THE MICROBIAL CONTAMINATION OF TAP WATER, WELL WATER AND RIVER WATER ASSOCIATED WITH WATER SOURCES AT IKPOBA HILL ENVIRONS.

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MICROBIOLOGY TECHNIQUES

THE DEPARTMENT OF SCEINCE LABORATORY TECHNOLOGY

FACULTY OF LIFE SCIENCE

UNIVERSITY OF BENIN

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A PROJECT SUBMITTED TO THE DEPARTMENT OF SCIENCE LABORATORY TECHNOLOGY, FACULTY OF LIFE SCIENCES, UNIVERSITY OF BENIN, BENIN CITY IN PARTIAL FULFILMENT OF THE REQUIREMENTS FOR THE AWARD OF THE DEGREE OF BACHELOR OF SCIENCE (B.Sc.) IN SCIENCE LABORATORY TECHNOLOGY (MICROBIOLOGY TECHNIQUES)

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CERTIFICATION

This is to certify that this project work carried out by **Perpetual Esegboyota IMONIOKENA (Miss)** with the matriculation number, **LSC2007310** of the department of Science Laboratory Technology (Microbiology Techniques), Life Sciences, University of Benin, Benin City, Edo State, Nigeria.

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DEDICATION

This book is dedicated to God Almighty whose unwavering love, guidance, direction and strength have fueled my journey of discovery.

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ABSTRACT

Clean water is essential for the health and survival of all life forms. Surface and underground water polluted by microbes and chemicals exacerbates issues of water scarcity. This continues to negatively affect the well-being of most people in developing countries like Nigeria and K-Vom, in Plateau State. Thus, this study aimed to determine the microbial contamination of tap water, well water and river water associated with water sources at ikpoba hill environs Benin City, Edo State, Nigeria. Five (5) samples were collected and analysed using standard microbiological procedures. Isolates were identified by microscopic, biochemical and carbohydrate fermentation characterizations**.** The nutrient agar (NA) count, which indicates the total heterotrophic bacterial population, showed that river water had the highest bacterial load (60–61 cfu/ml), followed by tap water samples (46–57 cfu/ml), while well water samples had comparatively lower bacterial counts (30–44 cfu/ml) and The bacterial count on MacConkey agar (MCA)**,** which is selective for Gram-negative enteric bacteria, was generally lower compared to the total heterotrophic count. Tap water recorded the highest counts (19–27 cfu/ml), while well and river water had very low counts (3–5 cfu/ml). The fungal count obtained on potato dextrose agar (PDA) also showed notable variation. River water again recorded the highest fungal load (52–58 cfu/ml), followed by tap water (31–42 cfu/ml) and well water (33–40 cfu/ml). The bacteria isolate included *Salmonella typhi*, *Escherichia coli*, *Shigella* spp., *Staphylococcus* spp., *Corynebacterium* spp., *Serratia marcescens*, *Citrobacter freundii*, *Klebsiella pneumoniae*, and *Klebsiella* spp and The fungal isolates obtained from the water samples exhibited distinct cultural and morphological characteristics that enabled their identification as *Saccharomyces* sp., *Fusarium* sp., and *Trichoderma* sp. Historical data show no improvement in water quality, emphasizing the need for individuals to treat water properly before consumption. The findings provide baseline data for local water authorities and serve as a wake-up call for adequate water treatment, storage interventions, and community education on water security. Additionally, this study offers a practical process for improving the quality of water stored in similar regions.

CHAPTER ONE

1.0 INTRODUCTION

1.1 Background of Study

Water remains one of the most essential natural resources, serving domestic, industrial, and agricultural needs (FAO, 2022). However, despite its importance to human survival and development, lack of access to safe drinking water is a major contributor to illness and death globally (Umar *et al*., 2020). Although significant strides have been made in improving water supply and sanitation, billions of people particularly in rural communities still suffer from inadequate access to potable water. Reports indicate that one in three people worldwide lack safe drinking water, two in five are without basic handwashing facilities, and over 673 million still practice open defecation (UN, 2022). Additionally, about 2 billion people consume water contaminated with fecal matter (WHO, 2019). Water scarcity currently affects more than 40% of the world's population and is expected to worsen, with about 1.7 billion people living in basins where water demand exceeds natural replenishment (UN, 2022). In Sub-Saharan Africa, about 42% of the population rely on unsafe water sources, while 72% lack basic sanitation services (Eberhard, 2019). Access to safe water is crucial in preventing gastrointestinal infections and safeguarding public health (Durmishi, 2012). Unfortunately, pollutants such as microorganisms, heavy metals, nitrates, and salts enter water bodies through untreated domestic, agricultural, and industrial waste discharges. Industrial effluents, including brine, significantly reduce water quality, making such water unsuitable for drinking or industrial applications unless further treated (Panagopoulos and Giannika, 2022). Recent studies have explored advanced treatment methods, including the use of *Chlorella vulgaris*, nitrifying-enriched activated sludge, and

ammonia-fed conventional activated sludge (CAS). Approaches such as nitrite-oxidizing bacteria (NOB) enrichment and nitratation strategies have shown improved nitrification efficiency and up to 50% reduction in microbial metabolites compared to conventional processes (Sepehria *et al*., 2020).

Even in the absence of human activities, natural factors can cause contamination. High levels of metals and chemicals that exceed permissible limits are harmful to health. Water pollution may also arise from flooding, weathering of rocks, climate conditions, and topography. To evaluate water quality, both physicochemical and microbiological parameters are assessed (Hadzi *et al*., 2015). Physical indicators include color, odor, temperature, pH, turbidity, and electrical conductivity. Chemically, substances such as iron, lead, mercury, chromium, and residual chlorine may be naturally present or introduced during water treatment. The World Health Organization (WHO) has set maximum allowable limits for these substances in drinking water (Lukubye and Andama, 2017).

On the microbial side, water quality is often assessed using indicator organisms (Abhishek *et al*., 2017). *Escherichia coli* (E. coli), a thermotolerant coliform, is widely accepted as the most reliable indicator of fecal contamination, while faecal coliform counts may be used where *E. coli* testing is not feasible (Abhishek *et al*., 2017). Other organisms, such as faecal streptococci, may also indicate recent contamination of water sources (Lukubye and Andama, 2017). Given these risks, regular monitoring of drinking water is essential to ensure that chemical and microbial contaminants remain within acceptable limits. Exceeding these limits can lead to severe health outcomes, including mutagenicity, growth defects, mortality, and structural abnormalities (Usman *et al*., 2020). The situation in Sapele, compounded by possible contamination from

effluents discharged by oil companies, underscores the need for thorough assessment of both physicochemical and bacteriological parameters of drinking water. This forms the basis for evaluating the potability of water and making recommendations aligned with WHO and Nigerian Standards for Drinking Water Quality (NSDWQ).

Edo State is located in southern Nigeria and is blessed with surface water resources, with rivers such as Ovia, Ose, Orhionmwon and Ikpoba rivers, being notable (Osimen and Anagha, 2020). Ikpoba River (also known as Oken River) is a fourth-order stream located in the rainforest belt of Edo State, southern Nigeria. It is of particular importance to Benin City the capital of Edo State with a population of over one million people (2006 Census). A major dam was constructed across the river at Okhoro Community, but the river remains exposed to pollution from industrial effluents, stormwater runoff, and drainage channels, particularly as it flows through Benin City. While agricultural activities such as farming and fishing dominate its upper reaches, industrial discharges, urban drainage, and waste from a government abattoir where about 50 cattle and goats are slaughtered daily also contribute significantly to its pollution load (Atuanya *et al*., 2012). The present study was therefore designed to evaluate whether the microbiological characteristics of Ikpoba River water fall within regulatory limits, with the ultimate aim of determining its suitability for human use and public health safety.

This research seeks to identify the microbial contamination of water from tap, well and riversat Ikpoba hill.

