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Microbial Quality of Water and Antibiotic Susceptibility Profiles of Enteric Bacteria Isolated From Hand-Dug Wells in Sabon Gida, A Semi-Urban Nigerian Community

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Abstract: In many semi-urban Nigerian communities like Sabon Gida, hand-dug wells are primary domestic water sources. However, poor sanitation and unregulated antibiotic use often compromise their safety. This study evaluated the microbial quality of water and antibiotic susceptibility profiles of enteric bacteria isolated from ten (10) hand-dug wells in Sabon Gida. Using standard microbiological techniques, Total Viable Counts (TVC), Total Coliform (TCC), and Faecal Coliform Counts (FCC) were determined. Isolates were characterized via biochemical testing, and susceptibility was assessed using the Kirby-Bauer disc diffusion method. All wells exceeded WHO and Nigerian drinking water standards. TVC ranged from 1.6 x 105 CFU/mL to 9.3 x 105 CFU/mL, while faecal coliforms (12 CFU/100mL–37 CFU/100mL) violated the zero-tolerance (0 CFU/100mL) safety threshold. Of the 23 isolates recovered, Escherichia coli was most prevalent (52.2%), followed by Klebsiella pneumoniae (34.8%) and Enterobacter aerogenes (13.0%). Susceptibility testing showed 100% resistance to Ampicillin and Tetracycline, and 91.3% to Amoxicillin/Clavulanate. Conversely, all isolates were sensitive to Gentamicin and Chloramphenicol. The presence of multi-drug resistant (MDR) enteric bacteria indicates significant faecal contamination and a high potential for waterborne disease transmission. Urgent community-wide water treatment, improved well construction, and stricter antibiotic stewardship are required to mitigate these public health risks.

Keywords: Antibiotic Resistance, Enteric Bacteria, Hand-Dug Wells, Microbial Quality, Nigeria, Sabon Gida.

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INTRODUCTION

Water is an indispensable universal solvent, essential for the continued existence of all living things, including humans. It is a basic need not just for drinking and domestic chores, but for the functioning of our industries, hospitals, and pharmaceutical companies (Malik et al., 2012). However, water is also a double-edged sword; while it sustains life, it is one of the most common vehicles for transmitting disease. It serves as a natural habitat for a wide variety of microorganisms such as bacteria, protozoa, algae, and viruses, many of which carry significant health risks that consumers are often unaware of until symptoms appear (McFadyen, 2014). Globally, the consumption of contaminated water remains a primary driver of enteric disease mortality, particularly in regions where monitoring systems are absent (Ashbolt, 2015).

Hand-dug water refers to groundwater that is obtained from wells dug into underground aquifers. It is a natural source of water commonly used for domestic, agricultural, and industrial purposes in areas where access to municipal water supply is limited or unavailable. The reliability of these shallow groundwater sources is increasingly questioned as rapid urbanisation often leads to the degradation of the surrounding soil and water table (Ocheri et al., 2017).

In many areas where municipal infrastructure has failed to keep pace with population growth, residents must rely on groundwater obtained from hand-dug wells (Adetunde & Glover, 2010). These wells tap into underground aquifers to provide water for domestic and agricultural use, but they are inherently vulnerable. In a community like Sabon-Gida, this gap has forced residents to become their own water engineers, digging shallow wells that sit dangerously close to pit latrines and open refuse dumps. This proximity creates an expressway for pathogens; during the rainy season, surface runoff carries faecal matter directly into these poorly protected sources. Recent studies have confirmed that such wells often act as a focal point for the convergence of chemical and biological pollutants, making them significantly more hazardous than protected boreholes (Okonko et al., 2022).

Microbial quality of water is a comprehensive measure of the safety and potability of a water source based on the presence or absence of a wide array of microorganisms, including bacteria, viruses, and protozoa. It serves as a vital biological index to determine the extent of faecal contamination and the overall sanitary integrity of a water supply. By identifying both specific pathogens (disease-causing agents) and indicator organisms (such

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as Escherichia coli and other coliforms), microbial quality acts as a predictive safety rating. It essentially tells us whether the water serves as a safe resource or a potential vehicle for waterborne diseases like cholera, typhoid, or viral gastroenteritis, thereby quantifying the health risk to the consuming public (World Health Organization, 2022).

