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ORIGINAL RESEARCH PAPER

Bacteriological quality characterization of a primary water source in Aba Oyo Community, Akure, Nigeria.

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A B S T R A C T

Access to safe water is a significant challenge in many communities in developing countries like Nigeria. This study examines the bacteriological quality of a primary water source in the Aba-Oyo Community in Akure, Ondo State. The community relies on a poorly managed well as its main source of water supply. The objective was to evaluate bacterial contamination and assess the water quality to determine its suitability for drinking. The research follows a cross-sectional design, combining quantitative and qualitative methods. Water samples were collected and analyzed using microbiological testing techniques to estimate bacteria concentration and dominant species. Key Informant Interviews were employed to provide insights into the water practices and prevalent diseases in the community. Results show high bacterial contamination, exceeding permissible limits, including coliform bacteria. Notably, Escherichia coli is absent. Various health-significant bacterial and fungal species were identified in the water samples. The Findings inform interventions for safe drinking water in Aba-Oyo and similar communities, contributing to the existing knowledge on water quality and public health in Nigeria. The study highlights the urgent need for improved water supply infrastructure, promotion of household water treatment options and safe sanitation practices in peri-urban areas of Nigeria.

Introduction

Water is a basic necessity and fundamental resource for life and plays a critical role in promoting public health and reducing the burden of waterborne diseases (Hatami, 2013). However, access to safe and clean water remains a significant challenge in many communities, particularly in developing countries like Nigeria (Iduseri, et al, 2021). One of the primary factors that contribute to poor water quality is contamination with bacteria and other microorganisms that can cause diseases (Ighalo and Adeniyi 2020; Nwinyi, et al, 2020, Pandey et al 2014).

In many rural and peri-urban communities in Nigeria, the bacteriological quality of water sources is often compromised due to inadequate sanitation practices and poor water supply infrastructure (Nwaiwu, Aduba, & Oni, (2020); Christenson, Bain, Wright, Aondoakaa, Hossain & Bartram (2014). In this context, it is essential to evaluate the bacteriological quality of primary water sources in these communities to ensure that they are safe for human consumption. The Aba Oyo community, located in Akure, Ondo State, Nigeria, is one such community where access to safe drinking water is a significant challenge (Lawal & Basorun (2015). The primary water source in Aba Oyo Community is a poorly managed shallow protected well which serves the entire community of about 400 persons in 42 households. Besides the communal well, there is a man-made pond which mostly serves other domestic use for the inhabitants of the community.

Aba Oyo is a peri-urban rural settlement located within the land area of Akure. The farming village has been displaced and its citizens peacefully evicted to a new location towards Aule village. The citing of big projects such as industrial

establishments and educational institutions, as in this case with the Federal University of Technology Akure (FUTA), often results in the extensive conversion of agricultural land to other uses as well as the development of squatter settlements. (Olujimi and Gbadamosi 2007). Aba Oyo community was initially located in the place now referred to as Alaba layout, sharing its northern boundary with FUTA but the migrant farmers were forced to migrate further away towards Aule village, to preserve their farming culture and their privacy, located northwest of FUTA. In 2005, Aba Oyo had 820 residential buildings (Olujimi and Gbadamosi 2007), while a pilot study showed 42 mud buildings which formed the Aba Oyo settlement in 2023. Despite all the years of encounters with urbanization and development, Aba Oyo seems to lack some of the most basic infrastructural facilities every community should have.

Therefore, this study aims to characterize the bacteriological quality of a primary water source in Aba Oyo Community, Akure, Nigeria, using standard microbiological techniques. This study will provide valuable insights into the quality of the primary water supply in the community and the extent of bacterial contamination of the water source and identify potential sources of contamination. The findings of this study will be useful in informing interventions aimed at improving the water quality and ensuring access to safe drinking water in the Aba Oyo community and other similar communities in Nigeria.

Statement of the research problem

The access to basic water supply in Nigeria is low. According to the Joint Monitoring Program by WHO and UNICEF, only 52% of the population in Nigeria has access to basic water supply services. The situation in rural areas is worse, with only 39% of the rural population having access to basic water supply (FMWR, 2021).

