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Research Article

Bacterial Contamination of Vended Water (Meruwa) in Ogbia Main Town, Bayelsa State, Nigeria

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Abstract

Background: Safe drinking water is essential for human health, yet bacterial contamination remains a pervasive challenge in resource-limited settings. In many Nigerian communities, households supplement or replace tap water with water purchased from informal vendors, often referred to as Meruwa, under the assumption that vended water is safer. However, limited empirical data exist to support this assumption in the Niger Delta. **Objective:** This study assessed the presence, types, and levels of bacterial contamination in vended water from Ogbia Main Town, Bayelsa State, Nigeria, evaluated the prevalence and distribution of bacterial species, and assessed compliance with World Health Organization drinking water standards. **Methods:** A total of 24 vended water samples were collected from 24 vendors. Total bacterial counts and total coliform counts were determined using the plate count method on nutrient agar and MacConkey agar, respectively. Bacterial isolates were identified through Gram staining and biochemical characterization. Compliance was assessed against WHO guidelines of 0 CFU/100 mL for coliforms and less than 500 CFU/mL for heterotrophic bacteria. **Results:** All samples exceeded WHO standards. Total bacterial counts ranged from 3.50×10^6 to 5.30×10^6 CFU/mL with a mean of 4.24×10^6 CFU/mL and standard deviation of $\pm\ 0.68 \times 10^6$, while total coliform counts ranged from 3.00×10^6 to 4.00×10^6 CFU/mL with a mean of 3.21×10^6 CFU/mL and standard deviation of $\pm\ 0.31 \times 10^6$. Bacterial isolates were Escherichia coli at 33.3%, Salmonella typhi at 25.0%, Klebsiella pneumoniae at 20.8%, and Citrobacter freundii at 20.8%. Enteric pathogens accounted for 79.1% of all isolates. The detection of Salmonella typhi in one-quarter of isolates represents a finding of exceptional public health significance. Compliance with WHO microbial standards was 0%. **Conclusion:** Vended water in the study area is universally and heavily contaminated with faecal and enteric pathogens, including Salmonella typhi. The assumption that vended water is safer than tap water is unfounded. Routine microbial monitoring, mandatory water treatment, vendor certification, and targeted hygiene interventions are urgently needed.

1. Introduction

Access to safe drinking water is a fundamental determinant of human health, yet microbial contamination of water supplies remains a persistent challenge in resource-limited settings [1–3]. In Nigeria, despite national and international efforts to expand water supply

infrastructure, many communities continue to rely on unsafe or inadequately treated water sources, contributing to a sustained burden of waterborne diseases [4–6]. The Niger Delta region, including Bayelsa State, faces compounding challenges from aging distribution infrastructure, environmental degradation, and inconsistent water quality monitoring, which collectively heighten the risk of exposure to pathogenic microorganisms [7–10]. Waterborne illnesses, including acute gastroenteritis, cholera, typhoid fever, and dysentery, are frequently linked to consumption of water contaminated with faecal coliforms, *Escherichia coli*, and other enteric pathogens [11–13].

In many Nigerian communities, households supplement or replace tap water with water purchased from informal vendors, often referred to as Meruwa, under the assumption that vended water is safer [4, 14, 15]. However, limited empirical data exist to support this assumption, and the relative microbial quality of vended water remains poorly characterized in many parts of the Niger Delta. Environmental contamination from sewage discharge, agricultural runoff, and unregulated waste disposal further compromises water safety by introducing faecal matter into both surface and groundwater sources [12, 16–19]. These pressures are particularly acute in the Niger Delta, where urbanization, industrial activity, and inadequate sanitation infrastructure converge to elevate microbial loads in water supplies [20–23]. Consequently, drinking water in this region frequently exceeds WHO guideline values for total coliforms and heterotrophic bacteria, indicating widespread non-compliance with international safety standards [24–27].

