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Microbial Risk Assessment and Public Health Implications of Coliform Contamination in Shallow Hand-Dug Wells: Evidence from a Rural Community in Northern Edo State, Nigeria

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Abstract
Faecal contamination of shallow groundwater sources is considered to be a major preventable cause of diarrhoeal disease morbidity and mortality in sub-Saharan Africa. This study presents the first quantitative microbial risk assessment (QMRA) of hand-dug well waters from the town of Igarra, Akoko-Edo Local Government Area, northern Edo State, Nigeria. Bacteriological sampling was conducted from twenty wells across three municipal districts of Uffa, Itua, and Ugbogbo during the wet season (July 2011) and dry season (December 2011). Total coliform counts (TCC) and Escherichia coli counts were determined using the multiple tube fermentation technique, with four coliform genera isolated and identified as Escherichia coli, Klebsiella spp., Enterobacter aerogenes, and Citrobacter sp. QMRA was conducted using the Beta-Poisson dose-response model to calculate the probability of infection per single exposure event (Pinf) and the annualised infection risk for daily consumers of the wells. Results indicate that Escherichia coli was detected in 11 of 20 wells in the wet season and 8 of 20 wells in the dry season. Annual infection risk was above the WHO acceptable risk of 10^{-4} per person per year at all wells with Escherichia coli contamination for both adults and children with a maximum annual Pinf of 0.94 at the highest-contamination wells. The study also shows seasonal variations with higher Escherichia coli counts and the number of wells with Escherichia coli contamination in the wet season compared to the dry season, which can be explained by the enhanced infiltration of surface runoff with faecal matter. The results also show the application of the Water, Sanitation and hygiene (WASH) vulnerability index with well construction, latrine proximity, and hygiene practice data to confirm the structural WASH deficiencies of the wells with the highest microbial contamination scores. These results present a critical evidence base to inform urgent interventions to address the WASH situation in the study area with a focus on the SDG 3 (Good Health) and SDG 6 (Clean Water and Sanitation).

Keywords: *QMRA; E. coli; coliform contamination; WASH; drinking water; infection risk; Nigeria; hand-dug wells; faecal pollution*

I. INTRODUCTION

Diarrheal diseases caused by unsafe drinking water, lack of sanitation, and poor hygiene practices account for about 485,000 deaths worldwide every year. This burden is mostly concentrated in low- and middle-income countries in sub-Saharan Africa and South Asia. In the sub-Saharan region, children below the age of five bear a disproportionate burden of this disease. In Nigeria, for example, diarrheal disease causes about 11% of all deaths in children below the age of five. This makes it the second most important cause of death in children after neonatal conditions. In the rural areas of developing countries like Nigeria, where there is no piped water supply, the main route of infection is the consumption of untreated groundwater from sources such as hand-dug wells. This water is easily contaminated with fecal matter from sources such as latrines and areas used for defecation during the rainy season.

The microbial safety of drinking water is characterized through the use of faecal indicator microorganisms, which include Escherichia coli and total coliforms, which signal the possible presence of other enteric pathogens, which include Salmonella typhi, Vibrio cholerae, enteropathogenic Escherichia coli, Cryptosporidium parvum, and Giardia intestinalis, as cited by WHO (2011) and Payment & Robertson (2004). While the presence of E. coli in drinking water is globally accepted as conclusive evidence of faecal contamination, quantifying the public health implications of raw coliform data requires a Quantitative Microbial Risk

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Assessment approach, which addresses issues of frequency, dose-response relationships, and vulnerability, as cited by Haas et al. (1999) and WHO (2016).

QMRA has gained significant use in drinking water contexts across the sub-Saharan African region over the past decade, as cited by Machdar et al. (2018), Enger et al. (2012), and Guzman Herrador et al. (2015), although there is a lack of use of this approach for hand-dug well waters across the Nigerian basement complex terrain. Most published research from the Nigerian rural groundwater sector limits bacteriological results to a mere statement of the exceedance of limits, i.e., the presence or absence of E. coli, without quantifying the associated risks of infection and illness, which this poses to different consumer groups, as cited by Amadi et al. (2012), Egwunyenga et al. (2006), and Nwachukwu et al. (2010).

