Journal of Science Research and Reviews
PRINT ISSN: 1595-9074
E-ISSN: 1595-8329
DOI: https://doi.org/10.70882/josrar.2025.v2i2.60
Homepage: https://josrar.esrgngr.org
Original Research Article

Assessment of Bacterial Contamination in Farmed Catfish and Wild Caught (*Clarias gariepinus*) (Burchell, 1822) and Water Sources in Zaria, Nigeria

***[1]Atawodi, Joy C., [1]Somdare, Peace O., [2]Okolo, Esther and [2]Bala, Hannatu**

[1]Department of Zoology, Federal University Lokoja, Kogi State, Nigeria.
[2]Department of Microbiology Federal University Lokoja, Kogi State, Nigeria.
*Corresponding Author's email: joyceciliaatawodi@gmail.com Phone: +2349166655062

KEYWORDS
Bacterial contamination,
Bacterial counts,
Dams,
Fish farms,
Pathogenic bacteria,
Public health implications,
Zaria Nigeria.

CITATION
Atawodi, J. C., Somdare, P. O., Okolo , E., & Bala, H. (n.d.). Assessment of Bacterial Contamination in Farmed Catfish and Wild Caught (Clarias gariepinus) (Burchell, 1822) and Water Sources in Zaria, Nigeria. *Journal of Science Research and Reviews*, *2*(2), 43-52. https://doi.org/10.70882/josrar.2025.v2i2.60

ABSTRACT
Catfish (Clarias gariepinus), obtained from both cultivated farms and natural environments serves as an important source of protein in Nigeria. Nevertheless, the presence of bacterial contamination in both fish and aquatic habitats presents considerable risks to public health. Evaluating the microbial quality of both farmed and wild catfish, as well as their water sources in Zaria is crucial for ensuring food safety and mitigating the threat of waterborne diseases. This study therefore, aimed at assessing the bacterial contamination levels in water and fish (*Clarias gariepinus*) from selected dams and fish farms in Zaria, Nigeria, and identified the bacterial species present. Water and fish organ samples (kidney and liver) were analyzed for bacterial and coliform counts over 12 months using standard culture methods. Results revealed significant variations in bacterial ($0.35x10^5$- $10.65x10^5$) and coliform ($0.8x10^4$-$9.0x10^4$) counts across months and sampling sites, with farm water samples exhibiting higher contamination levels than dam water. For the fish organs, however, the bacterial contamination rate of dam fish samples was higher ($12.62x10^5$) than the farm fish samples ($8.75x10^5$). Pathogenic bacteria were isolated from water and fish samples, including *Staphylococcus aureus*, *Escherichia coli*, *Salmonella typhi*, and *Klebsiella pneumoniae*. The findings reveal the public health risks associated with consuming contaminated fish and emphasize the need for improved water quality management and good food safety practices in the region.

INTRODUCTION

Bacterial Contamination in Aquatic Ecosystems

Fish is a vital source of protein in Nigeria, but its safety is compromised by bacterial contamination from polluted waterbodies. In Zaria, anthropogenic activities such as sewage discharge and agricultural runoff contribute to water pollution, increasing the risk of bacterial contamination in fish. Bacterial contamination in aquatic ecosystems is a global concern, particularly in developing countries where inadequate sanitation and poor waste management practices encourage water pollution. Waterbodies such as rivers, dams, and fish farms are often contaminated with pathogenic bacteria from human and animal waste, agricultural runoff, and industrial effluents (Bashir *et al*., 2020). These contaminants pose significant risks to aquatic organisms, including fish, which can serve as vectors for transmitting pathogens to humans through consumption (Adedeji *et al*, 2012).

In Nigeria, water pollution is a major environmental challenge, with studies reporting high levels of bacterial

contamination in rivers and dams used for fishing and domestic purposes (Dar *et al*., 2020). For instance, *Escherichia coli* and *Salmonella spp*. have been frequently isolated from water and fish samples in Nigerian water bodies, highlighting the prevalence of faecal contamination (Esonu *et al*., 2024). These findings expose the need for regular monitoring of water quality in order to mitigate public health risks.

Fish as a Vehicle for Bacterial Pathogens

Fish are highly susceptible to bacterial contamination due to their exposure to polluted water and improper handling practices during harvesting, processing, and storage (Suresh *et al*., 2022). Pathogenic bacteria such as *Staphylococcus aureus*, *Escherichia coli*, and *Salmonella typhi* have been isolated from fish tissues, including the kidney and liver, which are critical organs for detoxification and immune response (Aliyu *et al*., 2016). The presence of these pathogens in fish poses a significant risk to consumers, particularly in regions where fish is consumed raw or undercooked (Golden *et al*., 2023).

Fish is a major source of dietary protein in Nigeria, and *Clarias gariepinus* (African catfish) is one of the most commonly consumed species (Yahaya *et al*, 2021; Omoyinmi and Bello, 2023; Yashim *et al.,* 2025). However, studies have shown that fish from polluted waterbodies often harbour high levels of pathogenic bacteria, raising concerns about food safety (Abd El-Hack *et al*., 2022). For example, a study by Nwuzo *et al*. (2022) reported the isolation of *Vibrio cholerae* and *Shigella spp*. from fish in Nigerian rivers, highlighting the potential for waterborne disease outbreaks.

Sources of Bacterial Contamination in Waterbodies

The primary sources of bacterial contamination in waterbodies include untreated sewage, agricultural runoff, and industrial discharges (UNEP, 2022). In Nigeria, the lack of adequate wastewater treatment facilities and poor enforcement of environmental regulations contribute to the contamination of water resources (Nwankwo *et al*., 2023). For instance, a study by Ocholi (2024) found that waterbodies in Zaria were contaminated with faecal coliforms due to the discharge of untreated sewage from residential areas.

Fish farms are particularly vulnerable to bacterial contamination due to the high stocking densities and reliance on external water sources, which may already be polluted. Using contaminated water in aquaculture can lead to the bioaccumulation of pathogens in fish, posing risks to both consumers and farm workers. Poor hygiene practices during fish handling and processing can further increase contamination levels (Yohans et al, 2022).

Public Health Implications of Bacterial Contamination of Fish and Water

The consumption of contaminated fish can lead to foodborne illnesses, including gastroenteritis, typhoid fever, cholera etc (Odetokun et al, 2023). Pathogenic bacteria such as *Escherichia coli* and *Salmonella typhi* are known to cause severe infections, particularly in immunocompromised individuals and children (Khabo-Mmekoa *et al*., 2022). In Nigeria, however, the burden of foodborne diseases is exacerbated by limited access to clean water, inadequate healthcare facilities, and poor sanitation practices (Okafor, 2024).

