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Assessment of Bacterial Contamination of wells and Boreholes in selected Students' hostels in Nnamdi Azikiwe University, Awka Anambra State, Nigeria

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ABSTRACT
Access to safe drinking water is crucial for public health, yet many students rely on potentially contaminated wells and boreholes. which can lead to serious health issues. Understanding bacterial contamination levels is essential for effective interventions, ensuring students well-being. This study assesses the bacterial contamination of water in wells and boreholes at selected students hostels in Nnamdi Azikiwe University Awka, focusing on total microbial load, total coliform counts, and the prevalence of specific bacterial species. A total of sixteen water samples were analyzed, revealing microbial load counts ranging from $1.7x10^2$ CFU/ml to $2.78x10^3$ CFU/ml in well water and $2.0x10^2$ CFU/ml to $1.87x10^3$CFU/ml in borehole water. Mean microbial loads were notable higher in well water (890±317.478 CFU/ml) than in borehole water (525±197.935 CFU/ml), but no significant difference existed between the two sources (F=0.9518, P=0.3458). Both sources remained below the WHO safe limit for recreational water (2300 CFU/ml). Total coliform counts were within safety limit for borehole water (1.25±1.25 CFU/ml) but exceeded WHO safe limits of 126 CFU/ml for well water, with means of 318.75±223.178 CFU/ml. Biochemical identification revealed five bacterial species: *Escherichia coli*, *Enterobacter aerogenes*, *Klebsiella pneumoniae*, *Citrobacter freundii*, and *Proteus mirabilis*. *Klebsiella pneumoniae* was the most prevalent, found in 25% of samples, while *Enterobacter aerogenes* was least, detected in only 6.25% of samples. This study highlights the significant public health risks associated with bacterial contamination in university water sources, and underscores the need for regular monitoring and management efforts to ensure water quality and public health safety for hostel residents.

Keywords:
Bacterial contamination,
Well, Borehole,
Water, Total coliform

INTRODUCTION

Access to clean drinking water is a fundamental human right and essential for maintaining public health. In many university settings, particularly in developing countries, reliance on wells and boreholes for water supply is common; however, these sources often remain under-researched concerning their microbiological safety. Recent studies have highlighted alarming levels of bacterial contamination in drinking water sources, posing risks to the health of students and staff alike (Choda *et al*., 2025; Anekwe *et al*., 2026). For instance, a study conducted in a similar educational setting revealed that 70% of sampled borehole water exceeded the permissible limits of coliform bacteria, underscoring the potential for waterborne diseases (Igbinosa *et al*., 2026).

Despite recognition of the need for water quality assessments in educational institutions, gaps remain in the literature regarding specific contaminant profiles in university-hosted wells and boreholes. Most existing research has focused on urban or rural communities rather than on the unique contexts of university hostels, where the demographic and usage patterns differ significantly (Jimoh *et al*., 2025). This highlights an urgent need for localized studies to evaluate water safety in these environments, specifically targeting bacterial contaminants associated with improper sanitation and waste management practices (Rilwan, 2024).
Consequently, this study aims to assess the levels of bacterial contamination in selected wells and boreholes within university hostels.

By addressing this research gap, it seeks to provide critical information that can inform health interventions and promote safe water practices among students and staff.

MATERIALS AND METHODS

Study area

The research was conducted at Nnamdi Azikiwe University in Awka, Anambra State, Nigeria, located at geographical coordinates 6° 16' 0" North and 7° 3' 0" East. The university spans over 100 acres, featuring a rich variety of flora and fauna (Ogbodo et al., 2020). The area includes several streams, agricultural lands, numerous buildings, and forested regions. Awka is situated within Nigeria's tropical rainforest zone, experiencing two distinct seasons: the wet season from April to October and the dry season from November to March. The average temperature ranges from 28.5º C between June and December to 33º C from January to April (Okeke et al., 2021)