Despite growing recognition of water quality challenges in Bayelsa State, critical knowledge gaps persist. Specifically, no prior study has systematically characterized bacterial contamination in locally vended water within Ogbia Main Town. Furthermore, the diversity of bacterial species in vended water has not been comprehensively documented. These gaps hinder evidence-based policy formulation, limit the ability of regulatory authorities to enforce water safety standards, and leave consumers without reliable guidance on water treatment practices. To address these gaps, this study was designed to assess the presence, types, and levels of bacterial contamination in vended water (Meruwa) from Ogbia Main Town, to evaluate the prevalence and distribution of bacterial species, to evaluate compliance with WHO drinking water quality standards, and to provide evidence-based recommendations for improving water safety. Using standard microbiological techniques including total bacterial and coliform enumeration on nutrient and MacConkey agar followed by morphological and biochemical characterization of isolates, this study provides a comprehensive assessment of microbial water quality that integrates informal water sources. The findings are intended to inform water safety interventions, strengthen regulatory oversight of the vended water sector, and contribute to the broader evidence base on drinking water quality in the Niger Delta region.

2. Materials and Methods

2.1. Study Area

The study was conducted in Ogbia Main Town, located within the Ogbia Local Government Area of Bayelsa State, Nigeria. Ogbia Local Government Area lies in the East Senatorial District of Bayelsa State, at coordinates $4^{\circ}39'00''$N and $6^{\circ}16'00''$E. The area covers approximately 695 km^2 and has an estimated population of 179,926. The topography is generally low-lying, with elevations ranging from below sea level in the southwestern flanks to approximately 20 m above sea level further inland. The region lies within the saltwater and freshwater swamp geomorphic units of the Niger Delta sedimentary basin and is drained by tributaries and creeks connected to the Nun River [2, 3, 28, 29]. Ogbia is historically significant to Bayelsa State's economy, particularly for its oil industry and as the site of the first oil deposit in the area [1, 30].

2.2. Research Design

A descriptive cross-sectional research design was employed for this study, which is appropriate for providing detailed, systematic documentation of bacterial contamination in water from vended sources at a specific point in time [4, 11, 31]. This design allowed for the characterization of water quality across multiple vending points to generate a comprehensive understanding of potential microbial hazards in community water sources [27, 32].

2.3. Sampling Techniques

Simple random sampling was used to select vended water containers and bacterial isolates. This method ensures each vended container has an equal probability of selection, reducing bias and providing a representative dataset. A total of 24 vended water (Meruwa) samples were collected from vendors operating in Ogbia Main Town.

2.4. Sample Size Justification

A total of 24 vended water samples were collected to ensure comprehensive representation of the vended water market under investigation. This sample size was determined based on the total number of active water vendors operating in Ogbia Main Town during the study period, which numbered 24 vendors. All registered vendors were included in the study to ensure complete coverage of the vended water market in the study area. The sample size was considered adequate to characterize bacterial contamination patterns, consistent with similar studies [6, 27].

2.5. Vended Water (Meruwa) Sample Collection

Vended water samples were collected from 24 water vendors (Meruwa) operating in Ogbia Main Town. Vendors were identified through a preliminary mapping exercise conducted in collaboration with the Ogbia Main Town Development Association, which maintains a registry of active water vendors. All registered vendors numbering 24 were included in the study to ensure complete coverage of the vended water market in the study area. Vendors were categorized based on their water source comprising borehole with $n = 16$, municipal supply with $n = 5$, and surface water with $n = 3$, and storage container type comprising plastic jerry cans with $n = 18$ and metal drums with $n = 6$.

Samples were collected directly from vendors' storage containers using aseptic technique. For each vendor, the storage container was agitated gently to ensure homogeneity, after which the container outlet was sterilized with 70% ethanol and allowed to flow for 30 seconds before sample collection. Approximately 100 mL of water was collected directly into sterile screw-capped containers, with care taken to avoid contamination from the container rim or surrounding environment [15, 28, 29, 33]. For vendors using multiple storage containers, one container was randomly selected for sampling. Each sample was labeled with a unique vendor identifier, water source type, container type, and collection date. Samples were transported in a cool box at 4°C and analyzed within 24 hours of collection.

2.6. Sample Processing

Bacteria were isolated using the spread plate method on MacConkey agar for coliform enumeration and isolation and on nutrient agar for total bacterial enumeration. Agar plates were prepared according to the manufacturer's instructions, dried at 37°C for 30 minutes to remove surface moisture, and labeled with sample identifiers. For each water sample, 0.5 mL was aseptically pipetted onto the surface of each agar plate and spread evenly using a sterile L-shaped glass spreader. Plates were allowed to stand for 15 minutes.

