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Bacteriological Quality Of Surface Waters In The Adamawa Region-Cameroon

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Abstract: This study, which aimed to evaluate the microbiological quality of surface waters in the Adamaoua Region of Cameroon, was conducted in February 2025 during the dry season. During this period, the scarcity of water leads to the common use of streams by humans and animals. The samples collected in sterilized glass bottles and stored in a cooler containing ice packs were analyzed within 6 hours (maximum) using a Whagtech portable bacteriological analysis kit. The results obtained after 24 hours of incubation allowed the enumeration of more than 2000 CFU/100 mL in the 10 sampling stations. The rivers Mayo Saourou, Anam, Minin, Bella Fokou, Massin, Mbewe, and Lake Mbakaou also showed extremely high levels of microbial contamination compared to the Mbong, Maba, and Maour rivers. The populations of the localities adjacent to the studied rivers are daily exposed to waterborne diseases. These results highlight the consequences of animal fecal pollution on the microbiological quality of water and the urgent need to increase the number of improved water sources in these study sites in order to reduce health risks for vulnerable populations.

Keywords: Bacteriological quality, Surface waters, Adamawa, Cameroon.

Introduction

Access to drinking water is a crucial factor for both the socio-economic and environmental development of a population. This highly concerning issue for the international community is the subject of the sixth Sustainable Development Goal (UNRIC, 2020). The Adamawa Region, commonly referred to as the "water tower" of Cameroon, is not spared from the problem of access to quality water. In African countries, the supply of drinking water for humans is a critical problem (Abdullahi BM & Abdulrahman, 2015) especially in remote areas due to the hyper-centralization of public management services (Mpakam *et al*., 2006). As in other parts of Cameroon, but less so in the Central or Littoral Regions, the West does not have a continuous water supply system, which leads the majority of inhabitants to use surface water, wells, boreholes, and rivers as an alternative source of drinking water and for other water needs (Nkengfack *et al*., 2017). Studies conducted in similar areas of Cameroon have highlighted the poor bacteriological quality of these water sources (Yongsi, 2010). Waterborne diseases are generally the second leading cause of infant morbidity and mortality after malaria in Cameroon (INS *et al*., 2026), indicating non-compliance with bacteriological standards for drinking water for human consumption (World Health Organization, 2026). Morbidity and mortality rates from diarrheal diseases are higher among children under 05 years of age (INS *et al*., 2026). The germs responsible for these waterborne diseases are generally transmitted via the fecal-oral route and represent a major public health issue (World Health Organization, 2026). Microbiological contamination of water occurs in a context of poor waste management, including fecal matter (Bain *et al*., 2014). Coliforms can be used as indicators to monitor the microbiological quality of water (Nicholson *et al*., 2017), and their rapid detection is therefore crucial and should be easy to perform in order to assess water quality, especially in resource-limited countries such as Cameroon. Preventive public health approaches for drinking water must include a rapid assessment of the microbiological quality of water in order to guide water quality monitoring and treatment. In this perspective, this study aimed to investigate in the surface waters of the Region four bacterial groups and five bacteria of health interest, including Total Aerobic Mesophilic Flora (TAMF), Fecal Coliforms (FC), Total Coliforms (TC), Fecal Streptococci (FS), Vibrio, *Staphylococcus* spp., *Salmonella* spp., *Shigella* spp. and *Pseudomonas* spp.

1. Materials and Methods

1.1. Study Framework

The Adamawa Region, or the water tower of Cameroon, is located between 6-8 degrees North latitude and 10-16 degrees East longitude. It is a highland region with an average altitude of 1000 m and mountains with peaks nearly 2300 m high. It is in this Region that many of Cameroon's streams originate. The climate has two seasons: a rainy season lasting 6 months (May to October) and a dry season from November to April. Annual rainfall ranges between 1500 and 1800 mm (Mbogning *et al.,* 2011). Annual temperatures range between 24 and 32 °C and can reach 36 °C during the dry season, the period during which the study was conducted. In Adamawa, livestock farming mainly concerns cattle, sheep, oxen and goats (Fofiri Nzossie, 2013).

The sample points during the studies are represent to figure 1. Generally, the water of different points was using to drinking, domestic uses, Water consumption by oxen and the breeders.