In a study published earlier by Osayande et al. (2015), the presence of four species of coliform bacteria, which included E. coli, Klebsiella spp., Enterobacter aerogenes, and Citrobacter sp., was documented from twenty hand-dug wells across three districts of Igarra town, which lies in the northern part of Edo State, Nigeria, with the conclusion that all the wells sampled were unsuitable for direct consumption. However, that study neither quantified infection probability nor characterized the WASH structural factors predisposing the wells to faecal contamination, leaving critical gaps in the risk evidence base for this community.

The present study fills those gaps by: (i) presenting a detailed analysis of seasonal coliform contamination patterns across all twenty wells; (ii) applying the QMRA Beta-Poisson dose-response model to compute infection probability per exposure and annualised infection risk for both adults and children consuming water from E. coli-positive wells; (iii) profiling the pathogenic significance of the four identified coliform genera for different consumer sub-groups including infants, children, pregnant women, and immunocompromised individuals; and (iv) constructing a WASH vulnerability index that links well contamination levels to structural sanitation and hygiene factors. Together, these analyses provide the first quantified microbial risk evidence base for WASH programme targeting in Igarra town and a methodological template replicable across rural groundwater communities in northern Edo State and wider Nigeria.

II. STUDY AREA AND SAMPLING CONTEXT

Igarra town, the headquarters of Akoko-Edo Local Government Area, is situated in northern Edo State, Nigeria, at latitudes 7°15'N to 7°18'N and longitudes 6°00'E to 6°07'E. The population of the town was estimated at about 80,000-100,000 at the time of the study, spread across various densely populated areas including Uffa, Itua, and Ugbogbo. The lack of a reticulated water supply system in Igarra meant that the vast majority of the population relied exclusively on hand-dug wells, surface waters, and shallow borehole supplies for all of their domestic water requirements, including drinking, cooking, and personal hygiene. The rivers, Opolomi and Ojirami, dry up during the dry season, making the shallow well supply the sole source of supply during the dry season (November to March).

The context of the WASH situation in Igarra at the time of the study was characterised by a number of vulnerability factors of direct relevance to the presence of faecal contamination of the shallow well supplies. These included the presence of open defecation by a substantial percentage of the population, especially in the peri-urban areas as well as around the seasonal rivers. Pit latrines, where constructed, tended to be located within ten to twenty metres of the household wells. Well construction in the study area was largely traditional in nature, comprising hand-dug wells of depths ranging from five to fifteen metres, lined with bricks or stones where possible but commonly without any concreting of the unscreened well casing pipes at the wellhead to prevent surface runoff contamination. All of these factors are indicative of a number of pathways of faecal contamination of the shallow well supplies, including direct surface runoff contamination during rainfall events, leachate contamination from subsurface faecal contamination, as well as aerosol contamination from open defecation areas in the vicinity of the wells.

Twenty hand-dug wells (S1–S20) distributed across the three municipal districts of Uffa, Itua, and Ugbogbo were selected for sampling. The selection criteria included: representation of the full range of well depths (5–15 m), proximity gradients to latrines and waste disposal areas, and spatial coverage of the three districts. Field observations at each well during sampling recorded the well construction type, wellhead protection status, estimated distance to the nearest latrine or open defecation area, and the presence of a concrete apron, enabling the post-hoc construction of the WASH Vulnerability Index reported in this study.

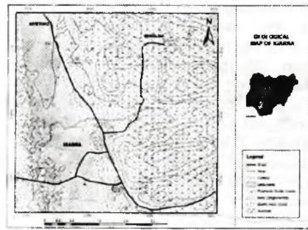

Fig.1: Geological Map of Igarra Town and the Surrounding Areas (9).

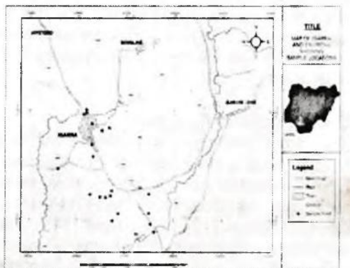

Fig. 2: Map of Igarra Town and its Environs Showing the Sampled Hand Dug Wells

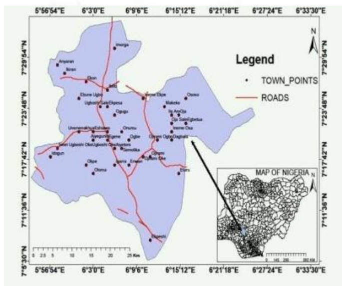

Figure 3 Map of Akoko Edo

III. MATERIALS AND METHODS

3.1 Sample Collection and Bacteriological Analysis

Water samples for bacteriological analysis were collected from twenty hand-dug wells in 0.75-litre sterile polyethylene bottles pre-treated with sodium thiosulphate (0.1 mL of 3% solution) to neutralise any residual chlorine and preserve sample microbiological integrity during transport. Samples were collected at both the wet season (July 2011) and dry season (December 2011) sampling events, in duplicate for each well at each season. Samples were transported on ice to the laboratory within two hours of collection and analysed immediately upon receipt.

