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Microbiological Investigation of *Harpadon nehereus* and *Otolithoides pama* Available in Local Markets of Dhaka City, Bangladesh

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Abstract

This study aimed to investigate the microbiological quality of two marine fishes collected from several local markets in Dhaka City, Bangladesh: *Otolithoides pama* (Poa fish) and *Harpadon nehereus* (Bombay duck). The total viable bacterial count ranged from 6.1×10^2 to 4.4×10^5 cfu/g, while coliform counts showed 40×10^1 to 2.03×10^3 cfu/g, and fungal counts showed 2.7×10^2 to 8.6×10^6 cfu/g, indicating high amounts of microbiological contamination from different sources. In addition, the Presence of *Vibrio spp.* and *Staphylococcus aureus* was detected, with concentrations ranging from 7.0×10^1 to 9.8×10^7 cfu/g. The examination of an *Otolithoides pama* sample revealed that both species of *Shigella* and *Salmonella* occurred TNTC (too numerous to count), thus indicating a source of significant contamination. The discovery of multidrug-resistant (MDR) organisms such as *Stenotrophomonas maltophilia*, *Acinetobacter baumannii*, and *Providencia alcalifaciens* by biochemical characterization further brings public health issues to the foray. Antibiotic test results indicated resistance to several commonly used antibiotics, i.e., co-trimoxazole, ciprofloxacin, and ceftriaxone, which seriously threatens antimicrobial resistance (AMR) in the food chain. Hence, enhanced hygiene practices, regulatory reinforcement, and the implementation of Hazard Analysis Critical Control Points (HACCP) in fish handling, storage, and transportation are urgently needed to protect consumer safety and minimize public health impacts associated with contaminated seafood.

Keywords: Antibiotic resistance, biochemical identification, fish contamination, food-borne pathogens, microbiological quality.

INTRODUCTION

Fish and fish products have been an important food source for nourishment by mankind over millions of years all over the world as it provides maximum nutrition, maximum digestibility, and the greatest benefit of key micronutrients such as omega-3 fatty acids, vitamins, and minerals (Atwa, 2017). Fish is the most preferred source of animal protein, contributing more than 60% of the Bangladeshi population's total animal protein intake (Belton, 2011). Moreover, fisheries play a crucial role in the country's economy, accounting for nearly 3.5% of the national GDP and over 25% of the agricultural GDP (Islam *et al.*, 2023). Thus, fish are crucial in terms of both diet and economy, and their safety and quality are vital to public health and economic stability.

The microbiological quality of fish and fishery products has become a significant health concern in developing countries, such as Bangladesh, where poor handling after harvesting, few storage facilities, and environmental contamination are prevalent (Novoslavskij *et al.*, 2016). Fish are very perishable, and microbial attacks occur from harvesting to retailing. Such contamination occurs when fish come into contact with polluted water during fishing, are subjected to improper transit handling, or are exposed to unsafe market conditions (V *et al.*, 2017). These factors

eventually favor the growth of some pathogens, bacteria, fungi, and parasites that can cause severe health problems to those who consume the infected fish.

According to several studies, fish were found to harbor pathogenic bacteria such as *Salmonella spp., Shigella spp., Vibrio spp., and Staphylococcus aureus* that pose a risk of foodborne disease (Faridullah *et al.,* 2022) (Lipi *et al.,* 2023). These bacteria have been connected to myriad illnesses ranging from gastroenteritis, typhoid fever, and dysentery to occasionally even neurological disorders (Rahman *et al.,* 2016) (Samia *et al.,* 2014). The emergence of antibiotic-resistant bacteria in fish and seafood has further aggravated food safety issues (Ahmed *et al.,*, 2010). The use of antibiotics in aquaculture has led to the dissemination of antibiotic-resistant genes (ARGs) into the environment, thus facilitating the spread of MDR bacteria to humans through the food chain (Sheng & Wang, 2021) (Talukdar *et al.,* 2023).

