

Survey and Identification of Biological Contaminants in Sources of Drinking Water in Biu Metropolis, Biu Local Government Area, Borno State, Nigeria

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ABSTRACT

Safe drinking water remains a public health priority in developing nations where untreated sources are commonly used. This study assessed the physicochemical and biological quality of drinking water from borehole, sachet, surface, and well water sources in Biu Local Government Area, Borno State. A total of 120 water samples were collected between April and September 2026 and analysed using standard methods. Physicochemical parameters differed significantly among sources ($p < 0.05$), with sachet water recording the lowest conductivity (278.48 $\mu\text{S}/\text{cm}$) and TDS (195.43 mg/L), while surface water had the highest (731.04 $\mu\text{S}/\text{cm}$ and 469.76 mg/L , respectively). Bacterial and fungal contaminants were detected across all sources. Borehole water contained the greatest number of presumptively identified bacterial types (20), while well water contained the fewest (14). Fungal genera including *Aspergillus*, *Penicillium*, *Fusarium*, *Candida*, *Rhizopus*, and *Cryptococcus* were detected, with sachet water containing the highest number of fungal types (13). Identifications were presumptive; confirmatory molecular methods and quantitative microbial enumeration were not performed. The findings indicate that water sources in the study area harbour bacterial and fungal contaminants of potential public health concern. Routine monitoring of physicochemical, bacteriological, and fungal parameters is recommended for all drinking-water sources in the study area.

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INTRODUCTION

Safe drinking water is essential for healthy living. Rivers, groundwater, aquifers, lakes, and other waterways are among the major sources of water for human use. Drinking-water sources are vulnerable to numerous pollutants arising from both natural and anthropogenic activities. This remains a global challenge, particularly in developing countries where poor sanitation persists and much of the population depends on rivers, streams, hand-dug wells, boreholes, and lakes for potable water (Koko *et al.*, 2024). Over the years, researchers have investigated the distribution, concentration, and risks associated with a wide range of chemical pollutants in drinking water, including inorganic contaminants such as heavy metals, inorganic anions, radionuclides, organic pollutants, and inorganic-organic pollutants. In addition, considerable research has documented the presence of microorganisms in drinking water. However, Pandey *et al.*, (2023) and Reinholds *et al.*, (2019) reported that information on the occurrence of fungal metabolites (mycotoxins) in drinking water remains scarce, particularly in Africa, with most available studies focusing on their presence in food.

Kwari (2015) identified water scarcity as one of the major environmental challenges confronting rural communities in northeastern Nigeria, particularly Borno State. In many rural communities across northern Nigeria, hand-dug wells and boreholes serve as the main sources of water for domestic and livestock use. However, the quality of water from these sources is not always known. Safe water is a basic necessity of life, and its unavailability or contamination can have serious public health implications, ranging from individual cases of disease to outbreaks of epidemics (Ibeto & Okoye, 2010). The physical and chemical contamination of groundwater by wastewater, pesticides, and fertilizers in Biu

has not been reported. However, contaminated water can harbour pathogenic organisms capable of causing infectious diseases. According to the World Health Organization (WHO), about 25,000 people died each day in 2008 as a result of consuming contaminated water. One out of every four hospital beds is reportedly occupied by a patient who has consumed contaminated water. More than 80% of diseases worldwide are related to contaminated water, while an estimated 5 billion infections occur annually in Africa, Asia, and Latin America as a result of contaminated water (Hiro *et al.*, 2013). Microbially contaminated water and food are also among the major causes of diarrhoeal diseases, affecting more than 1 billion children under five years of age worldwide (Fenwick, 2006).

Access to safe drinking water is essential for human health and well-being; however, many people worldwide, including in Nigeria, still face challenges in accessing clean and safe water sources (Mshelia *et al.*, 2023). In Biu Local Government Area, water is obtained from boreholes, wells, rivers and packaged/sachet water, however available information on the biological quality of these sources remains limited. Previous studies in the area have largely focused on groundwater availability, hydrogeological characteristics and physicochemical quality, with comparatively limited attention to the occurrence and characterization of bacterial and fungal contaminants across different drinking-water sources. This creates a need for an integrated assessment of the biological and selected physicochemical characteristics of commonly used water sources in the area. Therefore, this study aimed to assess the physicochemical characteristics and determine the occurrence of bacterial and fungal contaminants in selected drinking-water sources in Biu Local Government Area, Borno State.

The objectives of the study were: i. To determine the physical parameters, including pH, temperature (°C), total dissolved solids (TDS), electrical conductivity (EC), and dissolved oxygen (DO), of water samples collected from the selected study areas using portable meters. ii. To carry out a bacteriological study of water samples collected from the selected study areas. iii. To conduct biochemical studies of the bacterial isolates. iv. To identify the fungal spores present in the water samples. v. To determine the toxicology of the fungal spores present in the water samples.

