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Microbial Flora Associated with Different Body Parts of Nile Perch (*Lates niloticus*) from Kanye Dam, Kano State, Nigeria

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ABSTRACT
The distribution of microorganisms across body parts of fish reflects their interaction with the aquatic environment and serves as an important indicator of potential public health risks. This study examined the microbial diversity and distribution in different body parts of Nile perch (*Lates niloticus*) collected from Kanye Dam, using standard microbiological procedures including cultural characterization, Gram staining, biochemical identification, total viable bacterial count (TVC), total anaerobic count (TAC), total fungal count (TFC) and coliform enumeration. The head recorded the highest TVC (164.67 ± 59.38 CFU g^{-1}), while the gills exhibited the highest TFC (136.50 ± 5.26 CFU g^{-1}). Mean TAC values were highest in the head (153.83 ± 33.52 CFU g^{-1}) and scales (153.17 ± 25.46 CFU g^{-1}). Faecal coliform counts were identical (24 MPN/100 mL) across all body parts, whereas total coliform counts ranged from 12.40 to 13.33 MPN/100 mL. Cultural, Gram staining and biochemical analyses identified *Enterobacter spp.*, *Escherichia coli*, *Bacillus spp.*, *Staphylococcus spp.*, and *Shigella spp*. Gram-negative bacilli predominated in all samples, with Gram-positive bacteria occurring mainly in the gills and scales. *Enterobacter spp.* was the most frequently isolated organism, accounting for 100% of head isolates, 75% of gill isolates and 50% of scale isolates. The presence of indicator and potentially pathogenic bacteria highlight the need for improved hygienic handling practices and thorough cooking of Nile perch to safeguard public health.

Keywords: Bacterial Diversity, Food Safety, Freshwater Fish, Microbial Flora, Kanye Dam

INTRODUCTION

Fish constitute one of the most important sources of animal protein worldwide and play a vital role in ensuring food and nutritional security, particularly in developing countries (FAO, 2020). Besides providing high-quality protein, fish are rich in essential amino acids, polyunsaturated fatty acids, vitamins, and minerals required for normal human growth and health (FAO, 2018; Amosu *et al*., 2026)). In Nigeria, inland fisheries contribute significantly to household nutrition, employment, and income generation, with freshwater species accounting for a substantial proportion of domestic fish production (Olaifa *et al.,* 2022). Among these, Nile perch (*Lates niloticus*) is one of the most commercially valuable freshwater fish species because of its rapid growth, excellent flesh quality, high consumer acceptance and economic importance in both artisanal and commercial fisheries (Asnake, 2018). The species is widely distributed across African freshwater ecosystems, including rivers, lakes, reservoirs and dams, where it supports local livelihoods and food security (Basiita *et al.,* 2018). Despite its nutritional importance, the microbiological quality of fish remains a major concern because contamination can occur at different stages, from the aquatic environment to harvesting, transportation, processing and marketing (FAO and WHO, 2021).

Fish naturally harbour diverse microorganisms on their external and internal body surfaces, with microbial populations varying according to the anatomical site, surrounding water quality, handling practices and storage conditions **(**Akano *et al.*, 2025**)**. The skin (scales), gills and head are among the body parts most exposed to the aquatic environment and therefore serve as important ecological niches for microbial colonization. The gills continuously filter large volumes of water and are particularly susceptible to colonization by aquatic bacteria, while the skin and scales provide attachment surfaces for environmental microorganisms (Medina-Félix *et al.*, 2023). Some of these microorganisms constitute the normal microbiota of fish, whereas others are opportunistic or pathogenic species capable of causing spoilage or transmitting foodborne diseases to humans. Common bacterial genera isolated from freshwater fish include *Escherichia, Enterobacter, Pseudomonas, Aeromonas, Staphylococcus, Bacillus, Shigella, Salmonella,* and *Vibrio,* depending on the environmental conditions and sanitary status of the habitat.

