Bacteriological Quality of Mullet (*Mugil Cephalus*) in Ohiakwu River, Port Harcourt

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***Abstract*: - The bacteriological quality of the gastrointestinal tracts and gills of mullet (*Mugilcephalus*) in Ohiakwu River, Port Harcourt were evaluated quantitatively and qualitatively using standard bacteriological method. The results obtained showed that the fish used for this study were at adult stage. Heterotrophic bacteria were highest in the mullet gill than in other fish parts. In all, the bacterial count showed slight significant difference at P≥0.05. Seven (7) bacterial genera were identified (*Bacillus* species, *Vibrio* species, *Pseudomonas* species, *Shigella* species, *Escherichia* species, *Klebsiella* species and *Staphylococcus* species) with *Micrococcus* species and *Bacilluslentus* been the only species isolated in all samples during the study period. The investigation reveals a relatively high concentration of bacterial population in the mullet. The observation of high bacterialload in the mullet especially in the gills indicates that mullet pick up these bacteria from their environment when they feed. High bacterialload in fish gill and intestine is as a result of the fish high metabolic rates together with increase feeding activities. The presence of these organisms in the mullet especially in the gills and gastrointestinal tract can be transferred through the trophic level to humans when we consume these fishes. The knowledge of the microflora of mullet can assist in the management of abnormality that may arise as a prelude to the onset of bacterial diseases in the fish. This knowledge may be helpful in the storage of mullet since bacteria in the gastrointestinal tract may affect the quality and storage of the fish.**

***Keywords*: Mullet, Bacteria population, Ohiakwu River**

I. INTRODUCTION

Pathogenic microorganisms are synonymous with contaminated aquatic environment. When their population in the environment is minute, they are no threat, but at large population, they become threat to human and aquatic organisms. The amount to microorganisms in aquatic organisms is a reflection of the abundance of these organisms in the aquatic environment. Bacteria are common inhabitants of aquatic environment, whether river, ponds, streams, lake and even underground water systems. These bacteria are ubiquitous in nature. They have great impact on the aquatic system by causing disease in aquatic organisms as well as in humans [1].Bacterial diseases in fish generally do not develop simply as the result of exposing a host to an infectious agent. In most instances, disease occurs as the result of complex interactions between pathogen, fish and environmental stress, which affect the susceptibility of the host to disease [2].

Mullet (*Mugilcephalus*) feeding mechanism is neither exclusively carnivorous nor herbivorous as a result it possess a high risk for bacterial contamination. As an economically important species that contributes to fisheries in many countries including Nigeria and Port Harcourt in particular. Mullet lives near the bottom of the river, and its benthic feeding habits increase the risk of contamination[3]. The intestine and gill of mullet is a common route for the proliferation of bacteria due to its favourable condition [4]. This species also has commercial importance in Nigeria [5] and is commonly available in Port Harcourt waters. The evaluation of the bacterial population of mullet is used to assess the quality of the fish which can be used as a yardstick to determine the shelf life and quality of the fish [6]. The knowledge of the bacterial population in the gill, gastrointestinal tract and muscle of mullet provide firsthand information to develop mechanism that will forestall the possible outbreak of diseases. This study will be providing information in respect to bacterial populations present in mullet gills and intestine and also as a guide to public health.

II. OBJECTIVE

This study was carried out to determine the bacteriological population of the fish parts (intestine, gills and muscles).

III. METHODOLOGY

A total of 40 mullet (*Mugilcephalus*) samples were collected from the Ohiakwu River behind Rivers State University, Port Harcourt which lies within rectangular coordinates $N4^{0}46'50''$, $N4^{0}48'10''$ and $E6^{0}57'10''$, $E6^{0}57'30''$ (Figure 1) for a period of five (5) months (June to August covering the raining period and October to November covering the dry period. Sample area was divided into two (2); the upstream covering areas around Nigerian Agip Oil Company while the downstream covered areas around Eagle Island. The Ohiakwu River is a mixture of fresh and sea water which influences its system as it flows through it. The Ohiakwu River receives salt water from the Bonny River. The muscle, gills and intestines of the mullet were extracted by dissecting from the head to the abdomen and the weights of the muscle, gills and intestines were estimated using a digital weigh balance. The nearby land is populated by various human activities such as sand mining, abattoir, boat carving, wastewater discharges from sewage treatment plant, indiscriminate disposal of waste materials, etc.