MATERIALS AND METHODS

Study Area

This study was conducted in Biu Local Government Area (LGA) of Borno State, Nigeria. The LGA covers approximately 3,165–3,423 km² and is situated on the Biu Plateau, a volcanic formation with elevations ranging from 626 to 700 m above sea level. The area has a climate characteristic of the Northern Guinea Savannah zone. Biu has an annual temperature of approximately 32.16 °C (89.89 °F), which is 2.7% higher than the national average for Nigeria. The area receives about 500–700 mm of precipitation and records approximately 61.57 wet days annually, representing 16.87% of the year.

Five non-randomly selected communities were included in the study to assess the microbiological quality of drinking water across settlements with different environmental and human settlement characteristics. The communities were Galdimare, Dugja, Zarawuyaka, Buratai, and Sulumthla. Galdimare, located on a relatively flat part of Biu Town, is a densely populated and heavily built-up area. Dugja is located north/northwest of Galdimare at approximately the same elevation (629 m) and is similarly characterised by high-density development. Zarawuyaka, located east of Biu Town

at an elevation of about 697 m, is a peri-urban settlement where high-density residential development gradually gives way to low-density agricultural land. Buratai is a rural community along the Damaturu Road, approximately 25–30 km from Biu Town, with extensive open spaces and farmlands. Temporary streams also form in the area during the rainy season. Sulumthla is also a rural settlement.

Sample Collection

Samples were collected on 6 April, 13 May, 27 June, 3 July, 10 August and 17 September 2026. During each sampling occasion, one sample was collected from each of the four water-source types in each of the five selected communities. Thus, the total number of field samples was calculated as: 5 communities' × 4 water sources × 6 sampling occasions × 1 sample = 120 samples. The six sampling occasions provided temporal replication, with six observations obtained for each community × water-source combination. Water samples were collected aseptically from the selected sampling points using sterile containers. Each container was labelled with the sample identification code, water source, location, and date of collection. Each sample was assigned a unique identification code at the time of collection to facilitate laboratory processing and record keeping. Samples from wells and boreholes were collected using aseptic procedures to minimise contamination during sampling. Sachet-water samples were collected as sealed units from the selected sources. The collected samples were placed in a clean insulated cooler and transported to the laboratory for microbiological examination as soon as possible after collection. The samples were analysed for biological contaminants, including bacteria and fungi. The sampling areas were coded as follows:

Table 1: Codes of Areas of Study

S/N	Community (Code)	Sachet Water (SW)	Borehole Water (BW)	Well Water (WW)	River Water (RW)
1	Zarawuyaka Town (ZTW)	ZTW-SW	ZTW-BW	ZTW-WW	ZTW-RW
2	Gildamare (GDM)	GDM-SW	GDM-BW	GDM-WW	GDM-RW
3	Dugja Town (DTW)	DTW-SW	DTW-BW	DTW-WW	DTW-RW
4	Buratai (BRT)	BRT-SW	BRT-BW	BRT-WW	BRT-RW
5	Sulumthla (SLT)	SLT-SW	SLT-BW	SLT-WW	SLT-RW

Key: SW = Sachet Water; BW = Borehole Water; WW = Well Water; RW = River Water.

Physical Parameters Determination

Water samples for physical analysis were collected using 1000 mL wide-open plastic containers that were sterilised with distilled water. Each sample was transferred to a 1 L plastic container previously sterilised for onward transportation to the laboratory. Physical parameters measured were water temperature, specific conductivity, pH, total dissolved solids (TDS), and dissolved oxygen (DO). A portable dissolved oxygen analyser (Model JPB-607) and a portable conductivity, TDS, pH, and temperature meter (Model HI9813-5; Hanna Instruments, USA) were used at the sample collection point following the manufacturer's instructions. All data were collected and recorded at each sampling point. The probe was lowered to depth and allowed to equilibrate, after which readings for water temperature, specific conductivity, pH, TDS, and DO were taken. Measurements were displayed by pressing the stroke key, and readings were recorded for comparison with standards.

Research Design

The study employed a laboratory-based experimental design to investigate the occurrence, isolation, and identification of

bacterial and fungal contaminants in selected drinking-water sources. Water samples were collected from wells, boreholes, dam water, and sachet water within the study area and examined microbiologically in the laboratory. Bacterial examination involved culture, observation of colony characteristics, Gram staining, and biochemical characterisation, while fungal examination involved cultivation, macroscopic observation of colonies, and microscopic examination using Lactophenol Cotton Blue (LPCB).

Data Analysis

The laboratory results were entered into a spreadsheet or statistical software package for analysis. The occurrence of bacterial and fungal isolates was expressed as frequencies and percentages:

Occurrence (%) = (Number of samples positive for an organism / Total number of samples examined) × 100

The distribution of bacterial and fungal isolates among the different water sources and sampling locations was presented using tables and appropriate charts. Where statistical comparisons among water-source groups were required by

the study objectives, appropriate statistical tests were applied based on the nature of the data, with statistical significance set at $p < 0.05$. The method for analytical and statistical analysis was adapted from Sokal and Rohlf (2012). Collected data for water quality parameters were compiled using Microsoft Excel (version 2010) and analysed using SPSS version 22. All data obtained were analysed using analysis of variance (ANOVA) to test for significance, and means that differed significantly were separated using the least significant difference (LSD) at 5% probability level.