1.2 Aim of Study and objective of study

The aim of this study was to determine the microbial contamination of Tap water, Well water and River water associated with water sources at Ikpoba Hill Environs. Specific objective of this study were to:

1. Determine the heterotrophic microbial count from different water soures.
2. To isolate, enumerate and identify the microbial isolate from different water soures.
3. Determine the frequency distribuion of the microbial isolates from different water soures.
4. Determine the Fungi caracteristics

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Water borne

Water is one of the most vital natural resources on earth, essential for the survival of all living organisms, the functioning of ecosystems, human health, food production, and economic growth (Shafiq *et al*., 2013). Water is one of the most vital natural resources on Earth, covering about 71% of the planet's surface. It exists in different forms such as oceans, rivers, lakes, glaciers, and groundwater (Mishra, 2023). However, despite its abundance, only about 2.5% of the total water on Earth is freshwater. This limited fraction supports human needs for drinking, agriculture, and industry, while also playing a critical role in sustaining ecological balance. Freshwater resources are broadly categorized into surface water and groundwater (Mushtaq *et al*., 2020). Surface water, found in rivers, lakes, and reservoirs, is relatively easy to access and meets diverse human needs. Groundwater, in contrast, is stored in underground aquifers and serves as a crucial drinking water source, especially in areas where surface water is insufficient (Lewandowski *et al*., 2020).

According to (Arif *et al*., 2016), about 1.1 billion people lack access to safe drinking water globally, and millions of lives are lost annually to waterborne diseases. For water to be considered of good quality, it must be colourless, odourless, tasteless, and free from faecal contamination (Abel-Satar *et al*., 2017). The overall quality of water is determined by its physicochemical and biological properties, which are influenced by the geological characteristics of an area as well as human activities (Eyankware *et al*., 2018). Although water may be abundant, once it is contaminated, it becomes unfit for use. It is therefore preferable to have a smaller quantity of clean, safe water than an abundance of polluted water. In the past, especially before

Nigeria's independence, state and federal governments were directly responsible for providing free water for domestic use in many communities. Today, however, water supply has largely been left to individuals, leading to widespread reliance on personal boreholes for domestic needs. Similarly, residents of riverine areas depend mainly on surface water sources such as rivers and streams. Unfortunately, emphasis is often placed on water availability in terms of quantity rather than its quality (Ulakpa and Eyankware, 2021). Although many parts of the study area are richly endowed with water resources, pollution and contamination from various sources remain a major challenge (Orji and Egboka, 2016).

2.2 Microorganism in water

Microorganisms are predominantly present in surface water, while their occurrence in groundwater is relatively rare and often linked to direct contamination from surface water sources. According to (Daud *et al*., 2017), fecal contaminants such as *Escherichia coli* pose a major threat to water quality, particularly in unplanned urban areas where water supply management is left largely to individuals. Studies (Okuofu *et al*., 1990) have highlighted that bacteriologically polluted water is extremely hazardous to public health, as it can trigger outbreaks of diseases such as typhoid and cholera. A wide variety of microorganisms can be present in water; however, it is practically impossible to continuously monitor and identify all disease-causing organisms. Instead, coliform bacteria are commonly used as indicators to assess microbial contamination in water. While coliforms themselves may not always be pathogenic, their presence suggests the potential risk of waterborne pathogens (Odonkor and Ampofo, 2013). Furthermore, it was emphasized that the spread of pathogens is largely facilitated by untreated or

inadequately treated sewage, which is a major driver of waterborne infections. Many modern health issues have been linked to the ingestion of contaminated water (Vunain *et al*., 2017).

The quality of water is a critical factor for both public health and environmental sustainability. The presence of pathogenic bacteria in water sources poses a serious threat to human health. Commonly reported microorganisms include *Escherichia coli*, *Salmonella* spp., *Shigella* spp., and *Staphylococcus aureus*, all of which have been linked to outbreaks of waterborne diseases. In recent years, the emergence of antimicrobial resistance (AMR) in microorganisms isolated from water sources has raised further concern, as it complicates the treatment of infections and increases public health risks. Rivers are vital sources of water, supporting a wide range of uses including domestic consumption, industrial processes, agriculture, livestock production, and recreational purposes (Li and Wu, 2019). However, human activities contribute significantly to river water contamination, especially through the direct discharge of untreated effluents into rivers and streams. Globally, it is estimated that over 80% of wastewater is released into the environment without adequate treatment, leading to pollution by pathogenic microorganisms such as bacteria, viruses, protozoa, and helminths (Jung *et al*., 2014).

Microbial contamination of aquatic environments has become a major concern, threatening the sanitary quality of water used for drinking, recreation, and seafood harvesting. While pathogenic organisms are naturally present in ecosystems, fecal pollution resulting from anthropogenic activities is increasingly accelerating the deterioration of river systems and drinking water supplies worldwide (Páll *et al*., 2013). Several studies have documented microbial contamination of rivers caused by both human and animal activities, with particularly severe impacts noted in river sections near urban settlements (Chen *et al*., 2022). For instance, research conducted in

eight rivers serving as rural household water sources in northern South Africa reported bacterial indicator levels that exceeded drinking water quality guideline limits (Potgieter *et al*., 2020). Similarly, an investigation in the Kelani River Basin, Sri Lanka, revealed widespread contamination with total coliforms and *Escherichia coli* at nearly all sampled sites (Mahagamage *et al*., 2020). The continued reliance on fecal indicator bacteria as markers of water safety has, however, become increasingly debated within water quality and public health sectors (Dechesne *et al*., 2006). In developing countries, waterborne pathogens remain a major cause of gastrointestinal diseases in children, accounting for approximately 21% of under-five mortality, with an estimated 2.5 million child deaths annually linked to unsafe water (Bryce *et al*., 2005).

2.3 Water Pollution and Human Health Risks

Water pollution is a major global concern because it directly affects human health and overall wellbeing. Access to safe and clean water is essential for sustaining life, reducing the spread of waterborne diseases, and improving public health. Unfortunately, water quality is often compromised by a range of contaminants, making it unsuitable for everyday use. Both natural and human-related factors contribute to water pollution. Natural causes include microbial activity, geological processes, and naturally occurring pollutants within water sources. Human-related (anthropogenic) causes, however, arise from activities such as industrial processes, agricultural practices, poor waste management, and inadequate sewage systems. These practices increase contamination and reduce the safety of water supplies. Water pollutants can take different forms, including microorganisms, chemical substances, heavy metals, pesticides, pharmaceuticals, and emerging contaminants. For instance, household chemicals, agricultural runoff, and industrial effluents introduce toxic substances into water, many of which pose serious health risks.

Ongoing research continues to reveal the dangers of newly introduced pollutants such as modern pesticides, pharmaceuticals, and microplastics, which complicate water safety management (Guo *et al*., 2023)

Assessing health risks linked to contaminated water involves determining the likelihood of exposure to hazardous substances that may cause illness (Liu *et al*., 2022). This process typically includes four steps: identifying hazards, assessing exposure levels, determining pollutant concentrations, and applying mathematical models to evaluate human health risks (HHR) based on exposure and dose–response relationships (Xu *et al*., 2023) . To accurately predict the adverse effects on human health resulting from various situations, it is essential to have specific information for each pollutant, including a baseline incidence of morbidity or death, as well as concentration–response curves derived from studies on the health effects of the specific pollutant (Adimalla *et al*., 2018). Globally, water-related health issues are closely tied to both environmental and groundwater pollution (Li, 2018). Additionally, improper handling and the persistence of plastic trash result in the buildup in the environment of microplastics, the transmission of pollutants, and the leaching of hazardous additives (Revel and Chatel., 2018). Due to their proximity to the chemicals, heavy metals, drugs, pesticides, and other persistent organic contaminants previously stored in them, microplastics are frequently referred to as a combination of harmful agents (Carbery *et al*., 2020)

The decline in water quality has become a major global concern, largely driven by environmental changes and the increasing scale of human activities. Various factors such as natural processes, anthropogenic influences, and climate change contribute to this deterioration. Their impact is evident through rising levels of pollutants and contaminants in water bodies, which pose serious

risks to both human health and the environment. This makes regular monitoring and effective management of water quality essential to prevent further degradation (Yang *et al*., 2022). Human activities, including the improper disposal of pharmaceuticals, metabolic waste, industrial discharges, and municipal sewage, play a significant role in worsening water quality (Nsabimana and Li, 2023). Extensive research conducted worldwide has examined groundwater quality and its associated health risks, confirming that the consumption of contaminated water can cause severe adverse health effects (Li *et al*., 2019). Findings from these studies link pollutants in groundwater to a wide range of health problems such as obesity, diabetes, cancer, endocrine disruption, cardiovascular conditions, developmental disorders, and reproductive complications . The health consequences of water contamination are diverse and far-reaching. Depending on the type of pollutant, level of exposure, and duration, individuals may suffer from either acute or chronic health conditions. Short-term exposure can result in gastrointestinal infections, dehydration, and other life-threatening waterborne diseases, particularly among vulnerable groups such as children, the elderly, and immunocompromised individuals. Prolonged exposure, however, has been associated with more severe outcomes, including organ damage, developmental abnormalities, reproductive challenges, and an increased risk of cancer (Archer *et al*., 2021). Poor sanitation significantly contributes to the spread of various diseases, including diarrhea, cholera, dysentery, hepatitis A, typhoid, polio, and even stunted growth, which are leading causes of death in children under five years. One of the most common practices linked to poor sanitation is open defecation, where human waste is disposed of in fields, forests, rivers, beaches, or other open spaces. This practice leads to environmental contamination of soil, air, and water. Human feces contain numerous pathogenic organisms that can be transmitted through water, food, and flies, resulting in infections such as salmonellosis, cholera, dysentery, and

diarrhea. Since feces carry infectious agents that enter the digestive tract, the presence of *Escherichia coli* is widely recognized as an indicator of fecal contamination. For this reason, *E. coli* must be absent from safe drinking water and water used for sanitation purposes. Furthermore, contaminated water used in food processing can lead to foodborne infections, as seen in products such as ice cream and street-vended foods (Putri and Kurnia, 2018).