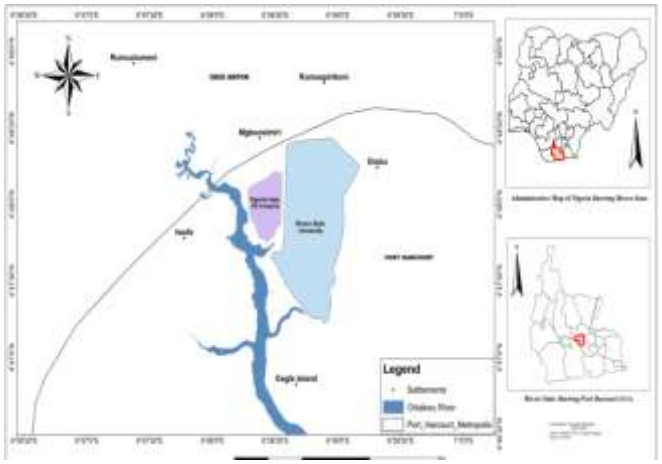

Figure 1: Map of Study Area

3.1 Cultivation and Enumeration of Microorganisms in Mullet

Enumeration of the various microbial populations in the mullet was done as described by [7]. Organic matter (intestines, gills and skin) samples were collected aseptically and stored at $4^{o}C$ until analysis. Each sample was homogenized using a Colwell stomacher and 5g of each sample was dissolved in 50ml of sterile normal saline to give an initial dilution of 1:10ml. 1ml of the samples were diluted serially in six-fold. Then, a 0.1ml aliquot of appropriate dilution of $l0^{-2}$ and $l0^{-4}$ were inoculated in duplicate onto already prepared sterile nutrient agar for total heterotrophic bacteria (THB), MacConkey agar for total coliform bacteria while mineral salt agar was used for hydrocarbon utilizing bacteria. Plates were evenly spread out with a sterile bent glass rod. Agar plates containing sample were incubated for 24 hours, 48hours and 120hours respectively. At the end of each incubation period, colonies were examined, counted and recorded. Counts of colonies was carried out only for plates with colonies from 30-300 [8] and representative colonies were sub-cultured onto sterile Nutrient agar plates to obtain pure cultures. Pure cultures were properly preserved in bijou bottles containing sterilized 10% glycerol and in agar slants. These were used for further identification tests.

3.2 Identification of Bacterial Isolates

Bacterial isolates were identified according to their physical, morphological, cultural and physiological properties according to methods as described by [8]. Various microbiological test conducted include Catalase Test, Coagulase Test, Methyl Red Test, Voges-Proskaeur Test, Indole Test, Starch Hydrolysis, Citrate Test, Oxidase Test and Sugar Fermentation.

3.3 Statistical Analysis

The data obtained for this study were analyzed using two-way analysis of variance to check for significance and Duncan multiple test was also used for mean separation.

IV. RESULTS AND DISCUSSION

The result of the mean physical characteristics of the mullet and the different mullet parts (intestine, gill and muscles) as presented in Figure 2 and Figure 3 showed that the mullet used for this study were adult. This result conforms to what [9] observed and as reported by [10]showed that mullets attain sexual maturity in 3 to 4 years at a size of about 30 cm. The physical characteristics of the mullet samples during the period of the study were compared. The result shows that there is a slight variation in the seasonal fish length, with the period of low rainfall having a higher fish length, weight and width than the period of higher rainfall (Figures 2 and 3).

