

## Multivariate Assessment of Waterborne Bacterial Contamination across Boreholes, Wells and Streams in Kuje Agro-Ecological Area, Nigeria

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### Abstract

Waterborne bacterial contamination remains a major public health concern in agroecological communities that rely on multiple water sources for domestic and agricultural use. This study assessed the distribution and interrelationships of selected waterborne bacteria across boreholes, hand-dug wells and streams in the Kuje agroecological area of the Federal Capital Territory, Nigeria, using multivariate statistical techniques. Water samples were collected from boreholes, wells, streams and a treated water control source and analyzed for *Escherichia coli*, *Salmonella* spp., *Shigella* spp. and *Pseudomonas* spp. using standard microbiological methods. Multivariate analysis of variance (MANOVA) was applied to evaluate differences in bacterial distributions across water sources, supported by Box's M test, Dunnett's post-hoc comparisons and Pearson correlation analysis. MANOVA results showed no statistically significant differences using Wilks' Lambda and Pillai's Trace ( $p > 0.05$ ); however, Roy's Largest Root revealed a significant multivariate effect ( $p < 0.05$ ), indicating subtle but meaningful variations in bacterial contamination patterns. Correlation analysis demonstrated significant positive associations among key bacterial indicators, suggesting shared contamination pathways linked to fecal pollution and environmental exposure. The findings highlight the value of multivariate statistical tools in water quality assessment and underscore the need for routine microbiological monitoring, improved sanitation practices and integrated water safety planning in agro-ecological communities.

**Keyword:** Waterborne bacteria; environmental monitoring; MANOVA; microbial water quality; Nigeria

### Introduction

#### Problem background and statement

Access to safe drinking water is essential for human health; however, microbial contamination of water sources remains a persistent challenge in many low- and middle-income countries. In agro-ecological areas, reliance on boreholes, hand-dug wells and surface waters increases vulnerability to contamination arising from agricultural runoff, open defecation, livestock activities and inadequate waste management systems.

Bacterial indicators such as *Escherichia coli* are widely used to assess fecal contamination, while pathogens including *Salmonella* spp., *Shigella* spp. and *Pseudomonas* spp. pose direct public health risks. The presence of these organisms in drinking water sources has been associated with outbreaks of waterborne diseases, particularly in rural and peri-urban communities.

Although several studies have evaluated microbial water quality in Nigeria and sub-Saharan Africa, many rely on univariate analytical approaches that may not adequately capture the complex interrelationships among multiple microbial indicators. Multivariate statistical techniques, such as multivariate analysis of variance

(MANOVA), allow for the simultaneous evaluation of multiple dependent variables and provide a more comprehensive understanding of contamination patterns.

This study therefore aimed to assess the distribution and interrelationships of selected waterborne bacteria across borehole, well and stream water sources in the Kuje agroecological area using multivariate statistical methods. The findings are intended to support evidence-based environmental monitoring and water quality management in similar settings.

### Materials and Methods

#### Study area

The study was conducted in the Kuje agro-ecological area of the Federal Capital Territory (FCT), Nigeria. Kuje Area Council is one of the six Area Councils of the Federal Capital Territory, with approximately between latitude 8°45'N and longitude 7°15'E, located in the southern part of FCT and shares boundaries with several states and local government areas (Figure 1). The area is characterized by a tropical savannah climate, mixed subsistence and commercial farming activities and dispersed rural settlements. Residents primarily depend on boreholes, hand-dug wells and surface water (streams) for

domestic and agricultural purposes. These water sources are potentially exposed to contamination from agricultural runoff, open defecation, livestock activities and inadequate waste disposal systems.

## Statistical analysis

Descriptive statistics were used to summarize bacterial concentrations across water sources. Multivariate analysis of variance (MANOVA) was applied to assess differences in bacterial distributions among water sources, with water source type as the independent variable and bacterial indicators as dependent variables. Box's M test was used to evaluate the assumption of covariance homogeneity. Where appropriate, Dunnett's post-hoc test was applied to compare each water source with the treated control. Pearson correlation analysis was used to examine interrelationships among bacterial indicators. Statistical significance was set at  $p < 0.05$ . Roy's Largest Root was emphasized due to its sensitivity in detecting dominant multivariate effects when dependent variables are correlated. Analyses were performed using SPSS software.

