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Unseen Threats in Our Water: Assessing Bacterial Contamination in Institutional Tap Water and Vended Water (Meruwa) in Otuogidi-Ogbia and Ogbia Main Town, Bayelsa State, Nigeria

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Abstract

Rationale: Safe drinking water is essential for human health, yet bacterial contamination remains a pervasive challenge in resource-limited settings. In the Niger Delta region of Nigeria, aging infrastructure, environmental degradation, and inadequate water quality monitoring contribute to persistent waterborne disease burden. However, no prior study has systematically characterized and compared bacterial contamination in both institutional tap water and informal vended water (Meruwa) in this region, leaving critical evidence gaps for policy and intervention. **Objectives**: This study aimed to: (i) assess the presence, types, and levels of bacterial contamination in tap water from Bayelsa State College of Health Technology and vended water from Ogbia Main Town; (ii) compare contamination levels and bacterial species distribution between the two water sources; (iii) evaluate compliance with World Health Organization (WHO) drinking water standards; and (iv) provide evidence-based recommendations for water safety interventions. **Methods**: A total of 47 water samples were analyzed, 23 tap water samples from six campus points and 24 vended water samples from vendors in Ogbia Main Town. Total bacterial counts (TBC) and total coliform counts (TCC) were determined using the plate count method on nutrient agar and MacConkey agar, respectively. Bacterial isolates were identified through Gram staining and biochemical characterization (catalase, coagulase, oxidase, citrate, urease, indole, Kligler iron agar, motility). Compliance was assessed against WHO guidelines (0 CFU/100 mL for coliforms; <500 CFU/mL for heterotrophic bacteria). **Results**: All samples exceeded WHO standards. Tap water TBC ranged from 3.50×10^6 to 5.00×10^6 CFU/mL (mean 4.32×10^6), and TCC ranged from 3.00×10^6 to 3.80×10^6 CFU/mL (mean 3.21×10^6). Vended water TBC ranged from 3.50×10^6 to 5.30×10^6 CFU/mL (mean 4.24×10^6), and TCC ranged from 3.00×10^6 to 4.00×10^6 CFU/mL (mean 3.21×10^6). No significant difference was observed between water sources for TBC ($p = 0.642$) or TCC ($p = 0.981$). Bacterial isolates from tap water included *Escherichia coli* (28.0%), *Staphylococcus aureus* (28.0%), *Pseudomonas aeruginosa* (20.0%), *Klebsiella pneumoniae* (12.0%), and *Enterobacter aerogenes* (12.0%). Vended water isolates comprised *E. coli* (33.3%), *Salmonella typhi* (25.0%), *K. pneumoniae* (20.8%), and *Citrobacter freundii* (20.8%). Species distribution differed significantly between sources ($\chi^2 = 24.18$, $p = 0.0005$). Compliance with WHO microbial standards was 0% for both water sources. **Conclusion**: Institutional tap water and vended water in the study area are universally and heavily contaminated with faecal and opportunistic pathogens, including *S. typhi*. Both water sources pose substantial health risks, and the widespread assumption that vended water is safer is unfounded. **Recommendation**: Immediate implementation of routine microbial monitoring, mandatory water treatment for both sources, vendor certification, and targeted hygiene interventions is essential to prevent waterborne disease outbreaks and protect public health. Thus, consumption of untreated water from either source carries risks of acute gastroenteritis, typhoid fever, and opportunistic infections, with particular vulnerability among

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children, the elderly, and immunocompromised individuals, representing a preventable public health crisis that demands urgent multisectoral action.

Keywords: bacterial contamination**;** *Escherichia coli*; *Salmonella typhi*; tap water; vended water; coliforms; microbial water quality; Niger delta; water safety; public health

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 (Raimi et al., 2017; Olalekan et al., 2018a, b, c; Oyibo et al., 2025). 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 (Agbendeh & Ogbonna, 2022; Nicholas & Raimi, 2025a, b; Iyoha et al., 2025). 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 (Olalekan et al., 2020; Raimi & Sawyerr, 2022; Raimi et al., 2022a, b, c; Opaminola & Raimi, 2025). 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 (Edberg et al., 1996; Raimi & Sabinus, 2017; Odipe et al., 2018). In institutional settings such as schools and colleges, where populations are concentrated and water consumption is high, contaminated water poses particular risks for outbreaks and endemic transmission (Justice-Alucho et al., 2021; El-Sheekh & Hamoud, 2021; Fekeda & Gutema, 2025; Omotoso et al., 2025). Moreover, 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 (Agbendeh & Ogbonna, 2022; Iman Alsarhan & Sedat Cam, 2023; Oyibo et al., 2025). However, limited empirical data exist to support this assumption, and the relative microbial quality of institutional tap water versus 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 (Odipe et al., 2018; Olalekan et al., 2022; Hameda-Khadem Zgair, 2024; Bear et al., 2024). 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 (Ifeanyichukwu et al., 2022; Clinton-Ezekwe et al., 2024a, b; Raimi et al., 2022a, b, c). 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 (Adesakin et al., 2020; Raimi et al., 2022b; Lateefat et al., 2022a, b; Fekeda & Gutema, 2025). Despite growing recognition of water quality challenges in Bayelsa State, critical knowledge gaps persist. Specifically, no prior study has systematically characterized and compared bacterial contamination in both institutional tap water and locally vended water (Meruwa) within Otuogidi-Ogbia and Ogbia Main Town. Furthermore, the spatial distribution of contamination across multiple campus tap points and the diversity of bacterial species in vended water have 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 with the following objectives: (i) to assess the presence, types, and levels of bacterial contamination in tap water from Bayelsa State College of Health Technology and vended water (Meruwa) from Ogbia Main Town; (ii) to compare contamination levels and bacterial species distribution between the two water sources; (iii) to evaluate compliance with WHO drinking water quality standards; and (iv) to provide evidence-based recommendations for improving water safety. Using standard microbiological techniques, including total bacterial and coliform enumeration on

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nutrient and MacConkey agar, followed by morphological and biochemical characterization of isolates, this study provides a comprehensive assessment of microbial water quality that integrates both institutional and 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. Methodology

2.1. Study Area

The study was conducted at Bayelsa State College of Health Technology, Otuogidi-Ogbia, a prominent institution focused on health education and training in Bayelsa State, Nigeria. The school is located within the Otuogidi community of Ogbia Local Government Area, East Senatorial District, at coordinates 4°39′00″N and 6°16′00″E. The area covers approximately 695 km² 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 (Olalekan et al., 2018a, 2018b, 2018c; Kader et al., 2023a, b). 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 (Olalekan et al., 2019a; Raimi et al., 2017).

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 taps and vended sources at a specific point in time (Edberg et al., 1996; Destiani & Templeton, 2018; Agbendeh & Ogbonna, 2022). This design allowed for the characterization of water quality across multiple sampling points to generate a comprehensive understanding of potential microbial hazards in both institutional and community water sources (Olalekan et al., 2019b; Fekeda & Gutema, 2025).

2.3. Sampling Techniques

Simple random sampling was used to select sampling points and bacterial isolates. This method ensures each water source or vended container has an equal probability of selection, reducing bias and providing a representative dataset. A total of 47 water samples were collected to ensure representation across all accessible taps and vendors, comprising 23 tap water samples from distinct points within the college campus and 24 vended water (Meruwa) samples from vendors operating in Ogbia Main Town.

2.4. Sample Size Justification

A total of 47 water samples were collected to ensure comprehensive representation of the water sources under investigation. This sample size was determined based on the total number of accessible tap water points within the college campus (23 points) and the number of active water vendors operating in Ogbia Main Town during the study period (24 vendors). The sample size was considered adequate to characterize bacterial contamination patterns and enable comparative analysis between water sources, consistent with similar microbiological water quality studies in resource-limited settings (Agbendeh & Ogbonna, 2022; Fekeda & Gutema, 2025; Nicholas & Raimi, 2025b).

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2.5. Tap Water Sample Collection

Water samples were collected aseptically using sterile 100 mL screw-capped plastic universal containers. Before collection, containers were sterilized by autoclaving at 121 °C for 15 minutes and rinsed with 70% ethanol, followed by sterile distilled water (Abdu et al., 2019; Bear et al., 2024). Each sample was labeled with a unique identifier denoting the source, sampling point, and date of collection. Tap water samples were collected from 23 distinct points across the Bayelsa State College of Health Technology campus, comprising: 5 samples from Boys' Hostel, 5 samples from the Water Board (point of entry into campus distribution system), 5 samples from Girls' Hostel A, 5 samples from Girls' Hostel B, 2 samples from the Library, and 1 sample from the Community Health Hall. The reduction from the originally planned 25 samples to 23 occurred because two sampling points (one from the Library and one from the Community Health Hall) were temporarily inaccessible due to ongoing maintenance activities during the collection period. All samples were collected after allowing water to run for 2 minutes to ensure representative sampling from the distribution system (Seki et al., 2024; Ulla et al., 2025). Samples were transported in a cool box maintained at 4 °C and analyzed within 24 hours of collection. Sample collection was conducted over a period of one week (Monday to Saturday) to capture typical weekly variation in water usage patterns.

2.6. 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 (n=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 (borehole, n=16; municipal supply, n=5; surface water, n=3) and storage container type (plastic jerry cans, n=18; metal drums, 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 (Oyibo et al., 2025; Seki et al., 2024; Kader et al., 2023a, b). 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.

2.7. Sample Processing

2.7.1. Culturing of Samples

Bacteria were isolated using the spread plate method on MacConkey agar (for coliform enumeration and isolation) and 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 to absorb the inoculum before inverted incubation at 37 °C for 24 hours (Destiani & Templeton, 2018; Bear et al., 2024; Edberg et al., 1996). Following incubation, distinct colonies were subcultured onto fresh nutrient agar plates to obtain pure isolates, which were subsequently inoculated into peptone broth for further biochemical characterization (Abdu et al., 2019; Fekeda & Gutema, 2025).