The result is that these wells become unintended reservoirs for enteric bacterial microbes like E. coli and Salmonella that belong in the gut, not in a glass of water (Nkere et al., 2011). To manage this risk, bacteriological water analysis is vital. It allows us to estimate the number of bacteria present and identify specific pathogens to ensure the water is safe for drinking, bathing, and swimming (Ngwa & Chrysanthus, 2013). Without this oversight, the community remains trapped in a persistent cycle of typhoid fever, cholera, and other diarrhoeal diseases (Amaechi, 2015). The detection of these indicator organisms serves as a definitive proxy for recent faecal contamination, signalling a failure in basic sanitation hygiene (Igharo et al., 2021).

However, finding the bacteria is only half the battle. A more modern and frightening challenge is that these bugs are learning to fight back. Through environmental exposure and the misuse of medications, many enteric isolates have developed resistance to the very drugs meant to kill them. This makes antibiotic susceptibility testing, the systematic evaluation of which antimicrobial agents remain effective, a public health necessity (CLSI, 2023). The emergence of Multi-Drug Resistant (MDR) strains within environmental water biofilms indicates that these sources are not just transmitting disease but are also facilitating the horizontal transfer of resistance genes (Olowe et al., 2022). If we do not understand these resistance patterns, we are essentially fighting a medical war with broken weapons. This study, therefore, aims to pull back the curtain on the microbial safety of Sabon Gida's water and provide a clear picture of the pharmacological challenges facing this semi-urban community.

2.0 MATERIALS AND METHODS

2.1 Study Area

The research was conducted in Sabon-Gida, a semi-urban community located within the Bungudu Local Government Area (LGA) of Zamfara State, Northwestern Nigeria (Latitude 12°08'05"N; Longitude 6°47'13"E). Situated within the Sudan Savannah vegetation zone, the area experiences a tropical climate characterised by a distinct wet season (May to September) and a prolonged dry season (October to April). The community is characterised by rapid population growth and a heavy reliance on shallow, often poorly

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lined hand-dug wells for domestic, agricultural, and industrial purposes, a dependency primarily driven by the limited reach and frequent failure of municipal water infrastructure. For this study, sampling sites were selected to represent diverse locations within the community, focusing particularly on wells in close proximity to potential contamination sources, such as pit latrines and open refuse dumps.

2.2 Collection of Samples

Following the sampling protocols outlined by the American Public Health Association (APHA, 2017), a total of thirty (30) water samples were collected from ten (10) selected wells across the community (three replicates per well). Samples were collected using sterile 500 mL glass bottles. For wells without integrated pumps, a sterile bottle was attached to a weighted rope, uncapped, and lowered into the well until air bubbles ceased to rise. For wells with drawing buckets, samples were collected directly from the residents' buckets. All samples were labelled (W1–W10), stored in an ice-packed cooler at 4 °C, and transported to the Microbiology Laboratory at the Federal University Gusau for processing within six hours of collection.

2.3 Media Preparation

All culture media, including Nutrient Agar (NA), Eosin Methylene Blue (EMB) Agar, MacConkey Agar (MAC), Methyl Red-Voges Proskauer (MR-VP) broth, Simmons Citrate Agar, and Mueller-Hinton Agar (MHA), were prepared according to the manufacturers' instructions. Sterilisation was achieved by autoclaving at 121 °C for 15 minutes. The media were allowed to cool to approximately 45 °C before being poured into sterile Petri dishes and allowed to solidify.

2.4 Microbiological Quality of Water Samples

The microbiological quality was assessed using standard plate count and filtration techniques.

2.4.1 Total Viable Count (TVC): The mesophilic plate count was performed using the spread plate method. Samples were serially diluted to 10^4, and 0.1 mL of each dilution was inoculated onto Nutrient Agar. A flamed glass spreader was used to distribute the inoculum evenly. Plates were incubated at 37 °C for 24-48 hours. Only plates containing between 30 and 300 colonies were counted and recorded as Colony Forming Units per millilitre (CFU/mL).

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2.4.2 Total and Faecal Coliform Counts: The membrane filtration technique was utilised to concentrate the microbial load. Briefly, 100 mL of each water sample was filtered through a 0.45 µm pore-size membrane under vacuum. The membranes were then aseptically transferred onto MacConkey agar (for total coliforms) and EMB agar (for faecal coliforms). Plates were incubated at 37 °C for 24 hours for the total coliforms and at 44 °C for 24 hours for the faecal coliforms (Brian & Catalina, 2015). Typical coliform colonies were observed, enumerated, and recorded. Metallic green sheen colonies on EMB agar were counted as presumptive coliforms. Results were expressed as CFU/100 mL.

