

A Geospatial survey of Disease-Causing Organisms in Some Selected Rural Domestic Water Sources of Southern Gombe Zone, Gombe State, Nigeria

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ABSTRACT

The study carried out a geospatial survey of disease-causing organisms in some selected rural domestic water sources of southern Gombe Zone, of Gombe State in North-eastern Nigeria. It sought to isolate *Escherichia Coli* 0157, *Salmonella Spp.* and *Shingella Spp.* from 12 purposively sampled rural water sources as well as determine seasonal concentration of these pathogenic microbes in the sample waters. The study also sought to depict spatial distribution of microbial contaminants in the sampled waters. The study adopts traditional microbiological culture methods using selective and differential culture media as well as biochemical tests for the isolation and determination of pathogenic microbes. Findings were presented in tables as well as maps and discussed descriptively. Major findings reveal that pathogenic *E.coli* prevalence is high, that is 75% in dry season and 83% for wet season. Results also shows that the highest concentration of *Salmonella spp* bacteria in the study area recorded is 103 cfu/ml and 128 cfu/ml for both wet and dry season respectively while the highest observation of concentration of *Shingella spp.* in the region is 86 cfu/ml in the wet season and 66 cfu/ml in the dry season. The study concludes that *E. coli* 0157, *Shingella Spp.* and *Salmonella Spp.* are prevalent in all type of water sources in the study area, they are also prevalent in wet and dry seasons.

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INTRODUCTION

The introduction of substances into water sources through pollution from human activity such as open defecation, agriculture (crop and livestock raising), industrial and domestic effluent significantly enhances the proliferation of bacteria into these waters (Edokpayi, et al, 2018). Microbial polluted waters are considered extremely dangerous for human consumption such as drinking, bathing, cooking or even swimming as they are absorbed into the human system orally, dermally, by wounds or body orifice causing health challenge (Some et al, 2021; Aqua-

Free, 2024). Hence, most standard benchmark of water quality pegged microbial permissible level at zero.

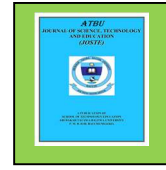
Pathogenic species of *Escherichia Coli* (usually called *E. coli* 0157), *Salmonella spp* and *Shingella Spp* are among predominant bacterial flora found in polluted waters causing illness in humans (Some et al, 2021). The *E coli* 0157 bacteria is the causative organism for a kind of diarrhoea, *Salmonella spp* on the other hand causes *Salmonellosis* and Typhoid, while *Shingella spp* is known to cause *Shingellosis* and Hemolytic Uremic Syndrome. Substantial number

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of illnesses and fatalities occur each year as a direct consequence of utilizing contaminated water sources. Diarrheal diseases stemming from polluted water alone account for approximately 3 million deaths annually (Almasi & Nouri, 2022). In specific instances, *Salmonella Spp* is considered the cause of over 93 million cases of illnesses and 155, 000 deaths globally, while *Shingella Spp* results in over 1.1 million deaths worldwide (Eng, et al, 2015; Logue, etal 2017).

Rural water quality deserves increased attention because it is a pertinent element in eliminating rural poverty (UN water 2011). Among major factors for rising rural poverty level and worsening poor rural condition in Nigeria is disease burden from water borne illnesses of rural population (Nigeria Bureau of Statistics, 2022). Huge amount of money needed by rural dwellers to improve their standard of living is spent in managing diseases whose causative organisms thrive in the water they consume.

Evaluating the microbial quality of domestic water is critical because its contamination by pathogenic bacteria constitutes a significant public health concern affecting populations globally (Alex & Kpormon, 2023). A considerable proportion of rural inhabitants depend on untreated water sources, such as streams, springs, ponds, dams, rivers, boreholes, and rainwater, which is much vulnerable to contamination by pathogenic microbes thereby transmitting diseases and elevating infant mortality rate. The 2021 Nigerian contamination status by source indicates that hand pump boreholes are 45%, motorised boreholes 49%, wells 75%, and springs 89%, this indicates the need for proactive measures to monitoring and surveillance of rural water sources to fore stop diseases outbreaks from contaminations (Fed. Min. of Water Resources, 2022).