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2.7.2. Morphological Characterization

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: a smear of each isolate was prepared on a clean glass slide, air-dried, heat-fixed, and sequentially stained with crystal violet (1 minute), Gram's iodine (1 minute), decolorized with 95% acetone-alcohol (10 seconds), and counterstained with neutral red (1 minute). Slides were examined under 100× oil immersion to determine Gram reaction and cellular morphology (Haciseyitoğlu et al., 2015; Fekeda & Gutema, 2025).

2.7.3. Biochemical Characterization

Biochemical testing was performed on all pure isolates using standard protocols to enable species-level identification. The following tests were conducted:

Catalase Test

A loopful of bacterial growth was transferred to a clean glass slide and mixed with 3% hydrogen peroxide. Immediate bubble formation indicated a positive catalase reaction (Haciseyitoğlu et al., 2015).

Coagulase Test

For Gram-positive isolates, the slide coagulase test was performed by emulsifying a loopful of colonies in a drop of rabbit plasma on a glass slide. Clumping within 10 seconds indicated a positive reaction (Raimi et al., 2022a, b, c).

Oxidase Test

Oxidase reagent (tetramethyl-p-phenylenediamine dihydrochloride) was applied to filter paper, and a loopful of bacterial growth was streaked onto the impregnated area. Development of a purple color within 30 seconds indicated a positive oxidase reaction (Haciseyitoğlu et al., 2015).

Citrate Utilization Test

Isolates were inoculated onto Simmons citrate agar slants and incubated at 37 °C for 24-48 hours. Growth with a color change from green to blue indicated positive citrate utilization (Fekeda & Gutema, 2025; Raimi et al., 2023).

Urease Test

Isolates were inoculated onto Christensen's urea agar slants and incubated at 37 °C for 24-48 hours. Development of a pink color indicated urease production (Olalekan et al., 2023).

Indole Production Test

Isolates were inoculated into tryptone broth and incubated at 37 °C for 24-48 hours. Kovac's reagent was added; development of a red ring at the surface indicated indole production (Fekeda & Gutema, 2025).

Kligler Iron Agar (KIA) Test

Isolates were stab-inoculated into KIA slants and incubated at 37 °C for 24 hours. The test assessed glucose and lactose fermentation (indicated by yellow color change in butt and slant, respectively), gas production (bubble formation or cracking of agar), and hydrogen sulfide (H_2S) production (black precipitate) (Haciseyitoğlu et al., 2015; Raimi & Sawyerr, 2022).

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Motility Test

Isolates were stab-inoculated into semi-solid nutrient agar (0.4% agar) and incubated at 37 °C for 24-48 hours. Diffuse growth radiating from the stab line indicated motility; growth confined to the stab line indicated non-motility (Fekeda & Gutema, 2025).

2.8. Sample Preparation for Bacteriological Enumeration

The standard plate count method was used to enumerate viable bacteria (Bear et al., 2024; Edberg et al., 1996). 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 15-20 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 24-48 hours (Destiani & Templeton, 2018; Fekeda & Gutema, 2025).

2.9. Determination of Bacteriological Quality

2.9.1. Total Bacterial Count (TBC)

Total bacterial counts were determined using nutrient agar plates. After incubation at 37 °C for 24-48 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 (>300 colonies) while higher dilutions yielded insufficient colonies (<30 colonies) for accurate quantification (Raimi & Sabinus, 2017; Bear et al., 2024). TBC was calculated using the formula:

$$\text{TBC (CFU/mL)} = \frac{\text{Number of colonies} \times \text{Dilution factor}}{\text{Volume plated (mL)}}$$

Results were expressed as colony-forming units per milliliter (CFU/mL). Plates with >300 colonies were recorded as "too numerous to count" (TNTC), while plates with <30 colonies were recorded as "too few to count" (TFTC) (Fekeda & Gutema, 2025).

2.9.2. Total Coliform Count (TCC)

Total coliform counts were determined using MacConkey agar plates, which selectively culture Gram-negative enteric bacteria and differentiate lactose fermenters (pink colonies) from non-fermenters (colorless colonies). After incubation at 37 °C for 24-48 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 (Olalekan et al., 2020; Fekeda & Gutema, 2025). TCC was calculated using the same formula as TBC:

$$\text{TCC (CFU/mL)} = \frac{\text{Number of pink colonies} \times \text{Dilution factor}}{\text{Volume plated (mL)}}$$

2.9.3. Confirmation of Coliforms and Faecal Coliforms

Presumptive coliform isolates from MacConkey agar were confirmed by subculturing onto eosin methylene blue (EMB) agar, where coliforms produce characteristic dark-centered colonies with a metallic sheen. For faecal coliform confirmation, isolates were inoculated into EC (Escherichia coli) broth and incubated at 44.5 °C for 24 hours. Gas production at this elevated temperature indicated the presence of thermotolerant (faecal) coliforms (Edberg et al., 1996; Fekeda & Gutema, 2025). *Escherichia coli* was confirmed using the indole test, where isolates producing indole from tryptophan were identified as *E. coli* (Haciseyitoğlu et al., 2015; Othieno Odwori & Wanambacha Wakhungu, 2023).

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2.10. Quality Control

Quality control measures were implemented throughout the study to ensure accuracy and reproducibility of results (Raimi et al., 2022a; Raimi & Sawyerr, 2022). Sterility checks were performed by incubating uninoculated nutrient agar and MacConkey agar plates at 37 °C for 24 hours; absence of growth confirmed media sterility. Positive controls using reference strains (*Escherichia coli* ATCC 25922, *Staphylococcus aureus* ATCC 25923, *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; coefficients of variation were consistently below 10%, indicating good analytical precision (Abdu et al., 2019; Henrietta et al., 2023; Bear et al., 2024; Abdulmalik & Mohammed, 2025).

2.11. Data Analysis and Statistical Methods

Data were entered into Microsoft Excel (Version 2021) and analyzed using SPSS (Version 27.0, 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 (Nicholas & Raimi, 2025b; Omotoso et al., 2025). For comparative analyses, tap water and vended water were treated as independent cohorts. Differences in TBC and TCC between water sources were assessed using independent samples t-tests after confirming normality with the Shapiro-Wilk test; for non-normally distributed data, the Mann-Whitney U test was employed. Differences in TBC and TCC across tap water sampling points were assessed using one-way analysis of variance (ANOVA), followed by Tukey's post-hoc test for pairwise comparisons where applicable. The association between water source (tap vs. vended) and bacterial species distribution was assessed using the chi-square (χ^2) test of independence. Statistical significance was set at $p < 0.05$ for all analyses (Raimi et al., 2022b; Olalekan et al., 2023). Compliance with WHO drinking water quality guidelines was assessed by comparing TBC, TCC, and faecal coliform presence against established benchmarks: total coliforms = 0 CFU/100 mL; faecal coliforms = 0 CFU/100 mL; heterotrophic plate count <500 CFU/mL (World Health Organization, 2022). Samples were classified as compliant if they met all three criteria; otherwise, they were classified as non-compliant.

2.12. Ethical Considerations

Ethical approval for this study was obtained from the Bayelsa State College of Health Technology Research Ethics Committee (approval number: BAYCHT/ERC/2024/017). Permission to collect water samples was obtained from the college administration and 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 (Elemuwa et al., 2025; Enang et al., 2025a).

3. Results

A total of 47 water samples were analyzed, comprising 23 tap water samples from Bayelsa State College of Health Technology, Otuogidi-Ogbia, and 24 vended water (Meruwa) samples from Ogbia Main Town (Table 1 & Figure 1 below). The total bacterial count (TBC) in tap water ranged from 3.50×10^6 to 5.00×10^6 CFU/mL, with a mean of 4.32×10^6 CFU/mL (SD ± 0.54×10^6), while the total coliform count (TCC) ranged from 3.00×10^6 to 3.80×10^6 CFU/mL, with a mean of 3.21×10^6 CFU/mL (SD ± 0.24×10^6). For vended water, TBC ranged from 3.50×10^6 to 5.30×10^6 CFU/mL (mean ± SD: 4.24×10^6 ± 0.68×10^6 CFU/mL), and TCC ranged from 3.00×10^6 to 4.00×10^6 CFU/mL (mean ± SD: 3.21×10^6 ±

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0.31 × 10^6 CFU/mL). Statistical comparison revealed no significant difference between tap and vended water for either TBC (independent samples t-test, p = 0.642) or TCC (p = 0.981), indicating that both water sources harbor comparable levels of microbial contamination despite their distinct supply chains and handling practices.

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

Water Source	n	Parameter	TBC (CFU/mL)	TCC (CFU/mL)
Tap Water	23	Mean ± SD	4.32 × 10^6 ± 0.54 × 10^6	3.21 × 10^6 ± 0.24 × 10^6
		Median (IQR)	4.40 × 10^6 (3.80-4.80 × 10^6)	3.20 × 10^6 (3.00-3.40 × 10^6)
		Range	3.50-5.00 × 10^6	3.00-3.80 × 10^6
Vended Water	24	Mean ± SD	4.24 × 10^6 ± 0.68 × 10^6	3.21 × 10^6 ± 0.31 × 10^6
		Median (IQR)	4.05 × 10^6 (3.80-4.80 × 10^6)	3.15 × 10^6 (3.00-3.35 × 10^6)
		Range	3.50–5.30 × 10^6	3.00-4.00 × 10^6
p-value[1]			0.642	0.981

[1] Independent samples t-test (Mann-Whitney U test for non-parametric comparison); no significant difference between tap and vended water for either TBC or TCC (p > 0.05). **Note:** All values exceed the WHO drinking water guideline of 0 CFU/100 mL for coliforms and heterotrophic plate count standard of <500 CFU/mL.

Figure 1. Descriptive statistics of Bacterial counts showing the Mean ± SD for both TBC and TCC across Tap and Vended Water samples.