2.5 Identification and Characterisation of Isolates

Pure cultures were obtained by sub-culturing distinct colonies onto MacConkey agar and Eosin Methylene Blue (EMB) agar. Isolates were characterised using Gram staining and observed under oil immersion (x100) for morphological features.

2.5.1 Gram staining

A thin smear of a colony was made with a drop of sterile distilled water on a clean microscope slide and allowed to air dry. The smear was heated and fixed by passing it over the Bunsen burner flame three times. The smear was flooded with crystal violet dye and allowed to stand for one minute, after which the dye was rinsed off with slow-running tap water. Gram iodine was added to cover the smear for another minute and rinsed with slow-running tap water. The smear was then decolourised with acetone briefly, and the smear was counterstained with safranin and allowed to stand for another minute before rinsing with slow-running tap water. The stained smear was allowed to air dry and was observed using an oil immersion objective lens at x100. The purple colour indicates Gram-positive bacteria, while the pinkish colour indicates Gram-negative bacteria. Gram-negative spore-forming rods indicate faecal coliform (Cheesbrough, 2010).

2.5.2 Biochemical Test

Identification was further confirmed through a series of biochemical tests as described by Cheesbrough (2010), including the catalase test, IMViC tests (indole, methyl red, Voges-Proskauer, and citrate utilisation), and the triple sugar iron (TSI) agar test (to observe gas/hydrogen sulphide production and carbohydrate fermentation).

2.6 Antibiotic Susceptibility Testing of the Isolates

Antibiotic susceptibility assessment of pure bacterial isolates using the disc diffusion method was adopted. The susceptibility of the enteric isolates was determined

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using the Kirby-Bauer disc diffusion method on Mueller-Hinton agar, strictly adhering to the Clinical and Laboratory Standards Institute (CLSI, 2023) guidelines.

2.6.1 Antibiotic used

The organisms were tested in vitro for susceptibility to the following commonly used antibiotics: Ampicillin (10 µg), Amoxicillin-clavulanic acid (30 µg), Chloramphenicol (30 µg), Cefotaxime (30 µg), Ciprofloxacin (5 µg), Streptomycin (10 µg), Gentamicin (30 µg), Ceftriaxone (30 µg), Tetracycline (30 µg), and Sulphamethoxazole/Trimethoprim (25 µg), with concentrations as recommended by the National Committee for Clinical Laboratory Standards (NCCLS, 2023).

2.6.2 Standardisation of Bacterial Inoculum

Using a sterile wire loop, three well-isolated colonies that were freshly grown for 24 hours on nutrient agar at 37°C were picked and emulsified in sterile 10 ml normal saline. The prepared turbidity was matched with 0.5 McFarland standards to have an equivalent suspension.

2.6.3 Disc Diffusion Susceptibility Test

A sterile swab was used to inoculate the suspension by streaking on the prepared and dried Mueller-Hinton agar plate evenly. It was then allowed to stand for 3 minutes. Sterile forceps were used to apply the disc; the plate was then incubated at 37°C for 24 hours. By using a metre ruler on the underside of the plate, the diameter of each zone of inhibition was measured in millimetres. Zone diameters for standards were compared with Clinical and Laboratory Standards Institute (CLSI, 2023) published limits; each isolate was classified as Sensitive, Intermediate, and Resistant. All intermediate organisms in this study were considered to be susceptible.

2.7 Statistical Analysis

The data obtained were expressed as means of triplicate determinations. Frequency of occurrence was calculated as a percentage of the total number of isolates recovered, and antibiotic susceptibility was calculated using a simple percentage.

3.0 RESULTS

Table 1 shows the assessment of microbial load across the ten sampled hand-dug water sources. The Total Viable Count (TVC) ranged from a minimum of 1.6 × 10^5 CFU/mL in well W2 to a maximum of 9.3 × 10^5 CFU/mL in well W9. Notably, several wells exhibited particularly high levels of microbial proliferation; specifically, wells W9 (9.3 × 10^5 CFU/mL), W7 (7.2 × 10^5 CFU/mL), and W4 (6.7 × 10^5 CFU/mL) showed

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the highest concentrations. In contrast, the lowest bacterial counts were recorded in W2 (1.6 × 10^5 CFU/mL) and W6 (2.2 × 10^5 CFU/mL), though even these remained within the 10^5 range.