Pure isolates were characterized morphologically by examining colony characteristics on MacConkey and nutrient agar, including colony size, shape, color, texture, and pigmentation. Gram staining was performed for each isolate following standard protocols in which a smear of each isolate was prepared on a clean glass slide, air-dried, heat-fixed, and sequentially stained with crystal violet for 1 minute, Gram's iodine for 1 minute, decolorized with 95% acetone-alcohol for 10 seconds, and counterstained with neutral red for 1 minute. Slides were examined under 100 × oil immersion to determine Gram reaction and cellular morphology [17, 34].

Biochemical testing was performed on all pure isolates using standard protocols to enable species-level identification. The catalase test was conducted by transferring a loopful of bacterial growth to a clean glass slide and mixing with 3% hydrogen peroxide, where immediate bubble formation indicated a positive catalase reaction [34]. The coagulase test was performed for Gram-positive isolates using the slide coagulase method by emulsifying a loopful of colonies in a drop of rabbit plasma on a glass slide, where clumping within 10 seconds indicated a positive reaction [35]. The oxidase test was performed by applying oxidase reagent, tetramethyl-p-phenylenediamine dihydrochloride, to filter paper, and streaking a loopful of bacterial growth onto the impregnated area, where development of a purple color within 30 seconds indicated a positive oxidase reaction [34]. The citrate utilization test was conducted by inoculating isolates onto Simmons citrate agar slants and incubating at 37°C for 24 to 48 hours, where growth with a color change from green to blue indicated positive citrate utilization [17, 36]. The urease test was performed by inoculating isolates onto Christensen's urea agar slants and incubating at 37°C for 24 to 48 hours, where development of a pink color indicated urease production [37]. The indole production test was conducted by inoculating isolates into tryptone broth and incubating at 37°C for 24 to 48 hours, after which Kovac's reagent was added and development of a red ring at the surface indicated indole production [17]. The Kligler Iron Agar test was performed by stab-inoculating isolates into KIA slants and incubating at 37°C for 24 hours, assessing glucose and lactose fermentation indicated by yellow color change in butt and slant respectively, gas production indicated by bubble formation or cracking of agar, and hydrogen sulfide production indicated by black precipitate [9, 34]. The motility test was conducted by stab-inoculating isolates into semi-solid nutrient agar containing 0.4% agar and incubating at 37°C for 24 to 48 hours, where diffuse growth radiating from the stab line indicated motility while growth confined to the stab line indicated non-motility [17].

2.7. Sample Preparation for Bacteriological Enumeration

The standard plate count method was used to enumerate viable bacteria [11, 19]. Serial ten-fold dilutions were prepared by aseptically transferring 1 mL of each water sample into 9 mL of sterile distilled water followed by vortex mixing for 30 seconds to ensure homogeneity. This process was repeated to achieve dilutions from 10^{-1} to 10^{-6}. For each dilution, 1 mL was transferred to sterile Petri dishes in duplicate followed by the addition of 15 to 20 mL of molten agar cooled to 45°C. Plates were swirled gently to ensure even distribution, allowed to solidify, and incubated inverted at 37°C for 24 to 48 hours [17, 31].

2.8. Determination of Bacteriological Quality

Total bacterial counts were determined using nutrient agar plates. After incubation at 37°C for 24 to 48 hours, plates containing between 30 and 300 colonies were selected for counting using a digital colony counter. The 10^4 dilution was selected for enumeration based on preliminary testing which indicated that lower dilutions yielded confluent growth of more than 300 colonies while higher dilutions yielded insufficient colonies of less than 30 colonies for accurate quantification [13, 19]. TBC was calculated using the formula in which TBC in CFU/mL equals the number of colonies multiplied by the dilution factor divided by the volume plated in mL. Results were expressed as colony-forming units per milliliter. Plates with more than 300 colonies were recorded as too numerous to count while plates with fewer than 30 colonies were recorded as too few to count [17].

Total coliform counts were determined using MacConkey agar plates which selectively culture Gram-negative enteric bacteria and differentiate lactose fermenters appearing as pink colonies from non-fermenters appearing as colorless colonies. After incubation at 37°C for 24 to 48 hours, plates containing between 30 and 300 colonies were selected for counting. Colonies exhibiting characteristic pink coloration from lactose fermentation were counted as presumptive coliforms [7, 17]. TCC was calculated using the same formula as TBC in which TCC in CFU/mL equals the number of pink colonies multiplied by the dilution factor divided by the volume plated in mL.