Table 2 & Figure 2 presents the total bacterial count (TBC) and total coliform count (TCC) across six distinct sampling points within the Bayelsa State College of Health Technology campus, comprising 23 tap water samples. The highest mean TBC was observed at the Community Health Hall (4.80 × 10^6 CFU/mL, n=1), followed by the Boys' Hostel (4.40 × 10^6 ± 0.55 × 10^6 CFU/mL, n=5) and the Water Board (4.34 × 10^6 ± 0.59 × 10^6 CFU/mL, n=5). The lowest mean TBC was recorded at Girls' Hostel B (4.18 × 10^6 ± 0.58 × 10^6 CFU/mL, n=5) and Girls' Hostel A (4.22 × 10^6 ± 0.49 × 10^6 CFU/mL, n=5). For TCC, the Water Board exhibited the highest mean (3.42 × 10^6 ± 0.33 × 10^6 CFU/mL), while the Boys' Hostel recorded the lowest (3.16 × 10^6 ± 0.21 × 10^6 CFU/mL). One-way analysis of variance revealed no statistically significant differences in TBC across sampling points ($F(5,17) = 0.32$, $p = 0.892$) or in TCC across sampling points ($F(5,17) = 0.84$, $p = 0.536$), indicating that despite observed numerical variations, bacterial contamination levels are uniformly elevated across all campus water access points.

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Table 2. Total Bacterial Count (TBC) and Total Coliform Count (TCC) by Sampling Point-Tap Water.

Sampling Point	n	TBC (CFU/mL)	TCC (CFU/mL)
		Mean ± SD	Mean ± SD
Boys' Hostel	5	$4.40 \times 10^6 \pm 0.55 \times 10^6$	$3.16 \times 10^6 \pm 0.21 \times 10^6$
Water Board	5	$4.34 \times 10^6 \pm 0.59 \times 10^6$	$3.42 \times 10^6 \pm 0.33 \times 10^6$
Girls' Hostel A	5	$4.22 \times 10^6 \pm 0.49 \times 10^6$	$3.18 \times 10^6 \pm 0.18 \times 10^6$
Girls' Hostel B	5	$4.18 \times 10^6 \pm 0.58 \times 10^6$	$3.20 \times 10^6 \pm 0.27 \times 10^6$
Library	2	$4.25 \times 10^6 \pm 1.06 \times 10^6$	$3.15 \times 10^6 \pm 0.07 \times 10^6$
Community Health Hall	1	4.80×10^6	3.40×10^6
Total	**23**	$\mathbf{4.32 \times 10^6 \pm 0.54 \times 10^6}$	$\mathbf{3.21 \times 10^6 \pm 0.24 \times 10^6}$

One-way ANOVA: TBC across sampling points, $F(5,17) = 0.32$, $p = 0.892$; TCC across sampling points, $F(5,17) = 0.84$, $p = 0.536$. No significant differences between sampling points.

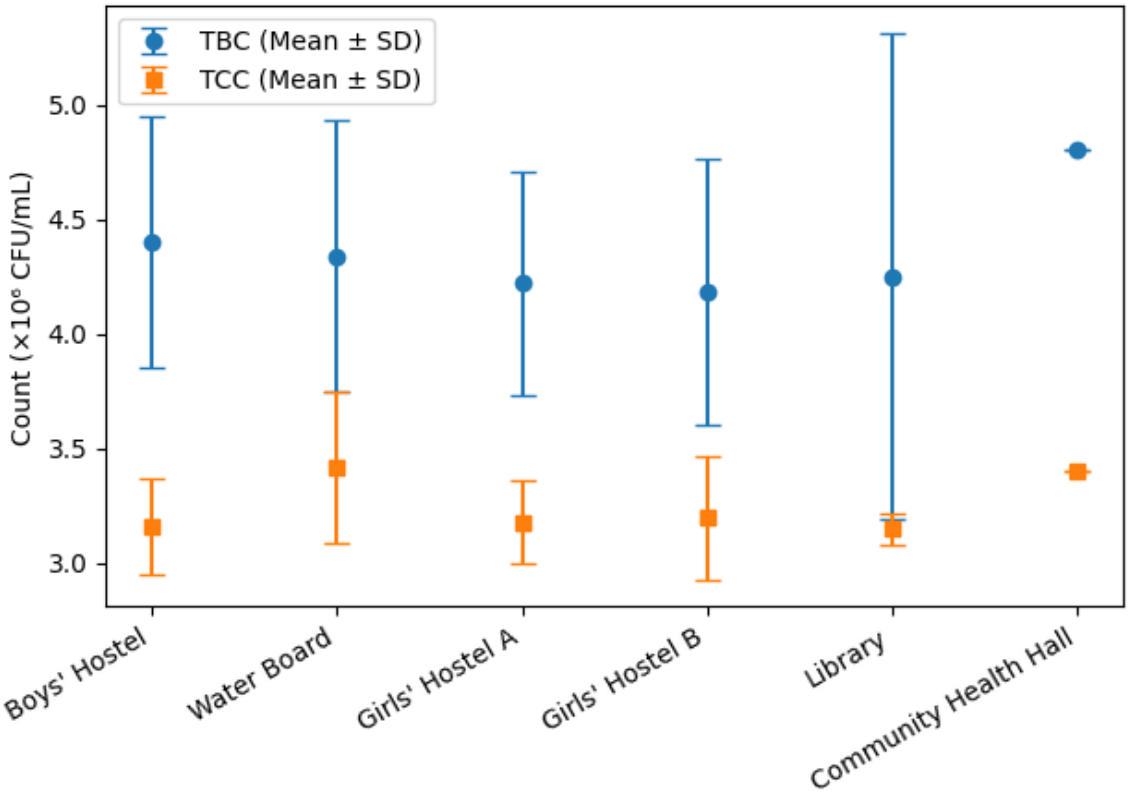

Figure 2. Bacterial Counts by Sampling Point (Tap Water).

Table 3 & Figure 3 presents the morphological and biochemical characteristics of 25 bacterial isolates recovered from tap water samples across the Bayelsa State College of Health Technology campus. The isolates were identified as five distinct species: *Escherichia coli* (n=7), *Staphylococcus aureus* (n=7), *Pseudomonas aeruginosa* (n=5), *Klebsiella pneumoniae* (n=3), and *Enterobacter aerogenes* (n=3). Gram staining revealed that all isolates except *S. aureus* were Gram-negative rods; *S. aureus* was identified as Gram-positive cocci. On MacConkey agar, *E. coli* and *S. aureus* produced pink colonies, while *P. aeruginosa* formed flat, opaque colonies, and both *K. pneumoniae* and *E. aerogenes* formed large, mucoid pink colonies. Biochemical profiling demonstrated species-specific patterns: *E. coli* was catalase-positive, indole-positive, and motile, with positive lactose and glucose fermentation; *S. aureus* was distinguished by positive coagulase and urease reactions; *P. aeruginosa* was uniquely oxidase-positive and citrate-positive while failing to ferment lactose or glucose; *K. pneumoniae* was citrate-positive, urease-positive, and produced gas from glucose; and *E. aerogenes* shared similar characteristics with *K. pneumoniae* but was urease-negative. All isolates were catalase-positive, and none produced hydrogen sulfide (H_2S).

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Table 3. Morphological and Biochemical Characteristics of Bacterial Isolates from Tap Water (n = 25 isolates).

Characteristic	*E. coli* (n=7)	*S. aureus* (n=7)	*P. aeruginosa* (n=5)	*K. pneumoniae* (n=3)	*E. aerogenes* (n=3)
Gram stain	– (rod)	+ (cocci)	– (rod)	– (rod)	– (rod)
MacConkey agar	Pink colonies	Thin pink colonies	Flat, opaque	Large mucoid, pink	Large mucoid, pink
Catalase	+	+	+	+	+
Coagulase	–	+	–	–	–
Oxidase	–	–	+	–	–
Citrate	–	–	+	+	+
Urease	–	+	–	+	–
Indole	+	–	–	–	–
Lactose fermentation	+	+	–	+	+
Glucose fermentation	+	+	–	+	+
H_2S production	–	–	–	–	–
Gas production	+	+	–	+	+
Motility	+	–	+	+	+

Key: + = positive reaction; – = negative reaction.

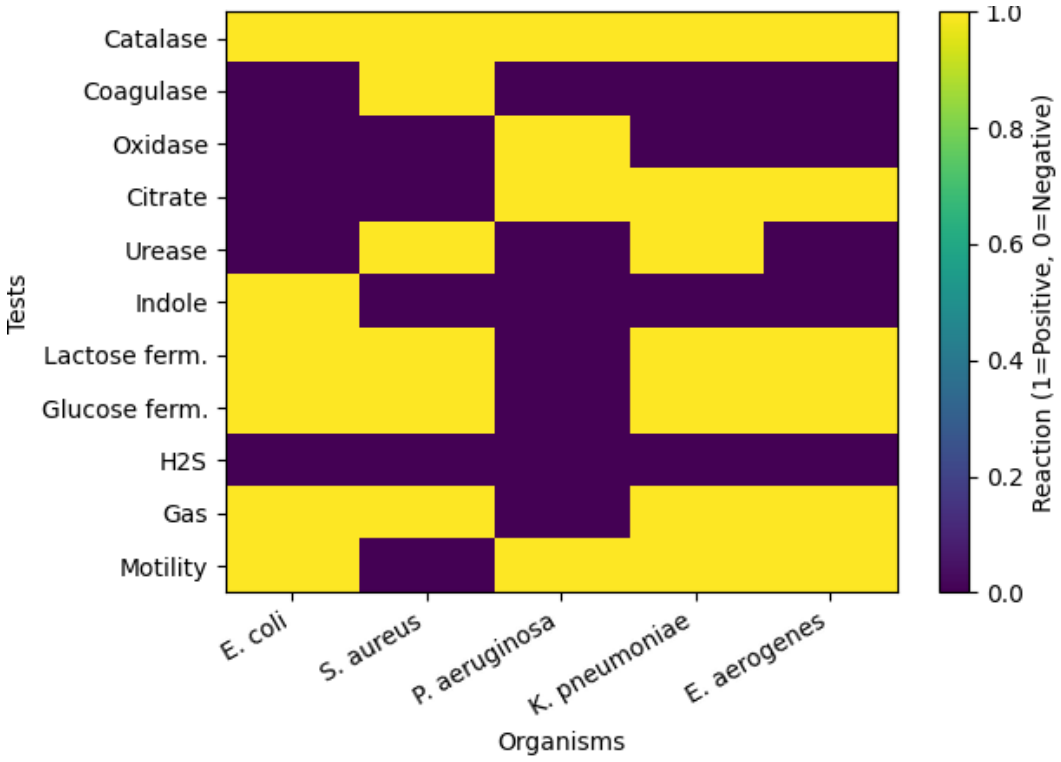

Figure 3. Heatmap matrix showing morphological and biochemical characterization data. **Notes:** Bright cells = **positive reactions**; Dark cells = **negative reactions**; Each column = organism profile; Each row = biochemical test.