Sampling protocol

For this study, a total of eight students hostels each with a functional wells and boreholes were identified for assessment of bacterial contamination. The hostels selected and their wells and bore holes were Dora Akunyili hostel (6°14’43.2564 N, 7°7’28.5464 E well, 14’43.34568 N, 7°7’28.61616 E borehole), Chukwuemeka hostel (6°14’47.84316 N, 7°6’37.54152 E well, 6°14’45.60612 N, 7°6’34.8192 E borehole), Oby Ezekwesili hostel (6°14’57.05268 N, 7°6’28.23876 E well, 6°14’51.26568 N, 7°6’17.34048 E borehole), Basil Oli hostel (6°14’44.18196 N, 7°6’40.3056 E well, 6°14’50.04636 N, 7°6’19.7622 E borehole), Ngozi Okonjo hostel (6°14’20.26356 N, 7°6’28.23876 E well, 6°14’50.04636 N, 7°6’19.7622 E borehole), Emelda hostel (6°14’58.05024 N, 7°6’25.4358 E well, 6°14’51.26568 N, 7°6’17.34048 E borehole), Miracle hostel (6°14’53.80836 N, 7°7’25.15404 E well, 6°14’57.9066 N, 7°7’25.3704 E borehole) and Anchor hostel (6°14’53.80836 N, 7°7’25.15404 E well, 6°14’52.5084 N, 7°7’27.35688 E borehole). The hostels were selected based on their status as active residential facilities, the confirmed presence of functional well and borehole water supply infrastructure, the high number of resident students dependent on these water sources, and their geographical distribution across different sectors of the university. Water samples were collected in the dry season to minimize variability due to seasonal changes in water quality. Sampling was conducted in early morning hours to 7am to 8am to reduce the influence of diurnal variations in water quality. All sampling equipment, including 1-lire capacity glass sampling bottles, were pre cleaned with hydrochloric acid (HCL) and rinsed with deionized water to prevent cross- contamination. Gloves were worn during the entire sampling process to avoid contamination from skin oil.

Sampling procedure

For each well, water samples were collected directly using a clean, sterilized glass sampling bottle. The bottles were submerged to a depth of approximately 1 meter below the water surface to ensure representative sampling. Each well was purged of at least three well volumes before sample collection to remove stagnant water. The bottle was sealed immediately after filling to minimize exposure to air. Each water sample was immediately stored following collection under cool conditions until analysis within 24 hours.

Prior to sampling, each borehole was purged by allowing water to flow for approximately 5 minutes before sample collection to ensure that stagnant water was flushed out. This is done to ensure that the samples reflected the current groundwater quality. Using pre-cleaned, glass sampling bottles, 1-liter samples was collected directly from the borehole outlet. Care was taken to avoid contamination by not touching the bottle openings and using gloves throughout the process. The bottle was sealed immediately after filling to minimize exposure to air. Collected samples were then stored under cool condition until analysis within 24 hours. The methodology used followed the standard procedures outlined by APHA, 2017; US EPA, 2017 to ensure accurate and reproducible results.

Sample preparation and culture-based isolation

Each sample was homogenized and thoroughly mixed and aliquots (0.1 mL) of appropriate dilutions were inoculated onto selective/differential media using the spread plate technique: MacConkey agar (for isolation of Gram-negative bacteria), Nutrient agar (for total heterotrophic counts). Plates were incubated at 37°C for 24–48 h, after which distinct colonies were sub-cultured to obtain pure isolates. This workflow is consistent with common protocols used in recent water bacteriological studies (Moges *et al*., 2024).

Identification of bacterial isolates

Pure isolates were characterized using Gram staining followed by standard biochemical tests: catalase, indole, citrate utilization, oxidase, methyl red (MR), Voges Proskauer (VP), nitrate reduction. Probable identities were assigned based on the combined Gram reaction and biochemical profiles (Abdulrahaman *et al*., 2024)

Microbial counts and prevalence reporting:

Microbial load (CFU/mL) and total coliform counts were determined from colony counts at the selected dilution level and recorded descriptively. Prevalence of identified pathogens across the water samples was expressed as frequencies and percentages (Holcomb *et al*, 2025).

Data analysis:
Data were analyzed using descriptive statistics (frequency and percentage). Where applicable, the association between water source types and contamination pattern was assessed using the Chi square test at $p < 0.05$. Statistical analysis was conducted using SPSS (version 25).

RESULTS AND DISCUSSION

Total Microbial Load of Water samples collected

All sixteen water samples analyzed showed measurable microbial contamination (Table 1). Total microbial load counts ranged from $1.7x10^2$ CFU/ml to $2.78x10^3$ CFU/ml in well water, and $2.0x10^2$ CFU/ml to $1.87x10^3$ CFU/ml in bore hole water. The mean microbial load for well water (890±317.478 CFU/ml) was higher than the mean microbial load for bore hole water (525±197.935 CFU/ml). There was no significant difference between total microbial load of well and borehole water samples ($F=0.9518$, $P=0.3458$, $P>0.05$). The mean well water and bore hole water microbial load were below the WHO safe limit for recreational water of 2300 CFU/ml.