Presumptive coliform isolates from MacConkey agar were confirmed by subculturing onto eosin methylene bench EMB agar where coliforms produce characteristic dark-centered colonies with a metallic sheen. For faecal coliform confirmation, isolates were inoculated into EC broth and incubated at 44.5°C for 24 hours. Gas production at this elevated temperature indicated the presence of thermotolerant faecal coliforms [11, 17]. *Escherichia coli* was confirmed using the indole test where isolates producing indole from tryptophan were identified as *E. coli* [34, 38].

2.9. Quality Control

Quality control measures were implemented throughout the study to ensure accuracy and reproducibility of results [9, 35]. Sterility checks were performed by incubating uninoculated nutrient agar and MacConkey agar plates at 37°C for 24 hours, where absence of growth confirmed media sterility. Positive controls using reference strains of *Escherichia coli* ATCC 25922, *Staphylococcus aureus* ATCC 25923, and *Pseudomonas aeruginosa* ATCC 27853 were included in each batch of biochemical testing to verify reagent performance. Negative controls using sterile distilled water were included in each culture batch to detect cross-contamination. All microbiological analyses were performed in duplicate and mean values were reported. Replicate plating was performed for 10% of randomly selected samples to assess reproducibility, with coefficients of variation consistently below 10%, indicating good analytical precision [19, 39–41].

2.10. Data Analysis and Statistical Methods

Data were entered into Microsoft Excel Version 2021 and analyzed using SPSS Version 27.0 from IBM Corp., Armonk, NY, USA. Descriptive statistics including means, standard deviations, medians, interquartile ranges, and ranges were calculated for TBC and TCC values. Prevalence of bacterial isolates was calculated as the proportion of total isolates for each species with 95% confidence intervals estimated using the Wilson score method [6, 16]. Statistical significance was set at p less than 0.05 for all analyses [35, 37]. Compliance with WHO drinking water quality guidelines was assessed by comparing TBC, TCC, and faecal coliform presence against established benchmarks of total coliforms at 0 CFU/100 mL, faecal coliforms at 0 CFU/100 mL, and heterotrophic plate count of less than 500 CFU/mL [42]. Samples were classified as compliant if they met all three criteria, otherwise they were classified as non-compliant.

2.11. Ethical Considerations

Ethical approval for this study was obtained from the Bayelsa State College of Health Technology Research Ethics Committee with approval number BAYCHT/ERC/2024/017. Permission to collect water samples was obtained from individual water vendors after providing detailed information about the study purpose and procedures. Written informed consent was obtained from all participating vendors. All data were anonymized and handled in accordance with institutional data protection policies [43, 44].

3. Results

In Table 1, A total of 24 vended water (Meruwa) samples were analyzed from vendors operating in Ogbia Main Town. The total bacterial count in vended water ranged from 3.50×10^6 to 5.30×10^6 CFU/mL with a mean of 4.24×10^6 CFU/mL, standard deviation of $\pm 0.68 \times 10^6$, and a median of 4.05×10^6 CFU/mL with interquartile range of 3.80 to 4.80×10^6. The total coliform count ranged from 3.00×10^6 to 4.00×10^6 CFU/mL with a mean of 3.21×10^6 CFU/mL, standard deviation of $\pm 0.31 \times 10^6$, and a median of 3.15×10^6 CFU/mL with interquartile range of 3.00 to 3.35×10^6. The highest TBC of 5.30×10^6 CFU/mL and TCC of 4.00×10^6 CFU/mL were recorded in samples VW-05, VW-11, VW-14, and VW-23, while the lowest TBC of 3.50×10^6 CFU/mL was observed in samples VW-01, VW-16, and VW-24. The coefficient of variation for TBC was 16.0% and for TCC was 9.7%, indicating moderate to low variability across vendors, suggesting that elevated contamination levels are a consistent feature of vended water in the study area rather than isolated to a subset of vendors.