Microbial contamination of fish is influenced by numerous environmental and anthropogenic factors, including water pollution, domestic sewage discharge, agricultural runoff, aquaculture practices, post-harvest handling, and market hygiene **(**Salama and Chennaoui, 2024**)**. Freshwater bodies receiving untreated municipal and agricultural wastes often contain elevated levels of faecal indicator organisms and pathogenic bacteria that readily colonize fish tissues. Consequently, fish may serve as reservoirs or vehicles for the transmission of foodborne pathogens if consumed raw or inadequately cooked. The presence of indicator organisms such as total coliforms and faecal coliforms is widely used to assess the sanitary quality of aquatic environments and fish products (Verma *et al.*, 2025**)**. Similarly, high total viable bacterial counts and fungal counts may indicate poor hygienic handling or prolonged storage, leading to reduced shelf life and increased public health risks. Therefore, microbiological assessment of different body parts of fish provides valuable information regarding contamination routes, hygienic quality,

and potential health hazards associated with fish consumption.

Increasing anthropogenic activities around freshwater reservoirs, including irrigation, livestock farming, domestic waste disposal, and recreational use, can negatively influence water quality and microbial communities. Previous studies have mainly focused on fish muscle contamination or general water quality, with limited information on microbial distribution among external and internal fish body parts that serve as major sites of environmental exposure and colonization (Lawal-Are *et al*., 2022a; Moruf, 2022; Lawal *et al*., 2026). Therefore, this study investigated the microbial flora associated with the head, gills and scales of Nile perch collected from Kanye Dam, Kano State, Nigeria, through microbial enumeration, bacterial characterization, and comparative assessment of microbial distribution.

MATERIALS AND METHODS

Study Area

The study was conducted using Nile perch (*L. niloticus*) obtained from Kanye Dam, Kano State, Nigeria. Kanye Dam is one of the important freshwater reservoirs in Kano State and supports artisanal fisheries that supply fish for domestic consumption and local markets. The dam receives water from surrounding catchments and serves multiple purposes, including fishing, irrigation, livestock watering and domestic activities. These anthropogenic activities may influence the microbial quality of the aquatic ecosystem through runoff, organic matter deposition, and environmental contamination. The tropical climate of Kano State, characterized by distinct wet and dry seasons, also influences the physicochemical and microbiological characteristics of the reservoir (Indabawa and Sindama, 2018).

Sample Collection

Twenty-Seven (27) apparently healthy adult Nile perch specimens were randomly obtained from artisanal fishermen immediately after capture at Kanye Dam. The fish were individually placed in sterile polyethylene bags and transported in an insulated ice box (4–8°C) to the Microbiology, Department of Bayero University, Kano, for analysis. Laboratory analyses commenced within 6 h of sample collection to minimize changes in microbial populations (Sinha *et al.*, 2017).

Sample Preparation

The external surfaces of the fish were gently rinsed with sterile distilled water to remove loosely attached debris without affecting the resident microbial flora. Using sterile dissecting instruments, samples were aseptically collected from three anatomical body parts, namely the head, gills and scales. Approximately 10 g of each tissue was excised separately and homogenized in 90 mL of sterile physiological saline (0.85% NaCl) using a sterile laboratory blender to obtain a 10^{-1} stock homogenate. Subsequent ten-fold serial dilutions were prepared for microbiological enumeration.

Determination of Microbial Load

Total viable bacterial count (TVC), total anaerobic bacterial count (TAC), total fungal count (TFC) and total and faecal coliform counts were determined using standard microbiological methods. For TVC, 1 mL aliquots from appropriate serial dilutions were inoculated into sterile Petri dishes using the pour plate technique with molten Plate Count Agar (PCA) cooled to approximately 45°C, mixed gently, and incubated aerobically at 37°C for 24–48 h before colonies were enumerated with a digital colony counter and expressed as colony-forming units per gram (CFU/g) (ICMSF, 2018). Total anaerobic bacterial counts were similarly determined on PCA, except that inoculated plates were incubated at 37°C for 48 h in an anaerobic jar containing a commercial GasPak anaerobic generating system, after which colonies were counted and expressed as CFU/g (APHA, 2017). Total fungal counts were determined by spread-plating 1 mL of appropriate serial dilutions onto Potato Dextrose Agar (PDA) supplemented with chloramphenicol (100 mg/L), followed by incubation at 25–28°C for 3–5 days before fungal colonies were counted and expressed as CFU/g (APHA, 2017). Total and faecal coliforms were enumerated using the Most Probable Number technique, in which serial dilutions (10^{-1}–10^{-3}) were inoculated into lactose broth tubes containing inverted Durham tubes and incubated at 37°C for 24–48 h. Tubes showing acid and gas production were regarded as presumptive positive for total coliforms, after which positive cultures were transferred into EC broth and incubated at 44.5 ± 0.2°C for 24 h. Gas production in EC broth confirmed the presence of faecal coliforms, and MPN values were obtained from standard MPN tables and expressed as MPN/100 mL (APHA, 2017).