It is alarming that studies have reported that most fish and shellfish sold in the local market have high levels of microbial contamination, particularly in Bangladesh (Acharjee *et al.,* 2021) (Md. Rokibul *et al.,* 2013). They reported the discovery of antibiotic-resistant strains, such as *Stenotrophomonas maltophilia, Acinetobacter baumannii,* and *Proteus hauseri,* in fish samples, which created concerns regarding the pathogens' infections that cannot be treated with conventional antibiotics (Sheng & Wang. 2021). Thus, the findings from these studies necessitate stringent monitoring and control measures to ensure and guarantee the safety of fish products while reducing risks associated with antimicrobial resistance.

The microbiological quality of fish is dependent upon many factors, including the water quality in which they are caught, the sanitary conditions during handling and processing, and the way the fish are stored and transported (Novoslavskij *et al.,* 2016). In Bangladesh, things have worsened because the fishing industry does not have enough infrastructure and regulatory controls, leading to the gross contamination of fish products (Islam *et al.,* 2023). The absence of a standard protocol for fish handling, storage, and transportation is another reason for the deterioration of fish quality, whereby the industry itself recognises the need for good hygiene practices (GHP) and the implementation of hazard analysis critical control points (HACCP) (World Health Organization. 2011).

This study has endeavored to evaluate the microbiological quality of *Harpadon nehereus* and *Otolithoides pama*, two fish species that are extremely common in Bangladesh, specifically for purposes of identifying potential sources of contamination and for developing strategies towards better food safety. It would further investigate the occurrence of pathogenic bacteria, as well as their antibiotic susceptibility, to determine antimicrobial resistance in the local fish supply chain.

The outcomes of these studies provide an insight regarding the microbiological safety of fish in the markets of Dhaka, ultimately contributing to evidence-based recommendations for fish handling, storage, and transportation practices. The research aims to enhance food safety, improve public health, and support the sustainability of Bangladesh's fisheries sector by addressing the challenges posed by microbial contamination and antibiotic resistance.

MATERIALS AND METHODS

Sample Collection and Preparation

Harpadon nehereus and *Otolithoides pama or* Poa and Loitta, sea fish samples were collected from North Jatrabari Wholesale Fish Market, Karwan Bazar Wholesale Fish Market, Muslim Bazar, Mirpur 12, Shwapno Super Shop, Mirpur 11.5, Sea Fish Corner, Mirpur 12, local fish markets in Dhaka city, Bangladesh. 6 samples were collected from different places and directly transferred from market to lab using sterile zip lock bags (V *et al.,* 2017).

Sample Processing

Harpadon nehereus and *Otolithoides Pama* were cut into small pieces, measured and then ground using a mortar and pestle (Bhakta *et al.,* 2021). All the equipment needed here should be sterile. Proper aseptic conditions should be maintained (World Health Organization 2011).

Sample preparation

The length and weight of the samples were recorded. Each sample was cut into various pieces, weighed 25g and homogenized in a sterile polybag. The homogenized sample was mixed with 225 mL of saline water (Lipi *et al.,*). Then, 1 mL of the homogenized suspension was diluted with 9 mL of normal saline, and serial dilutions (10-fold) were performed consecutively up to 10-6 (Rahman *et al.,*).

Microbiological analysis

Estimation of total viable bacteria (TVB)

The sample (0.1 mL) from 10^{-1} to 10^{-6} dilutions was spread onto nutrient agar (NA) to enumerate total viable bacteria (TVB). After spreading, the plates were incubated at 37 ° C for 24 hours (Nur *et al.,* 2020).

Estimation of total coliform count

The sample (0.1 mL) from 10^{-1} to 10^{-3} dilutions was spread onto on MacConkey Agar plates, a selective and differential media for coliform bacteria. After spreading, the plates were incubated at 37°C for 24 hours (R. R. Kamdi and P. Bhandari, 2015).

Estimation of total fungal count

The sample (0.1mL) sample was spread onto Sabouraud dextrose agar, and the plates were incubated at 25°C for 48 hours, which is favorable for fungal growth (Mamun *et al.*, 2017).

Estimation of Staphylococcus aureus count

The sample (0.1mL) from 10^{-1} to 10^{-3} dilutions was spread on Mannitol Salt media for *S.aureus* count, and the plates were incubated at 37°C for 24 hours (Uzoigwe *et al.*, 2021).