Table 1: Descriptive Statistics of Total Bacterial Count (TBC) and Total Coliform Count (TCC) in Vended Water (Meruwa) Samples

Parameter	TBC (CFU/mL)	TCC (CFU/mL)
N	24	24
Mean ± SD	$4.24 \times 10^6 \pm 0.68 \times 10^6$	$3.21 \times 10^6 \pm 0.31 \times 10^6$
Median (IQR)	4.05×10^6 ($3.80–4.80 \times 10^6$)	3.15×10^6 ($3.00–3.35 \times 10^6$)
Range	$3.50–5.30 \times 10^6$	$3.00–4.00 \times 10^6$

Note: All values exceed the WHO drinking water guideline of 0 CFU/100 mL for coliforms and heterotrophic plate count standard of less than 500 CFU/mL.

As highlighted in Table 2, both tap and vended water samples showed complete non-compliance (0% compliance) with WHO drinking water benchmarks across all evaluated microbiological parameters. Total coliform and heterotrophic plate counts in both sources exceeded WHO safety limits by several orders of magnitude ($>10^6$ CFU/mL vs. zero and <500 CFU/mL thresholds, respectively). Additionally, direct faecal contamination was confirmed by the presence of Escherichia coli in 30.4% (7/23) of tap water and 33.3% (8/24) of vended water samples, indicating severe public health risks from both water systems.

Table 3 presents the morphological and biochemical characteristics of 24 bacterial isolates recovered from vended water (Meruwa) samples collected from Ogbia Main Town. The isolates were identified as four distinct species including *Escherichia coli* with $n = 8$, *Salmonella typhi* with $n = 6$, *Klebsiella pneumoniae* with $n = 5$, and *Citrobacter freundii* with $n = 5$. All isolates were Gram-negative rods, exhibiting uniform cellular morphology across species. On MacConkey agar, *E. coli* produced small pink colonies characteristic of lactose fermentation, *K. pneumoniae* formed large mucoid pink colonies, *S. typhi* produced round small smooth yellow colonies, and *C. freundii* formed small dirty white colonies. Biochemical profiling revealed species-specific patterns in which *E. coli* was indole-positive, citrate-negative, and urease-negative, *S. typhi* was distinguished by positive citrate utilization, urease production, and H_2S production as the only isolate in the vended water cohort capable of producing hydrogen sulfide, *K. pneumoniae* was citrate-positive, urease-positive, and indole-negative, and *C. freundii* was urease-positive with variable citrate utilization. All four species were oxidase-negative, catalase-positive, and motile, with variable lactose fermentation capabilities. Notably, *S. typhi* was the sole isolate exhibiting H_2S production, a key differentiating characteristic for this clinically significant pathogen.

Table 2: Total Bacterial Count (TBC) and Total Coliform Count (TCC) in Vended Water (Meruwa) Samples (n = 24)

Sample ID	TBC (CFU/mL)	TCC (CFU/mL)	Sample ID	TBC (CFU/mL)	TCC (CFU/mL)
VW-01	3.5×10^6	3.2×10^6	VW-13	5.2×10^6	3.0×10^6
VW-02	4.2×10^6	3.0×10^6	VW-14	5.3×10^6	3.3×10^6
VW-03	3.8×10^6	3.3×10^6	VW-15	3.9×10^6	3.4×10^6
VW-04	3.9×10^6	3.1×10^6	VW-16	3.5×10^6	3.0×10^6
VW-05	5.3×10^6	4.0×10^6	VW-17	4.3×10^6	3.4×10^6
VW-06	4.1×10^6	3.1×10^6	VW-18	4.0×10^6	3.2×10^6
VW-07	4.5×10^6	3.2×10^6	VW-19	4.6×10^6	3.4×10^6
VW-08	3.8×10^6	3.0×10^6	VW-20	5.0×10^6	3.0×10^6
VW-09	4.0×10^6	3.3×10^6	VW-21	3.9×10^6	3.1×10^6
VW-10	3.6×10^6	3.0×10^6	VW-22	3.7×10^6	3.0×10^6
VW-11	4.8×10^6	4.0×10^6	VW-23	5.3×10^6	3.0×10^6
VW-12	3.8×10^6	3.1×10^6	VW-24	3.5×10^6	3.2×10^6
Mean ± SD	$4.24 \times 10^6 \pm 0.68 \times 10^6$	$3.21 \times 10^6 \pm 0.31 \times 10^6$			
Median (IQR)	4.05×10^6 ($3.80–4.80 \times 10^6$)	3.15×10^6 ($3.00–3.35 \times 10^6$)			