CHAPTER THREE

3.0 METHODOLOGY

3.1 Study area

This research was carried out in the Ikpoba Hill community. The Ikpoba Hill River is located at latitude 6.351°N and longitude 5.647°E. The tap water sample was collected at latitude 6.351°N and longitude 5.646°E, while the well water sample was obtained at latitude 6.352°N and

longitude 5.647°E.

Figure 3.1: Map of study area showing Ikpoba-Okha Local Government Area, Edo State, Nigeria

3.2 Sample Collection

A total of five water samples were collected from different sources within the Ikpoba Hill community for this study. The samples included two tap water samples, two well water samples, and one river water sample. The tap water samples were collected from household taps supplied by the local water distribution system, representing treated and piped water sources. The well water samples were obtained from hand-dug wells commonly used by residents as an alternative source of domestic water. The river water sample was taken directly from the Ikpoba Hill River, which serves as a major surface water body in the area. Each sample was aseptically collected in sterile containers, clearly labeled to indicate the source and sampling point. All samples were immediately transported to the laboratory under chilled conditions to prevent microbial growth and were analyzed within 24 hours of collection.

3.3 PREPARATION OF CULTURE MEDIA

The media used were prepared according to the manufacturer's instructions. The media used were Nutrient Agar and MacConkey Agar.

3.3.1 Preparation of Nutrient Agar

28 grams of nutrient agar (NA) powder was dissolved in 1 litre of distilled water in a conical flask covered with cotton wool and aluminium foil paper. It was mixed thoroughly and sterilized by autoclaving at 121ºC for 15 minutes. The medium was cooled to 45-50ºC and then dispensed aseptically into sterile petri dishes in the laminar flow.

3.3.2 Preparation of MacConkey Agar

55 grams of MacConkey agar (MCA) powder was dissolved in 1litre of distilled water in a conical flask covered with cotton wool and aluminium foil paper. It was mixed thoroughly and

sterilized by autoclaving at 121ºC for 15 minutes. The medium was cooled to 45-50ºC and then dispensed aseptically into sterile petri dishes in the laminar flow.

3.4 Isolation of bacteria

1ml of the sample was weighed and placed in 9ml sterile distilled water and allowed to stand for 30 minutes. The aliquot was then transferred aseptically to sterile petri plates. The prepared agar (for bacteria growth) was poured in aseptically and incubated at 37°C for 24 hours. After successful growth of microorganisms, the colonies were counted with a colony counter and the results per dilution count were recorded. The number of colony forming unit per milliliter was calculated with the formula:

$$\text{Cfu/ml} = \frac{number\ of\ colonies}{volume\ plated\ x\ dilution\ factor}$$

3.4.1 Pure culture

One single colony was identified and re-streaked as a primary inoculant on the surface of a nutrient agar plate medium. Pure cultures were checked from nutrient agar plates. After achieving a pure culture, the same colony was streaked onto a nutrient agar slant. These cultures were incubated at 37°C for 24 hours.

3.4.2 Cultural characteristics

Each colony morphology e.g., size, shape, margin, elevation, consistency, color, transparency was determined.

3.5 MORPHOLOGICAL TEST

3.5.1 Gram staining

Smears of the bacterial isolates were prepared and heat fixed on clean grease free slides. The smears were stained for one minute with crystal violet. This was washed out with distilled water. The slides were flooded with dilute Grams' iodine solution for one minute. This was washed off with distilled water and the smears were decolorized with 95% alcohol for 30 seconds and rinsed off with distilled water. The smears were then counter stained with safranin solution for one minute. Finally, the slides were washed off with distilled water, air dried and observed under oil immersion objective.

3.5.2 Catalase Test

This is a test to detect the presence or absence of catalase enzyme. The catalase enzyme catalyses the breakdown of hydrogen peroxide to release free oxygen gas and the formation of water. A few drops of freshly prepared 3% hydrogen peroxide were added onto the bacterial isolates smeared on a slide. The production of gas bubble indicated catalase enzyme positive.

$2\ H_2O_2 \rightarrow 2\ H_2O + O_2$

3.5.3 **Urease Test**

The urease test is used to determine the ability of an organism to split urea in the presence of the enzyme urease. The bacterial isolates were inoculated into slants of urea medium and incubated at 37ºC for 24-48 hours. Urease positive cultures produced a red-pink colour due to changes in the colour of the indicator

$NH_2CO.NH_2 + H_2O \rightarrow 2NH_3 + CO_2$

3.5.4 Citrate Utilization Test

This test is based on the ability of some organisms to utilize citrate as a sole source of carbon. This was carried out by inoculating the test organism in test tube containing Simon's citrate medium and this was incubated at 37ºC for 24 - 48 hours. The development of deep blue colour after incubation indicates a positive result.

3.5.5 Hydrogen Sulphide (H_2S) Test

Hydrogen sulphide production can be detected by incorporating a heavy metal salt containing (Fe2+) or lead (Pb2+) ion as H_2S indicator to a nutrient culture medium containing cysteine and sodium thiosulfate as the sulphur substrates. Hydrogen sulphide, a colourless gas, when produced reacts with sulphur metal salt (ferrous sulphate) forming a visible insoluble black sulphide precipitate.

3.5.6 Indole Test

Indole test is performed to determine the ability of the organism to split tryptophan molecule into indole. This test is performed to help differentiate species of the family enterobacteriaceae.

Kovac's reagent which contains hydrochloric acid, dimethylaminobenzaldehyde and amyl alcohol is used. Inoculate broth with the test organism and incubate for 18 – 24 hours at 37°C. Add 5ml of Kovac's reagent down the inner wall of the tube. Development of bright red colour at the interface of the reagent and the broth within seconds after adding the reagent is indicative of the presence of indole and is a positive test while absence is negative.

3.5.7 Sugar Fermentation Test

Each of the isolates was tested for its ability to ferment a given sugar with the production of acid and gas or acid only. The growth medium comprised of peptone water, sugar (1%) and the

indicator (bromocresol purple). The mixture was dispensed into test tubes and sterilized by autoclaving at 121°C for 15 minutes. After sterilizing, tubes were allowed to cool and then inoculated with the isolates and incubated at 37°C for 24hrs. Acid and gas production or acid only were observed after about 24 hours of incubation. Acid production was indicated by the change of the medium from purple to yellow colour indicated a positive test.

Sugars used are: lactose, sucrose, glucose, fructose, maltose, starch and sorbitol.

3.6 FUNGI PROCEDURE

3.6.1 Preparation of Potato Dextrose agar

39 grams of potato dextrose agar powder was dissolved in 1 litre of distilled water in a conical flask covered with cotton wool and aluminium foil paper. It was mixed thoroughly and sterilized by autoclaving at 121°C for 15 minutes. The medium was cooled to 45-50°C and before dispensing aseptically into petri dishes. Plates were then incubated for 72 hours at room temperature (25°C)

3.6.2 Isolation of fungi

1ml of the sample was weighed and placed in 9ml sterile distilled water and allowed to stand for 30 minutes. The aliquot was then transferred aseptically to sterile petri plates. The prepared agar (for bacteria growth) was poured in aseptically and incubated at 37°C for 24 hours. After successful growth of microorganisms, the colonies were counted with a colony counter.

3.6.3 Cultural Characteristics

Each colony morphology e.g., size, texture, color, reverse colour, was determined by physical examination.