Isolation and Purification of Bacterial Isolates

Distinct bacterial colonies obtained from the primary culture plates were subcultured repeatedly onto fresh Nutrient Agar until pure cultures were obtained. Pure isolates were preserved on Nutrient Agar slants at 4°C pending further characterization (ICMSF, 2018).

Cultural Characterization

Pure bacterial isolates were streaked onto selective and differential media, namely Mannitol Salt Agar (MSA), MacConkey Agar (MAC) and Eosin Methylene Blue Agar (EMB). Colony morphology, pigmentation, elevation, margin, consistency, and characteristic growth patterns were recorded after incubation at 37°C for 24 h. Preliminary identification of isolates was based on colonial characteristics and growth reactions on the selective media (ICMSF, 2018).

Gram Staining

Gram staining was carried out using the standard Gram staining procedure. Fresh bacterial smears were heat-fixed and sequentially stained with crystal violet, Gram's iodine, acetone-alcohol, and safranin. The stained smears were examined microscopically under oil immersion (×100 objective) to determine Gram reaction, cellular morphology and cellular arrangement (ICMSF, 2018).

Biochemical Characterization of Isolates

Presumptive bacterial isolates were identified using standard biochemical tests, including Indole, Oxidase, Catalase, Methyl Red (MR), Voges–Proskauer (VP), Citrate Utilization, Coagulase, and Starch Hydrolysis tests. Test results were interpreted according to standard bacteriological identification manuals to establish the probable identity of each isolate (APHA, 2017).

Statistical Analysis

Microbial counts were expressed as mean ± standard deviation (SD) of triplicate determinations. Data were analysed using IBM SPSS Statistics version 25.0. Differences among the head, gill, and scale samples were evaluated by one-way ANOVA, with Tukey's HSD test used for mean separation at $P < 0.05$.

RESULTS AND DISCUSSION

Microbial Load

Figure 1 shows that viable bacteria were recovered from all examined body parts of *L. niloticus*, with the head recording the highest mean total viable bacterial count (164.67 ± 59.38 CFU g^{-1}), followed by the gills (148.50 ± 94.86 CFU g^{-1}) and scales (143.83 ± 35.90 CFU g^{-1}). The higher bacterial load in the head may be attributed to its continuous exposure to surrounding water and accumulation of organic debris, while the large standard deviation observed in the gills indicates greater variation in microbial colonization among individual fish. Similar distributions have been reported in freshwater fish, where the head and gills often harbour higher bacterial loads because of direct environmental exposure and continuous water filtration (Chakma *et al.*, 2025). The relatively comparable bacterial counts across the three body parts further suggest that microbial contamination was widespread, reflecting the microbial quality of the aquatic habitat rather than localized contamination, in agreement with observations by Lawal-Are *et al*. (2022b) and Diner *et al.* (2025).

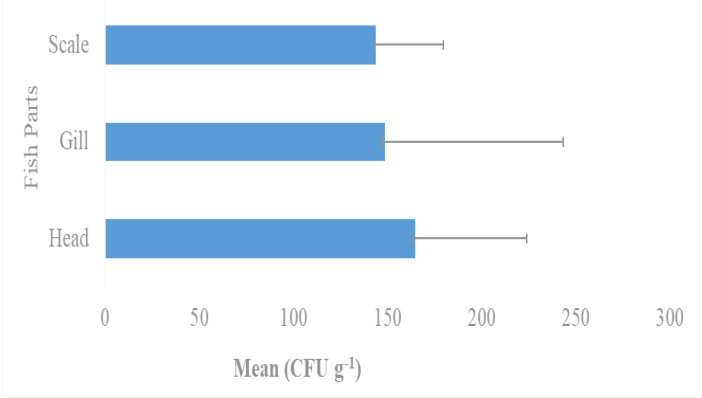

Figure 1: Total Viable Bacterial Count in Different Body Parts of Nile Perch from Kanye Dam, Nigeria