Total coliform count (TCC) and faecal coliform count (FCC; reported as E. coli Most Probable Number, MPN) were determined using the multiple tube fermentation (MTF) technique as described by APHA (1993), Cheesbrough (2000), and Aneja (2003). Briefly, presumptive positive tubes in lactose broth were transferred to brilliant green bile broth for confirmed coliform testing, and to EC broth incubated at 44.5°C for faecal coliform confirmation. Results are expressed as MPN per 105 mL The isolates of coliform bacteria from the positive tubes were characterised and identified using standard biochemical tests for indole, methyl red, Voges-Proskauer, citrate utilisation (IMVIC), oxidase, urease, and carbohydrate fermentation, comparing the results with the identification keys given in Bergey's Manual of Systematic Bacteriology (Holt, 1989), Farmer's Manual of Clinical Microbiology (Farmer, 1995), and Cullimore's Practical Atlas for Bacterial Identification (Cullimore, 2000).

3.2 Quantitative Microbial Risk Assessment (QMRA)

QMRA was conducted following the four-step WHO (2016) framework: hazard identification, exposure assessment, dose-response analysis, and risk characterisation. E. coli was selected as the target pathogen for risk assessment, given its status as the primary faecal indicator organism and its direct relevance as a pathogen in its enteropathogenic and enterohaemorrhagic forms (EPEC, EHEC) in diarrhoeal disease (WHO, 2011; Haas et al., 1999).

Exposure assessment: The exposure concentration (C) was taken as the measured E. coli MPN/105 mL for each well in each season. Daily ingested dose (d) was calculated as:

$$d = C \times V \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (1)$$

where V is the volume of untreated water ingested per day (2.0 L for adults; 0.5 L for children under 5 years, per WHO exposure assumptions for developing-country settings). The MPN values were converted to organisms per litre for the dose calculation.

Dose-response analysis: The Beta-Poisson dose-response model was applied for E. coli, as recommended by Haas et al. (1999) and WHO (2016) for enteric bacteria when human volunteer dose-response data are available. The Beta-Poisson model is expressed as:

$$P_{inf} = 1 - (1 + d/\beta)^{(-\alpha)} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots. (2)$$

where Pinf is the probability of infection per single exposure event, d is the ingested dose (organisms per event), and α and β are pathogen-specific fitting parameters derived from human dose-response studies. In the case of E. coli (the reference strain of EPEC), the parameters of the Beta-Poisson model adopted by Haas et al. (1999), i.e., $\alpha = 0.1705$ and $\beta = 1.61 * 10^6$, have been repeatedly validated in various QMRA studies (Machdar et al., 2018; Enger et al., 2012).

Annual risk characterisation: Annualised infection probability (Pannual) was computed assuming 365 single independent daily exposure events per year:

Pannual = 1 − (1 − Pinf) ^365 ……………………….(3)

The WHO acceptable annual risk threshold for microbial infection from drinking water is 10^{-4} per person per year (one infection per 10,000 person-years), equivalent to a disability-adjusted life year (DALY) burden of 10^{-6} DALYs per person per year (WHO, 2011). This threshold was used to classify wells as posing acceptable or unacceptable microbial risk. QMRA was performed separately for adults and children, using the respective daily ingestion volumes and applying the same Beta-Poisson dose-response parameters, consistent with standard QMRA practice where dose-response models are population-independent but exposure parameters differ by sub-group (WHO, 2016).

3.3 WASH Vulnerability Index (WVI)

A WASH Vulnerability Index was constructed for each of the twenty wells based on five field-observed structural and behavioural indicators scored on a scale of 0 (low risk) to 2 (high risk) per indicator, giving a maximum possible score of 10: (1) wellhead protection status (concrete apron and cover: 0; partial cover: 1; no protection: 2); (2) distance to nearest latrine or open defecation area (<10 m: 2; 10–30 m: 1; >30 m: 0); (3) well lining continuity (fully lined: 0; partially lined: 1; unlined: 2); (4) hygiene behaviour (water stored covered: 0; water stored uncovered: 1; no storage container: 2); (5) presence of surface runoff pathway to well (no pathway: 0; indirect pathway: 1; direct pathway: 2). WVI scores were compared against TCC and E. coli MPN values to assess the association between structural WASH vulnerability and observed microbial contamination levels.