Table 4 & Figure 4 presents the occurrence of bacterial isolates across six sampling points within the Bayelsa State College of Health Technology campus, based on 23 tap water samples. *Escherichia coli* was detected at all six sampling points: Boys' Hostel, Water Board, Girls' Hostel A, Girls' Hostel B, Library, and Community Health Hall, demonstrating its ubiquitous presence throughout the

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campus water distribution network. *Staphylococcus aureus* was detected at three sampling points: Boys' Hostel, Water Board, and Girls' Hostel A, but was notably absent from Girls' Hostel B, Library, and Community Health Hall. *Pseudomonas aeruginosa* was recovered exclusively from two sampling points: Water Board and Community Health Hall. *Klebsiella pneumoniae* was detected at three sampling points: Boys' Hostel, Girls' Hostel A, and Library. *Enterobacter aerogenes* was identified at two sampling points: Girls' Hostel B and Library. This spatial distribution reveals distinct patterns of bacterial occurrence, with *E. coli* serving as the only organism present across all sampling points, while the remaining four species exhibited variable and non-uniform distributions.

Table 4. Occurrence of Bacterial Isolates in Tap Water by Sampling Point.

Sampling Point	*E. coli*	*S. aureus*	*P. aeruginosa*	*K. pneumoniae*	*E. aerogenes*
Boys' Hostel (n=5)	+	+	–	+	–
Water Board (n=5)	+	+	+	–	–
Girls' Hostel A (n=5)	+	+	–	+	–
Girls' Hostel B (n=5)	+	–	–	–	+
Library (n=2)	+	–	–	+	+
Community Health Hall (n=1)	+	–	+	–	–

Key: + = detected in at least one sample from this point; – = not detected.

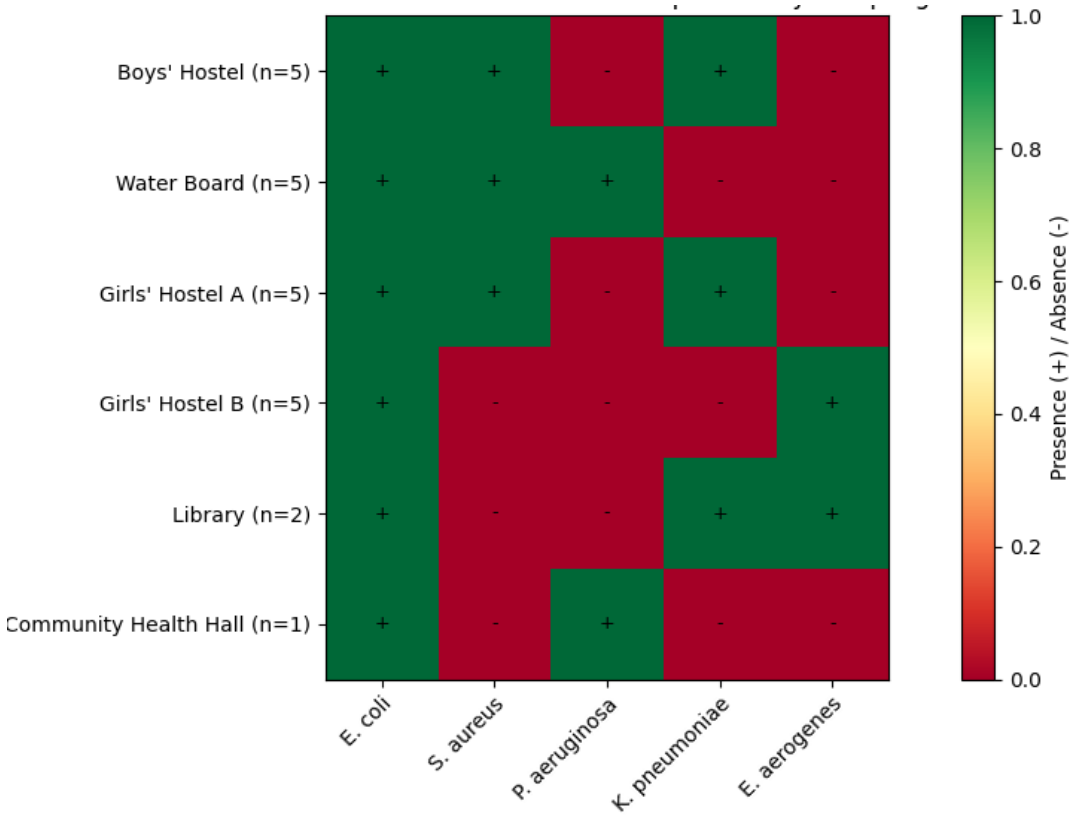

Figure 4. Occurrence of Bacterial Isolates in Tap Water by Sampling Point.

Table 5 & Figure 5 present the prevalence of bacterial isolates recovered from tap water samples across the Bayelsa State College of Health Technology campus, based on 25 bacterial isolates identified from 23 water samples. *Escherichia coli* and *Staphylococcus aureus* were the most prevalent species, each accounting for 7 isolates, representing 28.0% (95% CI: 12.1-49.4%) of the total isolates. *Pseudomonas aeruginosa* constituted 20.0% (5 isolates; 95% CI: 6.8-40.7%), while *Klebsiella pneumoniae* and *Enterobacter aerogenes* each accounted for 12.0% (3 isolates each; 95% CI: 2.5-31.2%). The predominance of *E. coli* and *S. aureus*, collectively representing more than half (56.0%) of all isolates, indicates that these two species are the dominant bacterial contaminants in the campus tap water

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supply. The prevalence pattern reveals a hierarchical distribution, with *E. coli* and *S. aureus* co-dominant, followed by *P. aeruginosa*, with *K. pneumoniae* and *E. aerogenes* representing the least frequently recovered species.

Table 5. Prevalence of Bacterial Isolates in Tap Water.

Bacterial Species	Number of Isolates	Prevalence (%)	95% Confidence Interval
Escherichia coli	7	28.0	12.1–49.4
Staphylococcus aureus	7	28.0	12.1–49.4
Pseudomonas aeruginosa	5	20.0	6.8–40.7
Klebsiella pneumoniae	3	12.0	2.5–31.2
Enterobacter aerogenes	3	12.0	2.5–31.2
Total	**25**	**100**	

Note: Prevalence calculated as (number of isolates of species / total isolates) × 100. Confidence intervals calculated using the Wilson score method for binomial proportions.

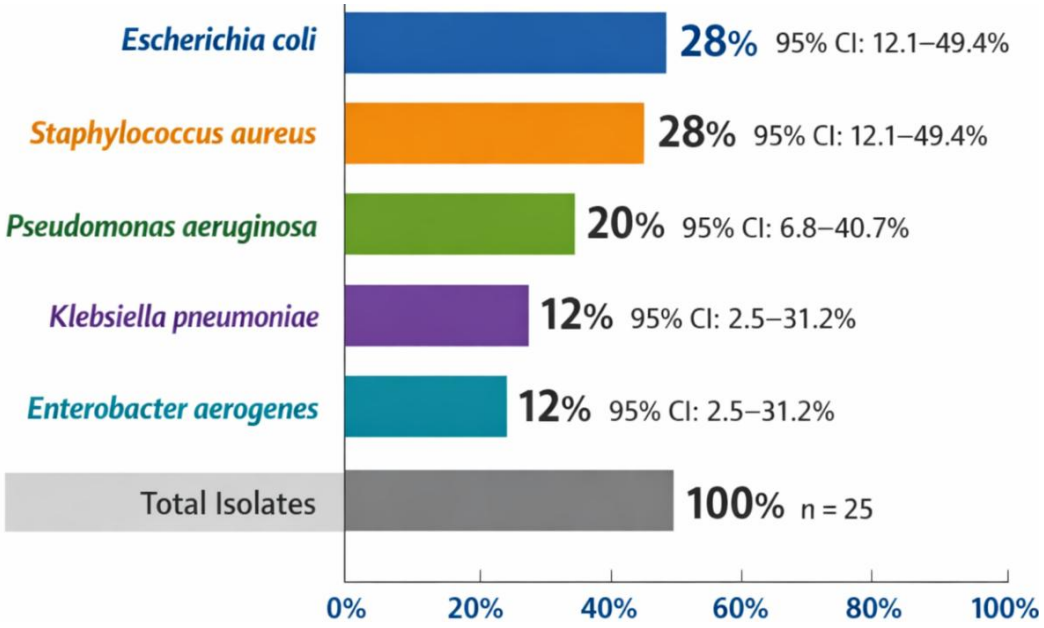

Figure 5. Prevalence of Bacterial Isolates in Tap Water.

Table 6 & Figure 6 present the total bacterial count (TBC) and total coliform count (TCC) for 24 vended water (Meruwa) samples collected from Ogbia Main Town. The TBC values ranged from 3.50 × 10^6 to 5.30 × 10^6 CFU/mL, with a mean of 4.24 × 10^6 CFU/mL (SD ± 0.68 × 10^6) and a median of 4.05 × 10^6 CFU/mL (interquartile range: 3.80-4.80 × 10^6). The TCC values ranged from 3.00 × 10^6 to 4.00 × 10^6 CFU/mL, with a mean of 3.21 × 10^6 CFU/mL (SD ± 0.31 × 10^6) and a median of 3.15 × 10^6 CFU/mL (interquartile range: 3.00-3.35 × 10^6). The highest TBC (5.30 × 10^6 CFU/mL) and TCC (4.00 × 10^6 CFU/mL) were recorded in samples VW-05, VW-11, VW-14, and VW-23, while the lowest TBC (3.50 × 10^6 CFU/mL) was observed in samples VW-01, VW-16, and VW-24. The coefficient of variation for TBC (16.0%) and TCC (9.7%) indicates 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.