## Results

### Distribution of waterborne bacteria

All sampled water sources exhibited detectable levels of bacterial contamination. *Escherichia coli* was detected across boreholes, wells and streams, with higher mean counts observed in surface water sources. *Salmonella* spp. and *Shigella* spp. were more frequently isolated from wells and streams, while *Pseudomonas* spp. was consistently detected across all water sources, including boreholes. The bacterial growths exhibited distinct morphological characteristics across the selective and differential media. (Figure 2).

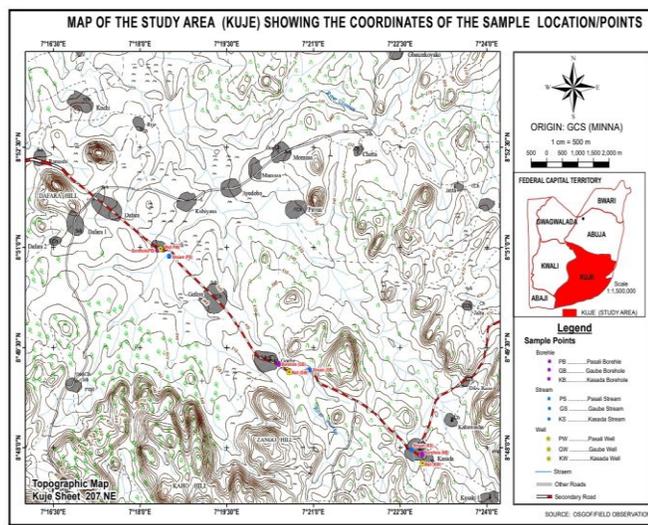


Figure 1: Map of the study area.

### Sample collection

A total number of 30 samples were randomly collected, 3 replicates of samples were collected in each area comprising of, 9 borehole samples, 9 hand-dug well samples, 9 stream samples and 3 treated water control samples using sterile 500 mL polyethylene bottles. Sample collection area coordinates are as follows; Gaube well (Lat: 8° 49' 08.094" N, Long: 7° 20' 32.036"E); Gaube stream (Lat: 8° 49' 10.669" N, Long: 7° 20' 53.927" E); Gaube borehole (Lat: 8° 49' 16.019" N, Long: 7° 20' 21.048" E); Passali well (Lat: 8°50'59.952"N, Long: 7°18'18.550"E); Passali stream (Lat: 8°50'56.271" N, Long: 7°18'28.158"E); Passali borehole (Lat: 8°50'56.271"N, Long: 7°18'28.158); Kasada well (Lat: 8°47'47.468"N, Long: 7°18'18.550"E); Kasada borehole (Lat: 8°47'54.686"N, Long: 7°18'18.550"E); Kasada stream (Lat: 8°47'59.016"N, Long: 7°18'18.550"E).

Sampling was conducted following standard procedures to avoid cross-contamination. For boreholes and wells, water was allowed to run for 2–3 minutes before collection. Stream samples were collected midstream at approximately 30 cm depth. All samples were transported in ice-packed containers to the laboratory and analyzed within 6 hours of collection.

### Microbiological analysis

Microbiological analyses were conducted using standard culture-based methods. Water samples were analyzed for *E. coli*, *Salmonella* spp., *Shigella* spp. and *Pseudomonas* spp. using selective and differential media following procedures recommended by the American Public Health Association. Presumptive isolates were identified based on colony morphology, Gram staining and biochemical tests. Bacterial concentrations were expressed as colony-forming units per 100 mL (CFU/100 mL).