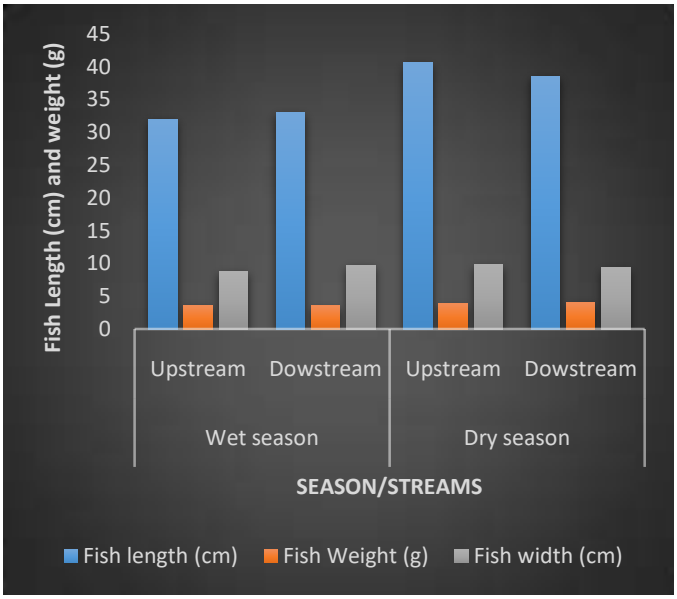

Figure 2: Comparison of the Physical Characteristics of the Mullet Samples

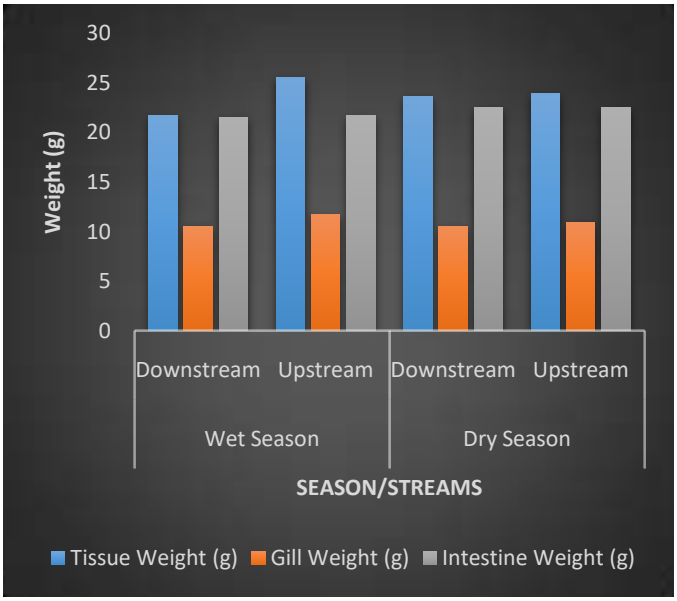

Figure 3: Comparison of the Weight of the Different Mullet Parts

In the different fish parts, the gill had the highest heterotrophic bacterialload during the period of the study, followed by the muscle during the period of high rainfall and intestine during the period of low rainfall. Despite the differences in the viable bacterial load, there was no significant differences in the bacterialload of the muscle and intestine but there was a significant difference in the gill at P = 0.05 during the period of the study (Figure 4).[11]had reported that bacterial present in fish is a reflection of those in the environment where the fish was obtained. [12]had reported heterotrophic bacterialload of above $3.0x10^3$cfu/ml in fishes. The result of this study also reported such bacterial load.