The use of protected wells for household drinking water supply in peri-urban settlements in southwest Nigeria is not uncommon. It is one of the main sources of drinking water for many households in the area (Ganiyu, Oyadeyi, & Adeyemi, 2021; Okoh, Miner, Ode, and Zoakah (2021). Protected wells are shallow wells that are constructed with a concrete lining to protect the water from contamination. They are often found in rural and peri-urban areas, where access to piped water supply is limited (Ighalo and Adeniyi 2020; Nwaiwu, Aduba, & Oni, (2020). However, the use of protected wells is not without risks. If not properly maintained, they can still be contaminated with bacteria and other harmful pathogens (Sharma &

Bhattacharya 2017). In addition, depending on the topography of the area, they may not provide enough water to meet the needs of a population, especially during dry seasons. Therefore, it is important to regularly test the water quality and maintain the wells to ensure that they provide safe drinking water (EPA, 2019).

Bacteriological quality is one of the important parameters of water potability. It is measured by the presence of a pollution indicator of organisms, particularly total germs (coliforms) and faecal coliforms (Escherichia coli) (Adamou, Ibrahim, Seyni, Adamou, Sanfo and Liersch. 2020; Cabral 2010). Total coliforms represent the density of the bacterial population in drinking water. Bacteriological water analysis estimates the number of bacteria present and, if needed, finds out what sort of bacteria they are (Hassan 2018; Cairncross 2017). The objective of the study is to determine the concentration of bacteria in the water samples and to draw inferences about the suitability of the water for drinking and domestic use.

The primary water source in Aba Oyo Community is not treated or adequately protected, and there are concerns about the quality of the water and the potential health risks associated with its use. Despite these concerns, there is limited information on the bacteriological quality of the primary water source in the Aba Oyo Community. There have been studies carried out which highlight the challenges associated with access to safe drinking water in rural and peri-urban communities in Nigeria (Shehu and Nazim 2022; Adewumi, 2023; Ishaku, Majid, Ajayi and Haruna, 2011). These studies provide evidence of the inadequate water supply infrastructure and poor sanitation practices that contribute to poor water quality. The studies also demonstrate the potential health risks associated with the consumption of contaminated water, including the prevalence of bacterial contamination and the incidence of waterborne diseases in Nigeria (Shehu and Nazim 2022), which highlights the need for further research on the quality of water sources in rural and peri-urban communities in Nigeria such as the Aba Oyo community in Akure, the capital city of Ondo State. Peri-urban communities in southwest Nigeria are often faced with challenges of safe water supply, owing to poor infrastructural development for delivering piped water to remote and informal settlements which were not planned as part of the city. This causes high dependence on alternative supplementary and mostly private sources, leading to poor health and social outcomes for the residents of such communities (Erhuanga et al, 2014; Okoye, Ngwu, and Ezeokonkwo (2017;

Aikowe and Mazancová, 2021). These challenges include poor water quality, inadequate access to safe water sources, insufficient quantity of water, and high cost of water supply (Iduseri, et al. 2021; Ishaku et al, 2011; Shehu et al, 2022). Therefore, the purpose of this study is to characterize the bacteriological quality of the primary water source in the Aba Oyo Community, identify potential sources of contamination, and provide valuable insights into the extent of bacterial contamination of the primary water source. The findings of this study will be useful in informing interventions aimed at improving the water quality and ensuring access to safe drinking water in the Aba Oyo community and other similar communities in Nigeria.

Research Questions

The following research questions were drawn to help guide the design and implementation of the study on the bacteriological quality characterization of the primary water source in Aba Oyo Community, Akure, Nigeria and contribute to the existing body of knowledge on water quality and public health in Ondo State, Nigeria.
1.	What is the level of bacterial contamination in the primary water source in the Aba Oyo Community, Akure, Nigeria?
2.	What are the dominant bacterial species found in the primary water source in Aba Oyo Community, Akure, Nigeria?
3.	What are the potential sources of contamination in the primary water source in the Aba Oyo Community, Akure, Nigeria?
4.	What are the risk factors associated with bacterial contamination of the primary water source in the Aba Oyo Community, Akure, Nigeria?
5.	What are the prevalent water-related diseases in Aba Oyo Community, as reported by the health workers in the Community Health Centre?

Aim and Objectives

The study aimed to examine the bacteriological quality of the communal well at the Aba-Oyo community in Ondo State, Nigeria, which serves as the primary source of drinking and domestic water in the community. The bacteriological assessment of domestic water– to determine water quality– is essential from a public health perspective. The results of such evaluations allow for informed actions to be taken by the relevant authorities, and ultimately, to prevent the outbreak of waterborne diseases such as cholera, diarrhoea, typhoid, and gastroenteritis (Ewuzie, Aku and Nwankpa, 2021).