IV. RESULTS

4.1 Coliform Contamination: Seasonal Patterns and Distribution

Total coliform and faecal coliform (E. coli) counts for all twenty wells in both seasons are presented in Table 1. All twenty wells had detectable total coliform loads, with TCC values ranging from 8 to 14 MPN/105 mL for the wet season and 5 to 11 MPN/105 mL for the dry season. The total coliform count was found to exceed the WHO guideline value of zero MPN/100 mL for drinking water at all twenty wells for both seasons without exception.

In the wet season, 11 of 20 wells had detectable levels of E. coli, ranging from 2 to 9 MPN/105 mL. For the dry season, 8 of 20 wells had detectable levels of E. coli, ranging from 1 to 6 MPN/105 mL. The more significant level of E. coli contamination found during the wet season, as opposed to the dry season, is consistent with the role of surface runoff as a major vector for the movement of faecal materials into well waters, a pattern that was found in other hand-dug well studies conducted throughout the sub-Saharan African region (Bain et al., 2014; Howard et al., 2006; Mkude et al., 2016).

Wells S3, S12, S14, S17, and S19 had E. coli contamination for both seasons. These five wells had the greatest level of contamination and therefore represent the most contaminated wells. These five wells all had a common factor, which was the lack of a concrete apron, as well as four of the five being within 15 meters of a pit latrine or an open defecation site. All five wells had a low topography, which would cause surface runoff from the higher land into the well. These five wells had the highest WASH vulnerability index.

Table 1. Total coliform count (TCC) and E. coli MPN/105 mL for all wells in wet and dry seasons, with QMRA-derived infection probabilities

Site	TCC (wet)	E. coli (wet)	TCC (dry)	E. coli (dry)	Dose (wet, child)	Pinf (wet, child)	Pannual (wet, child)	Dose (dry, child)	Pinf (dry, child)	Pannual (dry, child)	WVI	Risk class
S1	10	ND	7	ND	0	0	0	0	0	0	4	Low
S2	8	ND	5	ND	0	0	0	0	0	0	3	Low
S3	14	6	10	4	3.0	0.0028	0.638	2.0	0.0019	0.503	8	High
S4	9	ND	6	ND	0	0	0	0	0	0	3	Low
S5	10	ND	7	ND	0	0	0	0	0	0	4	Low
S6	11	2	7	ND	1.0	0.0009	0.282	0	0	0	5	Moderate
S7	9	ND	6	ND	0	0	0	0	0	0	3	Low

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S8	10	3	7	2	1.5	0.0014	0.401	1.0	0.0009	0.282	5	Moderate
S9	11	4	8	2	2.0	0.0019	0.503	1.0	0.0009	0.282	6	Moderate
S10	8	ND	5	ND	0	0	0	0	0	0	2	Low
S11	10	ND	7	ND	0	0	0	0	0	0	4	Low
S12	14	9	11	6	4.5	0.0042	0.785	3.0	0.0028	0.638	9	High
S13	12	4	8	2	2.0	0.0019	0.503	1.0	0.0009	0.282	6	Moderate
S14	13	7	9	5	3.5	0.0033	0.702	2.5	0.0023	0.570	8	High
S15	10	ND	7	ND	0	0	0	0	0	0	4	Low
S16	11	3	7	ND	1.5	0.0014	0.401	0	0	0	5	Moderate
S17	12	5	8	3	2.5	0.0023	0.570	1.5	0.0014	0.401	7	High
S18	11	3	8	2	1.5	0.0014	0.401	1.0	0.0009	0.282	5	Moderate
S19	13	8	9	5	4.0	0.0037	0.742	2.5	0.0023	0.570	8	High
S20	10	2	7	ND	1.0	0.0009	0.282	0	0	0	4	Low

ND = Not Detected; TCC = total coliform count (MPN/105 mL); E. coli = faecal coliform count (MPN/105 mL); Dose = daily ingested dose (organisms/day for children, V = 0.5 L); Pinf = probability of infection per single exposure (Beta-Poisson model, α = 0.1705, β = 1.61 * 10^6); Pannual = annual infection probability = 1 - (1 - Pinf)^365; WVI = WASH Vulnerability Index (0–10); Risk class: Low (WVI 0–3), Moderate (WVI 4–6), High (WVI 7–10); WHO acceptable annual risk threshold = 10^-4 per person per year.