Estimation of Salmonella spp. and Shigella spp. count

1 mL of homogenized fish sample was added to 9 mL of Selenite Cystine Broth for the selective enrichment of Salmonella and Shigella species. The broths were incubated for 6 h at 37°C. Then, 1 mL of enriched broth was subjected to a 10-fold serial dilution, ranging from 10-2 to 10-6, in 9 mL of normal saline. Then, 0.1 mL of the suspension was spread onto Salmonella-Shigella (SS) Agar plates, and the plates were incubated at 37°C for 24 hours. After being incubated at 37 °C for 24 hours, characteristic colonies were detected and counted (Faridullah *et al.*, 2022; Rivera *et al.*,).

Estimation of Vibrio spp. Count

1 mL of homogenized fish sample was added to 9 mL of alkaline peptone water for selective enhancement of vibrio spp. The broths were incubated for 6 h at 37°C. Then, 1 mL of enriched broth was subjected to a 10-fold serial dilution, ranging from 10-2 to 10-6, in 9 mL of normal saline. Then, 0.1 mL of the suspension was spread onto TCBS Agar plates, and the plates were incubated at 37°C for 24 hours. After being incubated at 37 °C for 24 h, characteristic colonies were detected and counted (Rahman *et al.*, 2016).

Gram staining

Some colonies from LB agar were selected for gram staining. Gram staining was done on a culture grown using a standard method. The growth from the culture plate is transferred onto a sterile, grease-free microscope slide after air-drying and fixed by passing it three times over the pilot flame of a Bunsen burner. The fixed smear was drenched with a crystal violet stain for 30 seconds. Washed off with tap water. Gram's iodine was poured and drained after 30 seconds. Acetone quickly decolorizes it and washes it on the spot. Then came neutral red (Counter stain) and was washed after about 60 seconds. After that, the slides are placed on a draining rack to air dry the smear. After this, a drop of immersion oil is placed on the smear and viewed using a microscope with oil immersion lenses(Ogheneoruese Onoharigho *et al.*, 2022)(Thairu *et al.*, 2014)(Paray *et al.*, 2023).

Biochemical Test

Seven colonies were selected from MacConkey agar for biochemical identification using VITEK 2.

Determination of antimicrobial susceptibility

This method was done on Muller Hington agar media. A bacteria lawn was created using a sterile wooden swab. Isolates were examined for antibiotic susceptibility by disc diffusion assay on Mueller Hinton agar against Co-trimoxazole (25 µg).disk-1, Gentamicin (10 µg).disk-1, Chloramphenicol (30 µg).disk-1, Ciprofloxacin (5 µg).disk-1, and Ceftriaxone (30 µg).disk-1 (Md. Rokibul *et al.*, 2013)**.** Antibiotics were placed on the MHA plates. The plates were incubated at 37°C for 24 hours. The zone of inhibition was measured and documented(Atwa, 2017).

Statistical analysis

Microbiological data were descriptively analyzed to obtain microbial contamination levels and antibiotic resistance patterns in *Otolithoides pama* and *Harpadon nehereus*. All the experiments were performed in triplicate. Total viable counts (TVC), coliforms, fungi, and pathogenic bacteria (Salmonella spp., Shigella spp., Vibrio spp., and Staphylococcus aureus) were expressed in terms of colony-forming units per gram (cfu/g). The data were presented as ranges based on triplicate tests. The disc diffusion method was used for antibiotic susceptibility testing on Mueller-Hinton Agar (MHA). At the same time, resistance patterns were calculated as percentages: Resistance (%) = (Number of resistant isolates / Total isolates tested) x 100, Intermediate susceptibility (%) = (Number of intermediate isolates/Total isolates tested) x 100, Overall sensitivity (%) equals to total number of tested isolates divided by number of sensitive ones.