Apart from the fact that rural households consume more microbial contaminated water in Nigeria compared to their urban counterparts according to Federal Ministry of Water Resources, the Gombe state government has also recently decried the practice of open defecation in many communities of the state which hindered effort to achieving an 'open defecation free state' status

among other state in Nigeria (Fed. Min. of Water Resources, 2022; Azubuike, January 2024). There is an observed widespread open livestock raising and open defecation among rural communities of southern Gombe zone as evidences abound in nearby bushes and river/stream banks, these make rural water sources vulnerable to most forms of faecal contamination from humans and animals, thus stirring curiosity as to microbial quality of water consumed within these areas.

Again, a random questioning of out-patient from primary health centres in Gombe south zone suggest substantial cases of gastro-intestinal illnesses and typhoid in addition to malaria as prevalent health challenges of the people of the region. Nwabor et al (2015), Logue et al (2017) and Some et al (2021), suggest these challenges could be from water sources consumed, hence the need for deeper insight on the possible causative factor for this development in the Gombe south zone.

Furthermore, although the seasonal variations, species diversity, source-route of contamination and concentration of microbial pollutant in domestic water is widely studied as shown by volume of literature in public domains, the spatial dimensions of these kind of environmental pollution is scantily studied. Therefore, this study seeks to geospatially survey the presence of disease causing organisms in rural domestic water sources of some localities in southern Gombe zone, it specifically;

1. Isolate *E. coli* 0157, *Salmonella spp* and *Shingella spp* in some selected water sources of the study area.
2. Determine the concentration of *E. coli* 0157, *Salmonella spp* and *Shingella spp* in some selected water sources of the study area.
3. Describe spatial and seasonal variations in concentration of *E. coli* 0157, *Salmonella spp* and *Shingella spp* in some selected water sources of the study area.

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MATERIALS AND METHODS

The study Area

The study was conducted in Gombe south Zone of Gombe state, Northeast Nigeria. The region is comprised of four local government areas, these include; Kaltungo, Shongom, Balanga and Billiri LGAs. It lies on 4,281sqKm total landmass and has a projected total population of 1,059,244 persons at 3.23% from

2006 national population and housing census data. The region is situated geographically between latitude 9°31' 27" N to 10°05' 44" N and Longitude 11°00' 00" E to 11°51' 18" E of the meridian and relatively commenced 60Km south of Gombe (The state Capital). Figure 1 below shows the map of the study area indicating sampling points and spatial expanse:

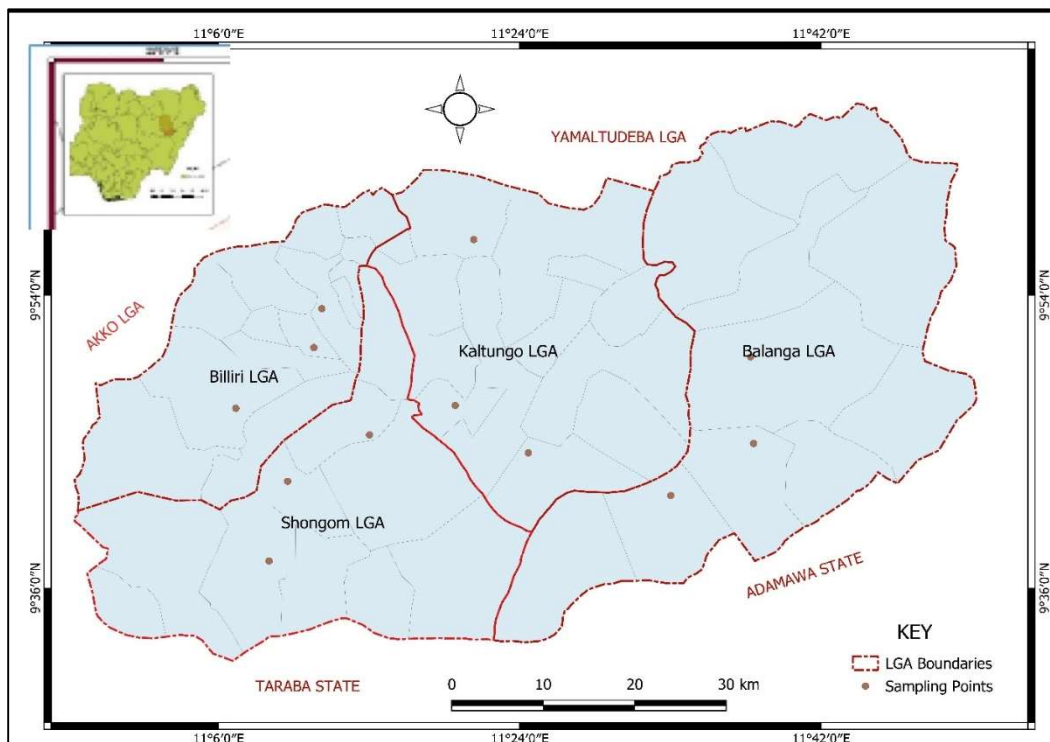


Figure 1. Map of the Study Area. Layout: Researchers, 2024(Data from Grid3).

