



Waterborne Pathogen Research: Examining *Shigella* Species in Fish Ponds of Uli Community

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Abstract	Article History
<p><i>Shigella</i> species are the primary cause of shigellosis, a highly infectious diarrheal disease that poses significant global health concerns due to its widespread impact and potential for outbreaks. This study investigates the prevalence of enteric <i>Shigella</i> species in fish ponds within the Uli community. A cross-sectional study was conducted, collecting samples from various fish-rearing locations using standard microbiological techniques. The analysis significantly ($p \leq 0.05$) revealed the presence of three <i>Shigella dysenteriae</i> strains: SD53, SD07, and SDBU. The distribution of these strains was as follows: 50% SD53, 19.44% SD07, and 30.56% SDBU. Notably, SD53 was the most predominant strain in the samples, and this was statistically significant ($p \leq 0.05$) when compared to other strains. The study highlights the presence of diverse <i>Shigella</i> species in fish pond water in Uli community, with SD53 being the most prevalent. Given these findings, community education is recommended as a crucial strategy for controlling the transmission of <i>Shigella</i> species. By raising awareness about the risks and prevention methods, the community can take proactive steps to mitigate the spread of these pathogens. This approach is essential for protecting public health and ensuring the safety of water sources in the community.</p> <p>Keywords: <i>Shigellosis, Microbiological, Strains, Predominant</i></p> <p>How to cite this paper: Iheukwumere, C. M., Ekesiobi, A. O., Iheukwumere, I. H., Okoli, U. O., Ejike, C. E., Dim, C. N., Ilechukwu, C. C., Ike, V. E., Okereke, F. O., Nwankwo, A. K., & Ochibulu, S. C. (2025). Waterborne Pathogen Research: Examining <i>Shigella</i> species in Fish Ponds of Uli Community. <i>IPS Interdisciplinary Journal of Biological Sciences</i>, 4(3), 125–129. https://doi.org/10.54117/ijbs.v4i3.65</p>	<p>Received: 16 May 2025 Accepted: 22 May 2025 Published: 29 Jun 2025</p> <p>Scan QR code to view*</p>  <p>License: CC BY 4.0*</p>  <p>Open Access article.</p>

Introduction

Fish constitutes an essential component of the human diet, serving as a major source of affordable animal protein, rich in

essential minerals and nutrients required for human sustenance (Njoku et al., 2015). It is widely considered one of the most reliable protein sources globally due to its broad acceptance

across religious and cultural boundaries. For example, fish is preferred among Muslim populations who abstain from consuming pork, thus making it a more universally acceptable alternative to red meat and other protein sources (Obire and Ariyo, 2015).

The rising demand for fish and its derivatives in Nigeria has driven increased fish production by both public and private sectors. Fish ponds vary significantly depending on location and climatic conditions. Seasonal temperature fluctuations, ranging from moderate warmth in summer to freezing conditions in winter, influence pond ecology. Generally, pond water exhibits a neutral pH around 7, but this can vary between 6 and 10 due to several environmental factors (Gorlach-Lira et al., 2013). The presence of large algal populations and aquatic plants significantly affects the pH, as these organisms absorb carbon dioxide during daylight through photosynthesis and release it during the night via respiration. Carbon dioxide reacts to form bicarbonate ions, which buffer pH fluctuations. However, excessive carbon demand by aquatic organisms can deplete bicarbonate ion concentrations, increasing the risk of rapid pH shifts.

Aquaculture systems range from small household ponds to large-scale commercial operations. The success of pond-based fish farming depends heavily on the physical, chemical, and biological characteristics of the water, in addition to effective nutrition management. These factors are closely interconnected and require continuous monitoring to prevent environmental degradation or contamination (Gorlach-Lira et al., 2013). To maximize productivity and profitability, fish farmers often employ strategies such as pond fertilization with organic manure to enhance natural food production. The resulting increase in fish production has contributed to improved dietary quality through diversified and nutrient-rich food sources.

Microorganisms play critical roles in aquatic ecosystems. They contribute to nutrient cycling and influence parameters such as pH, dissolved oxygen, and ammonia levels. The bacteriological quality of pond water is particularly important in managing fish health, as poor water quality can facilitate the spread of infectious diseases among farmed fish populations (Arifin et al., 2013). Pathogenic bacteria, especially species from the *Enterobacteriaceae* family, are influenced by environmental factors such as organic matter, nutrient salts, and oxygen levels. The abundance of these bacteria is closely tied to pond management practices and can directly affect both fish health and human handlers through occupational exposure.