Materials and Equipment

Materials used for the study included sterile sample containers, Petri dishes, test tubes, test-tube racks, inoculating loops, sterile pipettes and micropipette tips, membrane filters and filtration apparatus, cotton wool, aluminium foil, gloves, labels, marker pens, measuring cylinders, conical flasks, beakers, glass slides, cover slips, and other routine microbiological materials. The culture media used for bacterial examination included Nutrient Agar (NA), MacConkey Agar, Eosin Methylene Blue (EMB) Agar, Mannitol Salt Agar (MSA), Tryptic Soy Agar (TSA), Triple Sugar Iron (TSI) Agar, and other media used during bacterial isolation and characterisation. Sabouraud Dextrose Agar (SDA) was used for fungal isolation.

Reagents used included crystal violet, Gram's iodine, Gram decoloriser, safranin, Lactophenol Cotton Blue (LPCB), hydrogen peroxide, oxidase reagent, Kovac's reagent, Methyl Red reagent, citrate medium, indole medium, sterile physiological saline, distilled water, and immersion oil. The major equipment used included an autoclave, incubator, refrigerator, analytical balance, compound microscope, membrane filtration apparatus, vacuum pump, water bath, Bunsen burner, micropipette, pH meter, and other routine laboratory equipment.

Preparation of Culture Media

The culture media used for the isolation and identification of bacterial and fungal organisms were prepared from commercially available dehydrated media according to the manufacturers' instructions. The required quantity of each medium was weighed and suspended in the specified volume of distilled water. The suspension was mixed thoroughly and heated where necessary until the medium was completely dissolved.

The prepared media were dispensed into appropriate containers and sterilised by autoclaving at 121 °C for 15 minutes. Following sterilisation, the media were allowed to cool to a suitable temperature before being aseptically dispensed into sterile Petri dishes or test tubes, as required for the respective analyses. The prepared media were allowed to solidify and were examined for visible contamination before use. The preparation and handling of the media followed standard microbiological laboratory procedures (WHO, 2011, 2017)

Isolation of Bacteria

Bacterial isolation was carried out using appropriate culture media. Where membrane filtration was employed, 100 mL of the water sample was passed aseptically through a sterile membrane filter (0.45 µm pore size) using a membrane filtration apparatus. The membrane was subsequently transferred aseptically onto the appropriate culture medium for bacterial recovery. Nutrient Agar was used for general bacterial recovery, while MacConkey Agar and Eosin Methylene Blue Agar were used for the isolation and differentiation of Gram-negative enteric bacteria. Mannitol

Salt Agar was used in the characterisation of Gram-positive cocci, particularly suspected *Staphylococcus* species.

Bacterial Culture and Incubation

Following inoculation, the culture media were incubated at 37°C for 24–48 hours. After incubation, the plates were examined for visible bacterial growth. Distinct colonies were selected for further examination based on their observable colony characteristics.

Primary Isolation on Selective and Differential Media

Distinct bacterial colonies were selected according to their colony morphology and subcultured onto appropriate media for further characterisation. Nutrient Agar was used as a general-purpose medium for bacterial recovery and maintenance. MacConkey Agar was used to isolate and differentiate Gram-negative enteric bacteria based on observable growth and lactose fermentation characteristics. EMB Agar was used for further differentiation of Gram-negative enteric bacteria. MSA was used in the characterisation of suspected staphylococcal isolates.

Purification of Bacterial Isolates

Distinct bacterial colonies were picked aseptically and subcultured onto fresh agar media. The cultures were examined for uniform colony morphology, and repeated subculturing was carried out where necessary to obtain pure isolates. The purified isolates were maintained for subsequent Gram staining and biochemical characterisation.

Gram Staining

Gram staining was performed on purified bacterial isolates. A small portion of each isolate was emulsified in sterile water or saline on a clean glass slide to prepare a thin smear. The smear was air-dried and heat-fixed using the standard laboratory procedure. It was then treated sequentially with crystal violet, Gram's iodine, decoloriser, and safranin counterstain. The stained preparations were examined microscopically under the oil-immersion objective. The Gram reaction, cellular morphology, and arrangement of the bacterial cells were recorded.

Biochemical Characterisation of Bacterial Isolates

Biochemical characterisation was performed on the purified bacterial isolates using tests selected according to the observed Gram reaction and morphological characteristics. The tests recorded in the laboratory analysis included catalase, oxidase, coagulase, indole, Methyl Red (MR), Voges-Proskauer (VP), citrate utilisation, Triple Sugar Iron (TSI), motility, starch hydrolysis, and Mannitol Salt Agar (MSA) reactions. The specific tests applied varied according to the Gram reaction and morphological characteristics of each isolate.