selected. Samples were collected from open wells (3 sites), Springs (2 sites), Hand pump Boreholes

Sample Collection and Treatment

Samples for the study were collected twice, that is, in December 2023 and June 2024 to cover for dry and wet season respectively. This is necessitated by the fact that some of the selected water sources are surface water source with possible difference in seasonal quality. Samples were collected purposively from 12 sites in the 4 local government areas that made up southern Gombe zone. In each LGA, 3 sampling sites were

(4 sites), motorised Borehole (2 sites), and a River (1 site).

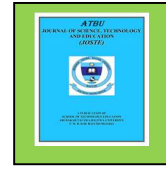
Samples were collected in a one-litre sterile plastic bottle aerobically and aseptically, and transported in a cool box to the laboratory for analysis within 5 hours from time of collection. Microbiological laboratory analysis was conducted at Gombe State College of Education Integrated Science Laboratory. In all sites geographic coordinates of each site was collected using

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Handheld GPS receiver (Garmin Etrex 30) for spatial differentiation purpose.

Culture Media and Biochemical Tests

Two selective and differential culture media were used in the study. Specifically, Sorbitol MackConkey Agar (SMAC) culture media was used for the isolation of Pathogenic *Escherichia Coli* (*E. coli* 0157) bacteria, while Xylose Lysine Deoxycholate Agar (XLD) culture media was used for the isolation of *Salmonella Spp* and *Shingela spp* from sample waters. For the confirmation of isolates from samples, Methyl red (MR) test, Urease test and Citrate Utilization test were used. The culture media preparation was done according to manufacturer's description with slight modification using lower media concentration to allow for easy visualisation of isolates on media as advised by Terones-Fernades, et al (2023). and reagent were prepared according to manufacturer's description.

Laboratory Procedures

Isolation and confirmation of *E.coli* 0157

Samples were gently rotated to mix adequately. A sterile pipet was used to transfer 1ml of sample into a sterile petri dish for pour plating. This was repeated to have duplicate petri dish for each site sample was collected from, 12ml-15ml of already prepared molten SMAC media cooled in a water bath at 48C -50C was then poured into the 1ml sample water in the petri dish. They were then gently swirled to mix sample and media evenly, the mixture is allowed to cool and solidify for 10 minutes. Petri dishes were tagged to avoid confusing with others, they are then inverted and incubated at 37C for 24hrs. Observation of growth showing colourless colonies on petri dishes are counted as presumptive *E.coli* 0157, when tested for biochemical reaction, isolates that are positive to MR test, Negative to citrate utilization test and Negative to urease test are confirmed as *E.coli* 0157.

Isolation and confirmation of *Salmonella spp* and *Shingella spp*

Samples were also gently rotated to mix adequately. A sterile pipet was used to transfer 1ml of sample into a sterile petri dish for pour plating. This was repeated to have duplicate petri dish for each site and each for *Salmonella spp* and *Shingella spp*, 12ml-15ml of already prepared molten XLD media cooled in a water bath at 48C - 50C was then poured into the 1ml sample waters in the petri dishes. They were then gently swirled to mix sample and media evenly, the mixture is allowed to cool and solidify for 10 minutes. Petri dishes were tagged to avoid confusing with others, they are then inverted and incubated at 37C for 24hrs.

Growths on petri dish showing black centered with slightly red colour translucent zone are counted as presumptive *Salmonella spp* and when few of these growths are picked and used for biochemical test using a sterile wire loop and tubes. A positive MR test, positive to citrate utilization test as well as negative urease test confirms the bacteria as *Salmonella spp*. Pink/red growth with yellow periphery on petri dishes are counted as presumptive *Shingella spp*, when test for biochemical reaction, isolates that are negative to MR test, Negative to citrate utilization test and Negative to urease test are confirmed as *Shingella spp* and recorded.

