercial activities, which contribute significantly to the river's pollution.

Sample Collection

Water samples for microbiological analysis were collected in sterilised glass bottles autoclaved prior to use. Each bottle was filled, leaving a 20 mm headspace to allow for effective shaking. Samples were transported in an icebox and analysed within 4 hours of collection. Sampling occurred twice weekly over an eight-week period.

Microbiological Analysis of Water Samples

Most Probable Number Technique

The presence of total and faecal coliforms was assessed using the multiple-tube fermentation technique, comprising presumptive, confirmed, and completed tests. For the presumptive test, 0.1 ml of each water sample was inoculated into five replicate test tubes, each containing 10 ml of sterile single-strength MacConkey broth and an inverted Durham tube. The tubes were incubated at 37°C for 24 hours. Gas production in the Durham tubes and a colour change to yellow indicated the presumptive presence of coliform bacteria. One ml from presumptive positive tubes was plated onto Eosin Methylene Blue Agar and incubated at 37°C for 24 hours. Dark blue colonies with a green metallic sheen suggested the presence of *Escherichia coli*. These colonies underwent biochemical tests, including oxidase, catalase, urease, motility, indole, and sugar fermentation tests (Hemraj et al., 2013).

Microbial Isolation

Bacteria were isolated using the spread plate method. Water samples underwent serial dilution, and 0.1 ml of 10^{-3} and 10^{-5} dilutions were uniformly spread onto nutrient agar using an L-rod. Plates were incubated at 37°C for 24 hours. Distinct isolates were subcultured and subjected to biochemical tests, including oxidase, catalase, urease, motility, indole, coagulase, methyl red, Voges-Proskauer, and sugar fermentation tests (Hemraj et al., 2013).

Isolation of Salmonella, Shigella sp., and Vibrio cholerae

For *Salmonella* and *Shigella*, 20 ml of water sample was enriched with 10 ml of sterile F broth and incubated at 37°C for 24 hours to enhance the growth of these low-concentration organisms. The enriched culture was streaked onto Salmonella-Shigella agar and incubated at 37°C for 24 hours. *Salmonella* colonies appeared colourless with a black center, while *Shigella* colonies were colourless without a black center.

For *Vibrio cholerae*, 20 ml of water sample was enriched with 10 ml of peptone water and incubated at 37°C for 24 hours. The enriched culture was streaked onto thiosulphate-citrate-bile-salt agar and incubated at 37°C for 24 hours. *Vibrio cholerae* colonies were 2–3 mm in diameter and yellow. Salmonella-Shigella agar and thiosulphate-citrate-bile-salt agar were used for selective growth of the target organisms.

Isolation and Characterisation of Fungi

Fungi were isolated using the spread plate method following serial dilution of the water samples. Aliquots of 0.1 ml from 10^{-3} and 10^{-5} dilutions were inoculated onto sterile potato dextrose agar supplemented with 1% streptomycin. Plates were incubated at 25°C for 48–72 hours. Pure cultures were obtained through subculturing and stored in agar slants. Fungal isolates were characterised using macroscopic, microscopic, and biochemical tests, with morphology determined according to Omomowo et al. (2015).

Results

The physicochemical properties of water samples from the Station Segment of the Asa River are presented in Table 1. Parameters include temperature, pH, total dissolved solids (TDS), dissolved oxygen (DO), biological oxygen demand (BOD), total solids (TS), and total suspended solids (TSS). The pH ranged from 7.47 to 8.95, temperature from 22.9 to 28.2°C, TDS from 630.0 to 793.5 mg/L, DO from 20.10 to 22.20 mg/L, BOD from 6.40 to 9.10 mg/L, TS from 486.2 to 816.1 mg/L, and TSS from 14.10 to 32.10 mg/L. Peak values were observed as follows: temperature in week 1 (26.95°C), pH in weeks 1 and 6 (8.95), TDS in weeks 1 and 6 (793.5 mg/L), DO in weeks 1 and 7 (22.20 mg/L), BOD in week 3 (9.10 mg/L), TS in week 7 (816.1 mg/L), and TSS in weeks 3 and 6 (32.10 mg/L).