3.6.4 Pure culture

One single colony was identified and re-streaked as a primary inoculum on the surface of a potato dextrose agar plate medium to make a pure culture. After achieving a pure culture, the same colony was streaked onto potato dextrose agar slant. These cultures were incubated at 25°C for 72 hours.

3.7 LACTOPHENOL COTTON BLUE MOUNTING OF FUNGI

Lactophenol cotton blue is a stain commonly used for making semi-permanent microscopic preparation of fungi. It stains the fungi cytoplasm and provides a light blue background, against which the wall of hyphae can readily be seen. It contains four constituents: phenol, which serves as fungicides; lactic acid, which act as a clearing agent; cotton blue, which stains the cytoplasm of the fungus; and glycerine, which gives semi- permanent preparation. A permanent preparation may be by incorporating polyvinyl alcohol in place of glycerine into the mounting medium.

For rapid and routine examination of almost all type of fungi, spores and spore bearing structures are tested out on a clean slide in a drop of mounting fluid (lactophenol cotton blue) and a cover-glass placed over the preparation which is then ready for microscopic examination.

3.7.1 PROCEDURE

Place a drop of lactophenol cotton on a clean slide. Transfer a small tuff of fungus, preferably with spore or spore boring structures into the drop on the slide using a flamed cooled needle. Gently tease using an inoculating needle. Mix gently the stains with the mold structures. Place a cover-glass over the preparation taking care to avoid trapping air bubbles in the stain.

3.7.2 OBSERVATION

Examine the preparation under low and high-power objectives. Describe the type of hyphae, conidiophore cell, conidia and their arrangement on the conidiophore / conidiogenous cells.

Draw a representative microscopic field under low power and high-power magnification. Identify the mold on the basics of characteristics features produced. The fungal cytoplasm is seen as a lightly stained blue region forming a layer inside the unstained cell wall of hyphae, conidiophores, phialides and conidia, that is conidia, that is surrounded by a light blue background on the slide.

Plate 3.1: Clearly labeled sample bottles containing tap, river, and Hand-dug well water collected for Microbial analysis

Plate 3.2: Gram staining reagents

CHAPTER FOUR

RESULT

The microbial analysis of the collected water samples revealed varying levels of heterotrophic bacterial and fungal growth across the different water sources. **Table 4.1** presents the total heterotrophic colony count for bacteria and fungi. The results showed that **river water** had the highest microbial load on all media (Nutrient Agar, MacConkey Agar, and Potato Dextrose Agar), with bacterial counts ranging from 56 to 61 cfu/mL on NA and 5 cfu/mL on MCA, while fungal counts ranged from 52 to 58 cfu/mL on PDA. **Tap water samples** showed moderate bacterial and fungal growth, whereas **well water samples** had comparatively lower counts. Among the tap water samples, Tap Water (1) recorded slightly higher counts than Tap Water (2), while Well Water (2) showed lower bacterial counts on MCA, indicating minimal presence of coliforms. **Table 4.2** shows the cultural characteristics of bacterial isolates obtained from the different media. The isolates exhibited diverse colony morphologies such as circular and irregular shapes, with elevations ranging from flat to raised and colors from cream to pink. Notable bacterial species identified included *Salmonella typhi, Escherichia coli, Shigella* sp*., Staphylococcus sp., Corynebacterium* sp*., Serratia marcescens, Citrobacter freundii,* and *Klebsiella* sp. **Table 4.3** summarizes the morphological, biochemical, and sugar fermentation characteristics used to confirm bacterial identities. The results revealed that most isolates were **Gram-negative rods**, except for *Staphylococcus sp.* and *Corynebacterium sp.*, which were **Gram-positive**. Biochemical tests such as indole, citrate, catalase, urease, and hydrogen sulfide production helped differentiate the organisms. All isolates fermented glucose and maltose, while variations were observed in lactose, sucrose, and starch

utilization. **Table 4.4** presents the cultural and morphological characteristics of fungal isolates. The fungi identified included *Saccharomyces* sp., *Fusarium* sp., *Trichoderma* sp., and *Saccharomyces* sp. formed creamy colonies with pseudohyphae and chlamydospores, *Fusarium sp.* produced woolly white colonies with orange spores and septate hyphae, while *Trichoderma sp.* developed green, powdery colonies with septate hyphae and conidiospores.

Overall, the results indicate that all water sources contained varying levels of microbial contamination, with the river water exhibiting the highest microbial load, suggesting possible environmental or anthropogenic pollution, while well and tap water samples showed relatively lower but still significant microbial presence.

TABLE 4.1: HETEROTROPHIC COLONY COUNT

	BACTERIA COUNT (NA)			BACTERIA COUNT (MCA)			FUNGI COUNT (PDA)		
SAMPLE NAME	**R1**	**R2**	**R3**	**R1**	**R2**	**R3**	**R1**	**R2**	**R3**
TAP WATER (1)	53	57	50	24	27	22	35	37	31
TAP WATER (2)	49	52	46	19	23	20	42	38	41
WELL WATER (1)	32	36	30	12	12	12	33	38	34
WELL WATER (2)	44	42	41	03	03	03	39	35	40
RIVER WATER	60	56	61	05	05	05	55	58	52

TABLE 4.2: CULTURAL CHARACTERISTICS OF BACTERIAL ISOLATES

Organism	Shape	Size	Elevation	Transparency	Margin	COLOUR	
						Agar 1 (NA)	Agar 2 (MCA)
Salmonella typhi	Irregular	Medium	Flat	Opaque	Undulate	Cream	-
Escherichia coli[1]	Irregular	Medium	Flat	Opaque	Lobate	Cream	-
Shigella sp.	Irregular	Small	Flat	Opaque	Undulate	Cream	-
Staphylococcus sp.	Irregular	Small	Flat	Translucent	Undulate	Cream	-
Corynebacterium sp.	Irregular	Small	Flat	Opaque	Lobate	Cream	-
Serratia marcescens	Circular	Medium	Flat	Opaque	Entire	-	Cream
Citrobacter freundii	Irregular	Medium	Flat	Opaque	Lobate	-	Cream
Klebsiella pneumoniae	Circular	Medium	Flat	Opaque	Entire	-	Cream
Escherichia coli[2]	Circular	Small	Flat	Transparent	Entire	-	Cream
Klebsiella sp.	Circular	Small	Raised	Translucent	Entire	-	Pink

Key: + =Present; - =Absent

TABLE 4.3: MORPHOLOGICAL, BIOCHEMICAL AND SUGAR TESTS OF BACTERIAL ISOLATES

	Salmonella typhi	*Escherichia coli*[1]	*Shigella sp.*	*Staphylococcus sp.*	*Corynebacterium sp.*	*Serratia marcescens*	*Citrobacter freundii*	*Klebsiella pnuemoniae*	*Escherichia coli*[2]	*Klebsiella sp.*
Gram stain	-	-	-	+	+	-	-	-	-	-
Cell type	Rod	Rod	Rod	Cocci	Rod	Rod	Rod	Rod	Rod	Rod
Cell arrangement	Clusters	Chains	Chains	Pairs	Clusters	Chains	Clusters	Chains	Clusters	Chains
Urease	-	-	-	+	-	+	-	+	-	+
Indole	-	+	+	-	-	-	-	-	+	-
Citrate	-	-	-	-	-	+	+	+	-	+
Catalase	+	+	+	+	+	+	+	-	+	-
H_2S	+	-	-	+	+	-	+	-	-	-
Lactose	-	+	-	+	-	-	+	+	+	+
Sucrose	-	+	-	+	+	+	+	+	+	+
Glucose	+	+	+	+	+	+	+	+	+	+
Fructose	-	+	+	+	+	+	+	+	+	+
Maltose	+	+	+	+	+	+	+	+	+	+
Starch	-	-	-	-	-	-	-	+	-	+
Sorbitol	+	+	-	-	-	+	+	+	+	+

Key: + =Present; - =Absent

TABLE 4.4: FUNGI CULTURAL CHARACTERISTICS

Cultural characteristics	**Morphological characteristics**		
Nature of colony	**Nature of hyphae**	**Spore type**	**Organism**
Cream colonies with pale reverse side	Pseudoyphae	Chlamydospore	***Saccharomyces sp.***
Wooly white colonies with orange spores	Septate	Conidiospore	***Fusarium sp.***
Green colonies with pale reverse side and powdery texture	Septate	Conidiospore	***Trichoderma sp.***