RESULTS

Prevalence of pathogenic bacteria and fungi in fish samples

The study of microbial with respect to *Harpadon nehereus* and *Otolithoides pama* fish sample have shown them to have an efficiently malkin pathogenic burden. *Otolithoides pama* displayed a total viable bacterial count ranging from 9.1×10^{2} cfu/g to 4.4×10^{5} cfu/g, while *Harpadon nehereus* exhibited a total viable bacterial count ranging from 6.1×10^{2} cfu/g to 1.73×10^{5} cfu/g. The complete coliform count, which is significantly larger, ranges from 40×10^{1} cfu/g to 1.54×10^{3} cfu/g in *Otolithoides pama* and from 50×10^{1} cfu/g to 2.03×10^{3} cfu/g in *Harpadon nehereus*. *Otolithoides pama* recorded a fungal load of 9.7×10^{2} to 8.6×10^{6} cfu/g, while the fungal load for *Harpadon nehereu* was between 2.7×10^{2} to 7.9×10^{6} cfu/g. There was an alarming presence of Staphylococcus aureus, ranging from 70×10^{1} cfu/g to 1.09×10^{6} cfu/g in *Otolithoides pama* and from 0 to 9.8×10^{7} cfu/g in *Harpadon nehereus*. *Vibrio spp.* were present in high numbers, while *Otolithoides pama* showed counts from 1.8×10^{3}

cfu/g to 2.67×10^8 cfu/g, and *Harpadon nehereus* showed counts from 9.3×10^4 cfu/g to 1.38×10^7 cfu/g. *Salmonella spp.* and *Shigella spp.* The infection rate was significantly high, with one sample of *Otolithoides pama* at a level beyond count, indicating severe contamination. *Salmonella* and *Shigella spp*. levels in *Otolithoides pama* ranged from 1.25×10^9 cfu/g to 1.58×10^6 cfu/g while in *Harpadon nehereus* they ranged from 1.29×10^7 cfu/g to 2.03×10^7 cfu/g. These data suggest that both fish species are heavily contaminated with harmful bacteria, posing a serious public health threat.

Table 1: Prevalence of Pathogenic Bacteria and Fungi in Fish Samples. Total Viable Count (TVC) of the *Harpadon nehereus* and *Otolithoides pama* sea fish samples. All experiments were performed in triplicate, and the results were reproducible

Fish Samples	Location	Total Viable Bacteria (cfu/mL)	Total Coliform Coumt (cfu/mL)	Total fungal count (cfu/mL)	*Staphylococcus* spp. (cfu/mL)	*Vibrio* spp. (cfu/mL)	*Salmonella* spp. & Shigella spp. (cfu/mL)
Otolithoides pama Sample 1	North Jatrabari Wholesale Fish Market	9.1×10^2	40×10^1	9.7×10^2	70×10^1	1.8×10^3	TNTC
Sample 2	Karwan Bazar Wholesale Fish Market	1.89×10^4	1.09×10^3	6.4×10^5	8.9×10^6	6.0×10^4	1.25×10^9
Sample 3	Muslim Bazar, Mirpur 12	4.4×10^5	1.54×10^3	8.6×10^6	1.09×10^6	2.67×10^8	1.58×10^6
Harpadon nehereus Sample 4	Karwan Bazar Wholesale Fish Market	1.73×10^5	2.03×10^3	7.9×10^6	9.8×10^7	9.3×10^4	1.29×10^7
Sample 5	Sea Fish Corner, Mirpur 12,	6.1×10^2	50×10^1	2.7×10^2	0	1.38×10^7	2.03×10^7
Sample 6	Shwapno Super Shop, Mirpur 11.5	8.0×10^3	4.3×10^2	3.4×10^6	4.4×10^3	6.9×10^6	1.85×10^7

Gram staining was done on isolates, and seven gram-negative bacteria were sent for further biochemical identification.

Table 2: Biochemical Identification of Isolates through Vitek 2

Isolate	Organism Identified	Positive Biochemical Markers	Negative Markers	Probability (%)	Confidence Level
1	*Stenotrophomonas maltophilia*	APPA, GGT, dMAL, ProA, CIT, lLATk, SUCT, PHOS, GGAA	ADO, PyrA, lARL, dCEL, BGAL, H_2S, BNAG, AGLTp, dGLU, OFF, BGLU, dMAN, dMNE, BXYL	91	High (Good Identification)
2	*Methylobacterium spp*	URE	All other tests negative	98	High (Excellent)
3	*Stenotrophomonas maltophilia*	APPA, GGT, dMAL, ProA, CIT, lLATk, SUCT, PHOS, GGAA	ADO, PyrA, lARL, dCEL, BGAL, H2S, BNAG, AGLTp, dGLU, OFF, BGLU, dMAN, dMNE, BXYL	98	High (Excellent)
4	*Acinetobacter baumannii complex*	ADO, lARL, dGLU, GGT, dMNE, CMT, BGUR, O129R, ELLM	APPA, dMAL, ProA, CIT, lLATk, SUCT, PHOS, PyrA, SAC, dTAG	87	Moderate (Acceptable)