Table 1: Total viable counts of well water samples (three replicates per well).

Sample	CFU /mL
W1	5.5×10^5
W2	1.6×10^5
W3	2.8×10^5
W4	6.7×10^5
W5	3.9×10^5
W6	2.2×10^5
W7	7.2×10^5
W8	6.4×10^5
W9	9.3×10^5
W10	4.0×10^5

Each result represents the mean of the three replicates per well.

KEYS: CFU/ml= Colonies Forming Unit per millilitre, W= well, W1-W10= Well 1 – Well 10.

Table 2 presents the Faecal Coliform Counts for the ten well water samples. The results reveal that Sample W9 contained the highest concentration of faecal coliforms at 37 CFU/100 mL, followed by Sample W7 at 34 CFU/100 mL, Sample W4 at 32 CFU/100 mL, and Sample W5 at 30 CFU/100 mL. In contrast, the lowest faecal coliform density was recorded in Sample W2, which showed 12 CFU/100 mL. While these represent the cleanest samples in this specific category, they still significantly exceed the World Health Organization (WHO) standard, which generally dictates that faecal coliforms should be non-detectable (0 CFU/100 mL) in any water intended for human consumption.

Table 2: Faecal Coliforms Count of Hand-dug Water Samples

Sample	CFU/100mL
W1	26
W2	12
W3	27
W4	32
W5	30
W6	28
W7	34
W8	23
W9	37

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W10	29

Each result represents the mean of the three replicates per well.

KEYS: Cfu/100 ml = colonies forming unit per hundred millilitre, W = well, W1-W10 = Well 1 - Well 10.

Table 3 presents the total coliform counts recorded across ten different well water samples. The results reveal varying levels of microbial loading, with all samples showing detectable levels of coliform bacteria. The highest level of contamination was observed in sample W9 (47 CFU/100 mL), followed by W10 at 43 CFU/100 mL, representing the upper threshold of coliform density in the studied wells. In contrast, sample W2 exhibited the lowest microbial count at 18 CFU/100 mL. The data indicate a significant distribution of coliforms across the board, with elevated levels also noted in wells W7 (41 CFU/100 mL) and W4 (39 CFU/100 mL).

Table 3: Total Coliform Counts of Hand-dug Water Samples

Sample	**CFU/100mL**
W1	32
W2	18
W3	37
W4	39
W5	38
W6	36
W7	41
W8	29
W9	47
W10	43

Each result represents the mean of the three replicates per well.

KEYS: Cfu/100ml= colonies forming unit per hundred milliliter, W1-W10= Well 1 – Well 10.

Table 4 shows the results of Gram reaction, biochemical characterisations, and identification of isolates. All isolates were confirmed as Gram-negative rods and exhibited a positive reaction for catalase, as well as an Acid/Acid (A/A) reaction on Triple Sugar Iron (TSI) agar. The differentiation of the species was achieved through the IMViC (Indole, Methyl Red, Voges-Proskauer, and Citrate) test: Escherichia coli showed positive for Indole and Methyl Red; negative for Voges-Proskauer and Citrate. This biochemical characteristic was the most frequent among the samples W1B, W2C, and W10B. Klebsiella pneumoniae showed negative for Indole and Methyl Red; positive for Voges-Proskauer and Citrate, appearing consistently in samples W1B, W3B, and W9C.

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Table 5 presents the frequency of occurrence for various coliform isolates identified in the study. Escherichia coli emerged as the most prevalent species, accounting for more than half of the total recovery, with a 52.2% occurrence rate. Following this, Klebsiella pneumoniae showed a significant presence, representing 34.8% of the isolates. In contrast, Enterobacter aerogenes was the least frequent coliform detected, contributing only 13.0% to the overall microbial profile. Collectively, these three species constituted a total recovery of 23 isolates across the samples evaluated.