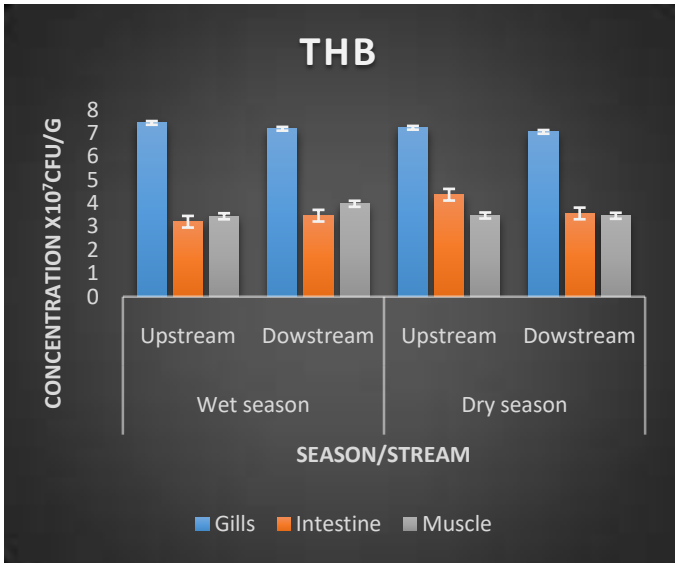

Figure 4: Comparison of Total Heterotrophic Bacterial Count in the Fish Parts

The mean total coliform bacterialload in the different fish parts showed that the coliform bacterialload varied in the different fish parts during the period of the study. In the upstream and downstream during the period of high rainfall, the gill coliform bacterialload were highest than in other fish parts with mean ±SD of 2.44±0.34 and 2.22±0.50 respectively while the period of low rainfallup stream and downstream mean±SD were 1.59±0.23 and 1.86±0.26 respectively. In the intestine during the period of high rainfall, the upstream and downstream mean±SD coliform bacterialload recorded were 1.40±0.30 and 1.36±0.19 while in the period of low rainfall, the coliform bacterialload were higher in the upstream and downstream with mean±SD of 2.03±0.64 and 1.66±0.47 respectively. The mean±SD upstream and downstream coliform bacterialload in the muscle during the period of high rainfall were 1.95±0.58 and 1.77±0.46 while during the period of low rainfall, it was 1.92±0.70 and 1.71±0.40. The coliform bacterialload showed slight significant differences at P = 0.05 across the season but no variation within season (Figure 5).[13]had reported a large coliform population in the gill and muscle of mullet which in line with the findings of this study.

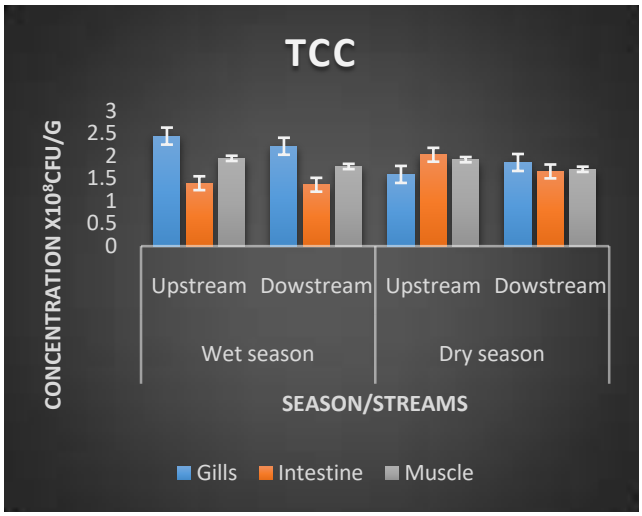

Figure 5: Comparison of Total Coliform Bacterial Count in the Fish Parts

The result of the Vibrio count of the various fish parts showed that in the gill, the mean Vibrio count in the upstream and downstream during the period of high rainfall were 2.57±0.34 and 2.44±0.32 while during the period of low rainfall, the upstream and downstream mean vibrio count in the gill were 2.39±0.37 and 2.57±0.24. The Vibrio count in the gill showed no significant differences at P = 0.05 during the period of the study. In the intestine, the mean Vibrio count in the upstream and downstream during the period of high rainfall were 2.14±0.28 and 2.13±0.33 while during the period of low rainfall, the upstream and downstream mean Vibrio count in the intestine were 2.14±0.25 and 2.12±0.30. In the muscle, Vibrio organisms were absent during the period of the study. The Vibrio count in the intestine showed no significant differences at P = 0.05 during the period of the study (Figure 6). [14] reported the presence of vibrio bacteria in the gill and intestine of fishes from brackish environment. This correspond with the result of this study.