Table 1: Microbial load of water samples from different sites

Sampling sites	No. of Bacterial colonies on plate	Dilution factor	Total Bacterial Count (CFU/ml)
Wells			
Dora Akuyili hostel (Well 1)	17	10^1	$1.7x10^2$
Chukwuemeka hostel (Well 2)	56	10^1	$5.6x10^2$
Oby Ezekwesili hostel (Well 3)	51	10^1	$5.1x10^2$ $x10^2$
Basil hostel (Well 4)	174	10^1	$1.74x10^3$
Ngozi Okonjo hostel (Well 5)	45	10^1	$4.5x10^2$
Emelda hostel (Well 6)	40	10^1	$4.0x10^2$
Miracle hostel (Well 7)	278	10^1	$2.78x10^3$
Anchor hostel (Well 8)	51	10^1	$5.1x10^2$
			Mean = 890±317.478
Bore holes			
Dora Akuyili hostel (Borehole 1)	20	10^1	$2.0x10^2$
Chukwuemeka hostel (Borehole 2)	21	10^1	$2.1x10^2$
Oby Ezekwesili hostel (Borehole 3)	187	10^1	$1.87x10^3$
Basil hostel (Borehole 4)	39	10^1	$3.9x10^2$
Ngozi Okonjo hostel (Borehole 5)	57	10^1	$5.7x10^2$
Emelda hostel (Borehole 6)	24	10^1	$2.4x10^2$
Miracle hostel (Borehole 7)	47	10^1	$4.7x10^2$
Anchor hostel (Borehole 8)	25	10^1	$2.5x10^2$
			Mean =525±197.935

Total Coliform Counts

All sixteen water samples analyzed showed measurable microbial contamination (Table 1). Total coliform count ranged from 0 CFU/ml to 1.84 $x10^3$ CFU/ml in well water, and 0 CFU/ml to $1.0x10^1$ CFU/ml in bore hole water. The mean total coliform count for well water (318.75±223.178 CFU/ml) was higher than the mean total coliform count for bore hole water (1.25±1.25 CFU/ml). There was no significant difference between the total coliform count of well and borehole water samples (F=2.0238, P=0.1767, P>0.05). The total coliform count for borehole water was below the WHO safe limit for recreational water of .126 CFU/ml, whereas the mean total coliform count for well water exceeded this limit.

Table 2: Total Coliform Count of water samples from different sites

Sampling sites	**No. of Bacterial colonies on plate**	**Dilution factor**	**Total Bacterial Count (CFU/ml)**
Wells			
Dora Akuyili hostel (Well 1)	0	10^1	0 (NG)
Chukwuemeka hostel (Well 2)	42	10^1	$4.2x10^2$
Oby Ezekwesili hostel (Well 3)	16	10^1	$1.6x10^2$
Basil hostel (Well 4)	12	10^1	$1.2x10^2$
Ngozi Okonjo hostel (Well 5)	1	10^1	$1.0x10^1$
Emelda hostel (Well 6)	0	10^1	0 (NG)
Miracle hostel (Well 7)	184	10^1	$1.84\ x10^3$
Anchor hostel (Well 8)	0	10^1	0 (NG)
			Mean = 318.75±223.178
Bore holes			
Dora Akuyili hostel (Borehole 1)	0	10^1	0 (NG)
Chukwuemeka hostel (Borehole 2)	1	10^1	$1.0x10^1$
Oby Ezekwesili hostel (Borehole 3)	0	10^1	0 (NG)
Basil hostel (Borehole 4)	0	10^1	0 (NG)
Ngozi Okonjo hostel (Borehole 5)	0	10^1	0 (NG)
Emelda hostel (Borehole 6)	0	10^1	0 (NG)
Miracle hostel (Borehole 7)	0	10^1	0 (NG)
Anchor hostel (Borehole 8)	0	10^1	0 (NG)
			Mean = 1.25±1.25

Biochemical Identification of Bacterial Isolates

Biochemical characterization of isolates (Table 3) revealed the presence of five bacterial species across the water samples: *Proteus mirabilis*, *Klebsiella pneumonia*, *Enterobacter aerogenes*, Citrobacter *freundii* and *Escherichia coli*. Identification was based on Gram reaction and biochemical test profiles, including catalase, indole, citrate utilization, methyl red, Voges–Proskauer, motility test, carbohydrate fermentation test, oxidase test and urease test.