Figure 2 shows that the head of *L. niloticus* recorded the highest mean total anaerobic bacterial count (153.83 ± 33.52 CFU g^{-1}), followed closely by the scales (153.17 ± 25.46 CFU g^{-1}), while the gills had the lowest count (133.67 ± 69.93 CFU g^{-1}). The greater variability observed in the gills suggests inconsistent anaerobic bacterial colonization among samples. The relatively higher anaerobic counts in the head and scales may reflect greater exposure to sediments and organic matter in the aquatic environment. Similar distributions of anaerobic bacteria on fish external surfaces have been reported in freshwater fish by Ruiz *et al.* (2025) and Diaz-Mateus *et al.* (2026), who attributed such variations to environmental exposure and habitat conditions.

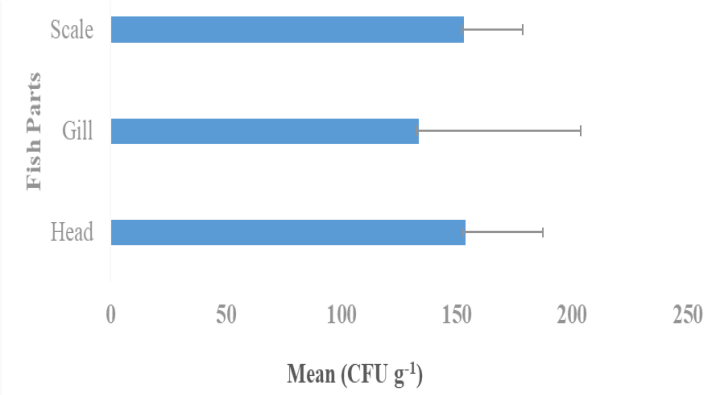

Figure 2: Mean Total Anaerobic Count in Different Body Parts of Nile Perch (*Lates niloticus*) from Kanye Dam, Nigeria

The mean total fungal count differed across the body parts of *L. niloticus* (Figure 3), with the gills recording the highest fungal load (136.50 ± 5.26 CFU g^{-1}), followed by the head (97.33 ± 25.86 CFU g^{-1}), while the scales had the lowest count (73.67 ± 26.77 CFU g^{-1}). The relatively high fungal burden and low variability in the gills suggest consistent colonization due to their continuous exposure to surrounding water. Similar findings have been reported in freshwater fish, where the gills harbour greater fungal populations because of constant contact with aquatic microorganisms (Diaz-Mateus *et al.*, 2026). Elevated fungal loads may also reflect environmental contamination and poor water quality (Moruf, 2022).

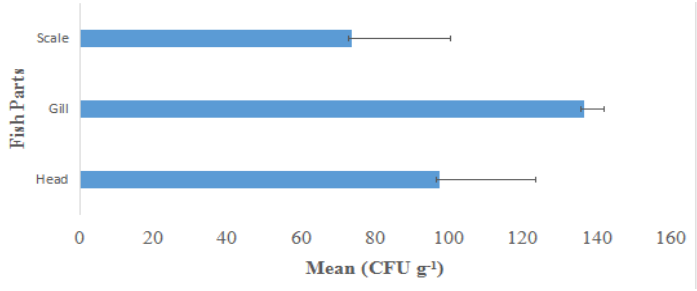

Figure 3: Mean Total Fungal Count in Different Body Parts of Nile Perch (*Lates niloticus*) from Kanye Dam, Nigeria

Figure 4 shows that the mean faecal coliform count was uniform across the head, gill and scale of *L. niloticus*, with each recording 24 MPN/100 mL, while total coliform counts varied only slightly, ranging from 12.40 MPN/100 mL in the head to 13.33 MPN/100 mL in the gill. The low standard deviations indicate consistent microbial contamination among the sampled body parts. The relatively higher coliform count in the gills may be attributed to their continuous contact with the surrounding water, making them more susceptible to microbial colonization. Similar findings have been reported in freshwater fish, where gills often harbour higher bacterial loads because of constant exposure to environmental microorganisms (Ruiz *et al.*, 2025). The detection of faecal coliforms across all body parts also suggests faecal contamination of the aquatic environment, consistent with observations by ICMSF (2018) that coliforms are reliable indicators of environmental sanitation and potential public health risk.