Plate 3.3: Nutrient agar plate

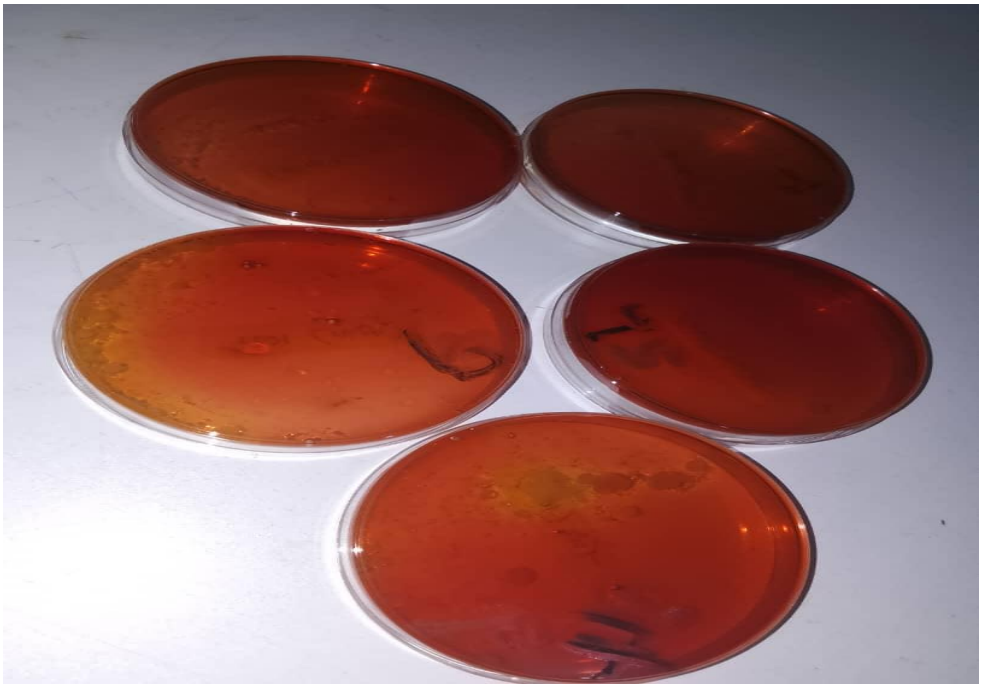

Plate 3.4: MacConkey agar plate

CHAPTER FIVE

DISCUSSION, RECOMMENDATIONS AND CONCLUSION

5.0 DISCUSSION

The quality of water has a direct impact on both mortality and morbidity, as water is essential for life and human survival depends on its availability. To be safe for consumption, drinking water must be free from harmful substances that can negatively affect health, such as pathogenic microorganisms, toxic minerals, and organic pollutants (Haydar *et al*., 2009). In many developing nations, a large portion of the population suffers from illnesses caused by either insufficient access to drinking water or the consumption of poor-quality water (Leeuwen, 2000).

The total heterotrophic bacterial (THB) counts obtained from the analyzed water samples (Table 4.1) indicated the presence of different heterotrophic bacteria in all the sampled water sources. According to the World Health Organization (WHO), the acceptable limit for heterotrophic bacteria in potable water should not exceed 100 cfu/mL (WHO, 2002). However, in this study, the THB counts were found to be lower than the WHO standard, suggesting that the water sources were not heavily contaminated and unsuitable for direct consumption. The bacterial counts ranged from (3–5 cfu/ml) in tap water and well water to (60–61 cfu/ml) in river water. These findings align with previous research conducted in Kaduna State (a neighboring state to Plateau), particularly in Samaru, Zaria (Adesakin *et al*., 2020), as well as other studies within Plateau State (Miner *et al*., 2015) and more recent results from Jos South LGA (Chukwu *et al*., 2023). The widespread contamination of water sources can be linked to improper waste disposal and poor sanitary conditions that are common in rural Nigerian communities. Such bacterial

pollution often results from the infiltration and runoff of waste and fecal matter, particularly during the rainy season—when this study was carried out (Adesakin *et al*., 2020).

Contaminated water is often associated with diseases such as typhoid, diarrhea, cholera, gastroenteritis, dysentery, and urinary tract infections (Nwidu *et al*., 2008). Among the different water sources examined, tap water had the lowest microbial load, likely due to treatment processes usually carried out before distribution. This observation corresponds with findings by (Jurbe *et al*., 2023), who reported tap water as the second least contaminated domestic water source in Jos and surrounding areas. The detection of *Escherichia coli*a primary indicator of fecal contamination further confirmed the presence of other enteric pathogens (Petridis, 1998). River water samples showed the highest microbial contamination, followed by tap water then well water. The high bacterial load observed in the river water may be attributed to direct contamination from surface runoff, domestic waste disposal, and human activities, which introduce organic matter that supports microbial growth. Similar observations were reported by **(**Okonko *et al*., 2008) who noted that open water sources such as rivers and streams often contain higher microbial populations due to continuous exposure to environmental contaminants. Microbial load in tap water could indicate leakages or contamination in the distribution system, possibly through corroded pipes or back-siphonage. Improper water distribution systems can lead to secondary contamination of treated tap water and in wellwater, this could be due to the fact that hand-dug wells are the main water sources in rural areas and are easily polluted by their surroundings. Contributing factors may include the absence of proper well seals, the use of dirty containers and ropes, and unhygienic practices during water collection, as reported by (Adesakin *et al*., 2020).and further supported by (Iduh, 2022).

The isolates presented in Table 4.2 exhibited a wide variety of colony morphologies that were consistent with the bacterial genera identified in this study. The organisms isolated included *Salmonella typhi*, *Escherichia coli*, *Shigella* spp., *Staphylococcus* spp., *Corynebacterium* spp., *Serratia marcescens*, *Citrobacter freundii*, *Klebsiella pneumoniae*, and *Klebsiella* spp. Analysis of the various bacterial isolates obtained from water sources within the study area and their associated health conditions (Table4.2) revealed that *Escherichia coli* was the most prevalent organism across all sampled locations. Although most strains of *E. coli* are harmless, some pathogenic strains are responsible for illnesses such as urinary tract infections, gastroenteritis, and neonatal meningitis, while others have been linked to food poisoning (Pormohammad *et al*., 2019) *Klebsiella* spp. was the next most abundant isolate and is known to cause diseases such as pneumonia, septicemia, spondylitis, and ankylosing (Ayandele *et al*., 2020)

The predominance of *Escherichia coli* (E. coli) among the bacterial isolates obtained from the study's water samples suggests fecal contamination across all the examined sources, likely resulting from the poor sanitary and hygienic conditions prevalent in the study area. Other gram-negative bacteria such as *Klebsiella* spp., *Salmonella typhi*, and *Shigella* spp. These microorganisms are known to cause a range of serious infections, including pneumonia, septicemia, salmonellosis, gastroenteritis, endocarditis, neonatal sepsis, wound infections, shigellosis, and dysentery. Staphycoccus aureus. It commonly leads to abscess formation and causes skin infections like Scalded skin syndrome, folliculitis, furuncle, carbuncle, impetigo and Toxic shock syndrome. Sometimes cause pneumonia, endocarditis, bacteremia and osteomyelitis. Some elaborate strains produce toxins that cause gastroenteritis, and Staphylococcal food poisoning (Ghalehnoo, 2018). Findings from related studies across different parts of the state

have similarly reported the occurrence of these pathogens in water sources, emphasizing their public health significance and the consequences of waterborne contamination (Miner *et al*., 2015)

The illnesses caused by these microorganisms are often difficult to treat with antibiotics, and hospitals are recognized as major hotspots for bacterial transmission when infected individuals receive treatment. Moreover, using contaminated water for washing or cleaning surfaces can further promote the spread of diseases within a community. Studies have shown that ultraviolet (UV) light sterilization alone is sometimes inadequate for completely eliminating certain bacterial species during water treatment. Gram-negative bacteria, in particular, are known to survive harsh environmental conditions such as low temperatures, chlorination, and nutrient deprivation by entering a viable but non-culturable (VBNC) state. Even in this dormant state, some of these organisms retain their pathogenic abilities, posing a continued threat to human health if not completely removed from water sources (Li *et al*., 2014). Therefore, it is strongly recommended that water undergo a combined and comprehensive treatment process before being deemed safe for consumption.