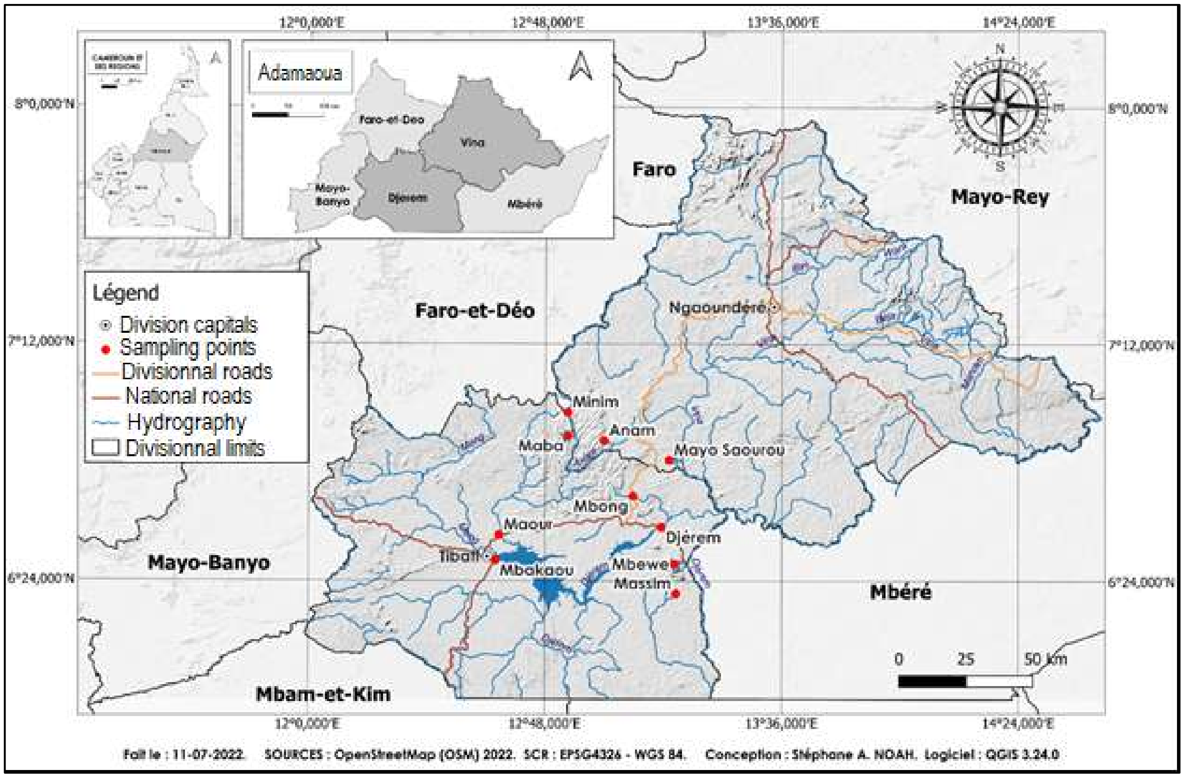

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Figure 1: Sampling points of the streams studied

1.2. Bacteria sampling and analysis methods

The methodological approach used for the microbiological analysis of samples in this study is the one recommended by Rodier *et al*. (2009). Given the sampling area coupled with the fact that sampling was carried out for 07 days and sampling locations were far apart, a portable bacterial analysis kit "Wagtech" was brought to the field (Figure 2A).

For each sampling location, water samples for bacterial analysis were collected in previously sterilized (flamed methanol) 100ml glass vials.

In the laboratory, isolation and testing for bacterial germs were carried out in stainless steel labelled Petri dishes containing the corresponding culture media broths after sampling, according to the recommendations of Rodier *et al*. (2009). Prior to incubation, water samples were filtered through a 0.45 µm porosity filter membrane having a manual vacuum pump. After filtration, the membranes were removed using sterile forceps and carefully placed on absorbent pads that were placed at the bottom of sterile Petri dishes containing corresponding culture medium previously prepared. The pads provide nutrients to specific bacteria for their development while inhibiting the multiplication of any non-targeted bacteria. After placing the lids on the Petri dishes, the dishes were placed in their racks and then placed in the incubator. The research protocol for groups of bacteria indicative of water quality and bacteria of health interest in collected water samples is described in Table 2 below.