Microbial loads, including total heterotrophic count (THC), total coliform count (TCC), total faecal count (TFC), and most probable number (MPN) values, are shown in Table 2. The THC was highest in week 3 (7.25×10^4 cfu/mL) and lowest in week 5 (2.70×10^4 cfu/mL). The TCC peaked in week 3 (6.05×10^4 cfu/mL) and was lowest in weeks 5 and 7 (1.85×10^4 cfu/mL). The TFC was highest in week 3 (3.40×10^4 cfu/mL) and lowest in week 5 (1.45×10^4 cfu/mL). MPN values, expressed per 100 mL, were highest in weeks 3 and 7 (0.94×10^4) and lowest in week 5 (0.30×10^4).

Bacterial isolates showed varying frequencies of occurrence (Figure 1). *Escherichia coli* was the most prevalent at 36.59%, followed by *Vibrio cholerae* (14.15%). *Salmonella* sp., *Streptococcus* sp., and *Staphylococcus aureus* each had a frequency of 11.71%, *Klebsiella pneumoniae* at 9.27%, and *Shigella* sp. was the least frequent at 4.87%.

Fungal isolates included *Rhizopus stolonifer* with the highest frequency of occurrence at 33.33%, followed by *Aspergillus fumigatus* at 26.67%. *Penicillium* sp. and *Aspergillus niger* each had the lowest frequency at 20% (Figure 2).

Antibiotic sensitivity tests (Figure 3) revealed that *Klebsiella pneumoniae* and *Staphylococcus aureus* exhibited multiple resistance, each resistant to at least three antibiotics (Ofloxacin, Nitrofurantoin, Gentamicin, Augmentin, Amoxicillin, Tetracycline, Ciprofloxacin, and Chloramphenicol). Ofloxacin was the

Table 1 Physicochemical parameters of water samples from Station Segment of Asa River

Week	T (°C)	pH	TDS (mg/L)	DO (mg/L)	BOD (mg/L)	TS (mg/L)	TSS (mg/L)
1	26.95	8.95	630.0	22.20	8.05	648.7	18.80
2	24.50	7.77	681.5	21.40	6.40	696.3	15.40
3	24.50	8.26	780.0	20.70	9.10	814.1	32.10
4	28.20	8.24	768.5	21.30	7.60	798.6	31.10
5	22.90	8.09	698.5	20.20	8.10	777.2	26.30
6	26.40	8.95	793.5	21.30	8.65	731.0	32.10
7	26.10	7.47	793.5	22.20	8.95	816.1	23.40
8	26.00	8.81	674.5	20.10	7.60	486.2	14.10

Keys: T (°C) – Temperature, TDS – Total Dissolved Solids, DO – Dissolved Oxygen, BOD – Biological Oxygen Demand, TS – Total Solids, TSS – Total Suspended Solids.

Table 2 Microbial load of water samples from Station Segment of Asa River

Week	THC (cfu/mL)	TCC (cfu/mL)	TFC (cfu/mL)	MPN/100mL
1	2.55×10^4	2.45×10^4	1.85×10^4	0.36×10^4
2	4.05×10^4	2.55×10^4	2.25×10^4	0.72×10^4
3	7.25×10^4	6.05×10^4	3.40×10^4	0.94×10^4
4	4.35×10^4	2.30×10^4	1.65×10^4	0.61×10^4
5	2.70×10^4	1.85×10^4	1.45×10^4	0.30×10^4
6	3.60×10^4	2.45×10^4	2.35×10^4	0.74×10^4
7	3.50×10^4	1.85×10^4	1.80×10^4	0.94×10^4
8	3.50×10^4	2.50×10^4	2.40×10^4	0.72×10^4

Keys: THC – Total Heterotrophic Count, TCC – Total Coliform Count, TFC – Total Faecal Count, MPN – Most Probable Number.