Methods of Analysis

The mean of duplicate petri dish count of observation is derived and recorded as average number of colony forming unit per one Millilitre of sample per season throughout the study. Descriptive statistical analytical tools such as sum, mean, frequency count as well as simple line graph were used in the study on a Microsoft Excel software (version 16). QGIS software (version 3.28) was used to plot Cfu/ml of results of the two seasons to geographic coordinates of the sample collection site in order to depict spatial and seasonal variation in colony count per millilitre.

RESULTS

Occurrence of Bacteria in water sources of the study area

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The Table 1 as follows presents the seasonal distribution of number positive cases of bacteria in the 12 sites used for this study from the

microbiological analysis of samples in the laboratory;

Table 1. Seasonal prevalence of some bacteria in some rural community waters of Southern Gombe

Name of Pathogenic Bacteria	No. of positive Results (out of 12 sites)	
	Dry season	Wet season
<i>Escherichia Coli 0157</i>	9 (75%)	10 (83%)
<i>Salmonella spp</i>	6 (50%)	7 (58%)
<i>Shingella spp</i>	5 (42%)	8 (67%)

Table 1 shows that pathogenic *E.coli* prevalence is high (75% - 83%) in all sample sites in all season and higher in the wet season. The Table 1 further shows that there is a moderate (50% -58%) prevalence of *Salmonella spp* in all sampled waters in the study area. On the other hand, Table 1also show fairly low and high prevalence of *Shingella spp* in the sample waters with 42% and 67% prevalence rate for dry and wet season respectively.

The laboratory analysis of water samples determined the concentration of individual pathogens of interest to this study, the observations' made are presented in tables, and maps as seen as follows;

Seasonal *E. coli 0157* concentration and Geospatial Distribution in the study Area

The Table 2 as follows indicates the seasonal concentration of pathogenic *E. coli 0157* in sampled waters of the study area;

Seasonal Concentration of Pathogenic Bacteria in the Study Area

Table 2. Average seasonal concentration of *E. coli 0157* in sample water per season

Sampled Site Code	Water Source	Longitude	Latitude	Dry season (cfu/ml)	Wet Season (cfu/ml)
BG1	Spring	11.63806	9.80411	73	81
BG2	Open well	11.60082	9.73211	90	103
BG3	Motorised Borehole	11.54040	9.70480	23	44
BR1	Hand pump borehole	11.17378	9.82149	07	04
BR2	Spring	11.18950	9.92908	30	57
BR3	Motorised Borehole	11.18950	9.91087	12	90
SH1	Hand pump Borehole	11.26233	9.78839	0	0
SH2	Hand pump Borehole	11.13736	9.69570	0	51
SH3	Stream/River	11.11833	9.64521	101	134
KT1	Open well	11.39557	9.93901	101	98
KT2	Open well	11.38150	9.79584	30	38
KT3	Hand pump Borehole	11.30619	9.81570	0	0

Source: Researchers Laboratory Analysis

Table 2 indicates that the highest colony counts per millilitre of water sample of *E. coli 0157* was recorded at SH3 (a stream) water source in the rainy season, there are cases of no *E. coli 0157* bacteria in the study area; 3 in dry season and 2 in wet season at SH1, SH2 and KT3which

are all hand pump borehole water sources. Table 2 also shows that there is a very colony concentration of *E.coli 0157* at BR2 of the study area.

In order to show the spatial distribution of *E.coli 0157* in selected waters of southern Gombe zone, figure 2 as follows is a map showing

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seasonal and locational variation of *E.coli* 0157 concentration in the study area:

