

**Original Article****Spatial assessment of microbiological pollution in the Emu stream of Lavun Local Government Area via inverse distance weighted interpolation**

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**ABSTRACT**

Access to safe drinking water is a critical challenge in rural Nigerian communities where populations rely on untreated surface water. This study evaluated microbiological pollution in the Emu stream, Lavun Local Government Area, Niger State, using Geographic Information Systems (GIS) and Inverse Distance Weighted (IDW) interpolation to map bacterial pathogens. Water samples were collected from four geo-referenced stations over an eight-month period from July 2021 to February 2022. Laboratory assessments using the Most Probable Number (MPN) technique revealed significant contamination across all points. The highest mean bacterial count occurred at Station 2 ( $5.4 \times 10^3$  CFU/mL), largely due to agricultural drainage, while the lowest was at Station 4 ( $4.3 \times 10^3$  CFU/mL). Ten bacterial species were isolated, including *Escherichia coli*, *Salmonella spp*, and *Staphylococcus aureus*. Stations 2 and 3 exhibited the highest microbial diversity. Findings indicate the Emu stream is unsafe for direct human consumption, as coliform levels exceed Nigerian Standard for Drinking Water Quality [12] and WHO guidelines. Spatial analysis confirmed that agricultural runoff and anthropogenic activities are the primary drivers of degradation. The study underscores the urgent need for water safety planning and environmental interventions to mitigate waterborne disease risks in the region.

**Keywords:** Emu Stream, *Escherichia coli*, Interpolation, Microbiological, Pollution

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**INTRODUCTION**

The global landscape of public health is inextricably linked to the integrity of freshwater ecosystems, particularly in

regions where industrialization and rapid population growth outpace the development of sanitation infrastructure. In the Nigerian context,

the contamination of surface water bodies remains a primary driver of waterborne morbidity and mortality, necessitating advanced diagnostic tools to monitor and manage these vital resources. The Emu stream, located in the Kusotachin village of the Lavun Local Government Area (LGA) in Niger State, serves as a critical hydrological artery for domestic, agricultural, and economic activities. However, the stream is increasingly subjected to intense anthropogenic pressures, ranging from agricultural runoff to direct fecal contamination. To address the invisibility of microbial spread, the integration of Geographic Information Systems (GIS) and Inverse Distance Weighted (IDW) interpolation provides a robust framework for mapping the spatial distribution of bacterial pathogens, thereby enabling targeted environmental interventions [16];[2].

Recent updates from the World Health Organization emphasize the necessity of robust regulatory systems and climate-resilient water safety plans [18]. These global initiatives aim to raise the percentage of safely managed drinking water services from approximately 71% to over 87% by 2025. In rural Nigerian communities like those in Lavun LGA, achieving these targets is complicated by fragmented institutional arrangements and limited monitoring capacity [3]. The reliance on untreated surface water sources like the Emu stream creates a vulnerability to pathogens such as *Escherichia coli*, *Salmonella spp*, and *Vibrio cholerae*, which are responsible for recurring outbreaks of cholera and typhoid fever [11];[1].

## MATERIALS AND METHODS

### Study area

The Emu stream is situated within the Guinea Savannah vegetation belt of North-Central Nigeria, characterized by a tropical climate with a distinct seasonality as shown on figure 1. The topography of the Lavun region influences the hydrological behaviour of the stream, with elevation gradients affecting water velocity, turbidity, and the transport of dissolved solids. The mean annual temperature of approximately 30.2 °C and rainfall levels between 1,200 and 1,300 mm create an environment conducive to the survival and proliferation of various microbial species. The inhabitants of Kusotachin village are predominantly agrarian, utilizing the Emu stream for the irrigation of food crops and the watering of livestock. Furthermore, the stream serves as a hub for domestic chores; women and children are frequently observed washing household utensils and doing laundry, activities that introduce detergents and organic residues into the ecosystem [15].

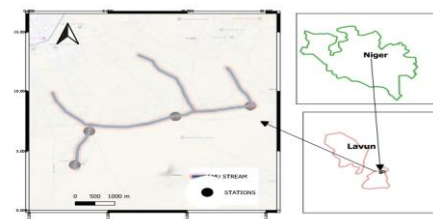


Fig.1. Base map of the study location: Emu stream

**Geomorphological Coordinates of Sampling Stations** To facilitate a comprehensive spatial assessment, four primary sampling points were established along the stream's course, reflecting diverse levels of human interaction and environmental impact. These stations are georeferenced using the Global Positioning System (GPS) to

ensure accuracy in the subsequent GIS-based IDW interpolation [15].

The assessment of microbiological pollution follows a rigorous laboratory sequence designed to identify and quantify indicator organisms. The methodology employs a three-tier approach: presumptive, confirmatory, and completed tests, ensuring that the findings are both quantitative and taxonomically accurate [6];[12].