The presence of antibiotic-resistant bacteria in fish and waterbodies further complicates the public health landscape. Studies have reported the isolation of multidrug-resistant strains of *Staphylococcus aureus* and *Klebsiella pneumoniae* from Nigerian water bodies, raising concerns about the effectiveness of conventional treatments for bacterial infections (Adebajo *et al*., 2020). This makes the need for a One Health approach to addressing the interconnected challenges of water pollution, food safety, and antimicrobial resistance an urgent matter (Aslam *et al.*, 2021; Suresh *et al.*, 2022). This study aimed to assess the bacterial contamination levels in water and fish from selected dams and fish farms in Zaria, identify the bacterial species present, and evaluate the implications for public health and food safety.

MATERIALS AND METHODS

Study Area

The study was conducted in Zaria, Nigeria, focusing on three selected dams (ZDM, SDM, ADM) and three fish farms (ZGF, SBF, BZF). These dams are used for fishing, domestic activities, and irrigation while the fish farms are backyard fish ponds that utilize water indiscriminately from any source possible.

Sample Collection

Water (n=144) and *Clarias gariepinus* fish (n=360) samples were randomly collected on a monthly basis throughout the year. Water from each of the three dams and three fish farms was aseptically collected into sterile bottles for analysis. For the fish samples, kidney and liver samples were aseptically collected into sterile tubes for bacterial analysis.

Microbial Analysis

Bacterial Isolation

Serial dilutions of water samples and tissue homogenates were prepared and a loop-full of each of the selected concentrations was inoculated in Nutrient Agar (NA), Mac Conkey Agar (MCA), Mannitol Salt Agar (MSA), Salmonella Shigella Agar (SSA) and Eosin Methylene Blue Agar (EMB) respectively by using spread plate technique. Plates were then incubated at 37°C for 24 hours, after which discrete

colonies were counted, multiplied by the dilution factor and computed as colony-forming units per milliliters (cfu/ml) for water samples while colony-forming units per gram (cfu/g) were recorded for fish organ samples (Murthy, 2021; Islam & Khanam, 2021).

Bacterial Identification

Isolated bacteria were identified by observing the growth characteristics, colony morphology, gram staining, motility and different biochemical tests using the procedure outlined by Chesebrough (2005); Omeji & Ojo (2017). Thereafter, the resultant appearances were compared with those of known taxa using the scheme of Cheesbrough (2010) and Bergy's Manual of Determinative Bacteriology (2000).

Data Analysis

Statistical analyses were conducted using Microsoft Excel. The data are presented as mean ± standard deviation (SD) and ANOVA was used to compare mean bacterial and coliform counts across months and sampling sites. Significance was set at $p < 0.05$.

RESULTS AND DISCUSSION

Results

Bacterial and Coliform Counts in Water Samples

The average monthly bacterial counts of water samples collected from selected dams and fish farms in Zaria and its surroundings are presented in Table 1. A significant variation ($p < 0.05$) was observed across the months, from January to December, at all sampling locations. The lowest bacterial count, recorded at ZGF in January, was 0.35×10^5, whereas the highest, noted at SBF in November, reached 2.63×10^6. When comparing the types of water sources, samples from farms exhibited higher bacterial and coliform counts than those taken from dams, as illustrated in Figure 1.

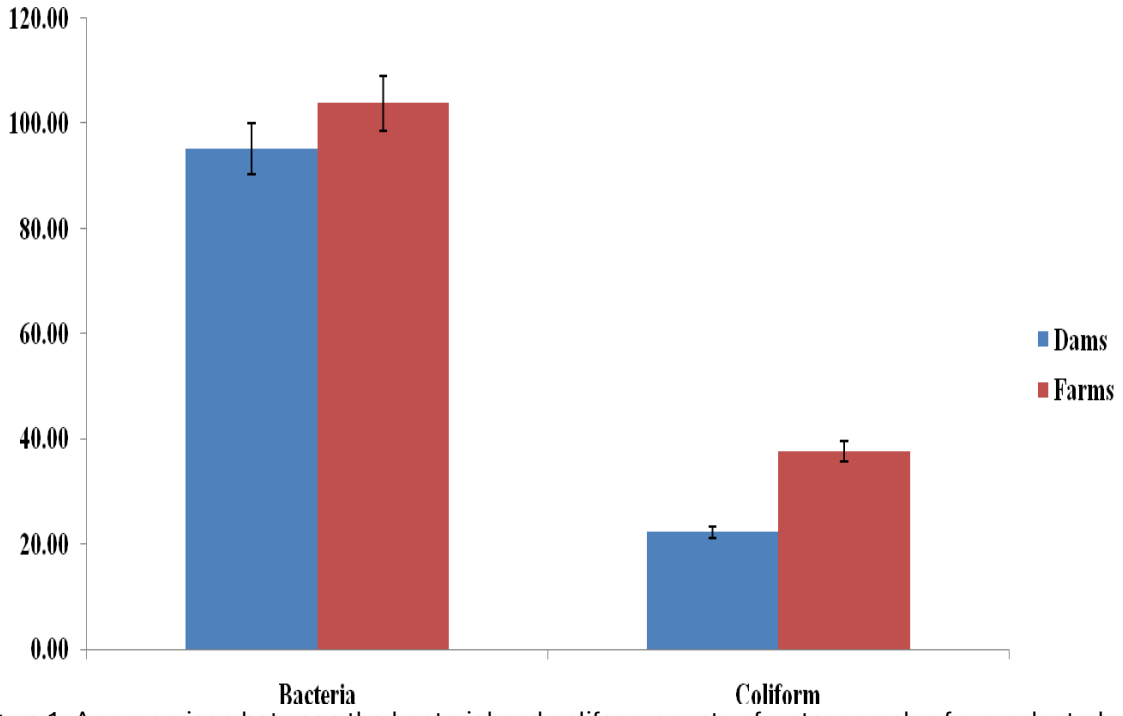

Figure 1: A comparison between the bacterial and coliform counts of water samples from selected Dams and fish farms in Zaria and its environs

Table 2 details the mean monthly coliform counts, expressed in colony-forming units per millilitre (cfu/ml), of water samples from the selected dams and fish farms in Zaria and its environs. The recorded coliform counts varied from 1.00×10^4, observed at ZDM in January, to 9.00×10^4, noted in July at BZF. No statistically significant changes were found in the coliform counts from ADM over the sampled months (January to December). In contrast, only minor fluctuations in coliform counts were documented for water samples from SDM and ZGF during September and October, respectively. Significant differences in coliform counts were noted for SBF and BZF throughout the study months. Overall, the average coliform count in farm water samples was greater than that of dam water samples (Figure 1)