Figure 5 shows that *Enterobacter spp*. predominated across all body parts of *L. niloticus*, accounting for 100% of isolates from the head, 75% from the gills, and 50% from the scales, whereas *Bacillus spp*. occurred only in the gills (25%), and *Shigella spp*. and *Staphylococcus spp*. were each isolated exclusively from the scales (25% each). This site-specific distribution suggests that different body parts provide distinct ecological niches for bacterial colonization. The predominance of *Enterobacter* spp. agrees with reports that members of the Enterobacteriaceae commonly colonize freshwater fish exposed to environmental and anthropogenic contamination (Diaz-Mateus *et al.*, 2026), while the occurrence of *Bacillus* and *Staphylococcus spp*. has also been documented in freshwater fish microbiota (Ruiz *et al.*, 2025).

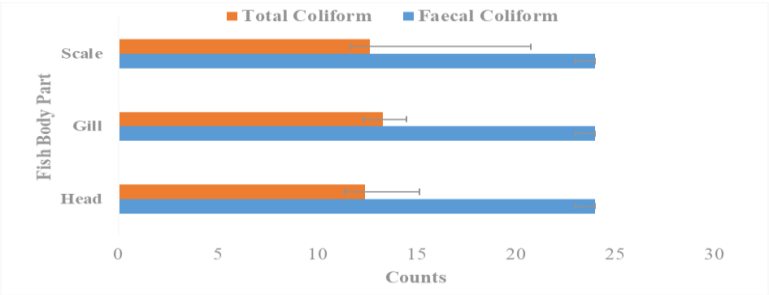

Figure 4: Mean Faecal Coliform and Total Coliform Counts (MPN/100 mL) in Different Body Parts of Nile Perch (*Lates niloticus*) from Kanye Dam, Nigeria

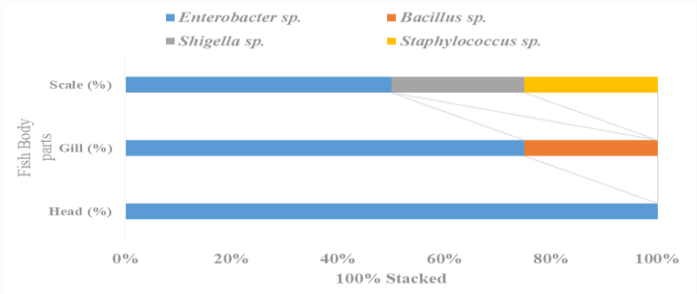

Figure 5: Frequency (%) of Bacterial Species Isolated from Different Body Parts of Nile Perch from Kanye Dam, Kano State, Nigeria

Table 1 showed that Enterobacter spp. predominated across all body parts of *L. niloticus*, as evidenced by the frequent occurrence of pink, moist colonies on MacConkey and EMB media, whereas the scales exhibited greater microbial diversity, harbouring *Enterobacter spp.*, *Shigella spp.* and *Staphylococcus spp*. The gills also contained *Bacillus spp*., reflecting intermediate diversity. The higher bacterial heterogeneity observed on the scales is expected because they are continuously exposed to surrounding water and suspended microorganisms. Similar predominance of Enterobacteriaceae and greater microbial diversity on external fish surfaces than internal tissues have been reported in freshwater fish by Lawal-Are *et al.* (2022c) and Ruiz *et al.* (2025), who attributed these findings to environmental exposure and water quality.

Table 1: Cultural Characteristics and Presumptive Identification of Bacterial Isolates Recovered from Different Body Parts of Nile Perch (*Lates niloticus*) from Kanye Dam

Body Part	Mannitol Salt Agar (MSA)	MacConkey Agar (MAC)	Eosin Methylene Blue Agar (EMB)	Presumptive Bacterial Isolates
Head	No growth	Predominantly pink, moist colonies; some plates showed no growth	Predominantly pink, moist colonies; occasional no growth	*Enterobacter* spp.
Gill	Mostly no growth; occasional pink colonies	Predominantly pink, moist colonies; some plates showed no growth	Pink, moist colonies and pink colonies with green metallic sheen; occasional no growth	*Enterobacter* spp.; *Bacillus* spp.
Scale	Mostly no growth; occasional pink, waxy colonies	Colourless, transparent colonies and pink, moist colonies; occasional no growth	Transparent colonies, pink, moist colonies, pink mucoid colonies; occasional no growth	*Enterobacter* spp.; *Shigella* spp.; *Staphylococcus* spp.