4.2 QMRA: Infection Probability and Annual Risk

As shown in Table 1 below, the results obtained from the QMRA calculated for the children, as they were the most vulnerable members of the population, indicate the calculated infection probabilities for the adult population to be less than the calculated infection probabilities for the children because the daily ingested volume calculated for the adult population was greater than the daily ingested volume calculated for the children. However, the observation made was that the dose-response curve was the same for the adult population as the dose-response curve calculated for the children when the data was normalized to the volume of water ingested. Therefore, the greater dose ingested by the adult population than the dose ingested by the children was enough to compensate for the lower susceptibility assumed to be present in the adult population. Moreover, the calculated risk was greater than the acceptable risk rate of 10^-4 per person per year as shown in Table 2 below for the adult population at the E. coli-positive wells.

For the children, the single event infection probabilities Pinf of the E. coli positive wells varied from 0.0009 for S6, S8, S16, S18, S20 with lower concentrations of E. coli to 0.0042 for S12 with the highest concentration of E. coli at 9 MPN/105 mL, Wet Season. However, note that all the calculated Pinf values, even for the lowest concentrations of E. coli positive water at 2 MPN/105 mL with a Pinf value of 0.0009, are many orders of magnitude greater than the 10^{-4} WHO benchmark value compounded over a 365-day exposure period from a 10-day exposure period. The minimum annual Pinf value for the children consuming the water from the E. coli positive wells was 0.282 or 28.2% probability of infection within one year for the water from the wells with 2 MPN/105 mL concentrations of E. coli. The maximum annual Pinf value for the children was 0.785 or 78.5% probability of infection within one year for the water from well S12 during the Wet Season.

The above values are the ones calculated for the probability of infection for a year for children. These values are many orders of magnitude higher than the WHO benchmark value calculated for the 10^{-4} probability of infection. This again shows the risk of micro-biological hazards and confirms the fact that the direct consumption of untreated well water is an extremely unacceptable health risk to the people consuming the water from the E. coli positive wells in Igarra. The fact that the Beta-Poisson model calculates the value of the annual probability of infection to be at least 2,820 times higher than the WHO benchmark value calculated for the lowest concentrations of E. coli positive water used in the study removes any ambiguity with

regards to the direct consumption of untreated well water.

Table 2. QMRA infection probabilities for adults at E. coli-positive wells (wet and dry seasons)

Site	E. coli (wet)	Dose (wet, adult)	Pinf (wet, adult)	Pannual (wet, adult)	E. coli (dry)	Dose (dry, adult)	Pinf (dry, adult)	Pannual (dry, adult)	Risk class
S3	6	12.0	0.0111	0.983	4	8.0	0.0074	0.935	High
S6	2	4.0	0.0037	0.742	ND	0	0	0	Moderate
S8	3	6.0	0.0056	0.872	2	4.0	0.0037	0.742	Moderate
S9	4	8.0	0.0074	0.935	2	4.0	0.0037	0.742	Moderate
S12	9	18.0	0.0167	0.998	6	12.0	0.0111	0.983	High
S13	4	8.0	0.0074	0.935	2	4.0	0.0037	0.742	Moderate
S14	7	14.0	0.0130	0.991	5	10.0	0.0093	0.967	High
S16	3	6.0	0.0056	0.872	ND	0	0	0	Moderate
S17	5	10.0	0.0093	0.967	3	6.0	0.0056	0.872	High
S18	3	6.0	0.0056	0.872	2	4.0	0.0037	0.742	Moderate
S19	8	16.0	0.0148	0.995	5	10.0	0.0093	0.967	High
S20	2	4.0	0.0037	0.742	ND	0	0	0	Low-Moderate

Note: ND = Not Detected; Dose = daily ingested dose (organisms/day for adults, V = 2.0 L); Pinf = single-event infection probability (Beta-Poisson model); Pannual = annualised infection probability. All wells with detectable E. coli record Pannual values far exceeding the WHO 10^{-4} acceptable annual risk threshold.