Table 2: The microbiological analysis protocol of water

Researched bacteria	**Culture media used**	**Incubation temperature (°C)**	**Volume of incubated sub-samples**
Total Aerobic Mesophilic Flora (TAMF)	Plate Count Agar (PCA)	30	1 ml ; 2 ml ; Filtration (25 ml ; 100 ml)
Total Coliforms (TC)	Lauryl sulfate	37	
Fecal Coliforms (FC)	Lauryl sulfate	44	
Fecal Streptococci (FS)	Bile esculin agar (BEA)	37	
Vibrio cholerae	Thiosulphate-Citrate-Bile-Sucrose (TCBS) Agar	37	
Vibrio parainfluenzae	Thiosulphate-Citrate-Bile-Sucrose (TCBS) Agar	37	
Staphylococcus aureus	Chapman Mannitol	37	
Salmonella	Salmonella-Shigella Agar (SS)	37	
Shigella	Salmonella-Shigella Agar (SS)	37	
Pseudomonas aeruginosa	Cetrimide + Glycerol	37	

2. RESULTS

2.1. General distribution of the abundance of the bacteria studied

The distribution of the abundance of four bacterial groups (Total Aerobic Mesophilic Flora (TAMF), Total coliforms, Fecal coliforms, and Fecal streptococcus) as well as five bacteria of sanitary interest (*Shigella* spp, *Salmonella* spp., *Vibrio cholerae*, *Vibrio parainfluenzae*, and *Pseudomonas* spp), expressed in Log10 (Abundance + 1) (Figure 2), allows for the visualization of data that can vary across several orders of magnitude and enables better comparison of bacterial distributions. This is a logarithmic transformation. Thus, the bacterium Pseudomonas and fecal streptococci, whose median is close to zero, are the very low-abundance organisms in the samples. They are followed by Salmonella spp., whose distribution is characterized by low abundance, then by fecal coliforms, Vibrio cholerae, and Vibrio parainfluenzae, which show moderate abundance in the samples. Finally, the Total Aerobic Mesophilic Flora (TAMF), *Shigella*, and total coliforms are distinguished by high and relatively consistent abundance across all samples (Figure 2).

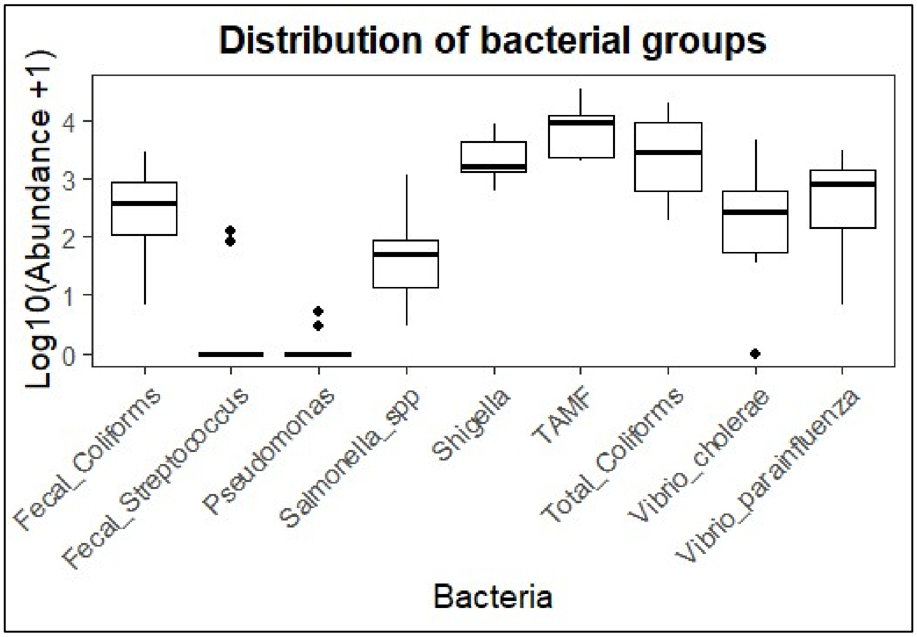

Figure 2: Distribution of bacterial groups and some bacteria of health interest in the different collected samples