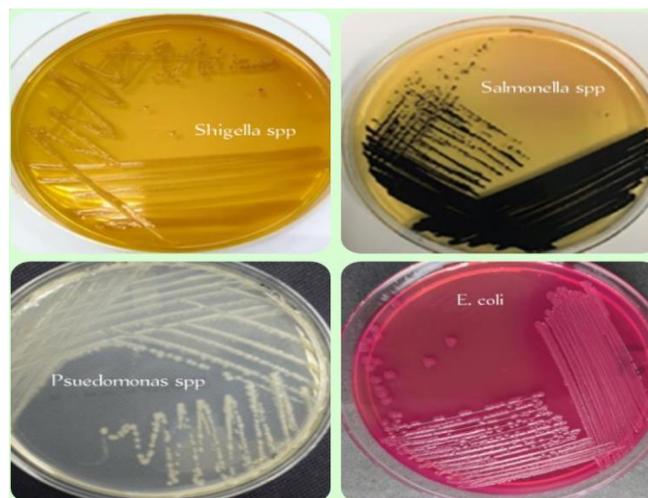


Figure 2: Bacterial growths on selective and differential media (*Shigella* sp, *Salmonella* spp, *Pseudomonas* spp and *E. coli*).

### Multivariate analysis of variance

MANOVA results indicated no statistically significant differences across most microbial parameters using Wilks' Lambda and Pillai's Trace ( $p > 0.05$ ). However, Roy's Largest Root test revealed a significant multivariate effect ( $p < 0.05$ ), suggesting that at least one linear combination of bacterial indicators differed among water sources. Box's M test confirmed homogeneity of covariance matrices, validating the MANOVA assumptions (Table 1).

Microbial Analysis Multivariate Tests						
Effect		Value	F	Hypothesis df	Error df	Sig.
Intercept	Pillai's Trace	.144	2.182 <sup>b</sup>	4.000	52.000	.084
	Wilks' Lambda	.856	2.182 <sup>b</sup>	4.000	52.000	.084
	Hotelling's Trace	.168	2.182 <sup>b</sup>	4.000	52.000	.084
	Roy's Largest Root	.168	2.182 <sup>b</sup>	4.000	52.000	.084
Water Source	Pillai's Trace	.301	1.507	12.000	162.000	.126 <sup>ns</sup>
	Wilks' Lambda	.711	1.577	12.000	137.871	.105 <sup>ns</sup>
	Hotelling's Trace	.388	1.637	12.000	152.000	.087 <sup>ns</sup>
	Roy's Largest Root	.334	4.513 <sup>c</sup>	4.000	54.000	.003*
b. Exact statistic *. The Test is significant at the .05 level. <sup>ns</sup> . The Test is not significant at the .05 level.						
c. The statistic is an upper bound on F that yields a lower bound on the significance level.						
Box's Test of Equality of Covariance Matrices <sup>a</sup>						
Box's M	77.878					
F	6.862					
df1	10					
df2	6173.992					
Sig.	.000*					
Tests the null hypothesis that the observed covariance matrices of the dependent variables are equal across groups.						
a. Design: Intercept + Water Source						

**Table 1:** Multivariate Tests.

### Post-Hoc comparisons

Dunnnett's post-hoc test showed no statistically significant differences between individual water sources and the treated control

for most bacterial indicators, although stream water consistently exhibited higher bacterial counts compared to boreholes and treated control water (Table 2).

Dunnnett Test for Multiple Comparisons							
Dependent Variable	(I) Water Source	(J) Water Source	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
						Lower Bound	Upper Bound
<i>Salmonella</i>	Borehole	Control	.0000 <sup>ns</sup>	7.13857	1.000	-15.9595	15.9595
	Well	Control	.3333 <sup>ns</sup>	7.13857	1.000	-15.6262	16.2928
	Stream	Control	9.0476 <sup>ns</sup>	7.08739	.306	-6.7975	24.8927
<i>E. coli</i>	Borehole	Control	.7778 <sup>ns</sup>	3.96456	.979	-8.0857	9.6412
	Well	Control	3.6111 <sup>ns</sup>	3.96456	.511	-5.2523	12.4746
	Stream	Control	4.3333 <sup>ns</sup>	3.93614	.397	-4.4666	13.1332
<i>Pseudomonas</i>	Borehole	Control	5.1667 <sup>ns</sup>	16.63639	.930	-32.0268	42.3602