In Uli community, fish farming plays a vital role in food security and economic livelihood. The growing demand for fish globally has highlighted the importance of maintaining a healthy aquaculture environment. Fish exist in a complex relationship with their biotic (living) and abiotic (non-living) environments, and changes in one component can significantly impact the others. Water used in fish ponds—particularly in intensive farming systems—often harbors diverse microbial populations, including opportunistic and pathogenic organisms that can affect fish, humans, and other aquatic life.

Contaminants in pond water have been linked to poor water quality, primarily due to the use of untreated surface water from rivers, streams, lakes, and runoffs in earthen ponds. While many concrete ponds use groundwater, the risk of microbial contamination remains. Notably, the presence of *Shigella* species, a genus known to cause human gastrointestinal infections, poses a public health concern in aquaculture settings. This study was undertaken to conduct a cross-sectional investigation of *Shigella* species in fish ponds within the Uli community.

Materials and Methods

Sample Collection

Sample collection, handling and transportation: The samples used for this study were drawn from the fish pond. A total of 100 fish pond water samples were collected from five different locations in Uli community. The fish pond water samples were collected with sterile containers. The containers were thoroughly washed with detergent, rinsed with water, and then rinsed with 70% ethanol and final rinsed three times with distilled water. The containers were placed inverted in order to drain the water inside them. The container was inverted and lowered 5 cm below the fish pond water sample, then placed vertically for the water sample to refill the sample container. This sample was covered immediately and kept in a cooler containing ice block, and this transported to the laboratory for immediate analysis (Iheukwumere et al., 2018).

Isolation of organisms:

One milliliter (1.0 ml) water sample was aseptically transferred into a sterile test tube (Pyrex) containing 9.0 ml of the diluent (sterile normal saline) and from this; ten-fold serial dilutions were made up to 10⁻³. One milliliter of the diluted sample (10⁻³) was plated on Petri dishes (60 mm OD × 55 mm ID × 13mm high) containing Deoxycholate Citrate agar medium (DCA/BIOTECH) using pour plate method. All the plates in triplicates were incubated inverted at 37±2°C for 24-48 h. (Iheukwumere et al., 2018).

Characterization and Identification of the Isolates

The isolates were sub cultured on nutrient agar (Biotech), incubated in inverted position at 37±2°C for 24 h. The isolates were characterized and identified using their colonial and morphological descriptions as described in the study published by Iheukwumere et al. (2018), Iheukwumere et al. (2025a), biochemical reactions as described in the study published by Iheukwumere et al. (2020), Iheukwumere et al. (2025b) and molecular characterization as described in the study published by Gabriela et al. (2014).

Prevalence and Distribution of the Isolates in the Stream Samples

The number each bacterial isolate in each sampling area were enumerated, and these were calculated in percentage of the occurrences. The bacterial that appeared in each sample location were detected and recorded as described in the study published by Iheukwumere et al (2021).

Statistical Analysis

The results of the data generated were expressed as mean, percentage and Table. Data were analyzed by two-way

Analysis of Variance (ANOVA) to determine the significance of the main effects and interactions at 95 % confidence level as published by Ekesiobi *et al.* (2017), and Abiodum *et al.* (2024a). Ekesiobi (2025), Abiodum *et al.* (2024b). Pairwise comparison of mean was done by Student “t” tests as described in the study published by Iheukwumere *et al.* (2018) Iheukwumere *et al.* (2025c), Iheukwumere *et al.*(2025d), Iheukwumere *et al.* (2025e) and Abiodum *et al.* (2024c).

Results

The occurrences of the Isolates in the sample is showed in Table 1. The study revealed that 36% of the samples were positive for shigella species. Sample c showed highest occurrences of the Test Organism whereas sample B recorded the lowest occurrences.

The cultural and morphological characteristics of the Isolates is shown in Table 2. The study revealed that the Isolates exhibited different appearances on Deoxychocolate citrate agar and similar elevation, Edge and surface. And also similar morphological characteristics on Gram reaction, cell morphology, Endospores and motile nature.

The biochemical characteristics of the Isolates revealed that the Isolates were Voges prokaurer, indole, Citrate, Hydrogen sulphide production, Urease, Dulcitol and Sucrose negative as shown in Table 3. The Isolates differ in their variation in utilization of sugars. They were all catalase and Glucose positive but differ in their abilities to utilize Lactose, Mannitol and Inositol.

The nucleic acid extracted from the Isolates showed the ratio of their absorbance at wave length of 260 nm and 280 nm using Nano drop was at the range of 1.80 —1.90, and this confirmed that the nucleic acids were DNA as shown in Table 4.