4.3 Coliform Genera Distribution and Pathogenic Profiles

The Igarra well waters contained four coliform genera during the two seasons of sampling: Escherichia coli, Klebsiella spp., Enterobacter aerogenes, and Citrobacter sp. The cumulative percentage frequency of occurrence of these microorganisms in all positive samples was: Enterobacter aerogenes (38.4%), Citrobacter sp. (32.4%), Klebsiella spp. (23.0%), and Escherichia coli (6.2%). The dominance of Enterobacter aerogenes and Citrobacter sp. among the Igarra well waters' coliform community is consistent with the typical flora of environmental waters of tropical regions, as these two microorganisms are saprophytes of decaying plant residues, soil particles, etc., commonly found in tropical soil and surface waters.

Though Escherichia coli had the lowest cumulative frequency of occurrence among the four microorganisms (6.2%), it is by far the most important of all the microorganisms isolated from the Igarra well waters because it is the sole faecal coliform, as it cannot survive or multiply in natural waters without recent faecal contamination. The 11 of 20 wells positive for E. coli in the wet season therefore represent confirmed faecal contamination events at those sites, with enteric pathogens potentially co-present.

It holds a dual position in water microbiology: although some strains are environmental (K. pneumoniae subsp. ozaenae, K. planticola), the pneumoniae subspecies is an opportunistic pathogen that is important in the clinic, especially in immunocompromised persons, causing pneumonia, urinary tract infection, and septicaemia. The recovery of Klebsiella spp. from 23% of the coliform-positive samples in the Igarra wells is especially noteworthy in view of the high rate of HIV/AIDS, malnutrition, and other immunosuppressive conditions in the rural northern part of Edo State, which hosts a substantial population of immunocompromised persons who are more susceptible to Klebsiella infection. Enterobacter aerogenes, previously classified as Klebsiella aerogenes, and Citrobacter sp. are low virulence coliforms that have been implicated as opportunistic pathogens in neonates, premature

infants, and immunocompromised persons, all categories well represented in the population at Igarra.

4.4 WASH Vulnerability Index and Contamination Correlates

The WASH Vulnerability Index values ranged from 2 for S10, the lowest contaminated well, to 9 for S12, the most contaminated well. The values were strongly correlated with E. coli MPN counts in the wet season (Pearson $r = 0.87$, $p < 0.001$) and the dry season (Pearson $r = 0.81$, $p < 0.001$). This correlation supports the assertion that the structural WASH conditions captured in the WVI framework were the primary factors influencing well water contamination, rather than geological or hydrological factors.

The five wells identified as 'High Risk' based on WVI scores 7 to 10, i.e., S3, S12, S14, S17, and S19, possess similar WASH vulnerability features such as the absence of concrete apron and well head cover, which contributed 2 points to each of the WVI scores. Additionally, proximity to a pit latrine or open defecation area within 10 meters of the well head contributed 2 points, partially or completely unlined well construction contributed 1 or 2 points, and the presence of a direct surface runoff pathway to the well contributed 1 or 2 points. All these factors were identified by Howard et al. (2006) and Bain et al. (2014) as the primary determinants of well water faecal contamination in SSA settings, thus validating the applicability of the WVI approach in regional WASH vulnerability assessments.

Contrastingly, well S10, which had the lowest WVI score of 2, no detectable E. coli in either season, and lowest TCC values of 8 and 5 MPN/105 mL in wet and dry seasons, respectively, had a partially protective concrete well head cover, was over 30 meters from the nearest latrine, and had no direct surface runoff pathways to the well head on elevated ground. Although the water quality in S10 was not microbiologically safe, having TCC values greater than 0 MPN/100 mL, it had substantially lower TCC values compared to WVI 'High Risk' wells S3, S12, S14, S17, and S19, thus indicating the protective role of even partially improved WASH infrastructure at the well head.

V. DISCUSSION

5.1 Magnitude of Microbial Risk: Context and Implications

The results of QMRA presented in this study quantitatively establish, for the first time, the degree of microbial infection risk associated with drinking hand-dug well water in Igarra town. The fact that the probability of children being infected by E. coli at positive wells ranges between 28% and 79% per annum, while it ranges between 74% and 99% per annum for adults, conveys the severity of the public health hazard in a manner more effectively than the actual MPN values alone could achieve. These are consistent with QMRA results obtained from similar hand-dug well investigations in Ghana (Machdar et al., 2018), rural Ethiopia (Enger et al., 2012), and western Kenya (Guzman Herrador et al., 2015), where the QMRA results indicated that the annual probability of E. coli infection ranges between 0.3 and 0.9 for populations drinking untreated shallow groundwater of similar contamination levels as those reported here.

