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## SHORT COMMUNICATION ASSESSMENT OF BACTERIAL LOAD IN DIFFERENT SACHET WATER SOLD WITHIN SULE LAMIDO UNIVERSITY, KAFIN HAUSA

\*Isah H. A. and Muhammad A. H.

Department of Biological Sciences Sule Lamido University Kafin Hausa Correspondence Author: <u>halimaisah84@gmail.com</u>; 08060743232

#### ABSTRACT

The research was conducted to assess the bacterial load in different sachet water sold at Sule Lamido University, Kafin Hausa. The samples were collected directly from manufacturers and the school shops. Eight water samples (A<sub>1</sub>, B<sub>1</sub>, C<sub>1</sub>, D<sub>1</sub>) collected from shop and (A<sub>2</sub>, B<sub>2</sub>, C<sub>2</sub>, D<sub>2</sub>) from the manufacturers were analyzed in triplicate using Serial dilution and pour plate methods on nutrient agar respectively. The isolates were identified using gram stain techniques and biochemical tests. It was found that the total bacterial load found in samples A<sub>1</sub>, A<sub>2</sub>, B<sub>1</sub>, B<sub>2</sub>, C<sub>1</sub>, C<sub>2</sub>, D<sub>1</sub> and D<sub>2</sub> were 108, 10, 88, 12, 204, 118, 50 and 10cfu respectively. Samples obtained from shops were comparatively observed to have high bacterial loads of 204cfu and this indicates the improper treatment, contamination during handling and distribution of the finished product at the shop. The organisms found were Staphylococcus spp, Streptococcus spp, Enterobacter spp and E.coli. Key words: Sachet water, Bacterial load, Sule Lamido,

## INTRODUCTION

Water is one of the most essential commodities for the survival of all lives. It is abundant in nature and occupies about 70% of the earth's crust (Kalpana *et al.*, 2011). Safe and readly available water is important for public health whether it is used for drinking, domestic, food production or recreational purposes. Improved water supply and sanitation as well as management of water resources can boost countries economic growth and greatly contribute to poverty reduction (WHO, 2019).

Contaminated water and poor sanitation are linked to transmission of diseases such as cholera, diarrhoe, dysentry, hepatitis A, typoid and polio (WHO 2019). The report also added that was in 2017, almost 829,000 people were estimated to die from diarrhoea which was mainly as a result of unsafe drinking-water, sanitation and hand hygiene.

Megarsa (2018) quoted WHO report that, about 80% of all the human diseases are cauesd by water and about 780 million people do not have access to a purified water source while an estimated 2.5 billion people lack access to improved sanitation worldwide (CDC, 2003).

Water is considered portable for human consumption or recreational activities when foreign enteric bacteria are not detected in a specific volume (100ml) of water (Abu *et al.,*  2020). The use of intestinal organisms as indicators of feacal contamination is a universally acceptable process for monitoring and assessing the microbiological safety of water supply before distribution. Two of the most widely accepted bacterial indicator organisms are *Escherichia coli* and *Streptococcus* due to their feacal linkages (Harwood *et al.*, 2004).

Though a water supply may pass all laboratory tests, we have to bear in mind that hazard may arise from pollution of the water source through cross-connection, back symphonage, leaks in mains and service reservoirs (Philip et al., 2018). The report indicates that there is isolation of some pathogenic organisms like Salmonella, Shigella and Escherichia coli from drinking water and most reported cases in Typhoid fever were not unconnected with drinking of sachet packaged water. Organisms which are well characterized and mostly present can include strains of Salmonella, Shigella, Leptospira, Enteropathogenic Escherichia coli, Francisella, Vibrio, Mycobacteria, Human enteric viruses, Cysts of Entamoeba histolytica, Giardia lamblia, or other pathogenic protozoans and larvae of various pathogenic worms. Salmonella strains have been frequently detected in drinking water sources and this have been correlated with outbreaks of Salmonellosis (Philip et al., 2018).

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Contaminated water supplies affect the growth and nutrition in young children adversely. Production of quality water product is increasingly difficult, because the demand for water is high and implementing universal standard for drinking water has not being followed to the letter, due to differences in sociological conditions, varying climates and other specific circumstances found all over the world. However, water treatments such as storage in open reservoirs, coagulation, filtration and treatment with chemicals can be used to improve quality of the product from the raw water (Funmilayo *et al.*, 2021).