The presumptive test utilizes the Multiple-Tube Fermentation (MTF) method to estimate the density of coliform bacteria in the water samples [17]. Measured volumes of water (10 mL, 1.0 mL, and 0.1 mL) are inoculated into MacConkey broth or Lauryl Sulphate Tryptose (LST) broth, which are selective media containing lactose and inhibitory agents for Gram-positive bacteria. The tubes contain inverted Durham tubes to capture gas production—a metabolic byproduct of lactose fermentation. Following an incubation period of 24 to 48 hours at 35–37 °C, a change in color from purple to yellow and the presence of gas bubbles indicates a positive presumptive result. The combination of positive tubes across the three dilutions is then cross-referenced with the Most Probable Number (MPN) index table to determine the coliform load per 100 mL of the sample.

Positive presumptive samples are subjected to a confirmatory test on Eosin Methylene Blue (EMB) agar and MacConkey agar. EMB agar is both selective and differential; it inhibits Gram-positive organisms and differentiates between lactose fermenters. *Escherichia coli* is identified by the characteristic metallic green sheen produced by its rapid lactose fermentation, while other coliforms like

*Enterobacter aerogenes* appear as large, pinkish-mucoid colonies. The completed test involves Gram staining and biochemical profiling of the isolates to confirm their identity beyond reasonable doubt. The Gram stain differentiates the bacteria based on their cell wall structure, with most waterborne pathogens being Gram-negative rods. Subsequent biochemical tests, including the IMViC series (Indole, Methyl Red, Voges-Proskauer, and Citrate), are used to distinguish between closely related species such as *E. coli*, *Klebsiella pneumoniae*, and *Salmonella typhi* [8];[15].

The use of GIS in this study focuses on the Inverse Distance Weighted (IDW) interpolation method to estimate unknown values at unsampled locations. IDW is a deterministic spatial interpolation technique that assumes that the influence of a measured variable decreases as the distance from the sampled location increases. This method is particularly useful for mapping bacterial gradients in rivers, where contamination levels typically follow a continuous model of spatial variation influenced by water flow and proximity to source points [16];[2].

## RESULTS

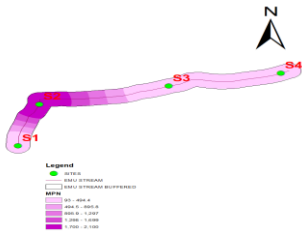
### Coliform Concentration and Most Probable Number (MPN) Data

The presumptive test results highlight extreme variation in bacterial density across the four stations. Station 2, identified as a point for agricultural drainage, exhibited the highest levels of contamination, while Station 4, characterized by lower direct human interaction, showed the lowest (though still non-compliant) levels as shown in Table 1.

Table 1: *Coliform concentration and most probable number (mpn) data*

| Sample Site      | 10 mL (+ tubes) | 1.0 mL (+ tubes) | 0.1 mL (+ tubes) | MPN per 100 mL | 95% Confidence Upper |
|------------------|-----------------|------------------|------------------|----------------|----------------------|
| S1 (Bridge)      | 3               | 2                | 1                | 150            | 440                  |
| S2 (Ag Drainage) | 3               | 2                | 3                | 2100           | 470                  |
| S3 (Washing)     | 2               | 1                | 2                | 120            | 350                  |
| S4 (Laundry)     | 3               | 2                | 0                | 93             | 350                  |

The IDW interpolation analysis indicated that the highest degradation occurs in areas heavily impacted by anthropogenic activities and agricultural drainage. Specifically, Station 2’s high count was attributed to agricultural runoff (fig. 2.)



The confirmatory and completed tests led to the isolation of several medically significant bacterial species. *Escherichia coli* was the most frequently isolated organism, present in all four sampling stations (100% frequency), followed by *Salmonella spp*, *Pseudomonas spp*, and *Klebsiella pneumoniae* as shown on Table 2.

Fig: 2 map showing IDW spatial interpolation of Emu stream

Table 2: *Bacterial isolate frequencies and pathogenic profile*

| Isolated Organism             | Morphology          | Frequency of Occurrence | Suspected Pathogenicity             |
|-------------------------------|---------------------|-------------------------|-------------------------------------|
| <i>Escherichia coli</i>       | Gram-negative rod   | 100% (4/4 stations)     | Gastroenteritis, Urinary infections |
| <i>Salmonella typhi</i>       | Gram-negative rod   | 50% (2/4 stations)      | Enteric/Typhoid fever               |
| <i>Pseudomonas aeruginosa</i> | Gram-negative rod   | 50% (2/4 stations)      | Opportunistic infections            |
| <i>Klebsiella pneumoniae</i>  | Gram-negative rod   | 50% (2/4 stations)      | Pneumonia, Bacteremia               |
| <i>Staphylococcus aureus</i>  | Gram-positive cocci | 100% (4/4 stations)     | Skin infections, Food poisoning     |

The biochemical profile of the isolates confirms the high prevalence of Enterobacteriaceae. The consistency of these results across multiple tests

(Catalase, Urease, Citrate, etc.) validates the diagnostic accuracy of the microbiological assessment (Tab. 3).