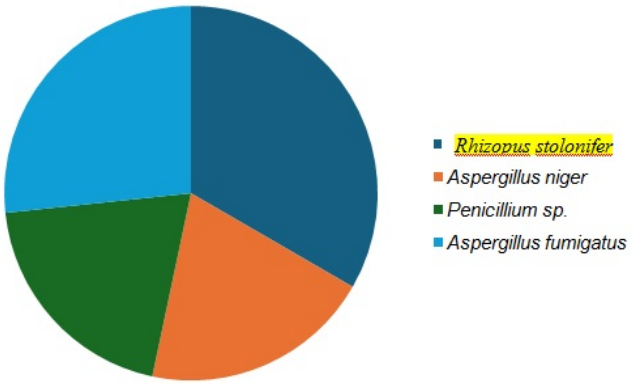

Figure 2 Fungal frequency of distribution from water samples obtained from Station Segment of Asa River

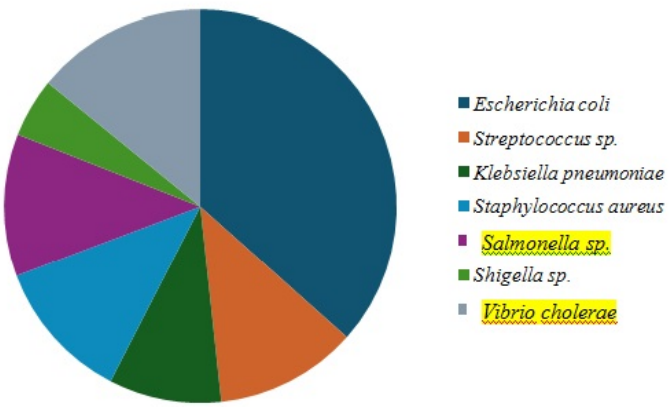

Figure 1 Bacterial frequency of distribution from water samples obtained from Station Segment of Asa River

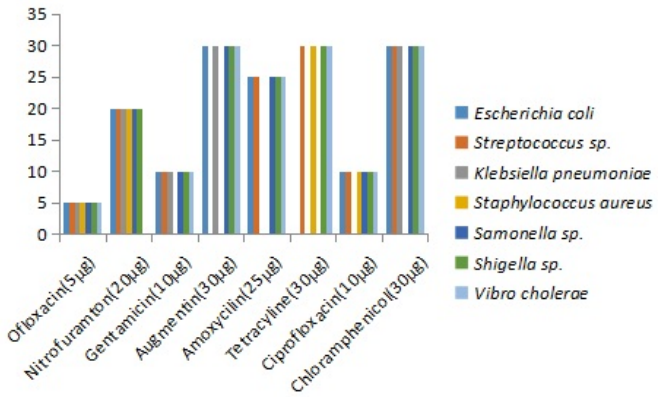

Figure 3 Antibiotic sensitivity of bacterial isolates obtained from Asa River water sample

most effective antibiotic, while Amoxicillin was the least effective. Variations in BOD and microbial counts across weeks were notable but not statistically analysed.

Discussion

The World Health Organization (2022) standards for potable water specify a pH of 6.8–8.5, dissolved oxygen of 6–8 mg/L, biological oxygen demand (BOD) of 6 mg/L, total suspended

solids (TSS) of 20 mg/L, and total dissolved solids (TDS) of 500 mg/L (WHO, 2022). The Asa River water samples exhibited values exceeding these standards. TDS (630.0–793.5 mg/L) and BOD (6.40–9.10 mg/L) consistently surpassed 500 mg/L and 6 mg/L, respectively. Total solids (486.2–816.1 mg/L) and TSS (14.10–32.10 mg/L) also indicated contamination. These findings align with Okonko et al. (2008) and Shittu et al. (2008), who reported elevated physicochemical parameters in contaminated water, exceeding WHO (2022) standards. The physicochemical parameters of the Asa River suggest significant contaminant presence.