Table 3: Biochemical characterization of bacterial isolates**.**

Isolate	Gram reaction	Cat	Mot	Ind	MR	VP	Cit	Lac	Glu	Suc	Fru	Mal	Oxi	Ure	Identity
1	- Rod	+	+	-	+	+	+	+	+	+	-	+	-	+	*Proteus mirabilis*
2	-Rod	+	-	-	+	-	+	+	+	+	(-)	+	-	+	*Klebsiella pneumoniae*
3	-Rod	+	+	-	-	+	+	+	+	+	+	+	-	-	*Enterobacter aerogenes*
4	-Rod	+	+	-	+	-	+	+	+	+	+	+	-	var	*Citrobacter freundii*
5	-Rod	+	+	+	+	-	-	+	+	var	-	-	-	-	*Escherichia coli*

Morphological and Colony Characteristics

Colony morphology and Gram staining supported biochemical identification of the isolates (Table 4). E. coli produced white, smooth, circular, translucent and convex colonies and appeared as Gram-negative rods. Klebsiella pneumonia formed opaque, cream colored, irregular, raised colonies with Gram-negative rods appearance, while *Enterobacter aerogenes* showed characteristic white, circular, convex colonies with Gram-negative rod morphology. *Proteus mirabilis* appeared as translucent, cream colored, circular raised colonies with Gram-negative rods appearance. *Citrobacter freundii* form opaque, grey shiny, circular, convex colonies.

Table 4: Morphological and colony characteristics of bacteria isolates

Isolate	Colony Color	Colony Shape	Margin	Elevation	Opacity	Gram	Identity
1	Cream	concentric	Entire	Raised	Transparent	- Rod	*Proteus mirabilis*
2	Cream	circular	Entire	Raised	Opaque	-Rod	*Klebsiella pneumoniae*
3	White	circular	Entire	Convex	Moist	-Rod	*Enterobacter aerogenes*
4	Grey/shiny	circular	Entire	Convex	Opaque	-Rod	*Citrobacter freundii*
5	Whitish	circular	Entire	Convex	Translucent	-Rod	*Escherichia coli*

Prevalence of Pathogenic Bacteria

The distribution of bacterial pathogens across the water sampling sites: well and borehole is presented in Table 5. A total of five species were detected across the sites. These were *Klebsiella pneumoniae, Enterobacter aerogenes, Citrobacter freundii, Proteus mirabilis* and *Escherichia coli. Klebsiella pneumoniae* was the most prevalent across the sites detected in 25% of samples, followed by *Proteus mirabilis, Escherichia coli* and *Citrobacter freundii* each occurring in 12.5% of samples. *Enterobacter aerogenes* was the least prevalent occurring in 6.25% of the samples. One (1) species were recorded in borehole water. This was *Klebsiella pneumoniae* occurring in 12.5 % of bore hole water samples. There was no significant difference in prevalence of bacteria species in borehole water (P= 0.4493). A total of five (5) species were recorded in well water. These were *Escherichia coli, Enterobacter aerogenes, Citrobacter freundii, Klebsiella pneumonia* and *Proteus mirabilis*.

Klebsiella pneumonia was the most prevalent in well water with 37.5 % occurrence, followed by *Proteus mirabilis, Citrobacter freundii and Escherichia coli* with 25% occurrence each. *Enterobacter aerogenes* was least with 12.5 % occurrence. There was no significant difference in prevalence of bacteria species in well water (P= 0.186).

Table 5: Prevalence of bacteria in water samples across study sites

	Wells								Boreholes								
Pathogens	Dora Akuyi Ilihostel (Well 1)	Chukwuemeka Ahostel (Well 2)	Oby Ezekwesili Hostel (Well 3)	Basil Hostel (Well 4)	Ngozi Okonjo Hostel (Well 5)	Eme Idah Hostel (Well 6)	Miracle Hostel (Well 7)	Anchor Hostel (Well 8)	Dora Hostel (Borehole 1)	Chukwuemeka Ahostel (Borehole 2)	Oby Ezekwesili Hostel (Borehole 3)	Basil Hostel Borehole 4)	Ngozi Okonjo Hostel (Borehole 5)	Eme Idah Hostel (Borehole 6)	Miracle Hostel (Borehole 7)	Anchor Hostel (Borehole 8)	Total Positive Samples (%)
Proteus mirabilis	-	-	-	-	+	-	+	-	-	-	-	-	-	-	-	-	2 (12.5%)
Klebsiella pneumoniae	-	+	+	-	-	-	+	-	-	+	-	-	-	-	-	-	4 (25%)
Enterobacter aerogenes	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	1 (6.25%)
Citrobacter freundii	-	-	+	-	-	-	+	-	-	-	-	-	-	-	-	-	2 (12.5%)
Escherichia coli	-	+	-	+	-	-	-	-	-	-	-	-	-	-	-	-	2 (12.5%)

The findings of this study provide critical insights into the bacterial contamination of well and borehole water in university hostels, which is crucial for public health, particularly among vulnerable populations such as students. The total microbial load and the presence of specific bacterial species highlight considerable contamination levels and underscore the need for ongoing monitoring and enhanced water management practices.