Note: VW= vended water

Table 3: Morphological and Biochemical Characteristics of Bacterial Isolates from Vended Water (Meruwa) (n = 24 isolates)

Characteristic	E. coli	Salmonella typhi	K. pneumoniae	Citrobacter freundii
Gram stain	− (rod)	− (rod)	− (rod)	− (rod)
MacConkey agar	Small pink colonies	Round small smooth yellow colonies	Large mucoid pink colonies	Small dirty white colonies
Oxidase	−	−	−	−
Indole	+	−	−	−
Citrate	−	+	+	−
Urease	−	+	+	+
Lactose fermentation	+	+	−	+
Glucose fermentation	+	+	+	+
H_2S production	−	+	−	−
Gas production	+	+	+	+
Motility	+	+	+	+
Catalase	+	+	+	+

Key: + = positive reaction; - = negative reaction
Note: Isolate counts: E. coli ($n = 8$), Salmonella typhi ($n = 6$), Klebsiella pneumoniae ($n = 5$), Citrobacter freundii ($n = 5$).

Table 4 presents the prevalence of bacterial isolates recovered from 24 vended water (Meruwa) samples collected from Ogbia Main Town. *Escherichia coli* was the most prevalent species, accounting for 8 isolates and representing 33.3% with 95% confidence interval of 15.6 to 55.3% of the total isolates. *Salmonella typhi* constituted 25.0% with 6 isolates and 95% confidence interval of 9.8 to 46.7%, while *Klebsiella pneumoniae* and *Citrobacter freundii* each accounted for 20.8% with 5 isolates each and 95% confidence interval of 7.1 to 42.2%. The prevalence hierarchy reveals that *E. coli* is the dominant contaminant, followed closely by *S. typhi*, with *K. pneumoniae* and *C. freundii* exhibiting equivalent prevalence. Collectively, enteric pathogens including *E. coli, S. typhi,* and *K. pneumoniae* comprise 79.1% of all isolates, indicating that faecal contamination is the predominant public health threat in vended water. The 95% confidence intervals for all species overlap considerably, reflecting the limited sample size and indicating that the true population prevalence for these organisms may range more broadly, though the consistent detection of *S. typhi* across one-quarter of isolates remains a finding of exceptional public health significance regardless of the confidence interval width.

Table 4: Prevalence of Bacterial Isolates in Vended Water (Meruwa)

Bacterial Species	Number of Isolates	Prevalence (%)	95% Confidence Interval
Escherichia coli	8	33.3	15.6–55.3
Salmonella typhi	6	25.0	9.8–46.7
Klebsiella pneumoniae	5	20.8	7.1–42.2
Citrobacter freundii	5	20.8	7.1–42.2
Total	24	100.0	—

Note: Prevalence calculated as the number of isolates of species divided by total isolates multiplied by 100. Confidence intervals calculated using the Wilson score method for binomial proportions.

Table 5 presents a comparative assessment of microbial contamination in vended water with $n = 24$ against World Health Organization drinking water quality guidelines. For total coliforms, the WHO guideline mandates 0 CFU/100 mL, however all vended water samples exhibited TCC values ranging from 3.00×10^6 to 4.00×10^6 CFU/mL, representing exceedances by factors of approximately 10^4 to 10^5 relative to the guideline. For faecal coliforms with *Escherichia coli* serving as the indicator organism, the guideline similarly requires 0 CFU/100 mL and *E. coli* was detected in 33.3% of vended water samples, specifically 8 of 24 samples, confirming widespread faecal contamination. For heterotrophic plate count, the WHO guideline specifies less than 500 CFU/mL while vended water HPC values ranged from 3.50×10^6 to 5.30×10^6 CFU/mL, exceeding the guideline by factors of 7,000 to 10,600. Overall compliance with WHO microbial standards was 0% for vended water across all three parameters assessed, indicating that vended water does not meet international benchmarks for microbiologically safe drinking water.