Table 1: Mean monthly bacterial count (cfu/ml) of water samples from some selected dams and fish farms in Zaria and its environs

Sapling site	Jan	Feb	Mar	Apr	May	Jun	July	Aug	Sept	Oct	Nov	Dec
ADM	$1.55X10^{5a}$	$2.25X10^{5a}$	$2.73X10^{5a}$	$2.75X10^{4a}$	$4.65X10^{5c}$	$8.50X10^{5c}$	$7.65X10^{5c}$	$2.0X10^{5a}$	$1.7\ X10^{5a}$	$2.80X10^{5a}$	$3.55X10^{5b}$	$7.40X10^{5c}$
ZDM	$5.10\ X10^{5a}$	$2.75\ X10^{5a}$	$2.75\ X10^{5a}$	$2.95\ X10^{5a}$	$4.30\ X10^{5a}$	$0.74X10^{4a}$	$2.95X10^{5a}$	$4.30X10^{5a}$	$9.50X10^{4a}$	$3.00X10^{5a}$	$4.4X10^{5a}$	$8.15\ X10^{4a}$
SDM	$3.15X10^{5a}$	$6.30X10^{5a}$	$9.55\ X10^{5a}$	$4.5\ X10^{4a}$	$4.5\ X10^{4a}$	$6.15\ X10^{5a}$	$1.00X10^{6a}$	$2.19\ X10^{6b}$	$2.3\ X10^{5a}$	$5.0\ 0X10^{5a}$	$7.2\ X10^{5a}$	$2.0\ X10^{5a}$
ZGF	$0.35\ X10^{5a}$	$5.85X10^{5abc}$	$10.65X10^{5bc}$	$1.25\ X10^{5ab}$	$6.45X10^{5abcd}$	$13.05X10^{d}$	$2.20X10^{5ab}$	$3.00X10^{5b}$	$10.05X10^{5d}$	$6.85X10^{5ad}$	$8.00X10^{5bd}$	$2.88X10^{5c}$
SBF	$3.55X10^{5a}$	$2.75X10^{5a}$	$1.85\ X10^{5a}$	$7.70X10^{5a}$	$3.95\ X10^{5a}$	$5.45\ X10^{5a}$	$6.25\ X10^{5a}$	$6.45\ X10^{5a}$	$1.5\ 0X10^{5a}$	$1.90\ X10^{5a}$	$2.63\ X10^{6b}$	$1.90\ X10^{6b}$
BZF	$6.00X10^{5abc}$	$1.32X10^{6c}$	$1.23X10^{6bc}$	$7.95X10^{5abc}$	$1.20X10^{6bc}$	$1.13X10^{5bc}$	$7.60X10^{5abc}$	$7.00\ X10^{4a}$	$4.45\ X10^{5ab}$	$3.80\ X10^{5ab}$	$5.85X10^{5abc}$	$5.00X10^{5abc}$

ADM=ABU Dam, ZDM=Zango Dam, SDM=Shika Dam, ZGF=Zango Farm, SBF= Sabo Farm, BZF=BZ Farm, cfu/ml = colony forming unit per millilitre. Values with different superscripts per row are statistically different (p≤0.05)

Table 2: Mean monthly coliform counts (cfu/ml) of water samples from selected dams and fish farms in Zaria and its environs between July, 2015 – June, 2016

Sampling site	Jan	Feb	Mar	Apr	May	Jun	July	Aug	Sept	Oct	Nov	Dec
ADM	$2.50x10^{4a}$	$1.70x10^{4a}$	$2.40x10^{4a}$	$1.50x10^{4a}$	$1.65x10^{4a}$	$1.75x10^{4a}$	$1.80x10^{4a}$	$1.35x10^{4a}$	$0.8x10^{4a}$	$4.10x10^{4b}$	$2.35x10^{4a}$	$1.90x10^{4a}$
ZDM	$1.0\ x10^{4a}$	$1.35\ x10^{4a}$	$5.70\ x10^{4c}$	$1.40\ x10^{4a}$	$1.7\ x10^{4a}$	$1.15\ x10^{4a}$	$2.6\ x10^{4ab}$	$2.45\ x10^{4ab}$	$1.0\ x10^{4a}$	$1.85\ x10^{4a}$	$2.15\ x10^{4ab}$	$4.75\ x10^{4bc}$
SDM	$1.05\ x10^{4a}$	$1.85\ x10^{4a}$	$2.05\ x10^{4a}$	$3.20\ x10^{4a}$	$3.10\ x10^{4a}$	$1.85\ x10^{4a}$	$3.00\ x10^{4a}$	$1.50\ x10^{4a}$	$5.50\ x10^{4c}$	$3.00\ x10^{4a}$	$2.70\ x10^{4a}$	$1.40\ x10^{4a}$
ZGF	$1.70\ x10^{4a}$	$2.90\ x10^{4a}$	$3.30\ x10^{4a}$	$5.10\ x10^{4a}$	$4.90\ x10^{4a}$	$2.98\ x10^{4a}$	$2.00\ x10^{4a}$	$2.35\ x10^{4a}$	$1.70\ x10^{4a}$	$3.65\ x10^{4b}$	$2.64\ x10^{4a}$	$3.70\ x10^{4a}$
SBF	$4.25\ x10^{4cde}$	$5.70\ x10^{4a}$	$2.35\ x10^{4abcd}$	$5.00\ x10^{4a}$	$1.40\ x10^{4ab}$	$1.90\ x10^{4abc}$	$2.90\ x10^{4a}$	$3.65\ x10^{4b}$	$3.35\ x10^{4bc}$	$8.00\ x10^{4c}$	$4.55\ x10^{4de}$	$7.25\ x10^{4a}$
BZF	$5.00\ x10^{4a}$	$4.6\ 0x10^{4ab}$	$4.20\ x10^{4ab}$	$3.15\ x10^{4ab}$	$1.20\ x10^{4a}$	$1.70\ x10^{4a}$	$9.00\ x10^{4b}$	$1.40\ x10^{4a}$	$2.50\ x10^{4ac}$	$1.75\ x10^{4a}$	$1.13\ x10^{4b}$	$2.80\ x10^{4ab}$

ADM=A.B.U Dam, ZDM=Zango Dam, SDM=Shika Dam, ZGF=Zango Farm, SBF= Sabo Farm, BZF=BZ Farm, cfu/ml= colony forming unit per milliliter. Values are expressed as means ± SEM (Standard error of means). Values with different superscripts per row are statistically different (p≤0.05)