This investigation was therefore carried out to identify health-threatening contamination in the water and inform water treatment interventions as a temporary measure while also informing the State and Federal Water Resources ministries and agencies, policymakers and donor agencies on the urgent need for a more permanent solution to the challenges of water supply faced by the citizens of Aba-Oyo.

Research Methods

A cross-sectional study that involves both quantitative and qualitative methods was the methodology adopted for this research.
The quantitative methods involved the collection of water samples from the primary water source in the community which were analyzed in the laboratory for the presence and concentration of bacteria in the samples. This involved the estimation of the total viable bacteria or fungi using Colony Forming Units (CFU) and Spore Forming Units (SFU) per millimetre (mL) of the sample. Also, specific bacterial strains were tested to determine the nature of the bacteria present in the water samples (Abulude, Akinnusotu, Adeoya, Mabayoje, Oluwagbayide, Arifalo, Adamu, 2023).

Key Informant interviews using semi-structured interview guides were engaged to gather qualitative data on the community's water usage practices, perceptions, knowledge about water quality and hygiene, and prevalence of water-related diseases. Community members were purposively selected for the interview using the accidental sampling of heads of households met on the day of the visit by the research team. A total of 6 persons were sampled in this group. The 3 health workers at the Community Basic Health Facility were also interviewed. This helped to provide insights into the community's behaviour and practices related to the use of the primary water source.

Overall, the designed methodology which combines quantitative and qualitative methods in a cross-sectional study would provide a comprehensive understanding of the bacteriological quality of the primary water source in Aba Oyo Community and the factors that contribute to water contamination in the community.

Bacteriological test procedures

The procedures used to determine the microbial load of the water samples in the laboratory included sterilization of all tools and equipment used using the autoclave and Bunsen burner, and cleaning with cotton wool soaked in ethanol. Various types of culture media were used, nutrient agar, MacConkey agar, eosin-methylene blue (EMB) agar, salmonella shigella agar, potato

dextrose agar, and BiGGY agar. Each of the agars was prepared and sterilized according to the manufacturer's specifications. The pour plate method was used to inoculate and culture the water samples, and the microbial colonies were enumerated by counting visible colonies and calculating the colony-forming unit (CFU) or spore-forming unit (SFU) per milliliter. Finally, the isolated colonies were identified using standard methods.

Preparation and sterilization of culture media

Different types of culture media were prepared and sterilized as detailed in (Koyo, B., 2017) using commercially-prepared media in sterile distilled water in conical flasks. Nutrient agar was prepared by stirring 28g of the medium, while MacConkey agar was prepared by swirling 50g of medium until dissolved. Salmonella Shigella agar was prepared by boiling and stirring 63g of medium and pouring it into sterile petri dishes, while Eosin methylene blue agar was prepared by swirling and sterilizing 37.5g of the medium, cooling it to 60°C, and shaking to restore the blue colour. Potato dextrose agar was prepared by sterilizing 39g of the medium. All media were sterilized by autoclaving at 121oC for 15 minutes.

Preparation and inoculation of samples

The Pyar and Peh (2014) pour plate method was used to prepare and inoculate samples. Water samples (3g) were added to test tubes with cooled sterilized water, mixed, and serially diluted. Dilutions were plated onto petri dishes and incubated for 24 hours for bacteria and 2-4 days for fungi at 37oC and 25oC, respectively. Colony counts were obtained, purified, and characterized using standard methods.

Enumeration of microbial colonies

Colony counting was carried out visually by counting the number of visible colonies that appeared on the plates. The calculation of colony forming unit (CFU) per ml for the bacteria and the spore forming unit (SFU) per ml for the fungi was based on the formula:

CFU/ml or SFU/ml = Number of colonies × dilution factor / ml of sample suspension

Isolation and Identification of Microorganisms
Isolation of Bacteria

The pour plate method was used for bacterial isolation through serial dilution of water samples using dilution factors 103 and 104. Aliquots from each dilution were inoculated into sterile petri dishes and salmonella-shigella agar, EMB agar, MacConkey agar, and nutrient agar were poured in. Incubation was done at 37oC for 24 hours. Colonies were sub-cultured on nutrient agar for characterization and the microbial load was measured using the indirect cell count method. The agar slant technique was used for the preservation of cultures by transferring the colony to the surface of a sloped agar slant, incubating at 37oC for 24 hours and refrigerating at 4oC until when needed.