The catalase test was used to determine catalase activity, while the oxidase test was used to assess oxidase activity. The indole test was used to determine indole production, and the Methyl Red test was used to assess acid production from glucose fermentation. Citrate utilisation was determined using citrate medium, while TSI was used to assess carbohydrate fermentation patterns, gas production, and hydrogen sulphide production. Motility, starch hydrolysis, and coagulase reactions were recorded where these tests formed part of the characterisation of the isolate. MSA reactions were also considered in the characterisation of relevant bacterial isolates. The biochemical reactions were recorded as positive or negative, while TSI reactions were recorded according to the observed reaction pattern, including

acid/acid (A/A), alkaline/acid (K/A), gas production, and hydrogen sulphide production where observed. The biochemical results were interpreted together with the Gram reaction, cellular morphology, and colony characteristics.

Isolation and Identification of Fungi

Fungal isolation was carried out separately from bacterial examination. Water samples were processed using the membrane filtration technique according to Standard Methods for the Examination of Water and Wastewater (American Public Health Association (APHA) 2017). A measured volume of 100 mL of each water sample was passed aseptically through a sterile membrane filter with a pore size of 0.45 µm and a diameter of 47 mm (APHA, 2017; Shrestha Khwakhali, 2024). The membrane was then aseptically transferred onto Sabouraud Dextrose Agar (SDA) supplemented with chloramphenicol (50 mg/L) to inhibit bacterial growth (Shrestha Khwakhali, 2024). The inoculated SDA plates were incubated aerobically at 20–25°C for 5–7 days (APHA, 2017). Plates were examined daily for visible fungal growth, and the number of colonies was counted and expressed as colony-forming units (CFU) per 100 mL of water sample (Shrestha Khwakhali, 2024).

Fungal colonies that developed on the culture media were examined macroscopically for characteristics such as colour, texture, colony size, margin, surface appearance, growth pattern, and reverse pigmentation. Distinct fungal colonies were subcultured onto fresh SDA plates where necessary to obtain pure cultures suitable for microscopic identification (Pitt & Hocking, 2009; Samson *et al.*, 1995). For microscopic identification, fungal isolates were examined using Lactophenol Cotton Blue (LPCB) preparations (Sigma-Aldrich, n.d.; Liofilchem, n.d.). A small portion of the fungal growth was transferred to a clean glass slide and prepared with LPCB before microscopic examination. The observed structures, including hyphae, septation, conidiophores, conidia, sporangia, rhizoids, and spore arrangement, were recorded and compared with recognised fungal identification keys (Pitt & Hocking, 2009; Samson *et al.*, 1995). Fungal isolates were identified on the basis of their macroscopic colony characteristics and microscopic morphology. Where the available characteristics did not adequately support species-level identification, the isolate was reported at the

appropriate genus level rather than being assigned an unsupported species name.

For bacterial isolates, identification was performed on the basis of colony characteristics, Gram reaction, cellular morphology, and biochemical characteristics. The observed characteristics and biochemical profiles were compared with recognised bacterial identification manuals, including Bergey's Manual of Determinative Bacteriology (Holt *et al.*, 1994) and Bergey's Manual of Systematic Bacteriology (Garrrity *et al.*, 2006). The identification was based on conventional cultural, morphological, and biochemical characteristics; isolates were regarded as presumptively identified as no additionally confirmatory method of was used. Where the available characteristics did not adequately support species-level identification, the isolate was reported at the appropriate genus level rather than being assigned an unsupported species name.

RESULTS AND DISCUSSION

The physicochemical parameters assessed in this study were pH, electrical conductivity (EC), total dissolved solids (TDS), temperature, and dissolved oxygen (DO). Table 2 shows the variability in EC and TDS across the four water sources (borehole, sachet, surface, and well water). The mean EC values for borehole, surface, and well water were 727.90, 731.04, and 677.58 µS cm⁻¹, respectively, while sachet water recorded a markedly lower mean EC of 278.48 µS cm⁻¹. WHO does not propose a health-based guideline value for EC because it does not pose a direct health risk to humans (WHO, 2017); however, an aesthetic reference value of 1500 µS cm⁻¹ is commonly applied (WHO, 2022). All mean EC values for the untreated sources fell below this aesthetic reference value. Similarly, mean TDS values were 410.73 mg L⁻¹ (borehole), 469.76 mg L⁻¹ (surface), 414.74 mg L⁻¹ (well), and 195.43 mg L⁻¹ (sachet). WHO (2022) states that TDS is “not of health concern at levels found in drinking-water” and does not propose a health-based guideline value; however, TDS may affect the acceptability of drinking water, with levels below 600 mg L⁻¹ generally considered satisfactory and those above 1000 mg L⁻¹ associated with noticeably poor taste (WHO, 2011, 2022). All TDS values in this study were below 500 mg L⁻¹ and therefore within the range considered acceptable for palatability.