Table 3: Mean monthly bacterial count (cfu/g) of organs (liver and kidney) samples of *C. gariepinus* from some selected dams and fish farms in Zaria and its environs

Sampling site	Jan	Feb	Mar	Apr	May	Jun	July	Aug	Sept	Oct	Nov	Dec
ADM	$7.30X10^{5d}$	$6.68X10^{5d}$	$4.42X10^{5abc}$	$5.48X10^{5bcd}$	$7.26X10^{5d}$	$5.46X10^{5bcd}$	$6.04X10^{5cd}$	$5.96X10^{5cd}$	$3.54X10^{5ab}$	$3.56X10^{5ab}$	$4.22X10^{5abc}$	$3.20X10^{5a}$
ZDM	$5.08\ X10^{5cd}$	$4.10X10^{4cd}$	$4.32\ X10^{5cd}$	$4.18\ X10^{5cd}$	$6.96X10^{5d}$	$8.22\ X10^{5e}$	$3.80X10^{4bcd}$	$3.34X10^{5abc}$	$3.80X10^{4bcd}$	$2.16\ X10^{5a}$	$2.98X10^{5abc}$	$2.60X10^{4ab}$
SDM	$1.38\ X10^{5a}$	$3.62X10^{5cd}$	$3.02\ X10^{5bc}$	$4.28\ X10^{5d}$	$4.72\ X10^{5d}$	$6.58\ X10^{5d}$	$4.30\ X10^{4d}$	$1.62\ X10^{5a}$	$2.80X10^{5bc}$	$1.32\ X10^{5a}$	$2.10\ X10^{4ab}$	$1.02\ X10^{5a}$
ZGF	$1.92\ X10^{4b}$	$2.20\ X10^{5a}$	$7.80\ X10^{5a}$	$2.22\ X10^{4bc}$	$3.18\ X10^{4cde}$	$6.00\ X10^{5d}$	$2.96\ X10^{4bcd}$	$3.76X10^{4bcd}$	$3.72X10^{5bcd}$	$3.70\ X10^{4bcd}$	$4.18\ X10^{4cd}$	$4.72\ X10^{4d}$
SBF	$4.50\ X10^{4cd}$	$3.90\ X10^{4bc}$	$2.24\ X10^{5a}$	$4.30\ X10^{4cd}$	$4.78\ X10^{4d}$	$4.30\ X10^{4cd}$	$4.50\ X10^{4cd}$	$3.90\ X10^{4bc}$	$2.24\ X10^{5a}$	$4.00\ X10^{4bcd}$	$3.40\ X10^{4b}$	$4.00\ X10^{4bcd}$
BZF	$1.78\ X10^{5d}$	$0.64\ X10^{4abc}$	$0.48\ X10^{4ab}$	$1.18\ X10^{5cd}$	$1.26\ X10^{5cd}$	$1.04\ X10^{5cd}$	$1.78\ X10^{5d}$	$0.64\ X10^{4abc}$	$0.42\ X10^{4ab}$	$0.36\ X10^{4ab}$	$0.28\ X10^{4a}$	$0.60\ X10^{4abc}$

ADM=A.B.U Dam, ZDM=Zango Dam, SDM=Shika Dam, ZGF=Zango Farm, SBF= Sabo Farm, BZF=BZ Farm, (cfu/g) = colony forming units per gram. Values with different superscripts per row are statistically different (p≤0.05)

Bacterial and Coliform Counts in Fish Organ Samples

Table 3 displays the average monthly bacterial counts for organ samples (kidneys and livers) of *C. gariepinus*. The lowest bacterial count recorded was 3.20 x 10^5 in December at ADM, whereas the highest count of 7.30 x 10^5 occurred in January at the same site. The January count showed a statistically significant difference ($p < 0.05$) compared to the counts from all other months studied.

In contrast, at ZDM, the pattern varied; no significant differences ($p < 0.05$) were found in bacterial counts from January (5.08 x 10^5) to April (4.18 x 10^5). The highest count was recorded in June at 8.22 x 10^5, which was statistically significant ($p < 0.05$), but this value also differed from the counts in January (1.38 x 10^5), August (1.62 x 10^5), October (1.32 x 10^5), and December (1.02 x 10^5). The mean coliform counts of organs of fish from the farms were higher than those from the dam (Figure 2).

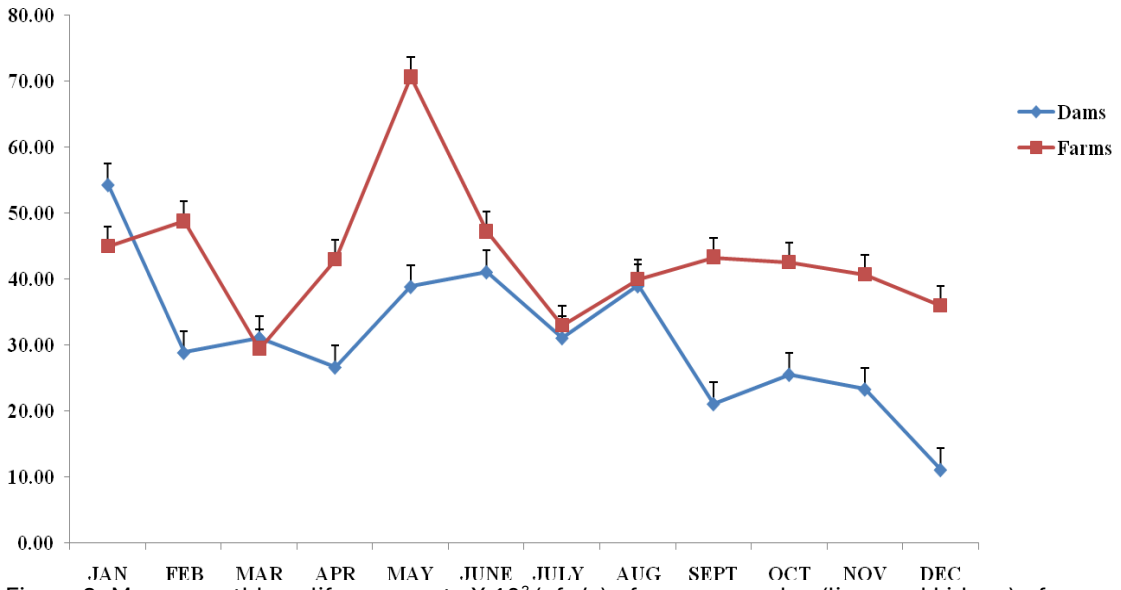

Figure 2: Mean monthly coliform counts X 10^3 (cfu/g) of organ samples (liver and kidney) of *Clarias gariepinus* from selected dams and fish farms in Zaria and its environs

Isolation and Identification of Bacteria from Water

The following bacteria were isolated from the water samples; *Staphylococcus aureus, Escherichia coli, Proteus spp., Bacillus subtilis, Pseudomonas spp., Klebsiella pneumoniae,* and *Salmonella typhi*. Having been detected in all the water samples collected from the dams and farms (Table 4).