The microbial load and diversity in the Station Segment of the Asa River were substantial. High microbial counts, comparable to those reported by Ogidi and Oyetayo (2013) (up to 10^5 cfu/mL), reflect river characteristics and pollution sources (Igbinosa and Aisien, 2020). Isolated species, including *Escherichia coli*, *Vibrio cholerae*, *Salmonella* sp., *Shigella* sp., *Klebsiella pneumoniae*, *Streptococcus* sp., and *Staphylococcus aureus*, are consistent with findings by Amoo et al. (2018) and Akinpele et al. (2014). These organisms indicate microbial contamination, posing public health risks if the water is used domestically (Caggiano et al., 2020; Akinbile, 2004).

Total coliform counts (1.85–6.05 $\times$ 10^4 cfu/mL) in all samples exceeded the WHO (2022) maximum permissible limit of 0/100 mL for drinking water. Faecal coliform counts (1.45–3.40 $\times$ 10^4 cfu/mL) further confirm contamination. While total coliform presence does not always indicate faecal contamination or pathogens (Adekunle and Eniola, 2008), these results align with Anthony and Renuga (2012), who detected coliforms in drinking water samples.

From eight samples, 41 isolates representing eight genera were identified, consistent with Anthony and Renuga (2012), who isolated similar species. This microbial diversity likely results from multiple environmental contamination sources, such as refuse dumping and industrial effluents (Hussain et al., 2013; Griffith et al., 2003; Arshad and Shakoor, 2017). *E. coli* was the most prevalent (36.59%), followed by *Vibrio cholerae* (14.15%), corroborating Asfaw et al. (2016). These bacteria thrive in water bodies impacted by refuse and industrial discharges (Abera et al., 2011; Amira and Yassir, 2011). *Klebsiella* sp., a slow-growing environmental bacterium, was also detected, posing risks to vulnerable populations (e.g., elderly, children, immunocompromised) if consumed (Chissaque et al., 2018; Antony and Renuga, 2012).

Fungal isolates included *Rhizopus stolonifer* (33.33%), *Aspergillus fumigatus* (26.67%), *Penicillium* sp. (20%), and *Aspergillus niger* (20%), consistent with Monika et al. (2017), who isolated similar fungi from drinking water. Fungal cell wall components and loads may cause allergies or opportunistic infections, particularly in immunocompromised individuals. *Aspergillus* sp. can lead to aspergillosis, and fungi are increasingly recognised as causative agents of respiratory, mucosal, and systemic infections (Moat et al., 2016).

Antibiotic susceptibility tests showed *Klebsiella pneumoniae* and *Staphylococcus aureus* exhibited multiple resistance to at least three antibiotics (Ofloxacin, Nitrofurantoin, Gentamicin, Augmentin, Amoxicillin, Tetracycline, Ciprofloxacin, Chloramphenicol). Ofloxacin was the most effective, while Amoxicillin and Ciprofloxacin were the least effective, aligning with Onifade and Ilori (2008). Multiple antibiotic resistance, also reported by Akinpele et al. (2014) in the Obere River, underscores public health risks from consuming water containing resistant organisms.

Conclusion

It can be concluded from the study of the Station segment of the Asa River that the water is heavily contaminated with faecal-originated microorganisms. The Station segment of the Asa River is unsatisfactory for drinking. Also, the presence of antibiotic-resistant microorganisms suggests that the Asa River is significantly contaminated and poses a public health risk, particularly if the water is used for domestic purposes.

Limitations of the Study

Variations were not assessed, potentially affecting microbial load.

Research Funding

The research did not receive any specific grant from funding agencies in the public, commercial, or non-profit sectors.