Table 2 shows that Gram-negative bacilli predominated in all body parts of *L. niloticus*, with the head containing exclusively Gram-negative rods, whereas both the gills and scales harboured Gram-negative and Gram-positive bacteria, indicating greater microbial diversity in these tissues. The gills contained Gram-negative bacilli and Gram-positive bacilli arranged in chains, while the scales exhibited Gram-negative short rods and clustered Gram-positive bacilli, reflecting increased environmental exposure. These findings agree with those of Diaz-Mateus *et al.* (2026), who reported that fish gills and skin generally harbour more diverse bacterial communities than other body parts because of continuous contact with surrounding water and suspended microorganisms.

Table 2: Gram Staining Characteristics of Bacterial Isolates Recovered from the Body Part of Nile Perch

Body Site	Gram Reaction	Cell Morphology and Arrangement	Remarks
Head	Gram-negative	Bacilli (rod-shaped bacteria)	All isolates consistently exhibited Gram-negative bacilli.
Gill	Gram-negative; Gram-positive	Gram-negative bacilli and short bacilli (short rods); Gram-positive bacilli arranged in chains	Predominantly Gram-negative bacilli with occasional Gram-positive chain-forming bacilli.
Scale	Gram-negative; Gram-positive	Gram-negative short bacilli (short rods); Gram-positive bacilli arranged in clusters	Gram-negative short bacilli predominated, with occasional Gram-positive clustered bacilli.

Table 3 presents the biochemical characteristics and presumptive identification of bacterial isolates recovered from the head, gill, and scale of *L. niloticus* collected from Kanye Dam. The biochemical characteristics confirmed the presence of *Escherichia coli, Enterobacter spp., Bacillus spp., Staphylococcus spp.,* and *Shigella spp.* in different body parts of *L. niloticus*. The head harboured *E. coli* (Indole+, MR+, Catalase+) and *Enterobacter spp*. (VP+, Citrate+, Catalase+), while the gills yielded *Bacillus spp*. (Catalase+, Citrate+, Starch hydrolysis+). The scales showed greater diversity with Staphylococcus spp. (Catalase+, Coagulase+) and *Shigella spp*. (MR+, Catalase+), indicating environmental and faecal contamination. Similar bacterial profiles have been reported in freshwater fish, where gills and scales are major sites of microbial colonization due to continuous environmental exposure and handling (ICMSF, 2018).

Table 3: Biochemical Characteristics and Presumptive Identification of Bacterial Isolates Recovered from Different Body Parts of Nile Perch from Kanye Dam

Source of Isolate	Presumptive Bacterial Isolate	Indole	Oxidase	MR	VP	Citrate	Catalase	Starch Hydrolysis	Coagulase
Head	*Escherichia coli*	+	–	+	–	–	+	–	–
	Enterobacter spp.	–	–	–	+	+	+	–	–
Gill	*Bacillus* spp.	ND	–	ND	ND	+	+	+	–
Scale	*Staphylococcus* spp.	ND	–	ND	ND	ND	+	–	+
	Shigella spp.	–	–	+	–	–	+	–	–

Keys: MR = Methyl Red; VP = Voges–Proskauer; ND = Not Determined; spp. = species (plural); (+) = positive reaction; (–) = Negative Reaction

CONCLUSION

The study revealed that *Lates niloticus* from Kanye Dam harbours diverse microbial communities across the head, gills, and scales. The head recorded the highest total viable bacterial count, the gills had the highest fungal count, while the scales exhibited the greatest bacterial diversity, dominated by Enterobacter spp. alongside *Escherichia coli, Bacillus spp., Staphylococcus spp.,* and *Shigella spp*. The detection of enteric pathogens and coliforms indicates possible environmental and handling-related contamination. These findings highlight potential public health risks and emphasize the need for routine microbiological surveillance, hygienic

fish handling, and thorough cooking before consumption to ensure consumer safety.

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