Table 4: Bacteria isolated from water obtained from selected dams and farms in Zaria and its environs

Isolated bacteria	Sampling sites					
	ADM	ZDM	SDM	ZGF	SBF	BZF
S.aureus	+	+	+	+	+	+
E. coli	+	+	+	+	+	+
Proteus spp	+	+	+	+	+	+
Bacillus subtilis	+	+	+	+	+	+
Pseudomonas spp	+	+	+	+	-	-
Klebsiella pneumoniae	+	+	+	+	+	+
Salmonella typhi	+	+	+	+	+	-
Aeromonas spp	+	+	+	+	+	+
Streptococcus faecalis	+	-	-	+	-	-
Shigella	-	+	+	-	+	-

Key: + = isolated, - = not isolated, ADM=A.B.U Dam, ZDM=Zango Dam, SDM=Shika Dam, ZGF=Zango Farm, SBF= Sabo Farm, BZF=BZ Farm.

Isolation and Identification of Bacteria from Fish Organs

The result of bacterial isolates from the liver and kidney of *Clarias gariepinus* sampled from the three dams and fish farms is presented in table 5. The isolated bacteria include *Staphylococcus aureus, Escherichia coli, Proteus spp, Bacillus subtilis, Pseudomonas spp, Klebsiella pneumonia* and *Salmonella typhi.* Bacterial isolation was reported for all the sampling sites. The bacterial load was higher in the farm samples than in the dams (Figure 3).

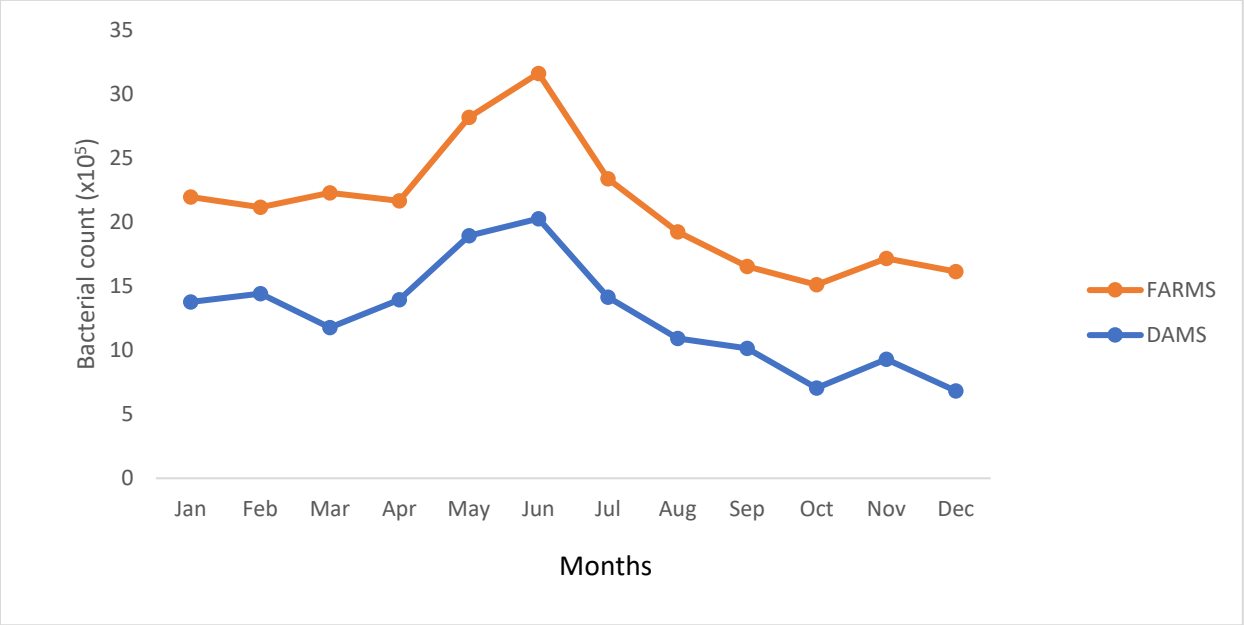

Figure 3: A comparison between the bacterial counts of organ samples from selected Dams and fish farms in Zaria and its environs

Table 5: Distribution of bacteria isolated from *Clarias gariepinus* obtained from selected dams and farms in Zaria and its environs

Isolated bacteria	Sampling sites					
	ADM	ZDM	SDM	ZGF	SBF	BZF
Staphylococcus aureus	+	+	+	+	+	+
Escherichia coli	+	+	+	+	+	+
Proteus spp	+	+	+	+	+	-
Bacillus subtilis	+	+	+	-	+	+
Pseudomonas spp	+	+	+	+	+	+
Klebsiella pneumoniae	+	+	+	+	+	+
Salmonella typhi	+	+	+	+	+	+

Key: + = Isolated, - = Not Isolated, ADM=A.B. U Dam, ZDM=Zango Dam, SDM=Shika Dam, ZGF=Zango Farm, SBF= Sabo Farm, BZF=BZ Farm

Discussion

The results of this study show that there are fluctuations of bacterial loads in water samples collected from various dams and fish farms in Zaria and its environs (Table 1). Throughout the different months, notable variations in bacterial counts were detected at the sampling locations, with the peak load observed in November at the SBF site ($2.63x10^6$), while the lowest count was recorded in January at the ZGF site ($0.35x10^5$). Most of the sampling sites demonstrated statistically significant differences in bacterial levels over the study months, apart from ZDM and SDM, which showed no significant variations ($p<0.05$). Furthermore, as seen in Figure 1, a comparison between the types of water sources indicated that farm water exhibited considerably higher bacterial and coliform counts compared to dam water ($p<0.05$). This is consistent with findings from previous studies, such as those by Adinortey *et al*. (2020) and Sheng & Wang (2021), who reported elevated microbial contamination in fish farm water compared to natural water sources. This would probably be due to organic waste from fish excreta, uneaten feed, and other anthropogenic inputs, which provide a continuous nutrient source for bacterial growth. The higher nutrient load in farm water can create favourable conditions for microbial proliferation,

especially when water is not properly treated or maintained.