Table 3: *Biochemical profile of the isolates*

| Isolate # | Gram Reaction | Catalase | Citrate | Urease | Voges-Proskauer | Organism Identified   |
|-----------|---------------|----------|---------|--------|-----------------|-----------------------|
| 1         | Negative rod  | +        | +       | -      | -               | <i>E. coli</i>        |
| 2         | Negative rod  | -        | +       | -      | -               | <i>S. typhi</i>       |
| 3         | Negative rod  | +        | +       | +      | -               | <i>Ps. aeruginosa</i> |
| 4         | Negative rod  | +        | +       | +      | +               | <i>K. pneumoniae</i>  |

## DISCUSSION

The integration of GIS-based spatial interpolation and microbiological data provides a nuanced understanding of the pollution patterns within the Emu stream. The findings indicate that the stream is not merely a passive conduit for water but a dynamic reservoir for bacterial pathogens, deeply influenced by the socio-economic activities of the surrounding community.

The universal presence of *Escherichia coli* across all stations is a definitive indicator of recent faecal contamination. This contamination can be traced to several anthropogenic mechanisms. First, the Bridge area (Station 1) and the Laundry area (Station 4) are high-traffic zones where human waste may enter the water through open defecation practices common in rural areas. Second, the presence of livestock such as ducks and cattle near the bridge introduces bovine and avian faecal matter. The IDW interpolation highlights these areas as high-intensity pollution zones, emphasizing that human behaviour is the primary driver of microbial risk. The isolation of *Salmonella typhi* at Stations 2 and 3 is particularly concerning, given its role as the causative agent of typhoid fever which is in agreement with [11]. Also, this is similar to the findings of [4] who observed that the total bacterial count result of the bottled water were

high, exceeding the acceptable range of  $1.0 \times 10^2$  CFU/ml recommended by E.P.A

and WHO which is the standard limit of total bacteria count for drinking water.

The presence of this pathogen in a stream used for domestic consumption and utensil washing creates a direct faecal-oral transmission pathway. Residents who wash their plates and cups at Station 3 may be inadvertently inoculating their food with pathogens, leading to chronic enteric infections within the village similar to the findings of [1] and [7].

Station 2 exhibited the highest MPN of 2100 per 100 mL, which is strongly correlated with its status as a discharge point for agricultural drainage. Modern agricultural practices in Niger State involve the use of organic and chemical fertilizers, which, when washed into the stream during rainfall events, increase the nutrient availability (nitrates and phosphates) for bacterial populations. This nutrient enrichment, combined with the warm tropical temperatures of the region, fosters the rapid proliferation of Gram-negative bacteria such as *Pseudomonas aeruginosa* and *Klebsiella pneumoniae* [14];[10]. This is in agreement with findings of [9], That the mean bacterial counts encountered in this study exceeds  $1.0 \times 10^2$  CFU/ml which is the standard limit of heterotrophic count for drinking water.

The spatial variance observed in the IDW maps confirms that Station 2 acts as a “source point” for downstream contamination. As the water flows toward Station 3, the concentration of these bacteria remains high, suggesting that the stream’s self-purification capacity is overwhelmed by the constant influx of organic and agricultural waste which is in agreement with the works of [14] and [2].

The physical parameters of the water—such as temperature (mean 28.5 °C) and pH (mean 6.8)—are within the acceptable ranges defined by the WHO (World Health Organization, n.d.). However, this “physical clarity” is deceptive. As noted in related studies, there is often little to no relationship between physical parameters and bacterial content; a stream may appear clear and taste unobjectionable while harbouring lethal concentrations of pathogenic microorganisms which agrees with the work of [5].

### CONCLUSION

The microbiological status of the Emu stream in the Lavun Local Government Area represents a profound challenge to public health and environmental security. The application of GIS-based Inverse Distance Weighted interpolation has provided a clear spatial narrative of the contamination, pinpointing hotspots of faecal pollution and agricultural runoff. The isolation of *Escherichia coli*, *Salmonella typhi*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* confirms that the stream is a significant vector for enteric and opportunistic diseases. The quantitative data shows that coliform levels (MPN > 100 to 2100 per 100 mL) are in direct violation of the Nigerian Standard for Drinking Water Quality and global WHO guidelines. This contamination is a consequence of

intense anthropogenic activities, including livestock watering, domestic washing, and agricultural drainage. To protect the population of Kusotachin and the broader Niger State, it is imperative to shift from reactive healthcare to proactive environmental management [18];[13].

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