The biochemical characteristics of the bacterial isolates obtained from the analyzed water samples are presented in Table 4.3. The positive reactions observed in the various biochemical tests—which reflect normal metabolic activities inherent in most living organisms or cells—indicate that the identified bacterial species are consistent with those commonly found in water and other aquatic environments. This observation aligns with the findings of Banwo (2006), who reported similar bacterial species in a study conducted on stream surface water in Wyoming, USA.

The biochemical characteristics of the bacterial isolates obtained from the various water samples (Table 4.3) revealed the presence of several Gram-positive and Gram-negative organisms commonly associated with contaminated aquatic environments. The positive biochemical reactions observed including catalase, citrate, and carbohydrate fermentation tests corroborate that the identified bacteria are consistent with those frequently encountered in natural and domestic water sources (Banwo, 2006). Similar findings were reported in more recent studies which confirmed that microbial contamination in surface and groundwater remains a major public health concern in Nigeria and other developing nations (Uduma *et al*., 2022; Tenebe *et al*., 2023). The presence of *Escherichia coli* and *Salmonella typhi* as dominant isolates in this study indicates faecal contamination of the sampled water sources. *E. coli* serves as a key indicator organism for waterborne contamination, reflecting the likely presence of other pathogenic enteric bacteria. Recent research across Nigeria supports this observation, revealing that borehole, well, and surface water samples often contain *E. coli* and coliforms above WHO permissible limits (Tenebe *et al*., 2023; Bakare-Abidola *et al*., 2025). Such findings emphasize that untreated or poorly treated water remains a major route for the transmission of typhoid fever, diarrhoea, dysentery, and gastroenteritis. The detection of *Pseudomonas aeruginosa*, *Klebsiella pneumoniae*, *Citrobacter freundii*, and *Serratia marcescens* further supports evidence of environmental pollution. These organisms are known opportunistic pathogens and are frequently isolated from hospital and household water sources. Their occurrence suggests possible runoff or seepage from contaminated waste materials and indicates poor hygiene and sanitary management within the study area. Similar findings were documented in a recent study on domestic water quality in Aluu community, Rivers State, where high counts of *Pseudomonas* and *Klebsiella* were recorded in borehole samples (Chukwuemeka *et al*., 2024). *Staphylococcus aureus* and

Enterococcus faecalis, the two Gram-positive isolates obtained, are also clinically important pathogens that may cause skin infections, urinary tract infections, and endocarditis when ingested or transmitted through contact. Their occurrence in water is an indication of cross-contamination from human or animal sources. This aligns with previous research by (Uduma *et al*., 2022), who found *Staphylococcus* species in untreated dam water in Jigawa State, suggesting that microbial contamination in drinking water sources persists despite public health interventions.

The biochemical profile of isolates such as *Salmonella typhi* (H_2S positive, lactose negative) and *Shigella* spp. (H_2S negative, indole positive) further confirms the presence of enteric pathogens, which pose serious health risks to consumers. These organisms have been widely reported in polluted water bodies across Nigeria and are associated with outbreaks of typhoid and bacillary dysentery (Bakare-Abidola *et al*., 2025). The isolation of *Bacillus subtilis* and *Corynebacterium* species, though not as pathogenic, suggests possible soil and environmental contributions to the microbial load. In summary, the results from this study are consistent with multiple contemporary findings across Nigeria, all emphasizing the urgent need for improved water treatment, regular monitoring, and public awareness regarding safe water handling practices (Tenebe *et al*., 2023; Chukwuemeka *et al*., 2024; Bakare-Abidola *et al*., 2025). These measures are essential to prevent outbreaks of waterborne diseases and ensure community health.

The fungal isolates obtained from the water samples exhibited distinct cultural and morphological characteristics that enabled their identification as *Saccharomyces* sp., *Fusarium* sp., and *Trichoderma* sp. These findings are consistent with recent reports that have documented the frequent occurrence of these fungal genera in water and aquatic environments

(Chukwuemeka Ogbuleka *et al*., 2024). The *Saccharomyces* species produced cream-colored colonies with pale reverse sides and pseudohyphae bearing chlamydospores. These characteristics are typical of *Saccharomyces cerevisiae* and related yeasts, which are known for their fermentative metabolism and adaptability to nutrient-rich environments (Costa *et al*., 2020). The presence of *Saccharomyces* sp. in the water samples suggests possible organic contamination, as this genus is often associated with decaying vegetation, sugar residues, and domestic waste discharge (Maria *et al*., 2022). Although *Saccharomyces* species are generally non-pathogenic, their detection indicates the existence of nutrients that can support microbial proliferation, which may indirectly affect water quality. The isolates identified as *Fusarium* sp. formed woolly white colonies with orange pigmentation and septate hyphae that produced conidiospores. This agrees with the descriptions of *Fusarium* morphology by (Jurbe *et al*., 2021), who reported similar cultural characteristics from water sources in Jos, Nigeria. *Fusarium* species are filamentous fungi commonly found in soil and water and are capable of producing mycotoxins harmful to humans and animals (Crous *et a*l., 2022). Their presence in water is of public health concern, as certain species such as *Fusarium solani* and *Fusarium oxysporum* can cause opportunistic infections in immunocompromised individuals and contribute to the deterioration of stored water quality (Tenebe *et al*., 2023). The *Trichoderma* sp. observed formed green, powdery colonies with septate hyphae and conidiospores. This observation corresponds with those of (Afonso *et al*., 2021), who found *Trichoderma harzianum* and related species prevalent in soil and aquatic habitats due to their saprophytic nature. *Trichoderma* species are known for their rapid growth, conidia production, and antagonistic ability against other microorganisms (Bakare-Abidola *et al*., 2025). Although they are generally considered beneficial in agriculture and biodegradation, their occurrence in domestic water suggests organic pollution

or soil run-off into the water system (Chukwuemeka Ogbuleka *et al*., 2024). The presence of these fungi in the analyzed water samples indicates possible environmental contamination from soil, decaying organic matter, or inadequate sanitation practices. According to (Tenebe *et al*., 2023), fungal presence in drinking water systems may result from poor storage conditions, biofilm formation, or post-treatment contamination. This observation aligns with the current study's findings, where the fungal isolates reflect the influence of human and environmental activities on microbial quality. Fungi such as *Fusarium* and *Trichoderma* are also indicators of high organic load and insufficient treatment processes (Maria *et al*., 2022). Their occurrence emphasizes the need for regular monitoring of both bacterial and fungal components of water to ensure safety and compliance with international drinking water standards (Bakare-Abidola *et al*., 2025). The detection of *Saccharomyces*, *Fusarium*, and *Trichoderma* species in the water samples suggests organic contamination and the possible presence of opportunistic pathogens. Proper treatment, safe storage, and continuous monitoring are essential to prevent fungal growth and safeguard public health.

5.1 CONCLUSION

The bacteriological analysis of the water samples revealed that all tested samples were contaminated with bacteria. Based on these findings, it can be concluded that the water requires proper treatment before consumption to prevent waterborne diseases. To address this issue, there is a pressing need to raise community awareness about preventive and treatment measures that can reduce the risks associated with using contaminated water. Public health education should emphasize simple and effective methods such as boiling water before drinking. Additionally, water distribution systems should use rust-resistant pipes (e.g., aluminum or steel) to prevent corrosion and leakage, which may further contaminate the water. Regular inspection and maintenance of pipe connections are essential to promptly detect and repair any leaks.

5.2 RECOMMENDATIONS

Based on the study's results, it is imperative that relevant agencies institute routine microbiological monitoring and evaluation of water sources within Ikpoba-Okha LGA. This should be performed to verify adherence to World Health Organization (WHO) and Nigerian Industrial Standards (NIS) for potable water. This could help to mitigate the current irregu larities in the quality of commercially accessible water. It is further recommended that, the inhabitants of the study area should be educated on the danger of their act in respect to the way sewage is disposed and related diseases that accompany the act is therefore advocated, It is necessary for water to be thoroughly treated be fore usage, Water exploration should leave in hand of state and federal government especially within rural communities, Microbial treatment should be carried out on water resources before consumption and Wells should be located far from domestic refuse waste, pit latrine, stagnant water and drainages.

REFERENCES

Abdel-Satar, A. M., Ali, M. H. and Goher, M. E. (2017). Indices of water quality and metal pollution of Nile River, Egypt. *Egyptian Journal of Aquatic Research* 43(1):21–29.

Abhishek, C., Pankaj, G., Ajit, V. and Tanu, J. (2017). Microbiological evaluation of drinking water sold by roadside vendors of Delhi, India. *Applied Water Science* 7: 1635–1644.