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Table 6. 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 (3.80-4.80×10^6)**	**3.15×10^6 (3.00-3.35×10^6)**			

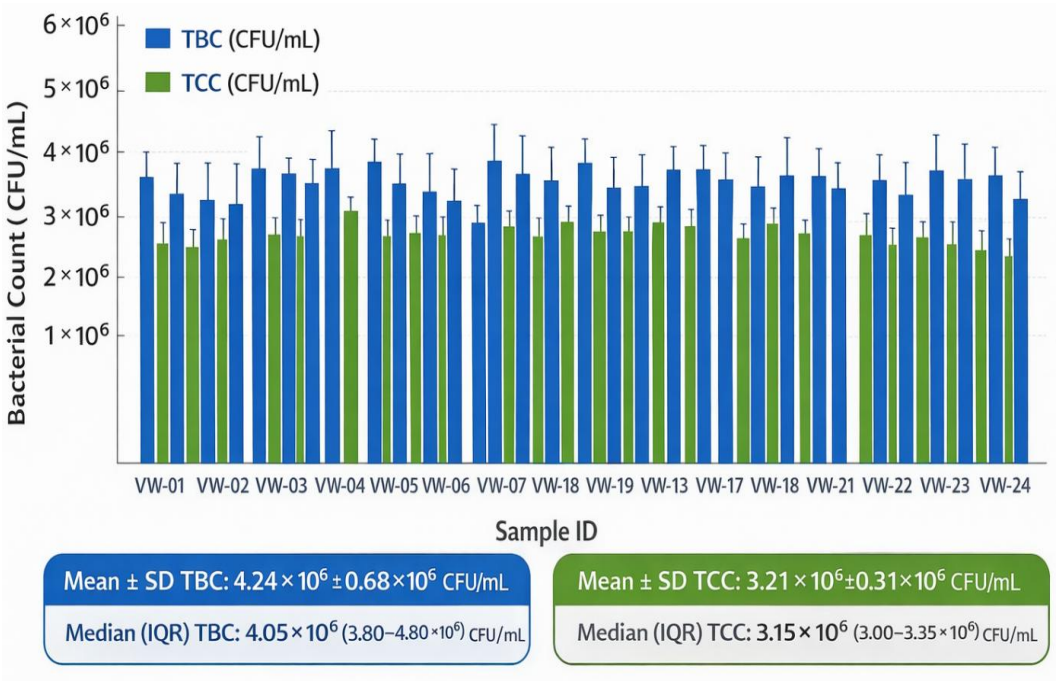

Figure 6. Total Bacterial Count (TBC) and Total Coliform Count (TCC) in Vended Water (Meruwa) Samples (n=24).

Table 7 & Figure 7 present 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: *Escherichia coli* (n=8), *Salmonella typhi* (n=6), *Klebsiella pneumoniae* (n=5), and *Citrobacter freundii* (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: *E. coli* was indole-positive, citrate-negative, and urease-negative; *S. typhi* was distinguished by positive citrate utilization, urease production, and H_2S production, the only isolate in the vended water cohort capable of producing

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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 7. 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	Large mucoid pink colonies	Round small smooth yellow 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).

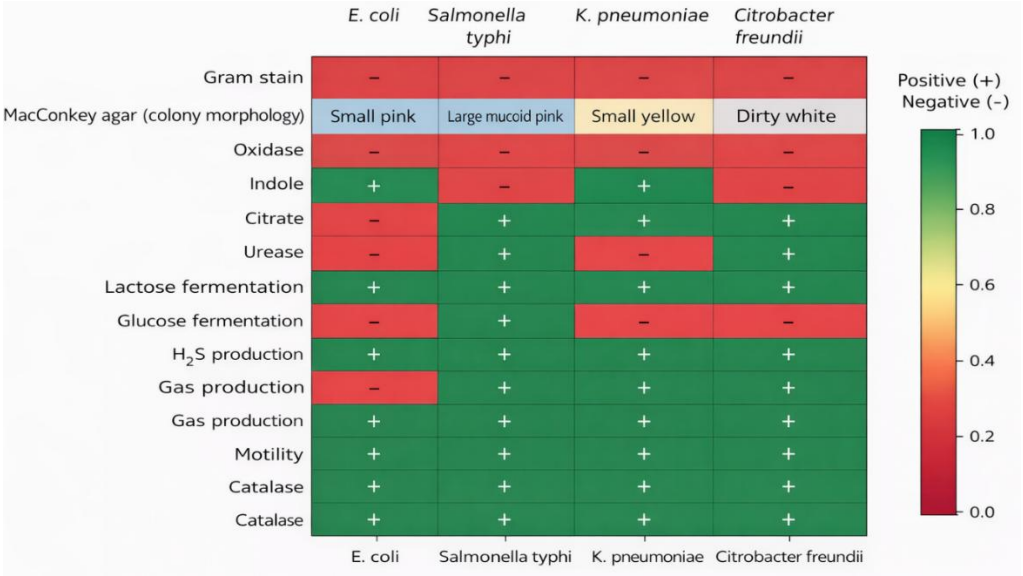

Figure 7. Morphological and Biochemical Characteristics of Bacterial isolates from Vended Water.

Table 8. & Figure 8 present 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, representing 33.3% (95% CI: 15.6-55.3%) of the total isolates. *Salmonella typhi* constituted 25.0% (6 isolates; 95% CI: 9.8-46.7%), while *Klebsiella pneumoniae* and *Citrobacter freundii*

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each accounted for 20.8% (5 isolates each; 95% CI: 7.1-42.2%). 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 8. 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**	

Note: Prevalence calculated as (number of isolates of species / total isolates) × 100.

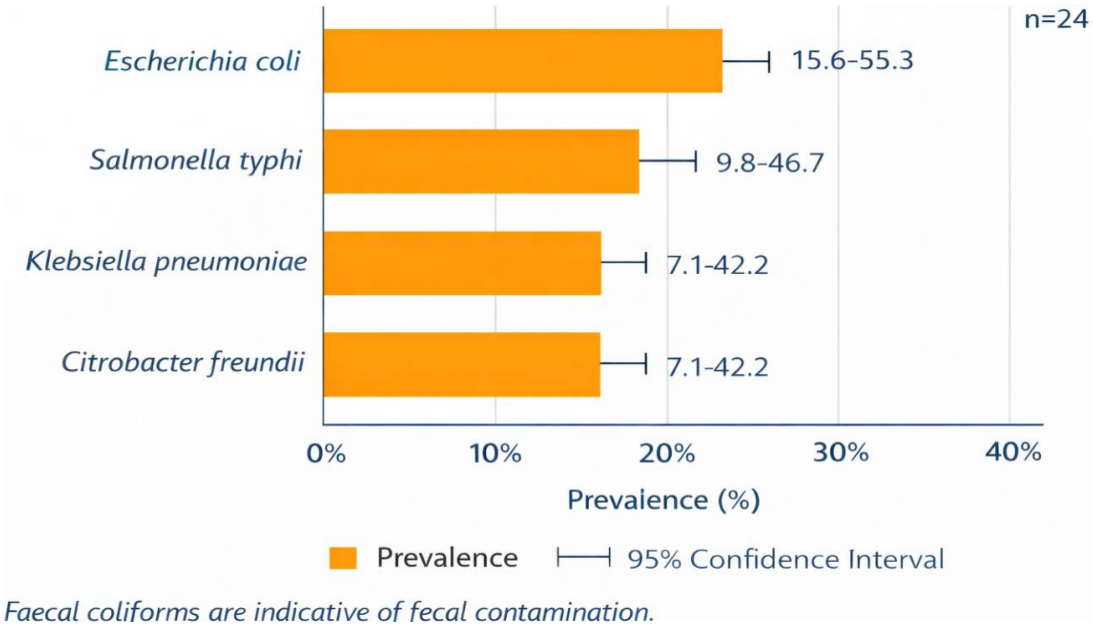

Figure 8. Prevalence of Bacterial Isolates in Vended Water (Meruwa).

Table 9 & Figure 9 present a comparative summary of bacterial isolates by water source, integrating data from 25 tap water isolates and 24 vended water isolates for a combined total of 49 isolates. *Escherichia coli* was the most frequently recovered species overall, accounting for 15 isolates (30.6% of the combined total), with comparable representation in tap water (7 isolates, 28.0%) and vended water (8 isolates, 33.3%). *Klebsiella pneumoniae* was the second most common overall (8 isolates, 16.3%), though its distribution varied by source: 3 isolates (12.0%) in tap water versus 5 isolates (20.8%) in vended water. Distinct species distributions were observed: *Staphylococcus aureus* (7 isolates, 28.0%), *Pseudomonas aeruginosa* (5 isolates, 20.0%), and *Enterobacter aerogenes* (3 isolates, 12.0%) were recovered exclusively from tap water. Conversely, *Salmonella typhi* (6 isolates, 25.0%) and *Citrobacter freundii* (5 isolates, 20.8%) were recovered exclusively from vended water. A chi-square test for association between water source and bacterial species distribution revealed a statistically

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significant difference ($\chi^2(6) = 24.18$, $p = 0.0005$), confirming that the microbial community composition differs substantially between tap water and vended water sources.

Table 9. Comparative Summary of Bacterial Isolates by Water Source.