Table 2: Mean ± SD of Physical Parameters of Water Samples According to Water Source

Water source	pH	Temperature (°C)	TDS (mg/L)	Conductivity (µS/cm)	DO (mg/L)
Borehole Water	7.37 ± 0.24 ^b	27.49 ± 0.91 ^a	410.73 ± 75.70 ^b	727.90 ± 178.44 ^a	2.62 ± 0.43 ^b
Sachet Water	8.02 ± 0.20 ^a	26.90 ± 0.75 ^b	195.43 ± 19.03 ^c	278.48 ± 96.94 ^b	5.83 ± 0.72 ^a
Surface water	7.36 ± 0.34 ^b	26.90 ± 0.75 ^b	469.76 ± 38.57 ^a	731.04 ± 89.89 ^a	6.21 ± 0.87 ^a
Well water	7.26 ± 0.29 ^b	27.39 ± 0.87 ^{ab}	414.74 ± 83.49 ^b	677.58 ± 187.15 ^a	2.40 ± 0.33 ^b
ANOVA p-value	<0.001	0.006	<0.001	<0.001	<0.001

Values are expressed as Mean ± SD (n = 30 per water source). Means bearing different superscript letters within a column differ significantly at p < 0.05 according to Tukey's HSD test.

Groundwater often tends to have higher EC and TDS than surface water because it contains more dissolved ions and minerals acquired as it moves through rocks and soils (Oyelude *et al.*, 2013). However, in this study, surface water had the highest EC and TDS, a pattern that may reflect direct runoff and anthropogenic inputs; sachet water had the lowest values, consistent with treatment processes such as filtration or reverse osmosis. EC was proportional to TDS in this study, consistent with the established relationship between these two parameters (Oyelude *et al.*, 2013). The Indian Council of Medical Research guideline for EC is 300 µS/cm as cited in IWA Publishing, n.d., and while the untreated sources

exceeded this value, WHO does not specify a health-based guideline for EC (WHO, 2017). The significantly lower EC in sachet water supports the interpretation that packaged water had undergone demineralisation or purification.

The average pH of the water samples (Table 2) shows that sachet water had the highest mean pH (8.02 ± 0.20), followed by borehole (7.37 ± 0.24), surface (7.36 ± 0.34), and well water (7.26 ± 0.29). All values fall within the WHO acceptable pH range of 6.5–8.5 for drinking water (WHO, 2017). In contrast to the sample format where groundwater was acidic, the groundwater sources in this study (borehole and well) were near-neutral to slightly alkaline. The weakly

alkaline pH of sachet water may be due to treatment-related alkalinity adjustment. The near-neutral pH of the untreated sources has implications for fungal growth. Wheeler et al. (1991) examined 61 isolates belonging to 13 toxigenic fungal species across the pH range 2–11 and found that *Aspergillus* species were more tolerant of alkaline pH while *Penicillium* species were more tolerant of acidic pH. Nearly all species studied were able to grow over the entire pH range examined. Therefore, the near-neutral pH range observed in this study (7.26–8.02) is unlikely to inhibit the growth of either genus. The optimal conditions for fungal biofilm formation in groundwater systems have been found to be neutral or weakly acidic at 28 °C with rich nutrition (Zhang et al., 2021). However, the same study noted that *Aspergillus niger*, *Penicillium polonicum*, and *Trichoderma harzianum* were not observed to form mature biofilms in actual groundwater within 120 hours, with carbon found to have the maximum effect on biofilm formation in actual groundwater, followed by nitrogen and phosphorus (Zhang et al., 2021). These findings suggest that while the physicochemical conditions of the water sources in this study may permit fungal survival, biofilm formation and mycotoxin production may be limited by nutrient availability.

Temperature varied significantly among sources (one-way ANOVA: $p = 0.006$), with borehole water recording the

highest mean (27.49 ± 0.91 °C) and sachet and surface water the lowest (26.90 ± 0.75 °C). These temperatures are within the mesophilic range that supports the growth of many waterborne bacteria and fungi. DO showed the strongest source-related difference ($p < 0.001$), with surface water (6.21 ± 0.87 mg/L) and sachet water (5.83 ± 0.72 mg/L) having significantly higher DO than borehole (2.62 ± 0.43 mg/L) and well water (2.40 ± 0.33 mg/L). WHO does not propose a health-based guideline value for DO in drinking water (WHO, 2017; WHO, 2011). The low DO in groundwater is expected due to limited atmospheric contact and microbial oxygen demand. The warm temperatures and variable DO conditions across sources provide an environment in which microorganisms can survive or persist, especially where treatment or handling is inadequate.

The physicochemical parameters indicate that the water sources are broadly acceptable in terms of pH, TDS, and EC. DO levels were notably lower in borehole and well water compared with surface and sachet water, though WHO does not propose a guideline value for DO in drinking water. The detection of bacterial and fungal contaminants across all sources including sachet water shows that physical compliance alone is insufficient to guarantee microbiological safety.