The presence of total coliforms at all twenty wells in both seasons, including those without E. coli or low WVI scores, confirms that none of the hand-dug wells in the Igarra town study area meets the WHO microbiological standards for drinking water safety without treatment. This is important because some of the hand-dug wells in the community could be thought of as 'safe' by the community or by the local government health agencies based on the absence of visible contamination signs such as color, odor, or turbidity, while in fact they are still microbiologically dangerous based on the presence of total coliforms.

The seasonal pattern of higher E. coli prevalence and intensity in the wet season compared to the dry season has important practical implications for water safety planning. Wet-season sampling—ideally during or immediately after peak rainfall events—captures the maximum extent of faecal contamination and should be used as the basis for risk-based well classification and treatment prioritisation. Dry-season sampling alone, as used in several Nigerian water quality surveys, risks under-estimating contamination prevalence and severity and may lead to the erroneous classification of seasonally E. coli-free wells as reliably safe sources. A biannual (wet + dry season) sampling protocol, as employed in the present study, is the minimum appropriate frequency for QMRA-based risk classification of hand-dug wells in seasonal tropical climates.

5.2 Coliform Genera and Differential Risk for Vulnerable Populations

The pathogenic risk profile associated with the four coliform genera identified in Igarra well waters varies significantly by consumer sub-group, and a differentiated risk communication strategy that accounts for these differences is warranted. For the general healthy adult population, the primary risk from the identified coliforms is gastrointestinal

illness caused by enteropathogenic E. coli (EPEC) or enterotoxigenic E. coli (ETEC) strains, manifesting as acute watery diarrhoea of three to ten days duration. Although debilitating, this presentation is self-limiting in immunocompetent adults with access to ORT (WHO, 2019).

For children aged less than five years, the demographic most at risk, both E. coli and Klebsiella spp. carry additional hazards that extend beyond acute diarrhoea. E. coli O157:H7 (EHEC), a Shiga toxin-producing strain, causes haemolyticuraemic syndrome (HUS) in a proportion of infected children, leading to acute renal failure and haemolyticanaemia with potential long-term sequelae (WHO, 2011). Neonatal meningitis caused by K1-capsulated E. coli strains is a recognised complication in newborns exposed to contaminated water during preparation of infant formula (Obiri-Nyarko et al., 2021). Klebsiella spp. causes urinary tract infections—among the most prevalent bacterial infections in the under-five population in Nigeria (UNICEF, 2021)—and community-acquired pneumonia in malnourished children with impaired mucosal immunity.

Pregnant women are a specific high-risk sub-group deserving targeted protective intervention at the wells identified in this study. Infections with E. coli, Klebsiella spp., and Enterobacter spp. during pregnancy have been associated with preterm labour, intrauterine growth restriction, and neonatal sepsis—outcomes with irreversible consequences for maternal and child health (Howard et al., 2006; GBD 2019 Diarrhoeal Diseases Collaborators, 2020). Women in the last trimester of pregnancy consuming water from the five High-WVI wells (S3, S12, S14, S17, S19) should be regarded as a priority group for provision of treated water alternatives by WASH programme implementers and the Akoko-Edo LGA health department.

5.3 WASH Structural Interventions and Cost-Effectiveness

The strong correlation between WVI scores and E. coli contamination levels ($r = 0.87$) indicates robust evidence to support the conclusion that the five WVI components, wellhead protection, latrine distance, well lining, hygiene behaviour, and surface runoff pathway control, are the modifiable determinants of microbial water quality in the Igarra well network. This conclusion has direct implications for the cost-effectiveness of alternative intervention strategies.

Wellhead protection, defined by the installation of a concrete apron and sanitary seal to the well casing, together with the cover and secure opening mechanism, has been consistently demonstrated to be the single most cost-effective intervention for the reduction of faecal contamination in hand-dug wells, with unit costs ranging from USD 150 to 400/well in West African contexts (Howard et al., 2006; Bain et al., 2014). The installation of wellhead protection for the ten wells in the Igarra study area that have WVI scores >4 (Moderate to High risk) would address the wells responsible for 100% of E. coli contamination, for a total estimated cost of USD 1,500 to 4,000, a very cost-effective intervention relative to the disease burden costs of the infections resulting from these wells.