Adesakin, T. A., Oyewale, A. T., Bayero, U., Mohammed, A. N., Aduwo, I. A., Ahmed, P. Z., Abubakar, N. D. and Barje, I. B. (2020). Assessment of bacteriological quality and physico-chemical parameters of domestic water sources in Samaru community, Zaria, Northwest Nigeria. *Heliyon* 6(8): e04637.

Adimalla, N., Li, P. and Venkatayogi, S. (2018). Hydrogeochemical evaluation of groundwater quality for drinking and irrigation purposes and integrated interpretation with water quality index studies. *Environmental Processes* 5(2):363–383.

Afonso, T. B., Simões, L. C.and Lima, N. (2021). Occurrence of filamentous fungi in drinking water: Their role in fungal–bacterial biofilm formation. *Research in Microbiology* 172(1):103791.

Archer, E., Volschenk, M., Brocker, L. and Wolfaardt, G. M. (2021). A two-year study of emerging micro-pollutants and drugs of abuse in two Western Cape wastewater treatment works (South Africa). *Chemosphere* 285 :131460.

Arif, S., Khan, U., Turab, A., Hussain, I., Habib, A., Mansoor, T., Mallick, D., Suhag, Z., Bhatti, Z. and Ahmed, I. (2016). Evaluation of solar disinfection of water intervention delivered through Lady Health Workers in reduction of diarrheal episodes in under-five children. *International Journal of Pedestrian Child Care* 1(1):1–7.

Atuanya, E. I., Nwogu, N. A., and Akpor, E. A. (2012). Effluent qualities of government and private abattoirs and their effects on Ikpoba River, Benin City, Edo State, Nigeria. *Advances in Biological Research* 6(5):196–201.

Ayandele, A. A., Oladipo, E. K., Oyebisi, O. and Kaka, M. O. (2020). Prevalence of multi-antibiotic resistant *Escherichia coli* and *Klebsiella* species obtained from a tertiary medical institution in Oyo State, Nigeria. *Qatar Medical Journal* (1): 9

Bakare-Abidola, T., Olaoye, J.and Adams, A. O. (2025). Isolation and identification of coliforms from public water supplies in Lagos State, Nigeria. *World Journal of Advanced Research and Reviews* 25(3):761–772.

Banwo,K. (2006).Nutrient load and pollution study of some selectedstations along ogunpa river in ibadan.*Master's dissertation, university of ibadan,ibadan* 107pp

Bryce, J., Boschi-Pinto, C., Shibuya, K.and Black, R. E. (2005). WHO estimates of the causes of death in children. *The Lancet* 365(9465):1147–1152.

Carbery, M., MacFarlane, G. R., O'Connor, W., Afrose, S., Taylor, H. and Palanisami, T. (2020). Baseline analysis of metal(loid)s on microplastics collected from the Australian shoreline using citizen science. *Marine Pollution Bulletin* 152, 110914.

Chen, S. S., Kimirei, I. A., Yu, C., Shen, Q. and Gao, Q. (2022). Assessment of urban river water pollution with urbanization in East Africa. *Environmental Science and Pollution Research* 29(29):40812–40825.

Chukwu, A. C., Duguryil, Z., Gambo, N. N., Lubis, S. and Kitka, D. (2023). Assessment of the physicochemical and bacteriological content of some drinking water sources in Jos South LGA in Northern Senatorial District of Plateau State, Nigeria. *Asian Journal of Applied Chemistry Research* 14(2):36–45.

Chukwuemeka-Ogbuleka, N. A., Owhonka, A., Kueniode, O. L. and Awari, V. G. (2024). Evaluation of bacterial contamination in domestic water sources in Aluu community, Rivers State, Nigeria. *Microbiology Research International* 12(3):73–77.

Crous, P. W., Sandoval-Denis, M., Costa, M. M., Groenewald, J. Z., van Iperen, A. L., Starink-Willemse, M., Hernández-Restrepo, M., Kandemir, H., Ulaszewski, B., de Boer, W., Abdel-Azeem, A. M., Abdollahzadeh, J., Akulov, A., Bakhshi, M., Bezerra, J. D. P., Bhunjun, C. S., Câmara, M. P. S., Chaverri, P., Vieira, W. A. S., Decock, C. A., … Thines, M. (2022). *Fusarium* and allied fusarioid taxa (FUSA) 1. *Fungal Systematics and Evolution* 9:161–200.

Daud, M., Nafees, M., Ali, S., Rizwan, M., Bajwa, R. A., Shakoor, M. B., Arshad, M. U., Chatha, S. A. S., Deeba, F. and Murad, W. (2017). Drinking water quality status and contamination in Pakistan. *BioMed Research International* 908183.

Dechesne, M., Soyeux, E., Loret, J. F., Westrell, T., Stenström, T., Gornik, V. and Medema, G. (2006). *Pathogens in source water (MicroRisk Project Report).*

Durmishi, B. (2012). Drinking water quality assessment in Tetova Region. *American Journal of Environmental Science* 8(2):162–169.

Eberhard, R. (2019). *Access to water and sanitation in Sub-Saharan Africa: Review sector report, investments, key findings to infrastructure future support to sector development.* GIZ.

Eyankware, M. O., Nnajieze, V. S. and Aleke, C. G. (2018). Geochemical assessment of water quality for irrigation purpose in abandoned limestone quarry pit at Nkalagu area, Southern Benue Trough, Nigeria. *Environmental Earth Sciences.*

Food and Agriculture Organization. (2022). *Land and water*. United Nations.

Ghalehnoo, Z. R. (2018). Diseases caused by *Staphylococcus aureus*. *International Journal of Medical and Health Research* 4(11):65–67.

Guo, W., Li, P., Du, Q., Zhou, Y., Xu, D. and Zhang, Z. (2023). Hydrogeochemical processes regulating the groundwater geochemistry and human health risk of groundwater in the rural areas of the Wei River Basin, China. *Exposure and Health.* 1-16

Hadzi, G. Y., Essumang, D. K.. and Adjei, J. K. (2015). Distribution and risk assessment of heavy metals in surface water from pristine environments and major mining areas in Ghana. *Journal of Health and Pollution* 5(9):86–99.

Haydar, S., Arshad, M. and Aziz, J. A. (2009). Evaluation of drinking water quality in urban areas of Pakistan: A case study of Southern Lahore. *Pakistan Journal of Engineering and Applied Sciences* 5:16–23.

Iduh, C. E. (2022). *Identification and antimicrobial susceptibility profile of pathogenic Escherichia coli in drinking water sources in Jos, Nigeria* (Doctoral dissertation).

Jung, A.-V., Le Cann, P., Roig, B., Thomas, O., Baurès, E. and Thomas, M.-F. (2014). Microbial contamination detection in water resources: Interest of current optical methods, trends, and needs in the context of climate change. *International Journal of Environmental Research and Public Health* 11(4): 4292–4310.

Jurbe, D. F., Bigwan, E. I., Ayanbimpe, G. M., Davou, V. K., Abashi, N. L., Raplong, H. H. and Fyaktu, E. J. (2023). Bacterial contamination of water sources for domestic use in Jos and environs. *World Journal of Advanced Research and Reviews* 19(1):375–385.

Jurbe, D. F., Bigwan, E. I., Ayanbimpe, G. M., Davou, V. K., Abashi, N. L., Raplong, H. H., & Fyaktu, E. J. (2021). Bacterial and fungal contamination of water sources for domestic use in Jos and environs. *Nigerian Journal of Microbiology* 35(2) 95–104.

Leeuwen, F. X. R. (2000). Safe drinking water: The toxicologist's approach. *Food and Chemical Toxicology* **38**(Suppl. 1):51–58.

Lewandowski, J., Meinikmann, K., and Krause, S. (2020). Groundwater–surface water interactions: Recent advances and challenges. *Water* **12**(1),:296.

Li, L., Mendis, N., Trigui, H., Oliver, J. D. and Faucher, S. P. (2014). The importance of the viable but non-culturable state in human bacterial pathogens. *Frontiers in Microbiology* 5:258.

Li, P. and Wu, J. (2019). Drinking water quality and public health. *Exposure and Health* 11(2):73–79.

Li, P., He, X. and Guo, W. (2019). Spatial groundwater quality and potential health risks due to nitrate ingestion through drinking water: A case study in Yan'an City on the Loess

Plateau of Northwest China. *Human and Ecological Risk Assessment: An International Journal* 25(1–2):11–31.