	Well	Control	9.7778 <sup>ns</sup>	16.63639	.740	-27.4157	46.9713
	Stream	Control	17.1429 <sup>ns</sup>	16.51713	.433	-19.7840	54.0697
<i>Shigella</i>	Borehole	Control	.7778 <sup>ns</sup>	17.32979	1.000	-37.9659	39.5215
	Well	Control	5.8889 <sup>ns</sup>	17.32979	.914	-32.8548	44.6326
	Stream	Control	19.6190 <sup>ns</sup>	17.20556	.375	-18.8469	58.0850
Based on observed means. The error term is Mean Square (Error) = 540.579.							
*. The mean difference is significant at the .05 level. <sup>ns</sup> . The mean difference is not significant at the .05 level.							
a. Dunnett t-tests treat one group as a control and compare all other groups against it.							
NB: All the microbial parameters show not a significant mean difference in water source; most of the MANOVA Tests criteria showed not significant except the Roy's Largest Root Test!							

**Table 2:** Dunnett test for multiple comparisons.

### Correlation analysis

Pearson correlation analysis revealed significant positive correlations between *E. coli* and *Salmonella* spp., as well as between

*Shigella* spp. and *E. coli* ( $p < 0.05$ ). These correlations indicate shared contamination pathways, likely linked to fecal pollution and environmental exposure (Table 3).

Correlation Matrix <sup>a</sup>					
		<i>Salmonella</i>	<i>E. coli</i>	<i>Pseudomonas</i>	<i>Shigella</i>
Correlation	<i>Salmonella</i>	1.000	.017	.443	.347
	<i>E. coli</i>	.017	1.000	-.111	.272
	<i>Pseudomonas</i>	.443	-.111	1.000	.354
	<i>Shigella</i>	.347	.272	.354	1.000
Sig. (1-tailed)	<i>Salmonella</i>		.448	.000	.004
	<i>E. coli</i>	.448 <sup>ns</sup>		.201	.019
	<i>Pseudomonas</i>	.000*	.201 <sup>ns</sup>		.003
	<i>Shigella</i>	.004*	.019*	.003*	
a. Determinant = .585 *. The correlation is significant at the .05 level. <sup>ns</sup> . The correlation is not significant at the .05 level.					
NB: All the correlation among microbial parameters shows significance except between <i>E. coli/Salmonella</i> and <i>Pseudomonas/ E. coli</i> .					

**Table 3:** Correlation matrix.

### Discussion

The presence of multiple bacterial indicators across all water sources demonstrates widespread microbial contamination within the Kuje agro-ecological area. The detection of *E. coli* confirms fecal pollution, consistent with previous studies in rural Nigerian and sub-Saharan African settings [1,2].

Although univariate differences among water sources were limited, the significant result obtained using Roy's Largest Root

highlights the utility of multivariate approaches in detecting subtle contamination patterns that may otherwise be overlooked. Roy's Largest Root was emphasized due to its sensitivity in detecting dominant multivariate effects when dependent variables are correlated. This supports the use of multivariate techniques in water quality assessment, as they capture complex interactions among multiple microbial indicators that may be overlooked by single-parameter analyses [3].

The observed correlations among bacterial indicators suggest common contamination sources, including agricultural runoff, livestock waste and inadequate sanitation infrastructure. The relatively uniform distribution of bacteria across water sources indicates diffuse environmental contamination, underscoring the need for integrated water safety planning rather than source-specific interventions alone [4-17].

## Conclusion

This study demonstrates that water sources; boreholes, hand-dug wells and streams in the Kuje agro-ecological area are contaminated with multiple waterborne bacterial indicators. While conventional univariate analyses showed limited differences, multivariate analysis revealed meaningful interrelationships among microbial parameters. The findings support the incorporation of multivariate analytical tools into routine environmental monitoring frameworks and highlight the importance of continuous microbiological surveillance, improved sanitation practices and integrated water resource management to reduce public health risks.