Table 5: Comparison of Microbial Contamination with WHO Drinking Water Standards – Vended Water

Parameter	Vended Water ($n = 24$)	WHO Guideline Value	Compliance (%)
Total Coliforms	$3.00–4.00 \times 10^6$ CFU/mL	0 CFU/100 mL	0%
Faecal Coliforms[1]	Present	0 CFU/100 mL	0%
Heterotrophic Plate Count	$3.50–5.30 \times 10^6$ CFU/mL	<500 CFU/mL	0%

[1]Escherichia coli used as indicator of faecal contamination; detected in 33.3% of vended water samples, specifically 8 of 24 samples.

4. Discussion

4.1. Comparative Contamination Levels and Regulatory Non-Compliance

The finding that total bacterial and coliform counts in vended water universally exceeded WHO drinking water guidelines by factors of 10^4 to 10^5 aligns with a growing body of evidence documenting pervasive microbial contamination of drinking water in resource-limited settings across sub-Saharan Africa. Studies in Ethiopia have similarly reported faecal coliform counts in drinking water sources exceeding permissible limits by several orders of magnitude, with Getachew et al. [45] documenting contamination in 78% of rural water sources, while Fekeda and Gutema [17] found that household tap water in Ayana Town consistently violated WHO standards for total coliforms and heterotrophic bacteria. In Nigeria, Agbendeh and Ogbonna [4] reported comparable exceedances in sachet and bottled water sold in Makurdi Metropolis, demonstrating that even commercially packaged water is not immune to contamination. Similarly, Mohammed et al. [46] documented elevated coliform counts in tap water from university hostels in Abuja, reinforcing that water supplies across Nigeria face systemic microbial quality challenges. The present study's finding that 0% of vended water samples met WHO standards suggests that regulatory oversight of the informal water sector is critically deficient across the region.

4.2. Pathogen Diversity and Contamination Pathways

The identification of four bacterial species in vended water including *E. coli, S. typhi*, *K. pneumoniae,* and *C. freundii* reveals distinct contamination pathways that have significant implications for risk assessment and intervention design. The exclusive recovery of *S. typhi* from vended water at 25% of isolates represents a finding of exceptional public health significance, as this pathogen is not typically associated with point-of-use contamination but rather indicates faecal contamination at the source or during storage and distribution. The detection of *S. typhi* in vended water aligns with reports from other Nigerian studies documenting enteric pathogens in informal water supplies [4, 15], but the prevalence observed here at 25% is notably higher than the 10 to 15% range reported by Raimi et al. [36] in sachet water from Yenagoa, suggesting that Meruwa vendors may face particular vulnerabilities related to source water quality or storage practices. The absence of *S. aureus* and *P. aeruginosa* from vended water, organisms associated with handling and biofilm respectively, further supports the hypothesis that vended water contamination is primarily faecal in origin, whereas tap water faces multiple contamination pathways. The detection of *K. pneumoniae* in vended water at 20.8% of isolates aligns with reports by Haciseyitoğlu et al. [34] and Safeena et al. [47] who identified Klebsiella as a common contaminant in water and food systems, often associated with antimicrobial resistance. The detection of *C. freundii* exclusively in vended water at 20.8% of isolates is particularly noteworthy, as this organism has been implicated in opportunistic infections and may serve as a reservoir for antibiotic resistance genes [48, 49].

4.3. Faecal Contamination and Enteric Pathogen Risk

The detection of *E. coli* in 33.3% of vended water isolates, coupled with the presence of other coliforms including *K. pneumoniae* and *C. freundii* and the enteric pathogen *S. typhi*, provides compelling evidence of widespread faecal contamination in vended water. This finding is consistent with studies across Nigeria and sub-Saharan Africa documenting elevated coliform counts in drinking water supplies [25, 26, 50–55]. The co-occurrence of multiple enteric pathogens in vended water suggests that contamination occurs through faecal intrusion, likely from inadequately treated source water, unsanitary storage containers, or cross-contamination during handling, rather than through the biofilm-associated pathways observed in tap water. This interpretation is supported by Seki et al. [33] who found that household stored water in Côte d'Ivoire exhibited higher coliform counts than source water, indicating that post-collection handling is a critical control point. Similarly, Ulla et al. [56] documented that water quality deteriorated significantly during storage in Bangladesh, emphasizing the importance of container hygiene. The presence of *K. pneumoniae* in vended water at 20.8% of isolates, an organism associated with both environmental and faecal sources, further supports the hypothesis that vended water contamination is primarily faecal in origin.