Discussion of Presumptive Bacterial Presence and Absence by Water Source

Table 3: Presence (+) or Absence (–) of Presumptive Bacterial Contaminants According to Water Source

Bacterial Organism	Borehole	Sachet	Surface	Well
<i>Escherichia coli</i>	+	+	+	+
<i>Klebsiella pneumoniae</i>	+	+	+	+
<i>Staphylococcus aureus</i>	+	+	+	+
<i>Bacillus subtilis</i>	+	+	+	+
<i>Bacillus</i> spp.	+	+	+	+
<i>Pseudomonas aeruginosa</i>	+	+	+	–
<i>Pseudomonas</i> spp.	+	+	+	–
<i>Salmonella</i> spp.	+	+	+	+
<i>Salmonella typhi</i>	+	+	+	+
<i>Shigella</i> spp.	+	+	+	+
<i>Shigella</i> spp.	+	±	±	±
<i>Vibrio cholerae</i>	+	+	+	+
<i>Proteus mirabilis</i>	+	+	–	+
<i>Proteus vulgaris</i>	+	+	–	+
<i>Enterobacter</i> spp.	+	+	+	–
<i>Enterococcus</i> spp.	+	+	+	–
<i>Staphylococcus epidermidis</i>	+	+	–	–
<i>Aeromonas</i> spp.	+	–	–	–
<i>Citrobacter freundii</i>	+	–	–	–
<i>Acinetobacter</i> spp.	+	–	–	–

Key: + = recorded in at least one sample from that source; – = not recorded in the dataset; All identifications were based on cultural and microscopic characteristics and require molecular confirmation.

Table 3 shows the distribution of presumptive bacterial contaminants across the four water sources. The data revealed that contamination was not confined to any single source but varied in composition and the number of organism types detected. Several organisms were detected across all four water sources, while others were restricted to specific sources or absent from certain sources.

Nine bacterial groups were recorded in every water source: *Escherichia coli*, *Klebsiella pneumoniae*, *Staphylococcus aureus*, *Bacillus subtilis*, *Bacillus* spp., *Salmonella* spp., *Salmonella typhi*, *Shigella* spp., and *Vibrio cholerae*. Their consistent presence across borehole, sachet, surface, and well

water indicates that these organisms are widely distributed in the study area and are not eliminated by the treatment or storage conditions associated with any single source. The detection of these organisms in sachet water, despite its processed nature, suggests that contamination may occur during packaging, handling, or storage, or that treatment did not fully remove them. This finding is consistent with studies by (Chukwuka et al., (2025); Oridikitorusinyaa et al., (2025) that reported *E. coli*, *Salmonella*, *Shigella*, *Vibrio*, and *Staphylococcus aureus* in sachet water samples. The presence of *E. coli* is particularly significant because it is the primary indicator of faecal contamination and the infectious dose for

enterohaemorrhagic *E. coli* (EHEC) may be as low as 10–100 organisms (Hara-Kudo & Takatori, 2011). Its detection in all four water sources could indicate that the water is not free from intestinal disease-causing pathogens.

Several organisms showed source-specific absences. *Pseudomonas aeruginosa* and *Pseudomonas* spp. were absent from well water but present in borehole, sachet, and surface water. *Proteus mirabilis* and *Proteus vulgaris* were absent from surface water but present in borehole, sachet, and well water. *Enterobacter* spp. and *Enterococcus* spp. were absent from well water but present in the other three sources. *Staphylococcus epidermidis* was absent from surface and well water but present in borehole and sachet water. *Aeromonas* spp., *Citrobacter freundii*, and *Acinetobacter* spp. were detected only in borehole water and were absent from all other sources.

Borehole water contained the greatest number of presumptively identified organism types, with all 20 organisms listed in the dataset recorded in at least one sample. This may reflect the absence of treatment, the influence of local hydrogeological conditions, or contamination pathways specific to borehole construction and maintenance. Sachet water contained 15 of the 20 organisms, including several that were absent from other sources, such as *Staphylococcus epidermidis*. This indicates that sachet water is not free from bacterial contamination despite processing. Surface water contained 16 organisms and was the only source, apart from borehole water, where *Pseudomonas* spp. and *Enterobacter* spp. were detected; however, it lacked *Proteus* spp. and *Staphylococcus epidermidis*. Well water had the fewest organism types detected (14), with notable absences including *Pseudomonas* spp., *Enterobacter* spp., *Enterococcus* spp., and *Staphylococcus epidermidis*.

Sources of water samples and treatment differences are likely contributors to the observed presence or absence patterns. Sachet water undergoes treatment processes such as filtration and disinfection, which may reduce or eliminate certain organisms, but post-treatment contamination can reintroduce others. Borehole and well water are groundwater sources that are not treated; their bacterial composition may reflect local aquifer conditions, soil and rock interactions, and contamination from surface infiltration. Surface water is directly exposed to environmental inputs, including runoff, wildlife, and human activities, which may explain its broad range of organism types and the presence of organisms such as *Pseudomonas* and *Enterobacter*.