Bacterial Species	Tap Water (n=25 isolates)	Vended Water (n=24 isolates)	Combined (n=49 isolates)
Escherichia coli	7 (28.0%)	8 (33.3%)	15 (30.6%)
Staphylococcus aureus	7 (28.0%)	0 (0%)	7 (14.3%)
Pseudomonas aeruginosa	5 (20.0%)	0 (0%)	5 (10.2%)
Klebsiella pneumoniae	3 (12.0%)	5 (20.8%)	8 (16.3%)
Enterobacter aerogenes	3 (12.0%)	0 (0%)	3 (6.1%)
Salmonella typhi	0 (0%)	6 (25.0%)	6 (12.2%)
Citrobacter freundii	0 (0%)	5 (20.8%)	5 (10.2%)

χ^2 test for association between water source and bacterial species distribution: $\chi^2(6) = 24.18$, $p = 0.0005$. Significant difference in bacterial community composition between tap and vended water.

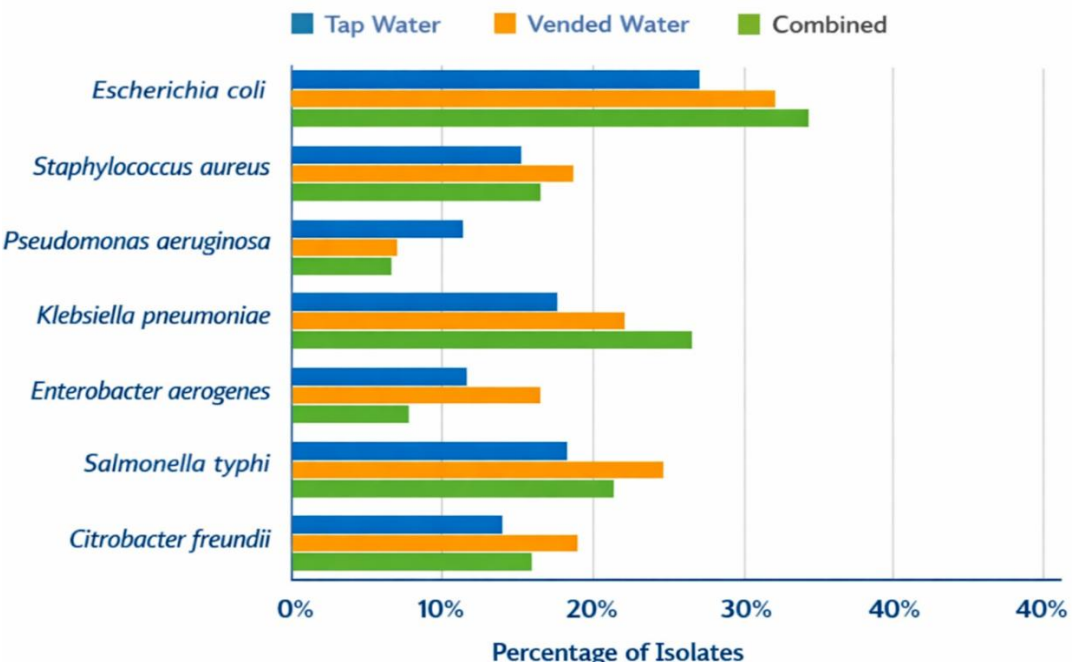

Figure 9. Comparison of Bacterial Isolates by Water Source.

Table 10 & Figure 10 present a comparative assessment of microbial contamination in tap water (n=23) and vended water (n=24) against World Health Organization (WHO) drinking water quality guidelines. For total coliforms, the WHO guideline mandates 0 CFU/100 mL; however, all tap water samples exhibited TCC values ranging from 3.00×10^6 to 3.80×10^6 CFU/mL, while vended water samples ranged 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; *E. coli* was detected in 30.4% (7 of 23) of tap water samples and 33.3% (8 of 24) of vended water samples, confirming widespread faecal contamination. For heterotrophic plate count (HPC), the WHO guideline specifies <500 CFU/mL; tap water HPC values ranged from 3.50×10^6 to 5.00×10^6 CFU/mL, and vended water 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 both water sources across all three parameters assessed, indicating that neither tap water nor vended water meets international benchmarks for microbiologically safe drinking water.

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Table 10. Comparison of Microbial Contamination with WHO Drinking Water Standards.

Parameter	Tap Water (n=23)	Vended Water (n=24)	WHO Guideline Value	Compliance (%)
Total Coliforms	3.00–3.80 × 10^6 CFU/mL	3.00–4.00 × 10^6 CFU/mL	0 CFU/100 mL	0%
Faecal Coliforms[1]	Present	Present	0 CFU/100 mL	0%
Heterotrophic Plate Count	3.50–5.00 × 10^6 CFU/mL	3.50–5.30 × 10^6 CFU/mL	<500 CFU/mL	0%

[1]*Escherichia coli* used as indicator of faecal contamination; detected in 30.4% (7/23) of tap water samples and 33.3% (8/24) of vended water samples.

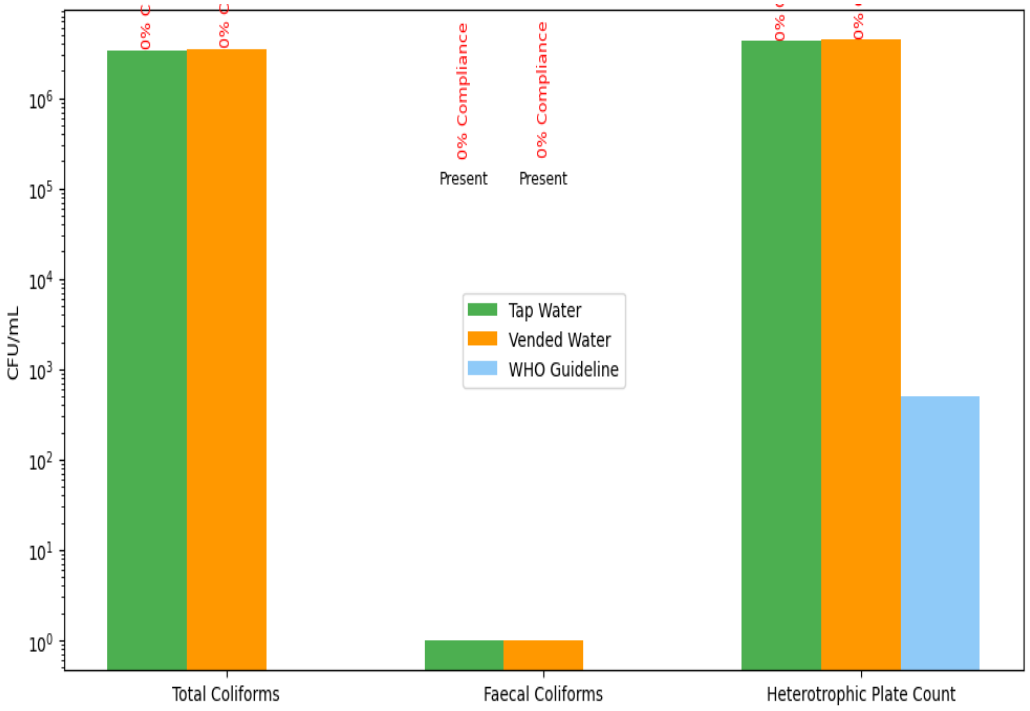

Figure 10. Comparison of Microbial Contamination with WHO Drinking Water Standards.

4. Discussion

4.1. Comparative Contamination Levels and Regulatory Non-Compliance

The finding that total bacterial and coliform counts in both tap and 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. (2018) documenting contamination in 78% of rural water sources, while Fekeda and Gutema (2025) found that household tap water in Ayana Town consistently violated WHO standards for total coliforms and heterotrophic bacteria. In Nigeria, Agbendeh and Ogbonna (2022) 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. (2023) documented elevated coliform counts in tap water from university hostels in Abuja, reinforcing that institutional water supplies across Nigeria face systemic microbial quality challenges. The absence of significant difference in contamination levels between tap and vended water in the present study corroborates findings from Côte d'Ivoire, where Seki et al. (2024) reported that household stored drinking water exhibited bacterial loads comparable to tap water, suggesting that

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post-collection handling practices may undermine source water quality regardless of origin. This equivalence challenges the widespread consumer assumption that vended water represents a safer alternative, a misconception that has been documented in other Nigerian studies by Olalekan et al. (2020) and Nicholas and Raimi (2025a, b), who noted that households often prioritize vended water under the belief that it undergoes more rigorous treatment. However, the present study's finding that 0% of vended water samples met WHO standards suggests that this assumption is unfounded and that regulatory oversight of the informal water sector is critically deficient across the region.

4.2. Spatial Uniformity and Distribution System Integrity

The demonstration of statistically uniform contamination across all six campus tap water sampling points, despite numerical variations, provides mechanistic insight into the nature of contamination within the institutional distribution system. This spatial homogeneity, with no significant differences in TBC or TCC between the Water Board (point of entry) and terminal taps in hostels and the library, strongly suggests that contamination occurs upstream or at the treatment stage rather than accumulating progressively through distribution. Similar patterns have been documented by Destiani and Templeton (2018) in London, where heterotrophic bacteria persisted throughout the distribution network despite treatment, indicating that biofilm formation within pipes can maintain stable bacterial populations regardless of water age. In the Nigerian context, Raimi and Sawyerr (2022) observed that groundwater quality in oil-producing communities exhibited spatial consistency across sampling points, attributing this to regional aquifer contamination rather than localized sources. The present study extends these observations by demonstrating that institutional tap water, even at the point of entry, fails to meet basic safety standards, a finding that aligns with Olalekan et al. (2020), who documented that drinking water challenges in the Niger Delta are systemic rather than localized. The detection of *Pseudomonas aeruginosa* at both the Water Board and Community Health Hall further supports the hypothesis of established biofilms within the distribution system, as *P. aeruginosa* is a recognized biofilm former capable of persisting despite intermittent disinfection (Morufu et al., 2021a, b, c; Morufu et al., 2022; Raimi et al., 2022a, b, c; Stephen et al., 2022; 2023; Wolf-Baca & Siedlecka, 2023). This contrasts with findings from high-income settings where distribution systems maintain water quality from treatment to tap (Schaffter & Parriaux, 2002; Webb, 2021; Jun et al., 2021), highlighting the infrastructure vulnerabilities that characterize resource-limited contexts. The uniformity of contamination across sampling points thus reflects not an absence of contamination sources but rather a systemic failure of water safety barriers from source to point of use.