2.2. Variation of total bacterial loads in the sampling points

The spatial variation in total bacterial load between the different sampling sites allowed for the simultaneous assessment of the central tendency (median), dispersion, and extreme values. A high spatial heterogeneity of bacterial loads was observed, indicating that microbiological contamination is not uniform across the studied sites. Depending on the level of distribution, it is possible to distinguish sites with a high bacterial load, showing the highest medians (Mbakaou, Mbewe, Massin, Anam, and Mbong), characterized by a generally high bacterial abundance, followed by sites with an intermediate bacterial load (Bella Fokou, Mayo Saourou, Maba, and Maour), characterized by a moderate bacterial abundance, and finally a site with a low bacterial load (Minin), characterized by low bacterial abundance and therefore relatively better microbiological quality compared to the other sites (Figure 3).

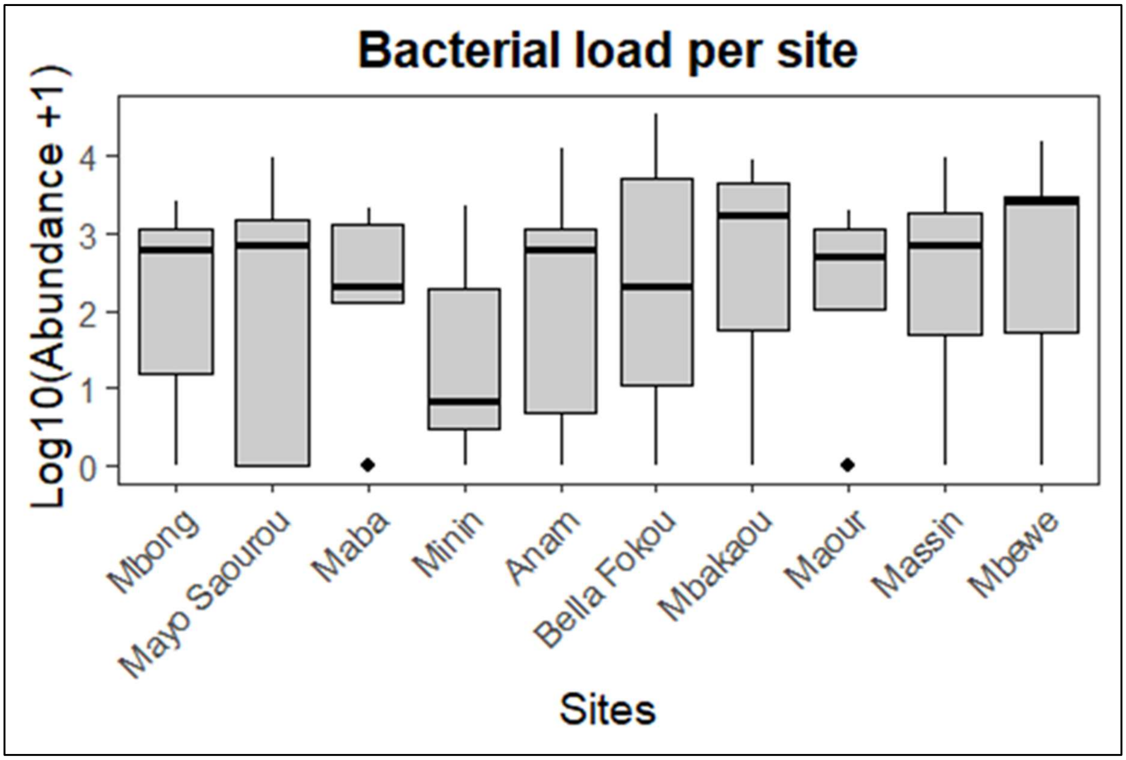

Figure 3: Spatial variation of the total bacterial load

2.3. Bacterial community heatmap

The heatmap of bacterial communities highlights a significant spatial variability in microbiological composition between the different sampling sites. The representation based on standardized data reveals gradients of bacterial abundance, allowing for the distinction of several groups of sites with distinct microbiological signatures. These variations, illustrated by colors (red/orange: high abundance, yellow: medium abundance, neutral tone: abundance close to the average, and blue: low abundance), allow for an assessment of the level of bacterial contamination. The dendrograms (trees) thus show the ecological similarity between sampling sites (on the left), on