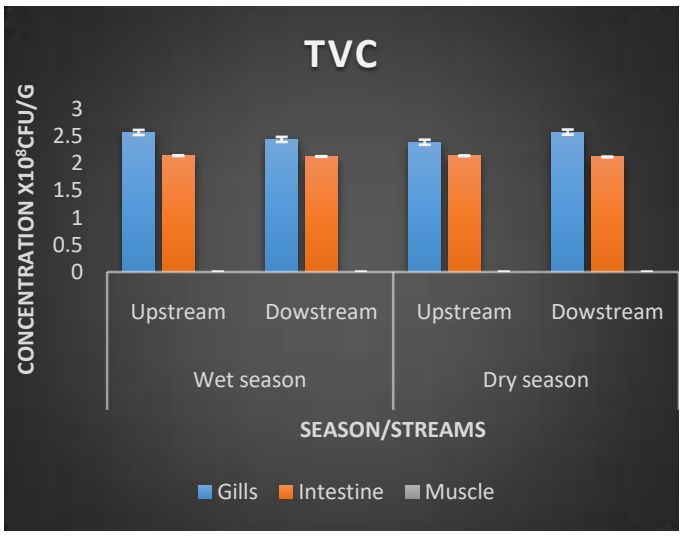

Figure 6: Comparison of Total Vibrio Count in the Fish Parts

The result of the *Pseudomonas* count of the various fish parts showed that in the gill, the mean *Pseudomonas* count in the upstream and downstream during the period of high rainfall were 2.49±0.57 and 2.66±0.74 while during the period of low rainfall, the upstream and downstream mean *Pseudomonas* count in the gill were 2.56±0.64 and 2.41±0.89. The *Pseudomonas* count in the gill showed no significant differences at P = 0.05 during the period of the study. In the intestine, the *Pseudomonas* organisms were absent during the period of the study. In the muscle, the mean *Pseudomonas* count in the upstream and downstream during the period of high rainfall were 4.14±0.55 and 3.69±0.41 while during the period of low rainfall, the upstream and downstream mean *Pseudomonas* count in the intestine were 3.31±0.72 and 3.59±0.67. The *Pseudomonas* count in the intestine showed no significant differences at P = 0.05 during the period of the study (Figure 7). [14] reported the presence of pseudomonas in the gill and intestine of fishes from brackish aquatic environment.

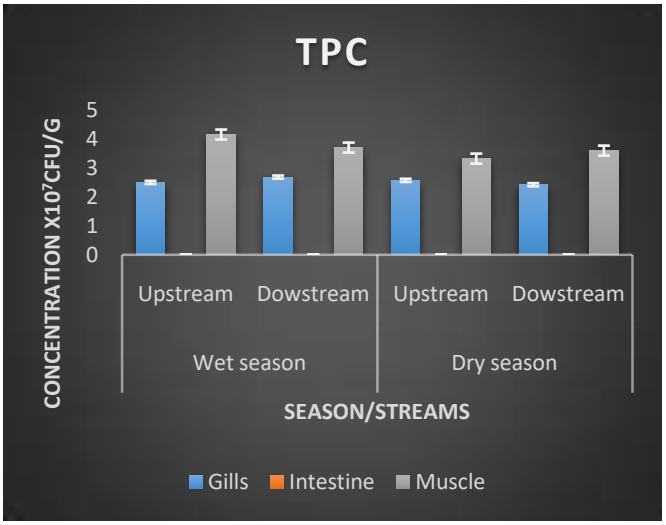

Figure 7: Comparison of Total Pseudomonas Count in the Fish Parts

V. CONCLUSION

The observation of high bacterialload in the mullet especially in the gills indicates that mullet pick up these bacteria from their environment when they feed. As reported by [14], high bacterialload in fish gill and intestine might be as a result of the fish high metabolic rates together with increase feeding activities. The presence of these organisms in the mullet especially in the gills and gastrointestinal tract can be transferred through the trophic level to humans when we consume these fishes[15]. The knowledge of the microflora of mullet can assist in the management of abnormality that may arise as a prelude to the onset of bacterial diseases in the fish. This knowledge may be helpful in the storage of mullet since bacteria in the gastrointestinal tract may affect the quality and storage of the fish.

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