4.3. Pathogen Diversity and Distinct Source Profiles

The identification of five bacterial species in tap water; *E. coli*, *S. aureus*, *P. aeruginosa*, *K. pneumoniae*, and *E. aerogenes*, and four species in vended water, *E. coli*, *S. typhi*, *K. pneumoniae*, and *C. freundii*, reveals distinct contamination pathways that have significant implications for risk assessment and intervention design. The detection of *S. aureus* exclusively in tap water (28% of isolates) and its absence from vended water points to point-of-use contamination through human handling, as *S. aureus* is a commensal organism shed from skin and mucous membranes (Edberg et al., 1996; Bear et al., 2024). This finding is consistent with studies by Raimi and Sabinus (2017) and Abdu et al. (2019), who identified *S. aureus* in environmental samples from Bayelsa State and attributed its presence to inadequate hygiene practices. Conversely, the exclusive recovery of *S. typhi* from vended water (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 (Agbendeh & Ogbonna, 2022; Oyibo et al., 2025), but the prevalence observed here (25%) is notably higher than the 10-15% range reported by Raimi et al. (2022a) in sachet water from Yenagoa, suggesting that Meruwa vendors may face particular vulnerabilities related to source water

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quality or storage practices. The presence of *P. aeruginosa* exclusively in tap water (20% of isolates) and its absence from vended water further supports the biofilm hypothesis, as this organism is known to colonize plumbing systems and resist routine disinfection (Zamorska et al., 2016; Destiani & Templeton, 2018; Raimi & Sawyerr, 2022). The statistically significant difference in species distribution between water sources ($\chi^2 = 24.18$, $p = 0.0005$) confirms that these distinct microbial communities reflect fundamentally different contamination pathways, faecal and handling-related for tap water versus predominantly faecal for vended water, a distinction that carries important implications for intervention targeting.

4.4. Faecal Contamination and Enteric Pathogen Risk

The detection of *E. coli* in 28% of tap water isolates and 33% of vended water isolates, coupled with the presence of other coliforms (*K. pneumoniae*, *E. aerogenes*, *C. freundii*) and the enteric pathogen *S. typhi*, provides compelling evidence of widespread faecal contamination across both water sources. This finding is consistent with studies across Nigeria and sub-Saharan Africa documenting elevated coliform counts in drinking water supplies (Abiye & Raimi, 2025a, b; Enang et al., 2025a, b; Afolabi & Raimi, 2021a, b; Adesakin et al., 2020; Odipe et al., 2018; Enoch, 2018; 2021). The presence of *K. pneumoniae* in both tap and vended water, 12% and 21% of isolates, respectively, aligns with reports by Haciseyitoğlu et al. (2015) and Safeena et al. (2022), 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 (21% of isolates) is particularly noteworthy, as this organism has been implicated in opportunistic infections and may serve as a reservoir for antibiotic resistance genes (Yamani & Elhadi, 2022; Yüksel Dolgun et al., 2024). 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. (2024), 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. (2025) documented that water quality deteriorated significantly during storage in Bangladesh, emphasizing the importance of container hygiene. 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.

4.5. 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 10-20% in untreated patients and the potential for chronic carriage and sustained community transmission (Gift & Olalekan, 2020, Gift et al., 2020; Petterson et al., 2021; Hejazi Dehaghani et al., 2025; Elemuwa et al., 2025). 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. (2017) and Enoch (2021) reported typhoidal *Salmonella* in surface water and beverages in Bayelsa State, but the prevalence observed in the present study (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 (Henry et al., 2019; Elemuwa et al., 2025; Nicholas & Raimi, 2025a, b), 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. (2025) and Omotoso et al. (2025), who identified gaps in water, sanitation, and hygiene infrastructure as key drivers of enteric

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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 (Awogbami et al., 2022; Oyibo et al., 2025; Opaminola & Raimi, 2025). The absence of molecular confirmation in this study (e.g., 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 (Fekeda & Gutema, 2025). 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. Thus, synthesizing the findings across water sources, the study reveals that while tap and vended water harbor quantitatively similar levels of bacterial contamination, their qualitative risk profiles differ substantially due to distinct pathogen communities shaped by different contamination pathways. For tap water, the presence of *S. aureus* (point-of-use handling), *P. aeruginosa* (biofilm formation), and enteric pathogens (*E. coli*, *K. pneumoniae*, *E. aerogenes*) indicates multiple barriers to safety: source water quality, distribution system integrity, and consumer hygiene all contribute to contamination. This multi-pathway profile is consistent with studies by Raimi et al. (2022c) and Clinton-Ezekwe et al. (2024a, b), who documented complex contamination patterns in Niger Delta water systems. For vended water, the exclusive presence of enteric pathogens, including *S. typhi*, and the absence of *S. aureus* and *P. aeruginosa* suggests a simpler but more clinically severe contamination pathway: faecal contamination at the source, during storage, or through handling, without the complicating factors of biofilm formation or human shedding. This distinction has important implications for intervention design, as strategies effective for tap water (e.g., biofilm management, tap hygiene) may be less relevant for vended water, where source water treatment and container sanitation are paramount. The comparable contamination levels between sources underscore that neither can be considered safe without treatment, and the distinct pathogen profiles argue against reliance on a single indicator organism for water quality monitoring (Edberg et al., 1996; Tachikawa et al., 2000; Singh et al., 2021; Soare et al., 2022; Shah & Sutar, 2025). The study's findings align with global calls for risk-based water safety planning that accounts for source-specific hazards and multiple barriers to contamination (Kassa, 2017; Lalumandier, 2000; WHO, 2022; Petterson et al., 2021). In the Nigerian context, these findings support the expansion of regulatory oversight to include informal water vendors, the implementation of point-of-use treatment strategies for all consumers, and sustained investment in water infrastructure to address the systemic vulnerabilities that permit persistent contamination (Olalekan et al., 2019a, b, Olalekan et al., 2020; Raimi & Sawyerr, 2022; Gbeghebo et al., 2023a, b). 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.

5. Study Limitations

While this study provides critical baseline data on bacterial contamination of tap and vended water in the study area, several methodological constraints must be acknowledged when interpreting the findings. First, the study was conducted over a single week, capturing only a snapshot of water quality at one point in time. Consequently, the results do not account for seasonal variability, which is particularly significant in tropical regions like the Niger Delta where rainy season conditions, characterized by increased rainfall, flooding, and surface water runoff, can substantially elevate bacterial loads through contamination of groundwater sources and intrusion into distribution systems. Conversely, dry season conditions may concentrate microbial contaminants due to reduced water flow and stagnation in pipes. Therefore, the findings presented here likely represent a minimum or maximum estimate depending on the season of collection, and future studies should

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incorporate longitudinal sampling across rainy and dry seasons to capture temporal dynamics and inform seasonal risk assessment. Furthermore, several analytical limitations affect the precision and completeness of bacterial characterization. All bacterial identifications were based on morphological and biochemical techniques, which provide presumptive identification but lack the confirmatory power of molecular methods such as 16S rRNA gene sequencing, polymerase chain reaction (PCR), or matrix-assisted laser desorption ionization–time of flight (MALDI-TOF) mass spectrometry. As a result, the potential for misidentification of closely related species, particularly within the Enterobacteriaceae family, cannot be excluded. Additionally, the plate count method employed for enumeration detects only culturable bacteria, thereby underestimating total bacterial presence by excluding viable but non-culturable (VBNC) organisms, which may retain pathogenicity and represent a hidden reservoir of infection risk. In light of these constraints, the findings should be interpreted as conservative estimates of contamination, and future investigations should incorporate molecular confirmation and culture-independent techniques such as quantitative PCR (qPCR) or metagenomic sequencing to achieve comprehensive characterization of the water microbiome and its associated health risks.

6. Summary of the Findings

This study systematically evaluated bacterial contamination in 23 tap water samples from six points within Bayelsa State College of Health Technology and 24 vended water (Meruwa) samples from Ogbia Main Town. The findings reveal uniformly elevated levels of microbial contamination across both water sources. Specifically, total bacterial counts ranged from 3.50×10^6 to 5.30×10^6 CFU/mL, while total coliform counts ranged from 3.00×10^6 to 4.00×10^6 CFU/mL. Notably, no statistically significant difference was observed between tap and vended water for either parameter ($p = 0.642$ for TBC; $p = 0.981$ for TCC), indicating that both water sources harbor comparable and equally hazardous levels of contamination. Furthermore, all samples exceeded World Health Organization drinking water guidelines, with a compliance rate of 0% across both sources, underscoring the universal failure to meet basic microbial safety standards. In addition to quantitative enumeration, species-level identification revealed distinct microbial communities between the two water sources. Tap water isolates comprised *Escherichia coli* (28.0%), *Staphylococcus aureus* (28.0%), *Pseudomonas aeruginosa* (20.0%), *Klebsiella pneumoniae* (12.0%), and *Enterobacter aerogenes* (12.0%), indicating a combination of faecal contamination, human handling-related contamination, and biofilm formation within the distribution system. Conversely, vended water isolates were exclusively enteric bacteria, including *E. coli* (33.3%), *Salmonella typhi* (25.0%), *K. pneumoniae* (20.8%), and *Citrobacter freundii* (20.8%). The presence of *S. typhi*, the causative agent of typhoid fever, in one-quarter of vended water isolates represents a finding of exceptional public health significance. Importantly, the bacterial species distribution differed significantly between water sources ($\chi^2 = 24.18$, $p = 0.0005$), demonstrating that while contamination levels are quantitatively similar, the qualitative risk profile differs substantially, with vended water posing a particularly severe threat due to the presence of a systemic enteric pathogen. Collectively, these findings establish that neither institutional tap water nor informal vended water in the study area is safe for human consumption without treatment, and they provide an evidence-based foundation for targeted water safety interventions.