The molecular identities of the Isolates revealed that Isolate E, F and G were *Shigella dysenteriae* strain 53-3937(SD53), *Shigella dysenteriae* strain 07-3308 (SD07) and *Shigella dysenteriae* strain BU53W (SDBU) as shown in Table 5

The study also revealed that SD53 showed highest occurrences in the studied sample whereas SD07 recorded the least occurrences as shown in Table 6.

Table 1: Occurrences of the Isolates in the studied samples

Sample	Number	P(%)	N(%)
A	20	7(35.00)	13(65.00)
B	20	4(20.00)	16(80.00)
C	20	13(65.00)	7(35.00)
D	20	5(25.00)	15(75.00)
E	20	7(35.00)	13(65.00)
Total	100	36(36.00)	64(64.00)

Table 2: Cultural and morphological characteristics of the Isolates

Parameter	E	F	G
Appearance on DCA	Colourless/pale	Pale	Colourless
Elevation	Convex	Convex	Convex
Edge	Smooth	Smooth	Smooth
Surface	Smooth	Smooth	Smooth
Gram reaction	—	—	—
Cell morphology	Rods	Rods	Rods
Endospore	—	—	—
Motility	—	—	—

Table 3: Biochemical characteristics of the Isolates

Parameter	E	F	G
Catalase	+	+	+
Voges prokaver	—	—	—
Indole	—	—	—
Citrate	—	—	—
H ₂ S	—	—	—
Urease	—	—	—
Glucose	+	+	+
Lactose	+/-	—	+/-
Mannitol	+/-	+/-	+
Dulcitol	—	—	—
Sucrose	—	—	—
Inositol	—	+/-	—

Table 4: Nano drop confirmation of the nucleic acids from the test isolates

Sample ID	Conc (mg/ml)	260 nm	280 nm	260/280
E	119.40	3.2271	1.7829	1.81
F	128.80	3.3522	1.8218	1.84
G	134.20	3.4220	1.8699	1.83

Table 5: Molecular identities of the isolates

Parameter	E	F	G
Max Score	6076	6076	7239
Total Score	6076	6076	15503
Query Cover (%)	100	100	100
E-Value	0.0	0.0	0.0
Accession No.	CP026780	CP026878	CP024469
Description	<i>Shigella dysenteriae</i> Strain 53-3937 (SD53)	<i>Shigella dysenteriae</i> strain 07-3308 (SD07)	<i>Shigella dysenteriae</i> strain BU 53W (SDBU)

Table 6: Prevalence of the isolates

Isolate	Number	Percentage (%)
SD53	18	50.00
SD07	7	19.44
SDBU	11	30.56
Total	36	100

Discussion

The presence of *Shigella dysenteriae* in the studied fish pond water samples could be traced from the management practices, poor handling and sanitary conditions attributed to the samples. Similar findings were reported by many researchers (Mandal *et al.*, 2009; Ampofo and Clerk, 2010; Knappett *et al.*, 2011; Sule *et al.*, 2016). Researchers had shown that poor hygiene can also harbour *Shigella dysenteriae* and this contributes to the contamination of water also stated that the high prevalence and high populations of enteric bacteria in fish pond water were evidence that the fish pond could be a principal source of enteric pathogens (Sule *et al.*, 2016 and Antunes *et al.*, 2018). Water contaminated by *Shigella dysenteriae* to humans can contribute to human waterborne illness through the water-food-human chain. This shows that a fish pond requires microbiological safety regulations to prevent microbial contamination of the product. The variation of *Shigella dysenteriae* from different locations of the fish ponds studied could be attributed to the nature and anthropogenic activities in the fish ponds (Knappett *et al.*, 2011).

The presence of *Shigella dysenteriae* strain 53—3937(SD53), *Shigella dysenteriae* strain 07—3308(SD07) and *Shigella dysenteriae* strain BU53W(SDBU) from studied fish pond water samples supported the occurrence of enteric bacteria in the samples. Traditionally, the laboratory detection of *shigella* species has relied on non-selective and/or selective enrichment and subsequent culture on selective media. The introduction of molecular techniques provides a more sensitive and rapid technique for detecting these bacteria.

Conclusion

The study has revealed the presence of which *Shigella dysenteriae* strain 53-3937(SD53), *Shigella dysenteriae* strain 07-3308(SD07) and *Shigella dysenteriae* strain BU53W(SDBU), of which SD53 was mostly encountered in the fish ponds water samples. The present study recommends community education as a better means of controlling the transmission of *Shigella* species.

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