Table 4: Gram reaction, biochemical characterisation and identification of isolates

Sample	Gram	Indole	Citrate	MR	VP	Catalase	TSI	Organism
W1B	-ve Rod	+	-	+	-	+	A/A	*Escherichia coli*
W1B	-ve Rod	-	+	-	+	+	A/A	*Klebsiella pneumoniaee*
W1C	-ve Rod	+	-	+	-	+	A/A	*Escherichia coli*
W2B	-ve Rod	+	-	+	-	+	A/A	*Escherichia coli*
W2B	-ve Rod	-	+	-	+	+	A/A	*Klebsiella pneumoniaee*
W2C	-ve Rod	+	-	+	-	+	A/A	*Escherichia coli*
W3B	-ve Rod	-	+	-	+	+	A/A	*Klebsiella pneumoniaee*
W3C	-ve Rod	-	+	-	+	+	A/A	*Enterobacter aerogenes*
W3C	-ve Rod	-	+	-	+	+	A/A	*Klebsiella pneumoniaee*
W4B	-ve Rod	+	-	+	-	+	A/A	*Escherichia coli*
W5B	-ve Rod	+	-	+	-	+	A/A	*Escherichia coli*
W5C	-ve Rod	+	-	+	-	+	A/A	*Escherichia coli*
W5C	-ve Rod	-	+	-	+	+	A/A	*Klebsiella pneumoniaee*
W6B	-ve Rod	+	-	+	-	+	A/A	*Escherichia coli*
W7B	-ve Rod	-	+	-	+	+	A/A	*Klebsiella pneumoniaee*
W7C	-ve Rod	-	+	-	+	+	A/A	*Enterobacter aerogenes*
W8B	-ve Rod	+	-	+	-	+	A/A	*Escherichia coli*
W8B	-ve Rod	-	+	-	+	+	A/A	*Klebsiella pneumoniaee*
W8C	-ve Rod	+	-	+	-	+	A/A	*Escherichia coli*
W9B	-ve Rod	+	-	+	-	+	A/A	*Escherichia coli*
W9C	-ve Rod	-	+	-	+	+	A/A	*Klebsiella pneumoniaee*
W9C	-ve Rod	-	+	-	+	+	A/A	*Enterobacter aerogenes*
W10B	-ve Rod	+	-	+	-	+	A/A	*Escherichia coli*

KEYS: W1-W10 = Well 1 – Well 10, A = Sample A, B = Sample B, C = Sample C, -ve = Gram negative, + = Positive, - = Negative, MR = Methyl Red, VP= Voges-Proskauer, TSI = Triple Sugar Iron, A/A = Acid slant/Acid butt with gas production, glucose sucrose and lactose fermentation.

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Table 6 presents the results of the Antibiotic Susceptibility testing of Bacterial Isolates from Hand-dug Water Samples in Sabon-Gida. The isolates demonstrated the highest sensitivity to Chloramphenicol (CHL) and Gentamicin (CN), with a 100% susceptibility rate across all species identified. Ciprofloxacin (CIP) and Ceftriaxone (CRO) also showed high efficacy, maintaining overall susceptibility rates of 86.9% and 78.3%, respectively. In contrast, all isolates (100%) exhibited complete resistance to Ampicillin (AMP) and Tetracycline (TET). Resistance to Amoxicillin/Clavulanate (AMC) was also nearly universal, with only two isolates of E. coli (16.7%) showing any sensitivity, while all Klebsiella and Enterobacter strains remained entirely resistant.

Table 5: Percentage Occurrence of Coliform Bacteria from Hand-dug Water Sample from Sabon-Gida

Isolates	Occurrence	% of Occurrence
Escherichia coli	12	52.2
Klebsiella pneumonia	8	34.8
Enterobacter aerogenes	3	13.0
Total	23	100

KEY: %= Percentage

Table 6: Antibiotic Susceptibility Patterns of Bacterial Isolates from Hand-dug Water Samples in Sabon-Gida

Hand-dug water Pathogens	Number of Isolates	Percentage (%) Susceptibility									
		AMP (10µg)	**AMC (30µg)**	**CHL (30µg)**	**CTX (30µg)**	**CIP (5µg)**	**CN (30µg)**	**STR (10µg)**	**TET (30µg)**	**CRO (30µg)**	**SXT (25µg)**
Escherichia coli	**12**	0(0.0)	2(16.7)	12(100)	7(58.3)	10(75.0)	12(100)	6(50.0)	0(0.0)	10(83.3)	8(66.7)
Klebsiella pneumonia	**8**	0(0.0)	0(0.0)	8(100)	5(62.5)	7(87.5)	8(100)	6(75.0)	0(0.0)	6(75.0)	5(66.7)
Enterobacter aerogenes	**3**	0(0.0)	0(0.0)	3(100)	1(33.3)	3(100)	3(100)	2(66.7)	0(0.0)	2(66.7)	1(33.3)
Total	**23**	**0(0.0)**	**2(8.7)**	**23(100)**	**13(56.5)**	**20(86.9)**	**23(100)**	**14(60.9)**	**0(0.0)**	**18(78.3)**	**14(60.9)**