The pour plate method with serial dilution was used to isolate bacteria from water samples. Dilutions were inoculated into sterile petri dishes with the different types of agars and incubated at 37oC for 24 hours. Uninoculated plates were used as controls for sterility. Colonies were sub-cultured on nutrient agar for characterization and viable counts were measured using the indirect cell count method. Agar slants were used for the preservation of cultures (Daniel and Daodu, 2016).

Isolation of Fungi

Fungi were isolated using the pour plate method and Potato dextrose agar. Serial dilutions of 10-3 and 10-4 were used, followed by incubation at 25°C for 2-3 days. The cultures were preserved using the agar slant technique in double-strength Potato dextrose agar in McCartney bottles, incubated at 28°C for 72 hours, and then refrigerated at 4°C.

Identification of Bacteria Isolate

Bacteria were identified using morphological, cultural, and biochemical characteristics according to the procedure highlighted in Beal, et al. (2013). To perform Gram staining, bacterial isolates were smeared on a slide with sterile water and heat-fixed. Crystal violet stain was applied for 1-2 minutes, followed by Gram's iodine for 1 minute. The slide was washed with 95% alcohol, rinsed with water, and counterstained with safranin for 1-2 minutes. After rinsing and drying, the slide was examined under a microscope with oil immersion (Oladeji and Odelade, 2016).

The biochemical characteristics tested involved the following tests to identify the presence of certain organisms: Coagulase Test, Indole Test, Oxidase Test, Methyl-Red Test, Voges-Proskauer Test, Citrate Utilization test, Motility Test, Sugar Fermentation Test and the Spore Staining test (Adamu et al., 2017; Daniel and Daodu 2016;). Carbohydrate Utilization tests were designed to detect the change in pH which occurs with the fermentation of the given carbohydrate. The carbohydrate tests performed are the Glucose (Dextrose) test, Lactose test, Sucrose test, Maltose test, Mannitol test, Xylose, Raffinose, Arabinose, Rhamnose, Ribose, Galactose, fructose and more (Adetunji et al., 2012).

Results
Analysis of water samples

The results presented in this section show the total viable organisms count measured in coliform units and presented in Table 1.

The pH, temperature and turbidity of the water sample were analyzed to ascertain its physiochemical properties. The temperature of the water sample was found to be 24 – 26°C. The sample had a cloudy whitish visual appearance with turbidity measurement of 7 – 10 NTU. The pH of the water samples ranged from 6.4 – 6.8.

The microbial load of the water samples was analyzed. Total bacteria count, total coliform and faecal coliform counts, as well as salmonella and fungi counts, were enumerated. The total bacteria count ranged from 182 - 187 x 10^4 cfu/ml in the samples analyzed. No faecal contamination was indicated as zero *E.coli* count was found in the samples. Fungi were found present in the samples at a mean count of 44 x 10^4.

Bacterial and spore species were isolated and identified in the sample. Some of the organisms encountered are of public health significance such as; pseudomonas aeruginosa, Citrobacter murliniae, Klebsiella (Enterobacter) aerogenes, and Serratia liquefaciens sp.

The results presented in Table 1 show the presence of bacterial and fungal coliforms but an absence of *E.coli*, indicating the possible absence of faecal contamination in the water source.

The bacteria and fungi count exceeds the maximum permissible microbiological limit as specified in the Nigerian Standard for Drinking Water Quality (NIS, 2015). The identified probable organisms present in the Aba-Oyo communal well water samples are presented in Table 2.

Qualitative survey results

The results of the Key Informant Interviews are presented in the chart in Figure 1

Discussion and Interpretation of Results
Microbial analysis of the well water sample

The results of the microbial analysis of three samples from the Aba-Oyo well which involved tests for the total viable bacterial count, total viable coliform count, total viable *E. coli* count, and total viable fungi count in the water sample as presented in Table 1 indicates that the mean total viable bacterial count for the three wells was 184 x 10^4 cfu/ml. This suggests a high level of bacterial contamination in the wells. The total viable coliform count was 22 x 10^4 cfu/ml, indicating the presence of coliform bacteria, which are commonly found in the intestines of humans and animals and can be indicative of faecal contamination. A positive total coliform test indicates unsanitary conditions and the possible presence of disease-causing organisms (Scherer, Feb. 2022).