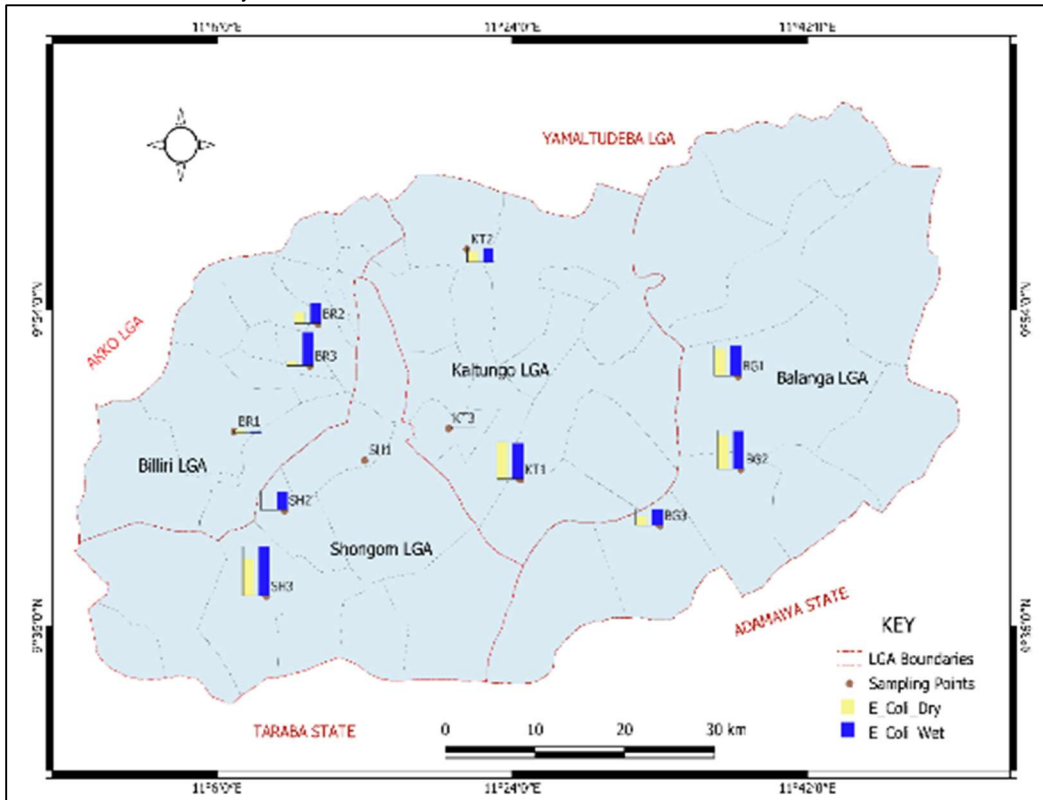


Figure 2. Spatial and Seasonal Distribution of *E. coli* 0157 in Southern Gombe Zone

Average Seasonal Concentration and Geospatial Distribution of *Salmonella* Spp.

The Table 3 as follows presents the average colony count of *Salmonella* spp in the 12 sites sampled for the study;

Table 3. Average concentration of *Salmonella* spp in cfu/ml

Site Code	Water Source	Longitude	Latitude	Dry season (cfu/ml)	Wet Season (cfu/ml)
BG1	Spring	11.63806	9.80411	84	60
BG2	Open well	11.60082	9.73211	38	33
BG3	Motorised Borehole	11.54040	9.70480	0	89
BR1	Hand pump borehole	11.17378	9.82149	14	28
BR2	Spring	11.18950	9.92908	103	128
BR3	Motorised Borehole	11.18950	9.91087	39	41
SH1	Hand pump Borehole	11.26233	9.78839	12	17
SH2	Hand pump Borehole	11.13736	9.69570	0	0
SH3	Stream/River	11.11833	9.64521	55	68
KT1	Open well	11.39557	9.93901	16	35
KT2	Open well	11.38150	9.79584	46	22

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KT3	Hand pump Borehole	11.30619	9.81570	0	0
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Source: Researchers Observation 2024.

Table 3 shows that the highest concentration of *Salmonella* spp bacteria in the study area was recorded at BR2 for both wet and dry season. During the dry season, 3 sites show no salmonella spp occurrence, they include BG3,

SH2, and KT3, while SH2 and KT3 also show no salmonella in the wet season.

The figure 3 as follows depicts the spatial and seasonal distribution of *Salmonella* Spp in the sampled water sources of the study area;