Physicochemical conditions may also play a role. Borehole water had the highest temperature and the lowest dissolved oxygen among the sources, while sachet water had the highest pH and the lowest TDS and conductivity. Surface water had the highest dissolved oxygen and the highest TDS, which may support aerobic and osmotolerant organisms. Well water had the lowest pH and the second-lowest dissolved oxygen. These physicochemical differences could potentially influence bacterial survival, but the present dataset does not permit statistical attribution of the observed presence/absence patterns to these parameters.

The presence/absence data showed that bacterial contamination is widespread across all four water sources in the study area. While some organisms are common to all sources, others are restricted to specific sources, and a few were detected only in borehole water. The patterns suggest that source type, treatment, and local environmental conditions influence bacterial community composition. These findings provide a descriptive baseline for understanding the distribution of bacteria in the water sources studied.

Discussion of Presumptive Fungal Presence and Absence by Water Source

Table 4: Presence (+) or Absence (–) of Presumptive Fungal Contaminants According to Water Source

Fungal organism	Borehole	Sachet	Surface	Well
<i>Aspergillus flavus</i>	+	+	+	+
<i>Aspergillus niger</i>	+	+	+	+
<i>Aspergillus</i> spp.	+	+	+	+
<i>Penicillium</i> spp.	+	+	+	+
<i>Rhizopus</i> spp.	+	+	+	+
<i>Mucor</i> spp.	+	+	–	+
<i>Mucor mucedo</i>	+	–	–	–
<i>Candida albicans</i>	+	+	+	+
<i>Candida</i> spp.	+	+	+	–
<i>Fusarium</i> spp.	+	+	+	+
<i>Cladosporium</i> spp.	–	+	+	–
<i>Trichoderma</i> spp.	–	+	+	–
<i>Trichoderma longibrachiatum</i>	–	+	–	–
<i>Cryptococcus</i> spp.	–	+	–	–

Key: + = recorded in at least one sample from that source; – = not recorded in the dataset. No fungal growth was recorded in selected samples. Fungal identifications are based on cultural and microscopic characteristics

Table 4 shows the distribution of presumptive fungal contaminants across the four water sources. The data show that fungal contamination was widespread but varied in composition among borehole, sachet, surface, and well water. Several organisms were detected across all four sources, while others were restricted to specific sources or absent from certain sources. Fungal identifications were presumptive, based on cultural and microscopic characteristics, and species-level confirmation was not performed for organisms reported only as "spp."

Seven fungal groups were recorded in every water source: *Aspergillus flavus*, *Aspergillus niger*, *Aspergillus* spp., *Penicillium* spp., *Rhizopus* spp., *Candida albicans*, and *Fusarium* spp. Their consistent presence across borehole, sachet, surface, and well water indicates that these fungi are widely distributed in the study area and are not eliminated by the treatment or storage conditions associated with any single source. The detection of these organisms in sachet water, despite its processed nature, suggests that contamination may occur during packaging, handling, or storage, or that treatment did not fully remove them.

Several organisms showed source-specific absences. *Mucor* spp. was absent from surface water but present in borehole, sachet, and well water. *Candida* spp. was absent from well water but present in the other three sources. *Cladosporium* spp. and *Trichoderma* spp. were absent from borehole and well water but present in sachet and surface water. *Mucor mucedo* was detected only in borehole water. *Trichoderma longibrachiatum* and *Cryptococcus* spp. were detected only in sachet water and were absent from all other sources.

No fungal growth was recorded in selected samples, particularly some surface and well-water samples. This absence of growth may reflect true absence of viable fungi, detection limits of the culture methods used, or unfavourable conditions for fungal growth during sampling or processing. Sachet water contained the greatest number of presumptively identified organism types, with 13 of the 14 organisms listed in the dataset recorded in at least one sample. This included organisms that were absent from other sources, such as *Trichoderma longibrachiatum* and *Cryptococcus* spp. The presence of these organisms in sachet water, despite its processed nature, indicates that fungal contamination can occur post-treatment or that treatment does not eliminate all fungal propagules.

Surface water contained 11 organisms and was the only source, apart from sachet water, where *Cladosporium* spp. and *Trichoderma* spp. were detected. However, it lacked *Mucor* spp. and *Mucor mucedo*. Borehole water contained 10 organisms, including *Mucor mucedo*, which was unique to this source, but lacked *Cladosporium* spp., *Trichoderma* spp., *Trichoderma longibrachiatum*, and *Cryptococcus* spp. Well water had the fewest organism types detected (10), with notable absences including *Candida* spp., *Cladosporium* spp., *Trichoderma* spp., *Trichoderma longibrachiatum*, and *Cryptococcus* spp.

Sources of water samples and treatment differences are likely contributors to the observed presence or absence patterns. Sachet water undergoes treatment processes such as filtration and disinfection, which may reduce or eliminate certain organisms, but post-treatment contamination can reintroduce others. Borehole and well water are groundwater sources that are not treated; their fungal composition may reflect local aquifer conditions, soil and rock interactions, and contamination from surface infiltration. Surface water is directly exposed to environmental inputs, including runoff, wildlife, and human activities, which may explain its broad range of organism types and the presence of organisms such as *Cladosporium* and *Trichoderma*.