7. Implications for Policy and Interventions

The findings of this study carry immediate and actionable implications for water safety management in the study area:

1. Vended water safety concerns
    - Salmonella typhi was detected in 25% of vended water samples but absent in tap water, challenging the assumption that vended water is inherently safer.

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- Regulatory authorities must extend water quality monitoring to the informal vending sector, including mandatory microbial testing and vendor certification programs targeting S. typhi in addition to standard coliform indicators.

2. Tap water contamination
   - Staphylococcus aureus was detected exclusively in tap water, particularly in hostel samples, suggesting point-of-use contamination from unclean taps and handling practices.
   - Immediate attention is needed for high-risk tap points (e.g., Boys' Hostel, Girls' Hostel A, and the Water Board) through disinfection and implementation of routine cleaning protocols using chlorinated disinfectants.
3. Prioritization in resource-limited settings
   - High-impact, low-cost interventions (e.g., household chlorination, ceramic filters, tap hygiene) offer immediate risk reduction.
   - Household-level interventions are cost-effective while systemic infrastructure upgrades are planned.
4. Infrastructure and systemic considerations
   - Elevated bacterial loads at the Water Board indicate contamination occurs at or before entry into the campus distribution system, necessitating rehabilitation of storage tanks and treatment facilities.
   - Detection of biofilm-forming Pseudomonas aeruginosa highlights the need for targeted flushing and hyperchlorination of specific pipe sections.
   - Comparable contamination levels in tap and vended water argue for an integrated regulatory framework treating both sources under unified microbial standards.

8. Conclusions

This study provides unequivocal evidence that both institutional tap water and informal vended water (Meruwa) in Otuogidi-Ogbia and Ogbia Main Town are universally and heavily contaminated with bacterial pathogens, with not a single sample meeting World Health Organization drinking water standards. The findings reveal a critical and previously unrecognized public health threat: while tap water harbors a mix of faecal, biofilm-associated, and human-handling-related organisms, vended water contains *Salmonella typhi*, the causative agent of typhoid fever, in one-quarter of samples, yet exhibits quantitatively similar contamination levels to tap water. This paradox fundamentally challenges the widespread assumption that vended water is safer and underscores the urgent need for regulatory oversight of the informal water sector. The absence of significant differences in total bacterial and coliform counts between sources, coupled with distinct pathogen profiles, demonstrates that reliance on enumeration alone is insufficient for risk assessment; species-level identification is essential to capture clinically significant threats. In a region where waterborne diseases remain endemic, these findings translate into a clear imperative: immediate implementation of point-of-use water treatment for all consumers, mandatory microbial testing of vended water with specific screening for *S. typhi*, targeted disinfection of high-risk campus taps, and sustained investment in water safety infrastructure. Without such action, the preventable burden of typhoid fever, diarrheal disease, and opportunistic infections will persist, disproportionately affecting the most vulnerable members of the community. The time for evidence-based intervention is now.

9. Health Significance

The detection of *Salmonella typhi* in one-quarter of vended water isolates represents the most clinically significant finding of this study, with profound implications for disease burden in the study population. Typhoid fever, caused by *S. typhi*, is a systemic illness characterized by prolonged fever, abdominal pain, hepatosplenomegaly, and, in severe cases, intestinal hemorrhage or perforation with case fatality rates of 10-20% in untreated patients. Unlike self-limiting diarrheal diseases, typhoid

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fever requires prompt antimicrobial therapy and carries the risk of chronic gallbladder carriage, enabling sustained community transmission. The presence of this pathogen in water sold to consumers, who purchase it under the assumption of safety, represents a preventable public health crisis. Compounding this risk, the co-occurrence of *Escherichia coli* and *Klebsiella pneumoniae* in both water sources indicates widespread faecal contamination, placing consumers at risk of acute gastroenteritis, urinary tract infections, and, in vulnerable populations, life-threatening sepsis. The burden falls disproportionately on children, the elderly, pregnant women, and immunocompromised individuals, for whom even low-dose exposure can precipitate severe clinical outcomes. Beyond immediate morbidity and mortality, the health significance of these findings extends to long-term consequences and systemic vulnerabilities. The detection of *Pseudomonas aeruginosa*, an opportunistic pathogen notorious for biofilm formation and antimicrobial resistance, in tap water signals the presence of established microbial communities within the distribution system that can serve as reservoirs for recurrent contamination despite intermittent disinfection. For individuals with cystic fibrosis, burns, indwelling medical devices, or compromised immune systems, exposure to *P. aeruginosa* poses risks of chronic colonization, difficult-to-treat infections, and increased healthcare utilization. Similarly, the prevalence of *Staphylococcus aureus* in tap water, a pathogen associated with skin and soft tissue infections, food poisoning, and invasive disease, highlights the intersection of water quality with hygiene practices, particularly in congregate living settings such as hostels. From a health systems perspective, the universal failure to meet WHO standards across both water sources suggests that waterborne diseases are likely endemic in the community, contributing to preventable outpatient visits, hospitalizations, and antimicrobial use that strain already limited healthcare resources. Addressing these risks through evidence-based water safety interventions represents not only a public health imperative but also a cost-effective strategy to reduce disease burden, protect vulnerable populations, and advance progress toward Sustainable Development Goal 6, ensuring universal access to safe and affordable drinking water. Thus, graphically it is represented (Figure 11 below) as:

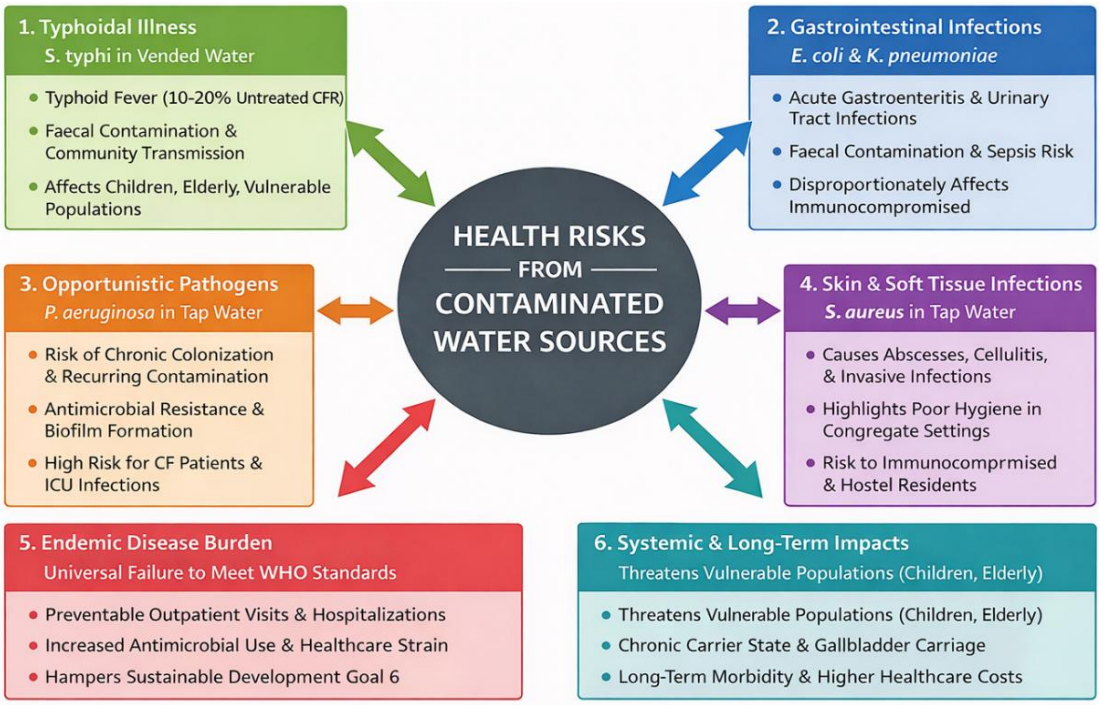

Figure 11. Integrated Framework of Waterborne Pathogens and Health Risks in Community Water Sources.

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10. Recommendations

10.1. Short-Term (0-6 Months)

- **Emergency disinfection of high-risk taps:** Hyperchlorinate taps in Boys' Hostel, Girls' Hostel A, and the Water Board; flush the Water Board line to disrupt biofilms.
- **Mandatory vended water chlorination:** Require vendors to add chlorine tablets to containers; subsidize tablets (~$0.05 per vendor per day).
- **Distribution of household water treatment supplies:** Provide chlorine tablets, ceramic filters, or boiling vessels to hostel students, prioritizing high-risk areas.
- **Targeted hygiene education:** Implement campus-wide campaigns on tap hygiene and safe handling; train vendors on sanitation and chlorination with certification.
- **Routine microbial monitoring:** Conduct monthly microbial testing of five sentinel tap points and all vendors; report results publicly.

10.2. Mid-Term (6-24 Months)

- **Rehabilitation of campus water storage and treatment facilities:** Upgrade chlorination systems, clean tanks, repair leaks or cross-connections.
- **Vendor certification and regulation:** Establish annual microbial testing and inspection for vendors; implement visible certification seals and quarterly spot checks.
- **Point-of-use filtration infrastructure:** Install communal filtration systems in high-traffic areas (Library, Community Health Hall, hostels).
- **Institutional Water Safety Plan:** Form a Water Safety Committee to oversee hazard mapping, monitoring, emergency response, and budgeting.
- **Enhanced laboratory capacity:** Enable low-cost microbial testing within campus or local diagnostic laboratories.

10.3. Long-Term (2-5 Years)

- **Distribution system rehabilitation:** Replace aging pipes, target biofilm-prone sections, and install backflow prevention devices.
- **Centralized treatment upgrade:** Implement continuous chlorination, UV disinfection, or ozonation with automated residual chlorine monitoring.
- **Integration of vended water into formal regulation:** Extend water quality oversight to informal vendors with licensing, routine testing, and enforcement.
- **Community-based water surveillance:** Establish volunteer-led monthly water quality testing linked to a central database for trend analysis.
- **Longitudinal research and evaluation:** Assess seasonal contamination patterns, intervention effectiveness, and molecular characterization of isolates; integrate findings into public health training.

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