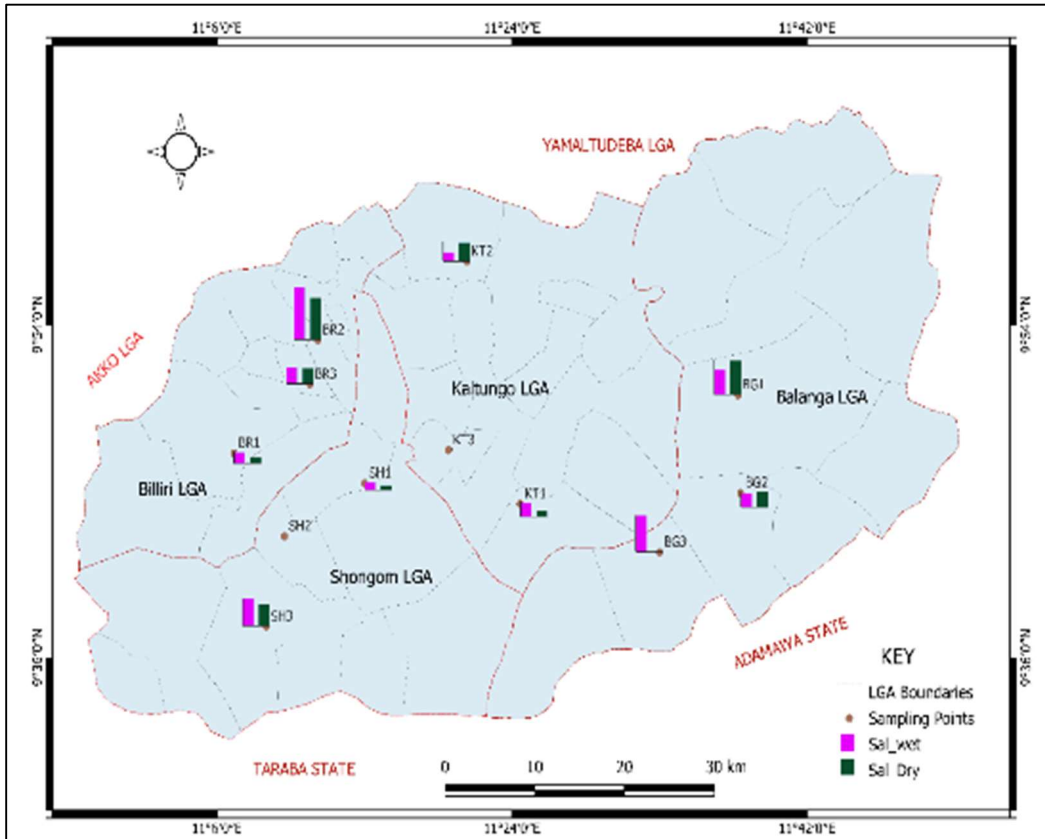


Figure 3: Spatial and seasonal distribution of *Salmonella* spp in Southern Gombe Zone.

Average Seasonal Concentration and Geospatial Distribution of *Shingella* Spp.

The Table 4 as follows demonstrates the distribution of *Shingella* spp per season as

observed in some sampled domestic water sites of Southern Gombe zone;

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Table 4. Average concentration of *Shingella spp* in the Study area

Site Code	Water Source	Longitude	Latitude	Dry season (cfu/ml)	Wet Season (cfu/ml)
BG1	Spring	11.63806	9.80411	0	0
BG2	Open well	11.60082	9.73211	66	81
BG3	Motorised Borehole	11.54040	9.70480	0	0
BR1	Hand pump borehole	11.17378	9.82149	0	0
BR2	Spring	11.18950	9.92908	34	82
BR3	Motorised Borehole	11.18950	9.91087	0	13
SH1	Hand pump Borehole	11.26233	9.78839	35	49
SH2	Hand pump Borehole	11.13736	9.69570	33	86
SH3	Stream/River	11.11833	9.64521	34	55
KT1	Open well	11.39557	9.93901	0	0
KT2	Open well	11.38150	9.79584	0	04
KT3	Hand pump Borehole	11.30619	9.81570	0	28

Table 4 revealed that seven water sites in the study area do not show the presence of *Shingella Spp* in the Dry season while four site do not show same in the wet season. The highest observation of concentration of *Shingella*spp as at the time of the study in the region is 86 cfu/ml in the wet season at SH2. Four sites show no

presence of *Shingella* throughout the period of the study.

The figure 4 as follows is a graphical representation of spatial and seasonal distribution of *Shingella spp* in the study areas at the time of the study;