KEYS: AMP - Ampicillin, AMC-Amoxycillin-clavulanic acid, CHL- Chloramphemicol, CTX-Cefotaxime, CIP-Ciprofloxacin, STR-Streptomycin, GN-Gentamicin,
CRO- Ceftriaxone, TET-Tetracycline, SXT-Sulphamethozazole/Trimethoprim, %- Percentage Susceptibility

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4.0 DISCUSSION

The microbial quality of hand-dug wells in Sabon-Gida reveals a high level of bacterial contamination that far exceeds both national and international safety benchmarks. In this study, the Total Viable Counts (TVC) ranged from 1.6 x 10^5 CFU/mL to 9.3 x 10^5 CFU/mL (Table 1). These figures significantly exceed the recommended limit of < 1.0 x 10^2 CFU/mL set by the Nigerian Standard for Drinking Water Quality (NIS 554:2015) and even exceed the 300 CFU/mL threshold often used as an upper limit for manageable microbial loading in untreated sources. Our findings align with the work of Ngwa and Chrysanthus (2013), who reported similarly high viable counts (0.2 x 10^5 CFU/mL to 7.3 x 10^5 CFU/mL) in well water from residential areas in Bambui. Such massive bacterial loads suggest that these sources are active reservoirs for opportunistic pathogens, likely fuelled by groundwater heavily enriched with organic matter and the infiltration of nutrients from the surrounding environment (Ocheri et al., 2017).

Total coliform counts ranged from 18 CFU/100 mL to 47 CFU/100 mL (Table 3), while faecal coliforms peaked at 37 CFU/100 mL in Well W9 (Table 2). The presence of faecal coliforms further highlights the sanitary deficit and the public health hazard. These values deviate sharply from the World Health Organization (WHO, 2022) guidelines, which mandate a zero-tolerance policy (0 CFU/100 mL) for coliforms in drinking water. This high coliform density is consistent with reports by Gambo et al. (2015), who attributed such contamination in Nigerian groundwaters to the percolation of sewage and inadequate maintenance of open wells. Even the cleanest samples in our study (W2) significantly breached these thresholds, confirming that the Sabon-Gida community is at risk of waterborne disease outbreaks. The high concentration in Wells W9, W7, and W4 suggests these sites are particularly vulnerable to enteric pathogens, likely due to the proximity of soakaways or pit latrines. This creates a dangerous cycle of transmission, where the lack of adequate separation between waste disposal and water sourcing facilitates the spread of illnesses such as cholera and typhoid fever (Bulus et al., 2021).

The biochemical characterisation identified an enteric profile dominated by Escherichia coli (52.2%), followed by Klebsiella pneumoniae (34.8%) and Enterobacter aerogenes (13.0%) (Table 5). The predominance of E. coli is particularly significant as a definitive indicator of faecal pollution, confirming that human or animal excreta may be directly entering the water system (Ashbolt, 2015). Similar microbial distributions have been documented by Idowu et al. (2011) in Shagamu. Furthermore, the Acid/Acid (A/A)

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reaction on Triple Sugar Iron (TSI) agar across all isolates confirms their robust ability to ferment lactose and glucose, a hallmark of the coliform group that suggests their viability and potential virulence. While K. pneumoniae and E. aerogenes are often environmental, they are known to cause community-acquired infections, including pneumonia and urinary tract infections, particularly in vulnerable groups like children and the elderly (Ashbolt, 2015). These contamination levels can be attributed to the shallowness and openness of the wells, the use of contaminated drawing containers, and the influence of surface runoff during rainy seasons, which facilitates the transport of pathogens from contaminated soil into the water table (Idowu et al., 2011; Ngwa & Chrysanthus, 2013).