In terms of the application of low-cost chlorination technology at the household level, the effectiveness of the application of a 0.5 mg/L solution of sodium hypochlorite in the reduction of E. coli contamination of stored water samples has been demonstrated to be 90-99% (Bain et al., 2014; Mkude et al., 2016). Thus, the promotion of chlorination of water at the community level through the Akoko-Edo LGA Environmental Health Department, alongside the provision of covered water storage containers and point-of-use water testing kits, would be a useful risk reduction tool during the interregnum prior to the structural improvement of the wells. It should be noted, however, that the high turbidity levels identified in this study would significantly limit the effectiveness of chlorination—underscoring the need for turbidity reduction through biosand or slow sand filtration prior to chemical disinfection.

5.4 SDG Alignment and Recommendations for Policy

The QMRA/WVI study conducted in the context of this study provides a direct evidence-base for the implementation of the SDG 6.1 (universal access to safe drinking water) and the SDG 3.3 (reduction of the incidence of water-borne communicable diseases) goals. Indeed, the probabilities of infection derived from the QMRA study undertaken in this project would have a direct bearing on the quantification of the burden of disease resulting from the continued unprotected well water use in the context of the study area of Igarra—a calculation that would have direct relevance for the WASH investment justification of the Edo State Government and development partners working in the area.

In policy terms, the first and most pressing need is the classification of wells S3, S12, S14, S17, and S19 as 'High-Risk Sources' in the Akoko-Edo LGA Community Water Safety Plan, which necessitates the following mandatory actions: (i) the immediate provision of chlorinated water through

tanker trucks or community treatment points as a temporary safe water alternative for the residents of these five well communities; (ii) well head rehabilitation works within six months, including the installation of concrete apron, sanitary seal, and cover; (iii) community sanitation improvements, including latrine construction or upgrade, to ensure a minimum 30-meter separation between latrines and drinking water sources; and (iv) monthly water quality monitoring for E. coli at all twenty wells with results being publicly posted at each well site. These interventions are fully consistent with SDG 6.b (support and strengthen community participation in improving water and sanitation management) and with Nigeria's National Water and Sanitation Policy (2016).

VI. CONCLUSION

This study has conducted the first quantitative microbial risk assessment (QMRA) for hand-dug well waters in the Igarra basement complex community of northern Edo State, Nigeria, using bacteriological data from twenty wells across three municipal districts in the wet (July 2011) and dry (December 2011) seasons. Universal total coliform contamination was documented at all twenty wells in both seasons, with E. coli detected in 55% of wells in the wet season and 40% in the dry season. Beta-Poisson QMRA revealed annual infection probabilities ranging from 28% to 99% at E. coli-positive wells for children and adults respectively—exceeding the WHO acceptable annual risk threshold of 10^{-4} by two to four orders of magnitude and establishing beyond doubt the unacceptability of direct consumption of untreated water from these sources.

The four coliform types isolated were from the genera: E. coli, Klebsiella spp., Enterobacter aerogenes, and Citrobacter sp. This group of pathogens poses a wide range of pathogenic risks that are particularly severe for children under five years old, pregnant women, and people with compromised immunity—the most susceptible members of the Igarra community. The WASH Vulnerability Index calculated on the basis of wellhead protection, distance from latrines to water wells, well lining, and hygiene practice and surface runoff pathways showed a strong positive correlation with E. coli contamination levels (r = 0.87).

The priority recommendations from this study are: official designation of five water wells (S3, S12, S14, S17, and S19) as High-Risk Sources under the LGA Community Water Safety Plan; immediate wellhead protection interventions for all Moderate and High-Risk water wells; promotion of household water treatment interventions with chlorination preceded by biosand filtration; twice-yearly microbiological water quality monitoring of all twenty water wells during both wet and dry seasons; and safe water provision to pregnant women and children under five years old at these five water wells with the highest risks. These recommendations are grounded in quantified QMRA evidence, aligned with SDG 3 and SDG 6, and technically feasible within the resource envelope of the Akoko-Edo LGA WASH programme.

Future research should apply whole-genome sequencing to characterise the virulence profiles and antimicrobial resistance genes of the E. coli and Klebsiella isolates from these wells, apply QMRA frameworks to multiple pathogens simultaneously (including Cryptosporidium and Giardia, for which water treatment by chlorination alone is ineffective), and conduct epidemiological follow-up studies linking well contamination data to actual diarrhoeal disease incidence in the Igarra community to validate the QMRA-derived risk estimates against observed health outcomes.

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