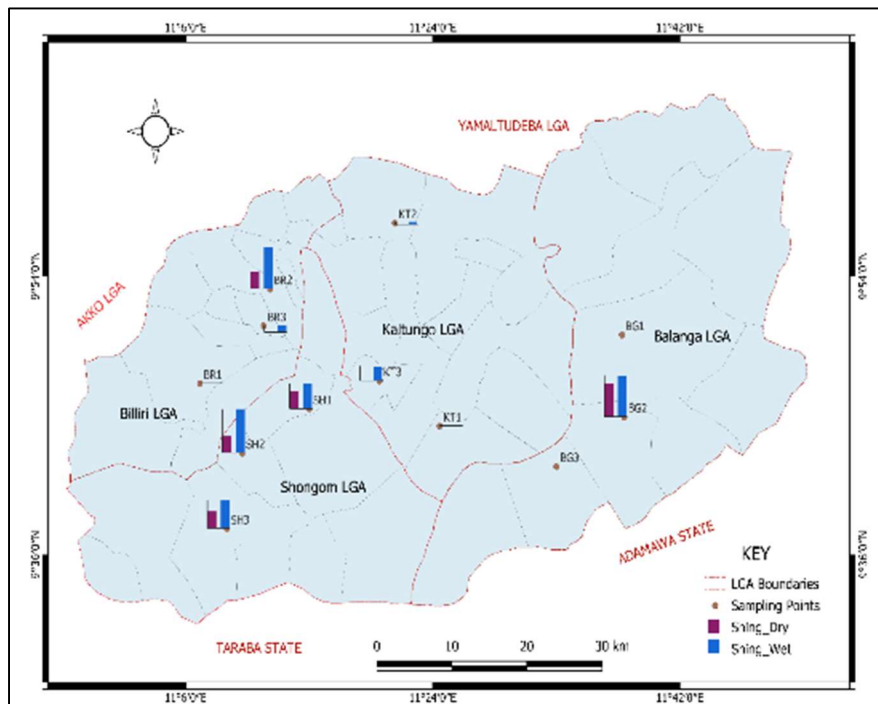


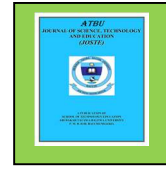
Figure 4. Spatial and Seasonal distribution of *Shingella Spp* in the Study Area

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DISCUSSION OF FINDINGS

The results of the study in regards the prevalence rate of *E. coli* is similar to the 70% of drinking water at source and point of consumption within households in Nigeria that are reported contaminated with *E. coli* (Fed. Min. of Water Resources, 2022). Although similar, the *E. coli* prevalence rate in the study area is higher than national values in both dry and wet season. The study results also agree with the conclusion of Abakpa et al (2015), that *E. coli* concentration is mostly found to be high in wet season than dry season.

On the other hand, results of the study differs with low positive results in some irrigation waters in Kano State and Plateau State, having 13% and 1.3% respectively identified by Abakpa et al (2015). The difference may be attributed to little or no contamination of irrigation water in the said location by livestock who are known to be the main reservoir of *E. coli* (Chigor et al, 2010). The difference may also be due to *E. coli* low survival rate and its susceptibility to survive changes in environmental conditions sustaining it, therefore, whenever detected, it implies acute concentration or a recent contamination (Abakpa et al 2015; Aqua-free, 2024).

Shingella spp are known to be salt tolerant and low temperatures increase their survival rate (Logue et al, 2017). When compared site by site with Danja et al (2024) who observed the salinity level of rural domestic waters in southern Gombe ranged between 0.13% to 1.35%, locations with higher salinity level did not influence shingella concentration as well locations with lower salinity levels.

The study agrees with Eng et al (2015) who posits that high concentration of *Salmonella spp* is mostly found in surface water than ground water and may come from soils, manure or animal faeces. Springs, Open wells, and Rivers in the study area show higher concentration of *Salmonella* than ground water sources such as motorised and hand pump boreholes. The study also agrees with Eng et al (2015), because *Salmonella Spp* exhibit seasonality pattern in rivers and other surface water sources.

Among the three bacteria studied, *Salmonella Spp* has the ability to survive UV light from sun, poor nutrient, changes in pH, and temperature and therefore required stringent attention during surveillance (Eng et al, 2015). Also, in the three microbes studied, contamination could arise from installation since there are negative cases in one season and positive in the other. Aqua-free (2024) noted that bacterial contamination can occur from installations and not necessarily the water source.

CONCLUSION

The study therefore concludes that *E. coli 0157*, *Shingella Spp.* and *Salmonella Spp.* are prevalent in all type of water sources in the study area, they are also prevalent in wet and dry seasons. The study also concludes that seasonality affects microbial concentration in the study area thereby calling for necessary action from concerned authorities to improve rural water quality by providing technology innovation suited for rural environment that will cut down microbial growth in domestic water.

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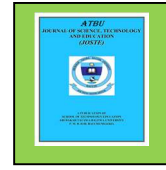
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