Packaged drinking water like the sachet water could be water from any potable source such as tap, well and rain, which may be subjected to further treatments like decantation, filtration, demineralization and other methods to meet established drinking standard. The aim of this study is therefore, to assess the bacterial load in different sachet water sold at Sule Lamido University, Kafin Hausa for exploitation towards ascertaining its quality.

## MATERIALS AND METHODS

Four Different samples of sachet water of different brands were commercially purchased from school shops and labelled as  $A_1$ ,  $B_1$ ,  $C_1$  and  $D_1$ . 500ml of each brand were also collected from the production site in a water sample bottles labelled  $A_2$ ,  $B_2$ ,  $C_2$ ,  $D_2$ . These were transported immediately to Biological Sciences Laboratory, Sule Lamido University, Kafin Hausa for analyses. Each sample was vigorously shaken and observed for turbidity, odor, shelf life, batch number and manufacturing dates.

#### Bioassay

#### **Total Viable Counts**

The analysis of total viable count (TVC) was done using the standard plate count method. The count represents the number of colonyforming units (CFUs) per ml of the sample. The reported count is the number of colonies counted multiplied by the dilution used for the counted plate. A high TVC count indicates a high concentration of microorganisms, which may indicate poor quality for drinking water. The bacteriological test was done within 2 hours of sample collection. The determination of total heterotrophic bacteria was done using serial dilution and pour plate technique. For this, tenfold serial dilution in sterile water was carried out for each water sample brought for testing. One ml from the 5<sup>th</sup> test tube was aseptically taken on two occasions and placed in two different sterile Petri dishes. Then, 15ml of nutrients agar (which was prepared as described

by the manufacturer) cooled to 50°C was added to each plate and mixed thoroughly. The mixtures were allowed to solidify and incubated at 37°C for 24 hours. After incubation, the number of bacterial colonies in both the plates was counted and the average was reported as CFUs per milliliter of the tested sample. The assay was done in triplicate (Uzma *et al.*, 2015).

# Characterization and Identification of Bacterial Isolates

**Pu**re forms of the bacterial isolates were characterized and identified based on their microscopic morphology and biochemical characterization as described by Cheesbrough (2006).

#### Gram stain

Gram's stain was used to stain the bacteria for microscopic examination to identify the morphology of bacteria. The colony were prepared on a microscopic slide using a drop of crystal violet solution which was allowed to stand for 1minute and then washed with water, the smear was flooded with iodine and was allowed for 1minute and then washed with water. The smear was flooded again with acid alcohol and it was then quickly washed with water, smear was finally flooded with safranin for 30secs and with water. The slide was then air dried and observed under the microscope using oil immersion (Bello *et al.*, 2014).

#### **Biochemical Test**

These tests were used to identify bacteria on the basis of their biochemical characteristics, namely; Catalase Test (James, 2001); Coagulase Test (Chidi *et al.*, 2006); Oxidase Test (James, 2001); Indole Test (Cheesbrough, 2006); Triple Sugar Iron Test (Funmilayo *et al.*, 2021).

#### **RESULTS AND DISCUSSION**

After physical examination, all the samples were found to be odorless and no visible particles seen and while noting the shell life as well as the batch number clearly stated, no date of production was provided.

#### **Bacterial viable count**

From the research conducted, it was found that there is bacterial growth at all the samples analyzed (Table 1). After conducting a bacterial viable count, samples  $A_1$  and  $A_2$  were found to be creamy with 108 and 10cfu respectively.  $B_1$ were golden and creamy with 88cfu while  $B_2$ ,  $C_1$ ,  $C_2$  were golden and milky with 12, 204,118cfu respectively. However,  $D_1$  were creamy and golden with 50cfu while  $D_2$  were milky and golden with 10cfu. It was indicated that sample C has the highest bacterial loadand this quantity was still accepted as it is within the range of maximum value accepted by CDC (2003), which specify that hetetrophic plate count should be less than 500cfu/ml.

#### **Identified organisms**

After 24hrs of incubation, the isolated organisms were identified based on their cultural appearance, microscopic appearance and biochemical tests (Table 2). They include *Staphylococcus aureus, Streptococcus spp, Escherichia coli* and *Enterobacter spp.* The *E.coli* was present in all the samples except sample D<sub>1</sub> and D<sub>2</sub>, Staphylococcus aureus was found in sample B<sub>1</sub>, B<sub>2</sub>, C<sub>1</sub>, D<sub>1</sub> and D<sub>2</sub>. *Streptococcus* was isolated in samples C<sub>1</sub> and C<sub>2</sub>. *Enterobacter spp* was only present in A<sub>1</sub> and A<sub>2</sub>

The presence of the *E.coli* in all the samples indicates that the water is not safe to drink because the composition is above the accepted value by CDC (2003), which stated that water should contain lessthan one coliform bacteria per milliliter. Coliform bacteria are organisms whose presence in the distribution system could indicate fecal contamination, in which *E. coli* is member and also it is a potential important human pathogene associated with a variety of The presence of *Enterobacter spp* which exist at higher temperature may be from its contamination due to the poor storage. Ogueri et al. (2020) stated that long storage of sachet

infectious diseases such as gastroenteritis and dysentery as stated by Uzoigwe and Agwa (2012).