References

Adekunle, A.S., & Eniola, I.T.K. (2008). Industrial effluents on the quality of the segment of the Asa River within an industrial estate in Ilorin, Nigeria. *New York Science Journal*, *1*, 17–21.

Akinbile, C.O. (2004). Borehole construction technology in the riverine areas: A case study of Igbokoda, Ondo State, Nigeria. *World Journal of Biotechnology*, *5*(1), 771–778.

Akinpele, A.T., Akinloye, O.M., Olukemi, B.C., & Adegoke, A.E. (2014). Antibiotics resistance pattern of isolated bacteria from Obere River in Orile-Igbon, Oyo State, Nigeria. *African Journal of Microbiology Research*, *8*(12), 1318–1321.

Alotaibi, E.L.S. (2009). Bacteriological assessment of urban water sources in Khamis Mushait Governorate, Southwestern Saudi Arabia. *International Journal of Health Geographics*, *8*, 16.

Amira, A.A., & Yassir, M.E. (2011). Bacteriological quality of drinking water in Nyala, South Darfur, Sudan. *Environmental Monitoring and Assessment*, *175*, 37–43.

Amoo, A.O., Adeleye, A.O., Bate, G.B., Okunlola, I.A., & Hambal, I.B. (2018). Water quality assessment of selected boreholes in Federal University Dutse Campus North-West, Nigeria. *Umaru Musa Yaradua University Journal of Microbiology Research*, *3*(2), 20–26.

Antony, R.M., & Renuga, F.B. (2012). Microbiological analysis of drinking water quality of Ananthanar Channel of Kanya Kumara district, Tamil Nadu, India. *An Interdisciplinary Journal of Applied Science*, *7*(2), 42–48.

Arshad, M., & Shakoor, A. (2017). Irrigation water quality. *Pakistan Journal of Agricultural Research*, *31*, 102–123.

Asfaw, H.S., Reta, M.A., & Yimer, F.G. (2016). High enteric bacterial contamination of drinking water in Jigjiga City, Eastern Ethiopia. *Ethiopian Journal of Health Development*, *30*, 118–128.

Bekuretsion, H., Hailekiros, H., Niguse, S., Asmelash, T., Abdulkader, M., Saravanan, M., & Brindhadevi, K. (2018). Bacteriological assessment of drinking water from hand-pump fitted borehole sources in Kola Tembien, Central Tigray, Northern Ethiopia.

Journal of Water Supply: Research and Technology-Aqua, *67*(8), 790–799.

Caggiano, G., Diella, G., Triggiano, F., Bartolomeo, N., Apollonio, F., Campanale, C., Lopuzzo, M., & Montagna, M.T. (2020). Occurrence of fungi in the potable water of hospitals, a public health threat. *Pathogens*, *9*, 783.

Chissaque, A., DeDeus, N., Vubil, D., & Mandomando, I. (2018). The epidemiology of diarrhea in children under 5 years of age in Mozambique. *Current Tropical Medicine Reports*, *5*, 115–124.

Eletta, O.A., Adekola, F.A., & Aderanti, M.A. (2005). Assessment of Asa River: Impact of waste discharge from soft drink plant into Asa River, Ilorin. *Nigerian Journal of Applied Science and Environmental Management*, *9*, 187–190.

Foppen, J.W. (2018). Microbial groundwater quality status of hand-dug wells and boreholes in the Dodowa area of Ghana. *International Journal of Environmental Research and Public Health*, *15*, 730.

Habtu, T., Samuel, S., & Zewdu, T. (2019). Bacteriological and physicochemical profile of water samples collected from river and stream water basins crossing Gondar town, North West Ethiopia. *Journal of Academic and Industrial Research*, *8*(2), 21–28.

Hassan, A., Kura, N.U., Amoo, A.O., Adeleye, A.O., Ijanu, E.M., Bate, G.B., Amoo, N.B., & Okunlola, I.A. (2018). Assessment of land fill induced ground water pollution of selected boreholes and hand-dug wells around Ultra-Modern Market Dutse North-West, Nigeria. *The Environmental Studies*, *1*(4), 1–10.