one hand, and the similarity in bacterial composition (at the top), on the other hand. This hierarchical classification highlights several ecological groups of sites. Group 1, consisting of heavily contaminated sites, notably includes Mbakaou, Anam, Bella Fokou, Mbewe, and Mayo Saourou. These sites are characterized by highly variable abundances of Total Aerobic Mesophyl Forms, *Shigella*, fecal coliforms, *Vibrio cholerae*, *Vibrio parainfluenza* and *Salmonella* spp., indicating high fecal contamination likely related to significant human pressure. Group 2, consisting of sites with intermediate contamination, includes notably Massin, Mbong, Maour, and Maba. It is characterized by a relatively low bacterial diversity, where the species *Vibrio cholerae*, *Vibrio parainfluenzae*, and *Salmonella* spp. are mainly observed. These environments could therefore be subject to diffuse pollution. Finally, group 3, consisting of the lightly contaminated site (Minin), is distinguished by the almost exclusive presence of fecal streptococci as the bacterial group detected in this environment, which could be related to a lower human impact. Beyond the ranking of sites, it is also possible to distinguish bacterial ecological associations. Thus, a first bacterial group of increased health interest consists of TAMF and fecal coliforms. A second group corresponds to opportunistic pathogenic bacteria, including *Shigella*, *Vibrio cholerae*, *Vibrio parainfluenza*, *Pseudomonas* spp, and *Salmonella* spp. Finally, a specific group of equally important health interest is represented by fecal streptococci (Figure 4).

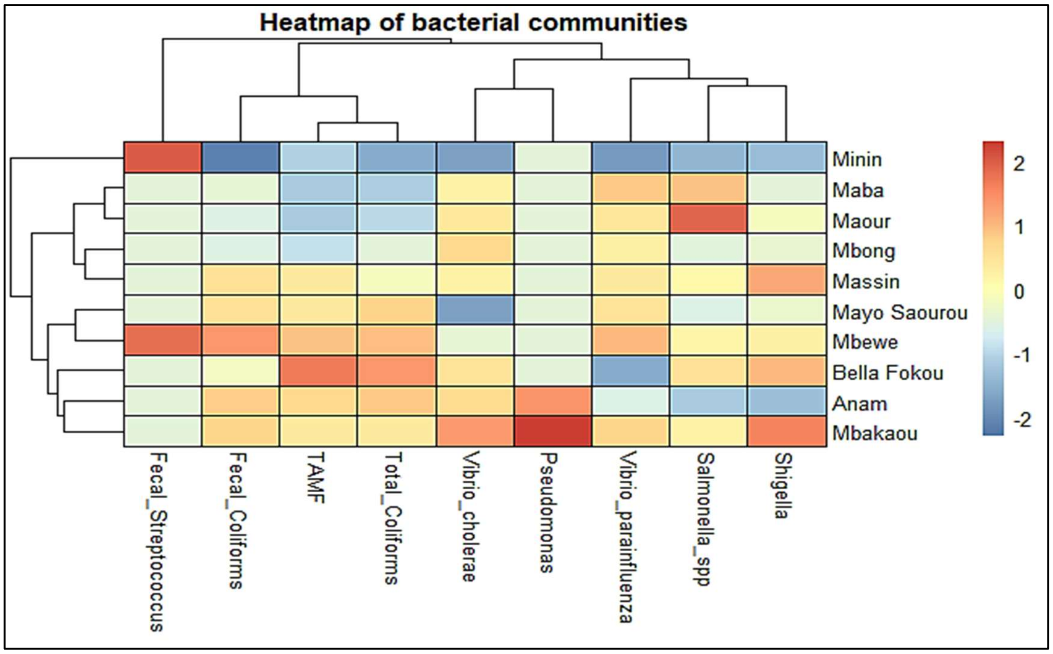

Figure 4 : Heatmap of the bacterial community identified in the different samples from the collection sites