The antibiotic results show a worrying level of contamination in the Sabon-Gida wells (Table 6). All identified species exhibited 100% resistance to Ampicillin and Tetracycline, alongside a staggering 91.3% resistance rate to Amoxicillin/Clavulanate. The 100% resistance to Ampicillin and Tetracycline means these common, affordable drugs are essentially useless for treating waterborne infections in this community. This total loss of efficacy in common first-line antibiotics reflects a broader environmental crisis fuelled by the unregulated sale and indiscriminate use of these drugs in semi-urban Nigerian communities (Adzitey, 2020). Because these drugs are inexpensive and accessible without prescription from unauthorised patent medicine shops, high selective pressure favours the survival of resistant strains in the human gut, which then leach into the shallow groundwater via pit latrines (Odonkor & Addo, 2018). From a clinical perspective, this means that should an outbreak occur, standard oral treatments may fail, leading to higher morbidity, prolonged hospitalisations, and increased mortality rates (World Bank, 2023).

While the resistance to beta-lactams was nearly absolute, the 100% susceptibility to chloramphenicol and gentamicin offers a critical clinical insight. In many settings, gentamicin remains effective because its status as an injectable drug makes it less prone to the self-medication abuse that plagues oral antibiotics. High susceptibility levels to the newer, more valuable antimicrobial compounds, such as phenicols and aminoglycosides, could yield good therapeutic outcomes. Our findings align with research in other parts of Sub-Saharan Africa, where aminoglycosides maintain high potency due to restricted administration routes (Nyandjou et al., 2017; Igharo et al., 2021). While high sensitivity to ciprofloxacin (86.9%) and ceftriaxone (78.3%) is encouraging for treating severe infections, the emergence of any resistance to these last-line defenses is a major red flag. If resistance genes continue to spread through horizontal gene transfer within well water biofilms,

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simple diarrhoeal diseases may become untreatable (Olowe et al., 2022). The variation in sensitivity between E. coli and K. pneumoniae further suggests that the "resistome" in Sabon-Gida's water is diverse and evolving, necessitating urgent interventions in waste management, improved well construction, and point-of-use water treatment.

5.0 CONCLUSION

The microbial quality of hand-dug wells in Sabon-Gida highlights a critical public health challenge, characterised by heavy microbial contamination and the proliferation of multi-drug resistant (MDR) enteric pathogens. Our findings reveal that none of the sampled wells met the international or national safety benchmarks for potable water. With total viable counts ranging from 1.6 x 10^5 CFU/mL to 9.3 x 10^5 CFU/mL, and coliform densities reaching up to 47 CFU/100 mL, every source significantly exceeded the zero-tolerance thresholds set by the World Health Organisation and the Nigerian Standard for Drinking Water Quality.

The identification of a classic enteric profile dominated by Escherichia coli (52.2%), Klebsiella pneumoniae (34.8%), and Enterobacter aerogenes (13.0%) serves as a definitive indicator of faecal pollution. The predominance of E. coli is particularly concerning, as it confirms that human or animal excreta are actively infiltrating the shallow groundwater table. This contamination is likely exacerbated by the open nature of the wells, the proximity of residential soakaways, and the influence of surface runoff during the rainy season.

Beyond the immediate risk of waterborne disease outbreaks, the antibiotic susceptibility profiles of these isolates are alarming. The 100% resistance observed against Ampicillin and Tetracycline, combined with near-universal resistance to Amoxicillin/Clavulanate, confirms that these wells are acting as environmental reservoirs for MDR strains. While the continued efficacy of Gentamicin, Chloramphenicol, and Ciprofloxacin provides some therapeutic alternatives, the loss of common first-line oral antibiotics poses a severe threat to community health management in this semi-urban setting.

RECOMMENDATIONS

Based on these findings, the following recommendations are made:

1. Residents of Sabon-Gida should be sensitised to the dangers of consuming untreated well water. The need to boil and filter water before consumption should be emphasised to prevent outbreaks of waterborne disease.

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2. Construction of wells should be done in accordance with World Health Organization recommendations with regard to their location and depth.

3. The well should have a protective covering to prevent contamination from runoff during rainfall, wind, and grazing animals.

4. The high levels of resistance observed necessitate better regulation of antibiotic use in the community to prevent the further selection and spread of resistant genes in groundwater sources.

5. The local Ministry of Health and environmental agencies should establish a periodic monitoring framework for groundwater quality in semi-urban communities to detect and respond to potential outbreaks before they escalate.

6. Future studies should focus on molecular characterisation (such as PCR or Whole Genome Sequencing) to track the specific plasmids responsible for the horizontal gene transfer of resistance observed in this study.

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