The results indicate that all sampled water sources exhibited measurable microbial contamination, with total microbial load counts ranging from 1.7 x 10^2 CFU/ml to 2.78 x 10^3 CFU/ml in well water and from 2.0 x 10^2 CFU/ml to 1.87 x 10^3 CFU/ml in borehole water. Notably, while both mean microbial loads were below the WHO safe limit of 2300 CFU/ml, the mean total coliform count for well water (318.75 ± 223.178 CFU/ml) significantly exceeded the WHO guideline of 126 CFU/ml for safe drinking water. This pattern of contamination is consistent with findings from other studies which similarly reported elevated coliform levels in well water sources in urban areas (Azubuike *et al*. 2025), suggesting a persistent issue of fecal contamination that poses health risks (Atemoagbo, 2024).

The average total coliform count in borehole water was found to be below the WHO safe limit, reflecting a generally safer status compared to well water. This conclusion is corroborated by studies such as that of Oyewale *et al*. (2025), which indicated borehole water is often less contaminated than well water, a trend attributed to better protection from surface pollutants. However, the absence of significant differences between the total microbial loads in the two sources suggests that both types of water are at risk of contamination from similar external factors, emphasizing the critical nature of environmental management practices.

Biochemical analyses revealed the presence of five notable bacterial species: *Klebsiella pneumoniae*, *Proteus mirabilis*, *Enterobacter aerogenes*, *Citrobacter freundii*, and *Escherichia coli*. Among these, *Klebsiella pneumoniae* emerged as the most prevalent species. Its ubiquitous presence, particularly within well water at 37.5%, underscores the risks associated with opportunistic pathogens that can cause severe infections, especially in immunocompromised individuals. The concerns regarding *K. pneumoniae* are supported by research from Sandu *et al*. (2025) and Bezerra *et al*. (2026), which emphasizes its potential as a significant pathogen contributing to healthcare-associated infections and gastrointestinal illnesses, particularly when environmental sanitation is compromised.

Morphological characterizations provided reliable identification of the isolates, supporting our findings and resembling the profiles published in prior research (Rocha *et al*., 2023). The implications of having multiple pathogenic bacterial species in both well and borehole water sources highlight the necessity for rigorous water safety assessments to mitigate health risks. Studies have shown that the presence of multiple bacterial species can compound the public health threat posed by waterborne pathogens (Yu *et al*., 2025).

The detection of *E. coli,* an indicator of fecal contamination in 12.5% of well water samples, aligns with numerous studies that underscore the critical role of *E. coli* as a marker for water safety. The findings are consistent with those of Saputra *et al*. (2025) and Hansen *et al*. (2026), who reported high prevalence rates of *E. coli* across similar water studies, indicating systemic fecal pollution and associated public health challenges.

The results underscore the importance of regular monitoring and stricter regulations concerning water quality, particularly in areas dependent on well and borehole water. Implementation of comprehensive water testing and appropriate sanitation measures are essential to ensure safe water access (WHO, 2023). Moreover, public awareness campaigns focusing on the proper management of water sources could help reduce contamination levels and improve community health outcomes (Alao *et al*., 2025).

The implications of these findings extend beyond the scope of mere microbial loads; they indicate significant gaps in water quality management that require urgent attention. The similarities in contamination profiles between well and borehole water suggest the necessity for comprehensive water safety initiatives that address potential sources of pollution. This may include improved sanitation facilities, regular water quality assessments, and public health campaigns to educate residents about safe water practices.

CONCLUSION

The wells and borehole water of selected students' hostels were assessed for heavy metal contamination. While the microbial loads of both well and borehole water remain within acceptable limits according to WHO guidelines, the concerning presence of pathogenic bacteria, particularly in well water, necessitates immediate action to safeguard public health. Enhancing water quality monitoring, implementing effective water management practices, and conducting further research into the sources of contamination will be crucial for improving public health in these communities.

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