Coliform bacteria include a large group of many types of bacteria that occur throughout the environment. They are common in soil and surface water and may even occur on your skin. Large numbers of certain kinds of coliform bacteria can also be found in waste from humans and animals. Most types of coliform bacteria are harmless to humans, but some can cause mild illnesses and a few can lead to serious waterborne diseases. Coliform bacteria are often referred to as "indicator organisms" because they indicate the potential presence of disease-causing bacteria in water. The presence of coliform bacteria in water does not guarantee that drinking the water will cause an illness. Rather, their presence indicates that a contamination pathway exists between a source of bacteria (surface water, septic system, animal waste, etc.) and the water supply. Disease-causing bacteria may use this pathway to enter the water supply. (Swistock and Sharpe, October 31, 2022)

The total viable *E.coli* count was nil, indicating that the water source is free of *E. coli*, an indicative organism for the presence of some coliform bacteria that can cause serious illness if consumed in water. *E. coli* is a type of faecal coliform bacteria commonly found in the intestines of animals and humans. A positive *E. coli* result is much more serious than coliform bacteria alone because it indicates that human or animal waste is entering the water supply (Swistock and Sharpe, October 31, 2022).

The total viable salmonella count was also nil, which is another positive result, as salmonella is a pathogenic bacteria that can cause severe illness in humans.

Lastly, the mean total viable fungi count was 44 X 10^4 cfu/ml, indicating the presence of fungal contamination in the samples. While some types of fungi can be harmless, others can cause illness or allergies in humans.

Overall, the results suggest that the Aba-Oyo community-owned well is contaminated with high levels of bacteria and fungi, and the presence of coliform bacteria indicates contamination, which poses a potential risk to human health. Further measures should be taken to ensure the safety of the water supply from these wells.

Microbial analysis Identification of specific microorganisms present in the well water sample

The data displayed in Table 2 shows the characteristics of several microorganisms isolated from the water sample from the well in Aba-Oyo. The characteristics analyzed include spore formation, Gram staining, shape, catalase production, gas production, H_2S production, lactose, sucrose, glucose, MR (methyl red) test, VP

(Voges-Proskauer) test, starch hydrolysis, casein hydrolysis, lipase hydrolysis, nitrate reduction, motility, indole production, citrate utilization, and utilization of various sugars, which were used to identify the bacterial species present in the water sample.

Based on the results, at least ten different species of microorganisms are present in the well water, as indicated by their different characteristics. These include Bacillus tequilensis, Pseudomonas aeruginosa, Bacillus trypoxylicola, Clostridium ramosum, Staphylococcus gallinarum, and Staphylococcus equorum subsp. equorum, Paenibacillus pectinilyticus, Citrobacter murliniae, Bacillus licheniformis, Klebsiella (enterobacter) aerogenes, and Seratia liquefaciens.

The similarity percentages provided in the table suggest that these species have similar genetic sequences to those in the database used for comparison. For example, Bacillus tequilensis has a similarity of 84.3%, while Pseudomonas aeruginosa has a similarity of 98.3%. These similarities suggest that the microorganisms identified in the well are closely related to the reference species and hence, most probable. In identifying the probable microorganisms present in the water sample, insight is provided into the ecological conditions and potential risks associated with the consumption and use of water from the Aba-Oyo well.

Health risks associated with identified organisms

Members of the genera Klebsiella, Enterobacter, Serratia, and others are mostly considered as environmental coliforms. Some other groups of coliforms are considered as "ubiquitous coliforms". However, while some coliforms in this group, including some species of Klebsiella, Enterobacter, and Citrobacter, may originate from faecal matter, they also can originate from environmental sources, making it difficult to determine if their presence is an indication of faecal contamination or not (Mena and Gerba, 2009).

P. aeruginosa is part of a large group of free-living bacteria that are ubiquitous in the environment. This organism is often found in natural waters such as lakes and rivers. P. aeruginosa can cause a wide range of infections and is a leading cause of illness in immunocompromised individuals (Mena and Gerba (2009).

While there is limited information on the potential health risks of Paenibacillus pectinilyticus, Bacillus tequilensis and Bacillus trypoxylicola; Bacillus licheniformis is known to be a common environmental bacterium that can cause infections in humans with weakened immune systems. Some Bacillus species can cause food poisoning and infection in humans.