The presence of coliform bacteria in drinking water generally suggests that the drinking water may have been contaminated with either humans or animals feaces. Coliform bacteria are enteropathogenic that interfere with human health (WHO, 2008). This result agreed with the work of Jumenten *et al.* (2020) where they found that *E.coli* contamination was due to unhygienic environmental conditions.

*Staphylococcus* aureus was present and this could be attrinuted to its commensal property. This finding is similar to that of funmilayo *et al.* (2021) were they isolated staphylococcus from the bottle water. Previous study according to Falegan *et al.*, (2021) reported that satchet water samples collected from five different manufacturers yielded 20.8% Staphylococcus aureus.

Some *Streptococcus spp* are associated with feacal origin due to its ability to withstand advance conditions. According to Standard Organization of Nigeria (SON) in Nigeria, thermo tolerant coliform (*E.coll*), faecal *Streptococcus* and *Clustridium perfringes* spore shuld be 0cfu/100ml in drinking water.

water under unfavourable environmental conditions and lack of good manufacturing practices (GMP) contribute to contamination.

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S/N	Sample	Colony count (cfu)			
1	A <sub>1</sub>	108			
2	A2	10			
3	B1	88			
4	B2	12			
5	<b>C</b> 1	204			
6	<b>C</b> <sub>2</sub>	118			
7	D1	50			
8	D <sub>2</sub>	10			

Table 2: Microscopic and Biochemical Characteristics of the Isolated organisms

Microscopic Diochemical characteristics								
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SH	CAT	COA	СТ	BH	IN	TSI	OX	ORG
Rod	+ve	*	-ve	+ve	+ve	+ve	-ve	E.coli
Rod	*	*	+ve	-ve	-ve	+ve	-ve	Enterobacter spp
Cocci in bunch	+ve	+ve	-ve	+VE	*	*	*	Staphylococcus aureus
Cocci in chain	-ve	-ve	*	+ve	*	*	*	Streptococcus spp
	SH SH Rod Rod Cocci in bunch Cocci in	Rod +ve Rod +ve Rod * Cocci in +ve bunch Cocci -ve in	Rod +ve * Rod +ve * Rod * * Cocci in +ve +ve bunch Cocci -ve -ve in	Ance <u>SH CAT COA CT</u> Rod +ve * -ve Rod * * +ve Cocci in +ve +ve -ve bunch Cocci -ve -ve * in	SHCATCOACTBHRod+ve*-ve+veRod**+ve-veCocci in+ve+ve-ve+VEbunch-ve-ve*+vein-ve-ve*+ve	SH CAT COA CT BH IN Rod +ve * -ve +ve +ve Rod * * +ve -ve -ve Cocci in +ve +ve -ve +VE * bunch Cocci -ve -ve * +ve * in	SHCATCOACTBHINTSIRod+ve*-ve+ve+ve+veRod**+ve-ve-ve+veCocci in+ve+ve-ve+VE**bunch-ve-ve*+ve**	SHCATCOACTBHINTSIOXRod+ve*-ve+ve+ve+ve-veRod**+ve-ve-ve+ve-veCocci in+ve+ve-ve+VE***bunch-ve+ve****Cocci-ve-ve*+ve**in-ve****

KEY: GR: Gram reaction, SH: Shape of the colony, CAT: Catalase test, COA: Coagulase test, CT: Citrate test, BH: Blood hemolysis, IN: Indole test, TSI: Triple sugar iron test, OXI: Oxidase test, ORG: organism identified

## CONCLUSION

The result of this study showed that all the water samples were not safe for drinking due to the presence of *E.coli* and *Streptococcus spp*. Which may occur due to the improper treatment and poor hygiene. Therefore, it is suggested that there should be periodic checks and analysis on the method and strategies used in the

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production and supply of the manufacturers' products. Also when coliforms and other bacteria are found, it is always recommended that an investigation should be carried out to identify the sources of the contamination as this can help to reduce the spread of water borne diseases.

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