3. DISCUSSION

The inhabitants of the studied area are mostly poor with limited capacities, including financial, to procure drinking water. They are therefore forced to turn to water sources that are dangerous to health and potentially highly polluted. Thus, for the assessment of drinking water safety, Fecal coliforms (FC) and other bacteria of sanitary interest are widely used as indicator organisms (Mabvouna Biguioh *et al*., 2020). In this study, bacteriological analyses revealed high levels of fecal contamination in the studied watercourses, with counts of Total Aerobic Mesophilic Flora, Fecal Coliforms, and Fecal Streptococcus (FS) exceeding 2,000 CFU/100 mL, 2,000 CFU/100 mL, and 100 CFU/100 mL, respectively. The high presence of Fecal Coliforms in the water samples to be analyzed is, according to several other studies, an indicator of possible fecal contamination of human or animal origin (Koffi-Nevry *et al*., 2012; Mengel *et al*., 2014; Mabvouna Biguioh *et al*., 2020; Thinasonke Duze *et al*., 2025). Similar results have been reported in the Western Cameroon region and in Yaoundé, where the high level of fecal coliforms in water sources was systematically associated with fecal contamination (Moussima Yaka *et al*., 2020 ; Mabvouna Biguioh *et al*., 2020). This result confirms the risk faced by the population when using the same water supply sources as livestock. Also, the high densities of FC would also be related to the high temperatures in the area, which range from 30 to 36 °C during the study period. According to An *et al*. (2002), the densities of fecal coliforms increase with high temperatures. By comparing the counts of these indicator organisms across the ten sampling stations, high numbers of fecal coliforms, Total Aerobic Mesophilic Flora, and Fecal Coliforms were observed in Mayo Saourou, Anam in the locality of Martap, Minin in Minim, Bella Fokou, Massin, Mbewe in the locality of Ngaoundal, and Lake Mbakaou in Tibati. This result is due to the high concentrations of human and animal populations around the mentioned watercourses. Notable effects on gastrointestinal health are expected in users of these waters in which concentrations range between 600 and 2,000 CFU/100 mL for total coliforms (DWAF, 1996; Thinasonke Duze *et al*., 2025).

The high presence of CF indicates the presence of bacterial pathogens such as *Salmonella*, *Shigella*, *Vibrio cholerae*, pathogenic *E. coli*, *Staphylococcus aureus*, and *Pseudomonas* (Tandlich *et al*., 2012). Indeed, *Salmonella*, *Shigella*, *Vibrio cholerae*, and *Vibrio parainfluenza* were detected in all the streams studied. The counts of these bacteria of health interest were consistent with the level of CF contamination. As indicated by the heatmap result, Mayo Saourou, Anam, Bella Fokou, Mbewe streams and Lake Mbakaou also showed extremely high levels of microbial contamination compared to the Mbong, Maba, Massim and Maour rivers. Worryingly, these pathogens are among the most important pathogens having a severe impact on public health. *Salmonella* is the etiological agent of typhoid fever, which is one of the main causes of intestinal diseases worldwide (Levantesi *et al*., 2012). Its survival and proliferation in streams are influenced by pollution and high temperatures, which accelerate its reproduction and dissemination (Reyes *et al*., 2025). High temperatures, between 30 and 36 °C during the dry season in the study area, would be favorable conditions for the proliferation of *Salmonella* sp. Consequently, the presence of this pathogen represents a significant concern for public health (Thinasonke Duze *et al*., 2025).

Shigella is a highly virulent pathogen that causes bacterial dysentery and continues to represent a significant disease burden worldwide, particularly in Asia and Africa (Zaidi *et al*., 2014). *Shigella* bacteria have been detected in all the streams studied, and their counts were much higher than those observed for *Salmonella*. Interestingly, Ekwanzala *et al*. (2017) made the same observation in the Apies stream in South Africa.

Finally, the presence of *Vibrio cholerae* in the studied watercourses, on the other hand, does not directly indicate the presence of a cholera epidemic. An infectious dose ranging from 10^3 to 10^{11} cells, depending on host conditions such as gastric acidity, is required to cause the disease (Nelson *et al.*, 2009).

Conclusion

The presence of these enteric pathogens in this urban river represents a serious public health risk, as the studied watercourses are used by communities for domestic needs, recreational activities for children, swimming, and laundry. High CF rates, as well as the detection of *Salmonella*, *Shigella*, and *Vibrio cholerae*, indicate significant health risks, particularly for communities living in localities adjacent to the studied watercourses. The presence of these enteric pathogens highlights the effects of the common use of watercourses with livestock on the degradation of water microbiological quality and the health of users. These results underscore the urgent need to create improved water points at the study sites in order to reduce health risks for vulnerable population.

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Declaration of conflict of interest

There is no conflict of interest between the authors or with a third party.

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