Li, P., He, X., Li, Y. and Xiang, G. (2018). Occurrence and health implication of fluoride in groundwater of Loess Aquifer in the Chinese Loess Plateau: A case study of Tongchuan, Northwest China. *Exposure and Health* 11(1):95–107.

Liu, L., Wu, J., He, S. and Wang, L. (2022). Occurrence and distribution of groundwater fluoride and manganese in the Weining Plain (China) and their probabilistic health risk quantification. *Exposure and Health* 14(3):263–279.

Lukubye, B. and Andama, M. (2017). Bacterial analysis of selected drinking water sources in Mbarara Municipality, Uganda. *Journal of Water Resource and Protection* 9(8):999–1013.

Mahagamage, M., Pathirage, M. and Manage, P. (2020). Contamination status of *Salmonella spp.*, *Shigella spp.*, and *Campylobacter spp.* in surface and groundwater of the Kelani River Basin, Sri Lanka. *Water* 12(8): 21-87.

Maria, U. B., Abubakar, M. M. and Muhammed, S. I. (2022). *Escherichia coli* and coliform bacteria as drinking water quality indicators at Warwade Dam, Dutse, Jigawa State, Nigeria. *FUDMA Journal of Sciences* 5(4):418–425.

Miner, C. A., Dakhin, A. P., Zoakah, A. I. and Afolaranmi, T. O., & Envuladu, E. A. (2015). Household drinking water: Knowledge and practice of purification in a community of Lamingo, Plateau State, Nigeria. *Journal of Environmental Research and Management* 6(10):230–236.

Mishra, R. K. (2023). Freshwater availability and its global challenge. *British Journal of Multidisciplinary Advanced Studies* 4(3): 1–78.

Mushtaq, N., Singh, D. V., Bhat, R. A., Dervash, M. A. and Hameed, O. B. (2020). Freshwater contamination: Sources and hazards to aquatic biota. In H. Qadri, R. Bhat, M. Mehmood, G. Dar (Eds.), *Fresh Water Pollution Dynamics and Remediation* (pp. 27–50).

Nwidu, L. L., Oveh, B., Okoriye, T. and Vaikosen, N. A. (2008). Assessment of the water quality and prevalence of waterborne diseases in Amassoma, Niger Delta, Nigeria. *African Journal of Biotechnology* 7(17) :2993–2997.

Odonkor, S. T. and Ampofo, J. A. (2013). *Escherichia coli* as an indicator of bacteriological quality of water: An overview. *Microbiology Research* 4(e2):5–11.

Okonko, I. O., Adejoye, O. D., Ogunnusi, T. A., Fajobi, E. A. and Shittu, O. B. (2008). Microbiological and physicochemical analysis of different water samples used for domestic purposes in Abeokuta and Ojota, Lagos, Nigeria. *African Journal of Biotechnology* 7(5):617–621.

Okuofu, A. C., Echafona, N. O. and Ayeni, O. G. (1990). Bacteriological and physicochemical examination of well waters in Ahmadu Bello University (main campus), Zaria, Nigeria. *Journal of the Nigerian Association of Hydrogeologists* 2(1):111–115.

Orji, E. A. and Egboka, B. C. E. (2015). The hydrogeology of Delta State, Nigeria. *The Pacific Journal of Science and Technology* **16**(2):257–268.

Osimen, E. C. and Anagha, L. I. (2020). Endoparasites of freshwater fishes from rivers in Edo State, Nigeria. *Sokoto Journal of Veterinary Sciences* **18**(4):197–204.

Páll, E., Niculae, M., Kiss, T., Șandru, C. D.and Spînu, M. (2013). Human impact on the microbiological water quality of rivers. *Journal of Medical Microbiology* 62(11):1635–1640.

Panagopoulos, A. and Giannika, V. (2022). Decarbonized and circular brine management/valorization for water and valuable resource recovery via minimal/zero liquid discharge (MLD/ZLD) strategies. *Journal of Environmental Management* **324**(8):116239.

Petridis, H. E. (1998). *E. coli O157:H7, a potential health concern*. University of Florida Cooperative Extension Service, Institute of Food and Agricultural Sciences (EDIS).

Pormohammad, A., Nasiri, M. J. and Azimi, T. (2019). Prevalence of antibiotic resistance in *Escherichia coli* strains simultaneously isolated from humans, animals, food, and the environment: A systematic review and meta-analysis. *Infection and Drug Resistance* 12:1181–1197.

Potgieter, N., Karambwe, S., Mudau, L. S., Barnard, T.and Traore, A. (2020). Human enteric pathogens in eight rivers used as rural household drinking water sources in the Northern Region of South Africa. *International Journal of Environmental Research and Public Health* 17(6):2079

Putri, A. M. and Kurnia, P. (2018). Identifikasi keberadaan bakteri coliform dan total mikroba dalam es dung-dung di sekitar kampus Universitas Muhammadiyah Surakarta [Identification of coliform bacteria and total microbes in Dung-Dung ice around Muhammadiyah University Surakarta]. *Media Gizi Indonesia* 13(1): 41–48.

Shafiq. A., Ayaz. A., Ihteram.U., Nadia. N., Ammar. A. and Nawab .A. (2013). How to cite this article: Bacteriological Biochemical Evaluation of the Springs water of district Buner, Khyber Pakhtunkhwa, Pakistan. International Journal of Advancements in Research and Technology 2 (7): 452-460.

Sepehria, A., Sarrafzadeh, M. H. and Avateffazeli, M. (2020). Interaction between *Chlorella vulgaris* and nitrifying-enriched activated sludge in the treatment of wastewater with low C/N ratio. *Journal of Cleaner Production* 247:119-164.

Tenebe, I. T., Babatunde, E. O., Eddy-Ugorji, C. C., Etu, E.-E. E., Ogarekpe, N. M., Ekeanyanwu, C. V., Diekola, O. A., Oladele, O. S. and Ezeudu, O. B. (2023). Bacterial contamination levels and brand perception of sachet water: A case study in some Nigerian urban neighborhoods. *Water* 15(9):1762.

Uduma, B. M., Abubakar, M. M. and Muhammed, S. I. (2022). *Escherichia coli* and coliform bacteria as drinking water quality indicators at Warwade Dam, Dutse, Jigawa State, Nigeria. *FUDMA Journal of Sciences* 5(4):418–425.

Ulakpa, R. O. E.and Eyankware, M. O. (2021). Contamination assessment of water resources around waste dumpsites in Abakaliki, Nigeria: A mini review. *Journal of Clean WAS* 5(1):13–16.

Umar, H. O., Okareh, O. T., Adeleye, A. O., Orifah, M. O., Amoo, A. O., Sabiu, N. and Gana, S. A. (2020). Consumers' perception of municipal water quality in Barnawa community of Kaduna State, Nigeria. *FUDMA Journal of Sciences* **4**(1):13–23.

United Nations (UN). (2015). *Sustainable Development Goals (SDG): Goal 6 – Clean Water and Sanitation.*

Usman, J., Nasir, A. G., Muhammed, Y., Muhammad, R., Musa, S. and Bello, A. E. (2020). Physicochemical analysis of well water utilized in Gusau Metropolis, Zamfara State. *International Journal of Science and Global Sustainability* **6**(2):73–81.

Vunain, E., Masoamphambe, E. F., Mpeketula, P. M. G., Monjerezi, M. and Etale, A. (2017). Evaluation of coagulating efficiency and waterborne pathogen reduction capacity of *Moringa oleifera* seed powder for treatment of domestic wastewater from Zomba, Malawi. *Journal of Environmental Chemical Engineering* **5**(3):103118.

World Health Organization (WHO). (2002). *Guidelines for drinking-water quality* (3rd ed.). World Health Organization.

World Health Organization. (2019). *National systems to support drinking-water, sanitation and hygiene: Global status report 2019 (GLAAS 2019 report)*. World Health Organization.

Xu, D., Li, P., Chen, X., Yang, S., Zhang, P., and Guo, F. (2023). Major ion hydrogeochemistry and health risk of groundwater nitrate in selected rural areas of the Guanzhong Basin, China. *Human and Ecological Risk Assessment: An International Journal* **29**(3):701–727.

Yang, Y., Li, P., Elumalai, V., Ning, J., Xu, F.and Mu, D. (2022). Groundwater quality assessment using EWQI with updated water quality classification criteria: A case study in and around Zhouzhi County, Guanzhong Basin (China). *Exposure and Health* 1–16.