The high bacterial and coliform counts in farm water could pose a risk to both fish health and public health, especially if water from these sources is used for irrigation or other domestic purposes. Possible implications of high bacterial loads in fish farms, may include a compromise in fish health, leading to increased susceptibility to infections, poor growth rates, higher mortality etc.

The higher bacterial load observed in the months of November and other rainy season months could be linked to the influx of organic material into the water, which serves as a nutrient source for bacterial growth. Previous studies have similarly indicated that environmental factors such as temperature, rainfall, and organic loading can promote bacterial proliferation in aquatic environments (Yu, 2025). For example, Abija *et al*. (2021) reported similar seasonal variations in bacterial contamination in fish farms in Calabar, Nigeria, with increased bacterial counts during the rainy season due to runoff and organic material accumulation.

Bacterial and Coliform Counts in Fish Organ Samples

There is significant variability in the bacterial counts of organ samples (kidney and liver) of *Clarias gariepinus* across different months and sampling sites. At ADM, the lowest bacterial count of 3.20 x 10^5 was recorded in December, while the highest count of 7.30 x 10^5 was observed in January. The significant difference ($p < 0.05$) in bacterial counts between January and all other months of the study suggests a possible seasonal influence on bacterial proliferation in the organs of the fish. This could be linked to changes in environmental conditions such as temperature, water quality, and organic matter availability, which may enhance bacterial growth in aquatic environments. The peak in January could also reflect higher bacterial activity following the rainy season, where nutrient influx from runoff can promote microbial proliferation.

In contrast, the trend observed in ZDM was different, with no significant variation ($p > 0.05$) in bacterial counts between January (5.08 x 10^5) and April (4.18 x 10^5). The highest bacterial count at ZDM was recorded in June (8.22 x 10^5), which was significantly different ($p < 0.05$) from the bacterial count in October (2.16 x 10^5). This indicates that while there were no significant fluctuations in bacterial counts for most of the months. June saw an increase that may be related to seasonal changes, such as water temperature or increased organic matter due to environmental factors. Furthermore, bacterial counts in April (4.28 x 10^5), May (4.72 x 10^5), June (6.58 x 10^5), and July (4.30 x 10^4) were not significantly different ($p > 0.05$), yet they were different from counts recorded in January (1.38 x 10^5), August (1.62 x 10^5), October (1.32 x 10^5), and December (1.02 x 10^5). This finding suggests that bacterial proliferation in the organ samples of *C. gariepinus* may follow a pattern influenced by seasonal shifts, but also potentially by site-specific factors such as the presence of organic waste, feed, and water management practices at each location. For example, higher bacterial counts in June at ZDM could indicate an influx of organic material or changes in water temperature, which favour microbial growth.

The observed differences in bacterial counts between the two sampling sites, ADM and ZDM, also suggest that site-specific factors, such as water quality, depth, or management practices, can influence bacterial dynamics in fish organs. This highlights the importance of considering both environmental and management factors when assessing the health and microbial load in aquaculture systems. The differences in microbial contamination levels between these sites may reflect variations in water handling, feeding practices, or pollution levels, all of which can influence the bacterial load in fish organs.

Coliform Count of Organ Samples (Kidney and Liver) of C. gariepinus

The coliform counts in kidney and liver samples of *C. gariepinus* from farms was significantly higher than those from dam samples (Afolabi *et al*, 2020), except for January. This suggests that environmental factors and aquaculture practices influence the microbial load in farmed fish, while natural water bodies like dams may offer more stable and cleaner conditions (Paredes-Trujillo & Mendoza-Carranza 2022).

Higher bacterial counts in farm samples align with previous studies that have attributed elevated coliform levels in farmed fish to factors such as high fish density, poor water circulation, and the use of contaminated feed (Afolabi *et al*, 2020). Conversely, the lower coliform levels in dam fish samples may be due to the larger, more dynamic nature of dam ecosystems, where water quality is typically better regulated through natural processes (Tiwari & Tiwari, 2022).

The exception in January, when dam samples had higher coliform counts, could be linked to seasonal changes in water quality, such as reduced water temperatures or increased runoff, which might temporarily elevate microbial levels in dam waters (Bohrerova *et al*., 2017). This highlights the need for further studies to examine the impact of seasonal fluctuations on bacterial populations in aquatic environments.

The higher bacterial load in farmed fish raises potential food safety concerns, as coliform bacteria can indicate contamination by more harmful pathogens (Adeyemi *et al.*, 2022). Consequently, effective management practices, including water quality monitoring and sanitation, are crucial in reducing the microbial risk associated with farmed fish (Alhaji *et al*., 2024).

Identified Bacterial Species

As observed in this study, the isolation of various bacterial species from water and fish samples reveals the significant risk of microbiological contamination in aquatic ecosystems and its implications for both fish health and public safety. The detection of bacteria such *as Staphylococcus aureus, Escherichia coli, Salmonella typhi, Klebsiella pneumoniae, Proteus spp., Bacillus subtilis, Pseudomonas spp.,* and *Aeromonas* spp. Shows the variety of pathogenic bacteria that can thrive in these environments. These results align with prior research that has similarly identified bacterial species in polluted water and fish, reinforcing the concept that such habitats serve as reservoirs for harmful microorganisms (Suresh *et al*., 2022; Pandey *et al*., 2014).

The detection of *Escherichia coli*, a common indicator of faecal contamination, suggests potential contamination of the water sources with faecal matter, which poses significant risks to human health, particularly if the fish are consumed raw or undercooked (Ava, 2020). Similarly, the presence of *Salmonella typhi* and *Klebsiella pneumoniae* is concerning, as these pathogens are associated with severe gastrointestinal and systemic infections in humans (Mumbo *et al*., 2023; Muhammed, 2024). The isolation of *Aeromonas spp. and Pseudomonas* spp., which are known to cause infections in both fish and humans, further highlights the dual threat of these bacteria to aquatic life and public health (Njoku *et al*., 2015; Govender *et al*., 2021).

The rarity of *Streptococcus faecalis*, isolated only from ADM and ZGF samples, may indicate localized contamination or specific environmental conditions favouring its presence in these areas.

The isolation of *Aeromonas spp. and Pseudomonas spp*. is particularly noteworthy, as these bacteria are not only pathogenic to fish but can also cause infections in humans, such as wound infections, septicemia, and gastrointestinal illnesses (Nolla-Salas *et al*,.2017). Their presence in aquatic environments is often linked to poor water quality and organic pollution, which can exacerbate their proliferation (Govender *et al*., 2021).