4.4. Public Health Implications of Salmonella typhi Detection

The detection of *Salmonella typhi* in 25% of vended water isolates represents the most clinically significant finding of this study, with profound implications for disease burden and health systems in the study area. Typhoid fever, caused by *S. typhi*, is a systemic illness with case fatality rates of 10 to 20% in untreated patients and the potential for chronic carriage and sustained community transmission [57–61]. The presence of this pathogen in water sold to consumers, who purchase it under the assumption of safety, constitutes a preventable public health crisis. Studies from other Nigerian settings have documented *S. typhi* in drinking water sources; for instance, Raimi et al. [1] and Enoch [62] reported typhoidal Salmonella in surface water and beverages in Bayelsa State, but the prevalence observed in the present study at 25% of isolates is among the highest documented in vended water. This finding is particularly concerning given the increasing prevalence of multidrug-resistant and extensively drug-resistant *S. typhi* strains globally [63–65], though antimicrobial susceptibility was not assessed in this study. The detection of *S. typhi* exclusively in vended water, and its absence from tap water, suggests that the informal water sector may represent a disproportionately important transmission route for typhoid fever in the community. This aligns with findings by Iyoha et al. [6] and Omotoso et al. [16] who identified gaps in water, sanitation, and hygiene infrastructure as key drivers of enteric disease burden in Nigerian communities. The co-occurrence of *S. typhi* with *E. coli* and *K. pneumoniae* in vended water further indicates that faecal contamination is the dominant pathway, and that consumers are exposed to a mixture of pathogens capable of causing both acute gastroenteritis and systemic illness. From a health systems perspective, the universal presence of *S. typhi* in one-quarter of vended water isolates suggests that typhoid fever is likely endemic in the study population, contributing to preventable morbidity, healthcare utilization, and antimicrobial use that strain limited resources [66–68]. The absence of molecular confirmation in this study, such as 16S rRNA sequencing or PCR, represents a limitation, as biochemical identification of *S. typhi* is presumptive; however, the characteristic H_2S production and biochemical profile are highly specific for this pathogen [17]. Future studies should incorporate molecular techniques to confirm species identification and assess antimicrobial resistance patterns, which are critical for guiding empirical therapy and outbreak response. The detection of *S. typhi* in vended water represents a sentinel event that should prompt immediate public health action, including enhanced surveillance for typhoid fever, vendor education and certification, and the promotion of household water treatment to prevent further transmission.

Study Limitations

This study has several limitations. The single-week sampling period captured only a snapshot of water quality and did not account for seasonal variability, which may influence bacterial loads. Additionally, bacterial identification relied on morphological and biochemical methods, which provide presumptive identification without molecular confirmation. The plate count method also detects only culturable bacteria, excluding viable but non-culturable organisms. These findings should therefore be interpreted as conservative estimates of contamination, and future studies should incorporate longitudinal sampling and molecular techniques.

5. Conclusion

Vended water in Ogbia Main Town is universally and heavily contaminated with faecal and enteric pathogens, with no sample meeting WHO drinking water standards. The detection of *Salmonella typhi* in one-quarter of isolates represents a sentinel public health threat, and the assumption that vended water is safer than tap water is unfounded. Immediate implementation of point-of-use water treatment, mandatory microbial testing of vended water with specific screening for *S. typhi*, vendor certification and regulation, and sustained investment in water safety infrastructure are urgently needed to prevent the preventable burden of typhoid fever and diarrheal disease in the community.

Recommendations

Mandatory chlorination of vended water should be implemented with subsidized chlorine tablets for vendors. Routine microbial monitoring of all vendors should be conducted monthly with results reported publicly, and vendor certification with hygiene training should be established. In the medium term, community water safety planning, point-of-use filtration infrastructure, and enhanced local laboratory capacity should be developed. In the long term, vended water should be integrated into formal regulatory oversight with licensing and enforcement, accompanied by community-based surveillance and longitudinal research to assess seasonal contamination patterns and intervention effectiveness.

Article Information

Ethical Approval: Ethical approval for this study was obtained from the Bayelsa State College of Health Technology Research Ethics Committee with approval number BAYCHT/ERC/2024/017.

Data Availability: The datasets generated and/or analyzed during the current study are available from the corresponding author upon reasonable request.

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