Staphylococcus is a common bacterium found on human skin and in the environment. While many strains are harmless, some can cause infections, particularly in individuals with weakened immune systems. Clostridium ramosum though a common gut bacterium in animals and humans, can cause severe infections in humans which can lead to sepsis, meningitis, and abscesses.

In conclusion, the presence of these microorganisms in water can pose various health risks, especially to individuals with weakened immune systems, making young children and the elderly easy targets. Proper treatment and disinfection of the water source as well as treatment and safe storage at households are necessary to reduce the risk of contamination and associated health risks.

Table. 1. Microbial analysis of coliform forming units in the Aba-Oyo communal well

Sample	Total Bacterial Cfu/ml	viable count	Total viable Coliform count Cfu/ml	Total viable E.coli count Cfu/ml	Total viable salmonella count Cfu/ml	Total viable Fungi count Cfu/ml
ABA-OYO WELL 1	183 X104		22 X104	Nil	Nil	45 X104
ABA-OYO WELL 2	187 X104		25 X104	<1	Nil	45 X104
ABA-OYO WELL 3	182 X104		19 X104	<1	Nil	43 X104
MEAN Value	184 X104		22 X104	Nil	Nil	44 X104

Table 2: Probable organisms present in the Aba-Oyo well water sample

S/N	SPORE	GRAM	SHAPE	CATALASE	GAS	H2S	LACTOSE	SUCROSE	GLUCOSE	M.R	V.P	STARCH HYDROLYSIS	CASEIN HYDROLYSIS	LIPASE HYDROLYSIS	NITRATE	MOTILITY	INDOLE	CITRATE	ARABINOSE	XYLOSE	MALTOSE	MANNITOL	GLYCEROL	FRUCTOSE	SORBITOL	GALACTOSE	ACID PRODUCTION	STARCH AS SUGAR	PROBABLE ORGANISMS
ABA-OYO WELL	+	+	rod	+	+	-	-	+	+	+	-	-	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	Bacillus tequilensis ~ similarity 84.3%
	-	_	sh. rod	+	+	-	-	-	+	+	-	-	-	-	+	+	+	+	-	-	-	+	+	+	-	+	+	-	Pseudomonas aeruginosa~ similarity 98.3%
	+	+	Long Rod	+	+	+	-	+	+	+	-	-	-	-	+	-	+	+	+	+	+	+	+	+	+	+	+	+	Bacillus trypoxylicola ~ similarity 74.4%
+	+		rod	+	+	-	+	+	+	+	-	+	-	-	-	+	-	+	+	+	+	+	+	+	-	+	+	+	Clostridium ramosum 96.5%
	_	+	cocci in clusters	+	+	+	-	+	+	+	-	-	+	-	+	+	+	+	+	+	+	+	+	+	+	+	-	+	Staphylococcus gallinarum ~ similarity 98.3%
	-	+	cocci in clusters	+	+	+	-	+	+	+	-	-	+	-	+	+	+	+	+	+	+	+	+	+	+	+	-	+	Staphylococcus equorum subsp. equorum ~ similarity 98.3%
	+	+	rod	+	+	+	-	+	+	-	+	+	+	-	+	-	+	+	+	+	+	+	+	+	+	+	+	+	Paenibacillus pectinilyticus ~ similarity 84.3%
	-	_	sh.rod	+	+	+	-	+	+	+	-	+	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	Citrobacter murliniae ~ similarity 97.6%/
	+	+	Long .rod	+	+	+	+	+	+	+	-	-	-	-	+	+	+	+	+	+	+	+	+	+	+	+	-	+	Bacillus licheniformis ~ similarity 79.4%

Findings from Qualitative data collected from the field survey

Basic background data about the community population and demographics were obtained via key informant interviews with members of the community and the community health centre workers.

The data is summarized below:
- 42 Households, Population of about 400 persons (49% male: 51% female; 64% Adult: 36% children under 15 years
- Major Occupation: Farming
- Government presence and public facilities: Basic Health Centre, LG Primary School
- Other sources of water: Man-made pond used for domestic purposes
- Sanitation practices: Open defecation
- Health challenges of greatest concern: Malaria

Basic Water Sources in the Community

The members of the community (100%) reported a lack of basic safe water supply facilities available in households and at the Health Centre.