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## Ethics Statement

Ethical approval was not required for this study as it involved environmental water sampling and did not include human or animal subjects.

## Conflict of interest

The author declares no conflict of interest.

## References

1. Adefisoye MA, Okoh AI (2017) Identification and antimicrobial resistance prevalence of pathogenic *Escherichia coli* strains from treated wastewater effluents in Eastern Cape, South Africa. *Microbiologyopen* 6(3): e00470. [Crossref] [GoogleScholar] [Pubmed]
2. Edokpayi JN, Rogawski ET, Kahler DM, Hill CL, Reynolds C, et al. (2018) Challenges to sustainable safe drinking water: A case study of water quality and use across seasons in rural communities in limpopo province, South Africa. *Water* 10(2): 159. [Crossref] [GoogleScholar]
3. Shrestha S, Kazama F (2007) Assessment of surface water quality using multivariate statistical techniques: A case study of the Fuji River Basin, Japan. *Environmental Modelling & Software* 22(4): 464-475. [Crossref] [GoogleScholar]
4. APHA (2017). Standard methods for the examination of water and wastewater. 23<sup>rd</sup> edn. American Public Health Association.
5. Bain R, Cronk R, Wright J, Yang H, Slaymaker T, et al. (2014) Fecal contamination of drinking-water in low- and middle-income countries: A systematic review. *PLoS Medicine* 11(5): e1001644. [Crossref] [GoogleScholar]
6. Cabral JPS (2010) Water microbiology: Bacterial pathogens and water. *International Journal of Environmental Research and Public Health* 7(10): 3657-3703. [Crossref] [GoogleScholar]
7. Douterelo I, Fish KE, Boxall JB (2018) Succession of bacterial communities in drinking water distribution systems. *Water Research* 141: 475-484. [Crossref]
8. Eze VC, Nwagwe NC (2016) Microbiological and physicochemical characteristics of water sources in rural communities of Anambra State, Nigeria. *Journal of Applied Sciences and Environmental Management* 20(2): 393-399.
9. Leclerc H, Schwartzbrod L, Dei-Cas E (2002) Microbial agents associated with waterborne diseases. *Critical Reviews in Microbiology* 28(4): 371-409. [Crossref] [GoogleScholar]
10. Odonkor ST, Ampofo JK (2013) *Escherichia coli* as an indicator of bacteriological quality of water: An overview. *Microbiology Research* 4(1): e2. [Crossref] [GoogleScholar]
11. Olasoji SO, Oyewole NO, Abiola B, Edokpayi JN (2019) Water quality assessment of surface and groundwater sources in rural areas of Ogun State, Nigeria. *Environmental Monitoring and Assessment* 191: 281.
12. Oloruntoba EO, Sridhar MKC (2017) Bacteriological quality of drinking water in rural communities of Nigeria. *African Journal of Biomedical Research*, 20(3): 285-292.
13. Ojekunle ZO, Ojekunle OV, Adeyemi AA, Taiwo AG, Sangowusi OR, et al. (2020) Evaluation of surface water quality indices and ecological risk assessment in Nigeria. *Environmental Science and Pollution Research* 27: 31617-31628. [Crossref] [GoogleScholar]
14. Okoh AI, Odjajare EE, Igbinsola EO, Osode AN (2007) Wastewater treatment plants as a source of microbial pathogens in receiving watersheds. *African Journal of Biotechnology* 6(25): 2932-2944. [Crossref] [GoogleScholar]
15. WHO (2017) Guidelines for drinking-water quality. 4<sup>th</sup> edn. World Health Organization. [GoogleScholar]
16. World Health Organization (2022) Guidelines for drinking-water quality. 4<sup>th</sup> edn. WHO.
17. WHO & UNICEF (2023) Progress on household drinking water, sanitation and hygiene 2000–2022. WHO/UNICEF Joint Monitoring Programme.