Hemraj, V., Diksha, S., & Avneet, G. (2013). A review on commonly used biochemical tests for bacteria. *Innovare Journal of Life Science*, *1*(1), 1–7.

Hussain, T., Roohil, A., Munir, S., Ahmed, I., Khan, J., Edel-Hermann, V., Kim, K.Y., & Anees, M. (2013). Biochemical characterization and identification of bacterial strains, Pakistan. *African Journal of Microbiology Research*, *7*(16), 1579–1590.

Igbinosa, I.H., & Aisien, T.E. (2020). Bacteriological quality and virulence capacity of water indicator pathogens from roof-harvested rainwater in peri-urban communities in Benin City, Edo State. *Journal of the Nigerian Society for Experimental Biology*, *20*(1), 1595–6938.

João, B. (2017). Fungal contaminants in drinking water regulation? A tale of ecology, exposure, purification and clinical relevance. *International Journal of Environmental Research and Public Health*, *14*(6), 636.

Luyt, C.D., Tandlich, R., Muller, J.W., & Wilhelmi, S.W. (2012). Microbial monitoring of surface water in South Africa, as an overview. *International Journal of Environmental Research and Public Health*, *9*, 2669–2693.

Ogidi, C.O., & Oyetayo, V.O. (2013). Antibiotic sensitivity pattern of microorganisms isolated from remnant foods and wastewater from restaurants. *FUTA Journal of Research in Sciences*, *2*, 209–216.

Okonko, I.O., Adejoye, O.D., Ogunnusi, T.A., Fajobi, E.A., & Shittu, O.B. (2008). Microbiological and physicochemical analysis of different water samples used for domestic purposes in Abeokuta and Ojota, Lagos State, Nigeria. *African Journal of Biotechnology*, *7*(3), 617–621.

Omomowo, L.O., Omomowo, O.I., Adeeyo, A.O., Adebayo, E.A., & Oladipo, E.K. (2015). Bacteriological screening and pathogenic potential of soil receiving cassava mill effluents. *International Journal of Basic and Applied Science*, *3*(4), 26–36.

Onifade, A.K., & Ilori, R.M. (2008). Antibiotic sensitivity of human pathogenic microbes from different water sources from Akure Metropolis, Ondo State, Nigeria. *Environmental Research Journal*, *2*(3), 104–106.

Onuorah, S., Igwemadu, N., & Odibo, F. (2019). Bacteriological quality assessment of borehole water in Ogbaru Communities, Anambra State, Nigeria. *Universal Journal of Clinical Medicine*, *7*(1), 1–10.

Oyediran, A.O., Adeyi, A.A., & Akindele, beta-blockerS.O. (2018). Microbiological quality of river water in Ilorin, Nigeria. *Journal of Water and Health*, *16*(3), 439–448.

Proctor, C.R., & Hammes, F. (2015). Drinking water microbiology—from measurement to management. *Current Opinion in Biotechnology*, *33*, 87–94.

Shittu, O.B., Olaitan, J.O., & Amusa, T.S. (2008). Physico-chemical and bacteriological analyses of water used for drinking and swimming purposes in Abeokuta, Nigeria. *African Journal of Biomedical Research*, *11*, 285–295.

Sohlberg, E., Bomberg, M., Miettinen, H., Nyyssönen, M., Salavirta, H., Vikman, M., & Itävaara, M. (2015). Revealing the unexplored fungal communities in deep groundwater of crystalline bedrock fracture zones in Olkiluoto, Finland. *Frontiers in Microbiology*, *6*, 573.

Upton, M. (2016). Domestic shower hose biofilms contain fungal species capable of causing opportunistic infection. *Journal of Water and Health*, *14*, 727–737.

WHO. (2022). *Guidelines for drinking-water quality: Fourth edition incorporating the first and second addenda*. Geneva, Switzerland.