The Primary water source is the communal well, especially during the dry season. Rainwater harvesting is more commonly used as a source of water during the rainy season. Some (67%) of the respondents reported fetching drinking water from newly-dug private-owned wells at building construction sites near the community. However, the private wells are mostly open for fetching for a few hours in the morning (Once-a-day access). The respondents also reported having access to a community-owned pond (which fits the description

of a man-made or dug-out pond). The pond provides water for domestic activities like washing clothes (83%), cooking (50%), doing dishes (67%), and sometimes drinking (50%). Visual observation from the surroundings of the pond shows that a cottage palm oil refinery and processing point is sited very close to the pond which is believed to supply water for the washing, boiling and processing of the palm oil. Also, animals have access to the pond, which is not fenced and the surroundings are bushy.

Interviews with the health workers revealed that the Health Centre also lacked access to basic water supply. The workers (100%) reported paying community youngsters to fetch a few buckets of water for the daily running of the Centre. They complained of the health risks associated with the lack of adequate access to water in the facility to wash hands, do laundry, clean the Centre and keep the toilets clean.

On the time taken to collect water, the respondents reported an average of between 15-20 minutes. The actual distance depends on the location of the household. Visual observation showed that the communal well is located a short distance away from the cluster of houses, in a clearing surrounded by farmlands. For most households (83%), young females (in their teenage years) were responsible for fetching water for the household. For the other households, younger boys collected the water from the source.

None of the respondents reported treating the water from this well or any other sources (private wells and rainwater). Even though visual observation showed the well water was lightly cloudy and the pond water very turbid.

Sanitation practices in the community

Many of the households (83%) reported not having access to basic sanitation facilities. However, the staff at the Health Centre reported that none of the households had a toilet/ latrine on the premises and that they all practised open defecation. They also reported that although the Health Centre was fitted with a water-closet (WC) type toilet facility, they (the health workers) were sometimes forced to practice open defecation as well, when they do not have a sufficient supply of water in a day.

It was reported that the children defecated openly within the surrounding of the premises. It is usually left unattended in 100% of the cases for animals (dogs) to clear it. While the adults used the nearby bushes.

Common/prevalent diseases in the Community

The Health Centre staff reported the most prevalent diseases in the community were malaria and typhoid fever, from their records. They reported that the members of the community did not mostly regard diarrhea as an illness that required medical attention at the Centre. So, they did not visit the Health Centre for diarhea and related illnesses, rather they self-medicated by getting medications from the Chemist/ local pharmacies or resorted to using herbal/home remedies.

The members of the community (67%) believed that their community well supplied them with clean water which was safe for consumption. They claim they have always used it and do not fall sick from drinking it. The other 33% reported that they preferred not using the community well for drinking, and they reported waking early to fetch from the newer wells in neighbouring construction sites. However, they (100%) would desire greater access to water supply within their premises to make it easier to fetch water even after dark.

Sanitary Inspection of the well site

Visual observation of the areas surrounding the well shows that the well is located away from activities that can contaminate it. No signs of human or animal excreta were seen anywhere near the well. There was no refuse dump site anywhere near the well. The palm oil processing site is located a few hundred meters away from the well.

However, the maintenance of the well appears to be very poor. The well has a wooden cover which is mostly broken off, leaving most of the top of the well uncovered. Also, the top rings of the well are mostly covered in green matter (algae) and insects and organic life forms such as cockroaches can be seen crawling around the insides of the well cover. Though there is a dedicated fetcher attached to the well, it seems to lack frequent washing.

The well also appears poorly constructed; there is no flooring around the well head to prevent the pooling of water at the well. The surrounding is bushy and could possibly harbour open defecation within a few meters from the well. Lastly, the well is not fenced off to avoid animals having direct access to the well.

Fig. 1. Qualitative data collected from key informant interviews

Figure 2: Water sources in Aba-Oyo a) The well b) The well opening with cover c) The pond

Conclusion

The qualitative data collected indicates the well is not suited for consumption and domestic purposes such as bathing because there can be risks of infections through the skin and via inhalation. The sanitation practices of the households indicate a risk of contamination of water at the households.

Therefore, it is advised that interventions be designed to educate the people on good sanitation and hygiene practices, disinfect the community-owned well, as well as provide an alternative source of water or a household treatment option as a temporary measure to meeting the safe water needs of the Aba-Oyo community. This study recommends that the Local and State Governments in partnership with donor agencies, provide basic water supply access to the Aba-Oyo Primary Health Centre, in a matter of utmost urgency, to secure the health of the workers, prevent the spread of diseases, and enhance the health of the people of Aba-Oyo.

Conflict of interest

The author declares that there was no conflict of interest.

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