The rarity of Streptococcus faecalis, which was isolated only from ADM and ZGF samples, may indicate localized contamination or specific environmental conditions that favour its survival. This finding is consistent with studies suggesting that *S. faecalis* is less commonly associated with aquatic environments compared to other enteric bacteria, and its presence may reflect point-source contamination (Igbinosa *et al*., 2020). The diversity of bacteria in the water samples, for both farmed and wild (dam) sources, was similar to those found in the fish samples. This agrees with the work of Njoku *et al*., (2015) and Abdelsalam *et al* (2021) who reported that the microbial load of water often reflects the microbial flora of the fish in the water body.

CONCLUSION

This study revealed high levels of bacterial contamination in fish and water from selected waterbodies in Zaria, Nigeria. Because pathogenic bacteria pose significant public health risks, it is important to emphasize the need for regular monitoring of the quality of fish-holding water. It is also recommended to implement good aquaculture practices to reduce bacterial contamination. Further research is recommended to explore the sources of contamination and develop mitigation strategies.

REFERENCES

Abd El-Hack, M. E., El-Saadony, M. T., Ellakany, H. F., Elbestawy, A. R., Abaza, S. S., Geneedy, A. M., & El-Tarabily, K. A. (2022). Inhibition of microbial pathogens in farmed fish. *Marine Pollution Bulletin*, *183*, 114003

Abija, F., Harry, T., & Nwankwoala, H. (2021). Seasonal Variation in Abundance, Distribution and Environmental Impacts of Geomicrobiological Communities in the Lower Calabar River Channel, Calabar, Nigeria. *Journal of Earth and Environmental Science Research. SRC/JEESR-178. https://doi.org/10.47363/JEESR/2021(3), 153*.

Abdelsalam, M., Ewiss, M. Z., Khalefa, H. S., Mahmoud, M. A., Elgendy, M. Y., & Abdel-Moneam, D. A. (2021). Coinfections of Aeromonas spp., Enterococcus faecalis, and Vibrio alginolyticus isolated from farmed Nile tilapia and African catfish in Egypt, with an emphasis on poor water quality. *Microbial Pathogenesis*, *160*, 105213.

Adebajo, S. O., Ojo, A. E., Bankole, P. O., Akintokun, A. K., & Olagunju, T. (2024). Seasonal Variation on Multidrug-Resistant Microorganisms from Water Sources in Alabata Community, Ogun State, Nigeria. *FUOYE Journal of Pure and Applied Sciences (FJPAS)*, *9*(3), 1-16.

Adedeji, O. B., Okerentugba, P. O., Innocent-Adiele, H. C., Okonko, I. O., Ojeniyi, S. O., Adejoro, S. A., & Mohamed, S. A. (2012). Benefits, public health hazards and risks associated with fish consumption. *New York Science Journal*, *5*(9), 33-61.

Adeyemi, F. M., Ojo, O. O., Badejo, A. A., Oyedara, O. O., Olaitan, J. O., Adetunji, C. O., ... & Akinde, S. B. (2022). Integrated poultry-fish farming system encourages multidrug-resistant gram-negative bacteria dissemination in pond environment and fishes. *Aquaculture*, *548*, 737558.

Adinortey, C. A., Aheto, D. W., Boateng, A. A., & Agbeko, R. (2020). Multiple antibiotic resistance-coliform bacteria in

some selected fish farms of the central region of Ghana. *Scientifica*, *2020*(1), 6641461.

Afolabi, O. J., Oladele, O. O., & Olususi, F. C. (2020). Assessment of bacterial loads of *Clarias gariepinus* (Burchell, 1822) obtained from cultured and natural habitats. *The Journal of Basic and Applied Zoology*, *81*, 1-7.

Alhaji, N. B., Odetokun, I. A., Jibrin, M. S., Lawan, M. K., & Kwaga, J. (2024). Antibiotic resistance and mitigation using One Health lens in aquaculture of Northern Nigeria. *Onderstepoort Journal of Veterinary Research*, *91*(2), 2165.

Aslam, B., Khurshid, M., Arshad, M. I., Muzammil, S., Rasool, M., Yasmeen, N., ... & Baloch, Z. (2021). Antibiotic resistance: one health one world outlook. *Frontiers in cellular and infection microbiology*, *11*, 771510.

Austin, B. (2006). The bacterial microflora of fish, revised. *The scientific world journal*, *6*(1), 931-945.

Ava, A., Faridullah, M. Lithi, U.J. and Roy, V.C. (2020). Incidence of Salmonella and Escherichia coli in fish farms and markets in Dinajpur, Bangladesh. Bangladesh J. Sci. Ind. Res. 55(1), 65-72, 2020. www.banglajol.info

Bashir, I., Lone, F. A., Bhat, R. A., Mir, S. A., Dar, Z. A., & Dar, S. A. (2020). Concerns and threats of contamination on aquatic ecosystems. *Bioremediation and biotechnology: sustainable approaches to pollution degradation*, 1-26.

Bergey, D.H and Holt, J.G (2000) Bergey's Manual of Determinative Bacteriology 9th Edition. Philadephia: Lippincot Williams and wilkins, 2000, 787.

Bohrerova, Z., Park, E., Halloran, K., & Lee, J. (2017). Water Quality Changes Shortly After Low-Head Dam Removal Examined With Cultural and Microbial Source Tracking Methods. *River Research and Applications*, *33*(1), 113-122

Cahill, M. M. (1990). Bacterial flora of fishes: a review. *Microbial ecology*, *19*, 21-41.

CheesbrougM,(2010) District Laboratory Practice in Tropical Countries, part 2, Second edition update, 2010, p187-195.

Dar, G. H., Bhat, R. A., Kamili, A. N., Chishti, M. Z., Qadri, H., Dar, R., & Mehmood, M. A. (2020). Correlation between pollution trends of freshwater bodies and bacterial disease of fish fauna. *Fresh water pollution dynamics and remediation*, 51-67.

Esonu, D. O., Kabir, J., Jatau, I. D., Lawan, M. K., Yusuf, M. S., Aliyu, M. B., & Yusuf, F. L. (2024). Occurrence of Cryptosporidium Oocysts in Faeces, Milk and Water Sources in Sedentary Fulani Herds in Selected Local Government Areas of Kaduna State, Nigeria. *Folia veterinaria*, *68*(3), 7-20

Golden, O., Araújo, A. C., Caldeira, A. J., & Santos, M. J. (2023). Raw fish consumption in Portugal: Commonly consumed fish species and associated risk factors for anisakiosis. *Food Control*, *145*, 109457.