Physicochemical conditions may also play a role. Sachet water had the highest pH and the lowest TDS and conductivity, which may influence the survival of different fungal groups. Borehole water had the highest temperature and the lowest dissolved oxygen among the sources. Surface water had the highest dissolved oxygen and the highest TDS, which may support aerobic and osmotolerant fungi. Well water had the lowest pH and the second-lowest dissolved oxygen. These physicochemical differences could potentially influence fungal survival, but the present dataset does not permit statistical attribution of the observed presence/absence patterns to these parameters.

The presence/absence data show that fungal contamination is widespread across all four water sources in the study area. While some organisms are common to all sources, others are restricted to specific sources, and a few were detected only in sachet or borehole water. The patterns suggest that source type, treatment, and local environmental conditions influence fungal community composition. These findings provide a

descriptive baseline for understanding the distribution of fungi in the water sources studied.

Fungal Toxicology in Water Samples

The fungal genera detected in the water samples; *Aspergillus*, *Penicillium*, *Fusarium*, *Candida*, *Mucor*, *Rhizopus*, *Cladosporium*, *Trichoderma*, and *Cryptococcus* include species that are recognised as opportunistic pathogens, mycotoxin producers, or allergenic agents. In the present study, *Aspergillus*, *Penicillium*, and *Fusarium* are of particular interest because some species within these genera are capable of producing mycotoxins. *Candida*, *Cryptococcus*, and *Fusarium* also contain species associated with opportunistic infections, particularly among immunocompromised individuals. In addition, fungi such as *Aspergillus*, *Penicillium*, and *Cladosporium* are recognised as important sources of fungal allergens and may affect susceptible individuals, including those with asthma or other atopic conditions. Globally, fungal diseases constitute an important health burden, with millions of people affected by invasive mycoses, allergic fungal sinusitis, allergic bronchopulmonary aspergillosis, and other fungal infections (Novak Babič et al., 2018).

The distribution of fungi among the different water sources in this study also showed some source-related differences. Sachet water contained the greatest number of presumptively identified organism types, with 13 of the 14 fungal organisms detected. It also contained *Trichoderma longibrachiatum* and *Cryptococcus* spp., which were not detected in the other water sources examined. This finding suggests that processing and packaging did not completely prevent the occurrence of fungal propagules in the sachet water. Borehole and well water, although untreated, each contained 10 fungal organisms. The detection of *Mucor mucedo* only in borehole water, together with the absence of *Candida* spp. from well water, further indicates differences in the fungal populations associated with individual water sources.

Fungal concentrations were not quantified in the present study, and mycotoxins were not analysed. In addition, fungal identification was based on cultural and microscopic characteristics and was therefore presumptive. Consequently, the detection of a potentially toxigenic or pathogenic genus does not, by itself, establish the presence of a specific mycotoxin or demonstrate a direct health risk to consumers. Further studies involving quantitative fungal counts, molecular confirmation of species, and targeted analysis of important mycotoxins such as aflatoxins, ochratoxin A (OTA), deoxynivalenol (DON), and zearalenone (ZEN) would provide stronger evidence for assessing the health significance of these findings. Nevertheless, the occurrence of several fungal genera with recognised pathogenic, toxigenic, or allergenic potential across the sampled water sources indicates the need for continued attention to fungal contamination in drinking-water quality assessment in the study area.

CONCLUSION

This research has demonstrated variations in the physicochemical characteristics and occurrence of bacterial and fungal contaminants among the assessed drinking-water sources of Buratai, Galdimare, Dugja, Zarawuyaka and Sulumthla communities of Biu Local Government Area. The measured pH, temperature, total dissolved solids, electrical conductivity and dissolved oxygen values varied significantly among the water sources. Bacterial and fungal contaminants were also detected across the assessed sources, with bacterial isolates identified presumptively from their cultural,

morphological, microscopic and biochemical characteristics, while fungal isolates were identified based on their macroscopic and microscopic morphological characteristics. The detection of bacterial contaminants, including organisms presumptively identified as *Escherichia coli*, *Salmonella* spp., *Shigella* spp. and *Vibrio cholerae*, indicates the need for appropriate microbiological monitoring and treatment of drinking-water sources. However, the presence or number of organism types detected in this study should not be interpreted as a direct measure of microbial concentration or used alone to rank the relative health risks of the different water sources. Similarly, the fungal findings indicate the occurrence of fungal contaminants but do not by themselves establish pathogenicity or direct health effects.

These findings provide baseline information on the physicochemical characteristics and microbial occurrence of selected drinking-water sources in the study area. Further studies involving quantitative microbial enumeration, confirmatory identification methods and broader water-quality assessment would provide additional evidence for evaluating drinking-water quality and potential public-health implications in Biu Local Government Area.

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