Govender, R., Amoah, I. D., Adegoke, A. A., Singh, G., Kumari, S., Swalaha, F. M., ... & Stenström, T. A. (2021). Identification, antibiotic resistance, and virulence profiling of Aeromonas and Pseudomonas species from wastewater and surface water. *Environmental monitoring and assessment*, *193*(5), 294.

Igbinosa, E. O., Beshiru, A., & Odjadjare, E. E. O. (2020). Diversity, antimicrobial characterization and biofilm formation of Enterococci isolated from aquaculture and slaughterhouse sources in Benin City, Nigeria. *Ife Journal of Science*, *22*(3), 51-63.

Islam, M. S., & Khanam, S. (2021). Characterization of Bacteria from Poultry Environment. *LAP Lambert Academic Publishing, Germany*.

Khabo-Mmekoa, C. M., Genthe, B., & Momba, M. N. B. (2022). Enteric pathogens risk factors associated with household drinking water: A case study in Ugu District Kwa-Zulu Natal Province, South Africa. *International Journal of Environmental Research and Public Health*, *19*(8), 4431.

Mohammed, I. U. (2024). Isolation and identification of pathogenic bacteria from commercially marketed fish in Wukari, North-Eastern Nigeria. *European Journal of Microbiology and Infectious Diseases*, *1*(2), 66-66.

Mumbo, M. T., Nyaboga, E. N., Kinyua, J. K., Muge, E. K., Mathenge, S. G., Rotich, H., & Njiru, J. M. (2023). Antimicrobial resistance profiles of Salmonella spp. and Escherichia coli isolated from fresh Nile tilapia (Oreochromis niloticus) fish marketed for human consumption. *BMC microbiology*, *23*(1), 306.

Murthy, R. K. (2021). *Introductory Microbiology-I*. Sankalp Publication.

Njoku, O. E., Agwa, O. K., & Ibiene, A. A. (2015). An investigation of the microbiological and physicochemical profile of some fish pond water within the Niger Delta region of Nigeria. *African journal of food Science*, *9*(3), 155-162.

Nolla-Salas, J., Codina-Calero, J., Vallés-Angulo, S., Sitges-Serra, A., Zapatero-Ferrandiz, A., Climent, M. C., ... & Masclans, J. R. (2017). Clinical significance and outcome of Aeromonas spp. infections among 204 adult patients. *European Journal of Clinical Microbiology & Infectious Diseases*, *36*, 1393-1403.

Nwankwo, I. L., Abam, T. K., & Giadom, F. D. (2023). Challenges of groundwater development and supply in the Niger Delta, Nigeria. *Journal of Water Resource and Protection*, *15*(6), 247-275.

Nwuzo, A. C., Igwe, P. C., Aniokete, U. C., Nomeh, O. L., Nwojiji, E. C., Chukwuemeka-Odi, L. O., & Nwokporo, N. R. (2024). Assessment of Bacterial Contamination of Fish from Aquaculture Sources and Its Public Health Implications in Abakaliki, Ebonyi State, Nigeria. *Journal of Applied Sciences and Environmental Management*, *28*(12), 4153-4160.

Ocholi, Y. (2024). Bacteriological quality of drinking water from wells located near municipal solid waste dumps and liquid waste sites in Zaria, Kaduna State, Nigeria. *Urban Water Journal*, *21*(7), 907-915.

Odetokun, I. A., Adetona, M. A., Ade-Yusuf, R. O., Adewoye, A. O., Ahmed, A. N., Ghali-Mohammed, I., ... & Fetsch, A. (2023). S taphylococcus aureus contamination of animal-derived foods in Nigeria: a systematic review, 2002—2022. *Food Safety and Risk*, *10*(1), 6.

Okafor, C. A. (2024). Impact and interventions of waterborne and foodborne illnesses caused by bacterial pathogens in Nigeria: A review. *Food and Health*, *10*(4), 316-322

Oluoch-Otiego, J., Oyoo-Okoth, E., Kiptoo, K. K. G., Chemoiwa, E. J., Ngugi, C. C., Simiyu, G.,& Opiyo, M. A. (2016). PCBs in fish and their cestode parasites in Lake Victoria. *Environmental monitoring and assessment*, *188*, 1-11

Omeji, S., & VU, A. J. O. (2017). Bacteriological profile of water sample and selected fish species from lower river Benue, Nigeria. *Octa Journal of Biosciences*, *5*(2).

Omoyinmi, O., & Bello, T. T. (2023). A Review of the Efficiency of Alternative Feed Sources for Cultured Catfish Species in Nigeria.

Paredes-Trujillo, A., & Mendoza-Carranza, M. (2022). A systematic review and meta-analysis of the relationship between farm management, water quality and pathogen outbreaks in tilapia culture. *Journal of Fish Diseases*, *45*(10), 1529-1548.

Sheng, L., & Wang, L. (2021). The microbial safety of fish and fish products: Recent advances in understanding its significance, contamination sources, and control strategies. *Comprehensive Reviews in Food Science and Food Safety*, *20*(1), 738-786.

Suresh, J. I., Janani, M. S., & Sowndharya, R. (2022). Bacterial diseases in fish with relation to pollution and their consequences—a global scenario. In *Bacterial Fish Diseases* (pp. 113-131). Academic Press.

Tiwari, P., & Tiwari, M. P. (2022). Evaluation of water quality and dam for sustaining the fish population dynamics. *Applied Water Science*, *12*(9), 233.

World Health Organization, UNEP United Nations Environment Programme, & World Organisation for Animal Health. (2022). *One health joint plan of action (2022–2026): working together for the health of humans, animals, plants and the environment*. World Health Organization.

Yahaya, T. O., Oladele, E. O., Abiola, O. R., Ologe, O., & Abdulazeez, A. (2021). Carcinogenic and non-carcinogenic risks of heavy metals in Clarias gariepinus (African catfish) obtained from Bariga section of Lagos Lagoon, Nigeria. *Iranica Journal of Energy & Environment*, *12*(1), 61-67.

Yashim, E. Y., Dambo, A., & Adole , A. . (2025). Effect of some Processing Methods on the Proximate Composition of some Frozen Marine Fishes. *Journal of Science Research and Reviews*, *2*(1), 127-132.

Yohans, H., Mitiku, B. A., & Tassew, H. (2022). Levels of Escherichia coli as bio-indicator of contamination of fish food and antibiotic resistance pattern along the value chain in Northwest Ethiopia. *Veterinary Medicine: Research and Reports*, 299-311.

Yu, H. (2025). Climate Change Unveils Hidden Microbial Dangers. Environmental Science and Ecotechnology, 100544.