5	*Proteus hauseri*	PyrA, dGLU, dMAN, SAC, dTAG, TyrA, lLATk, SUCT, PHOS	APPA, ADO, lARL, dMNE, BGUR, O129R, CIT, URE, dTRE	N/A	Low (Requires Confirmation)
6	*Acinetobacter baumannii complex*	ADO, lARL, dGLU, GGT, dMNE, CMT, BGUR, dTRE, URE	APPA, dMAL, ProA, CIT, lLATk, SUCT, PHOS, PyrA, SAC, dTAG	86	Moderate (Acceptable)
7	Providencia alcalifaciens	ADO (+), lARL (+), dGLU (+), GGT (+), OFF (+), dMNE (+), PHOS (+), CMT (+), O129R (+), ELLM (+)	APPA (-), PyrA (-), H2S (-), BNAG (-), TyrA (-), URE (-), dSOR (-), SAC (-), dTAG (-), dTRE (-),	99	High (Excellent)

Isolate 1 and Isolate 3: *Stenotrophomonas maltophilia*, with probabilities of 91% and 98%, respectively. This bacterium is recognized as both a spoilage organism and an opportunistic pathogen, suggesting that contaminated seafood may pose a concern.

Isolate 2: *Methylobacterium spp.* Identification was made with a likelihood of 98%, which is an excellent result. However, mainly environmental organisms, the occasional case regarding opportunistic infections demands further exploration.

Isolates 4 and 6: *Acinetobacter baumannii* complexes were discovered at an intermediate confidence level of 87% and 86%, respectively. The existence of these multidrug-resistant bacteria suggests that they may have been transmitted through handling, storage, or contaminated source water.

Isolate 5: *Proteus hauseri* was identified with a very low confidence, needing further confirmation tests. The species is known to be associated with various foodborne diseases, which indicates possible *faecal* contamination.

Isolate 7: *Providencia alcalifaciens* confirmed at 99% confidence. This microorganism is known to cause gastroenteritis, and its presence in fish samples raises serious public health concerns. The presence of these bacteria calls for strict adherence to hygiene standards in fish markets to control microbial contamination and ensure seafood safety.

Table 3: Antibiotic Resistance Patterns of Isolates

Isolate No.	CoTrimoxazole (COT 25)	Gentamicin (GEN 10)	Chloramphenicol (C30)	Ciprofloxacin (CIP5)	Ceftriaxone (CTR30)
1	(S)	(S)	(S)	(S)	(S)
2	(S)	(S)	(S)	(S)	(S)
3	(R)	(S)	(S)	(S)	(I)
4	(S)	(S)	(S)	(S)	(I)
5	(S)	(S)	(I)	(S)	(I)
6	(S)	(S)	(S)	(S)	(I)
7	(S)	(S)	(S)	(S)	(S)
8	(S)	(S)	(S)	(S)	(S)
9	(S)	(S)	(S)	(S)	(S)
10	(S)	(R)	(S)	(S)	(R)
11	(S)	(S)	(S)	(S)	(S)
12	(R)	(S)	(S)	(S)	(S)
13	(S)	(S)	(S)	(S)	(S)
14	(S)	(S)	(S)	(S)	(S)
15	(R)	(I)	(I)	(S)	(S)
16	(S)	(S)	(S)	(S)	(S)
17	(R)	(I)	(S)	(S)	(S)
18	(S)	(S)	(S)	(I)	(S)

The antimicrobial susceptibility test yielded varying results for different antibiotics, including sensitivity, resistance, and intermediate responses, among the bacteria. A total of 18 isolates were evaluated against the five commonly used antibiotics: Co-trimoxazole COT 25, Gentamicin GEN 10, Chloramphenicol C30, Ciprofloxacin CIP 5, and Ceftriaxone CTR 30.

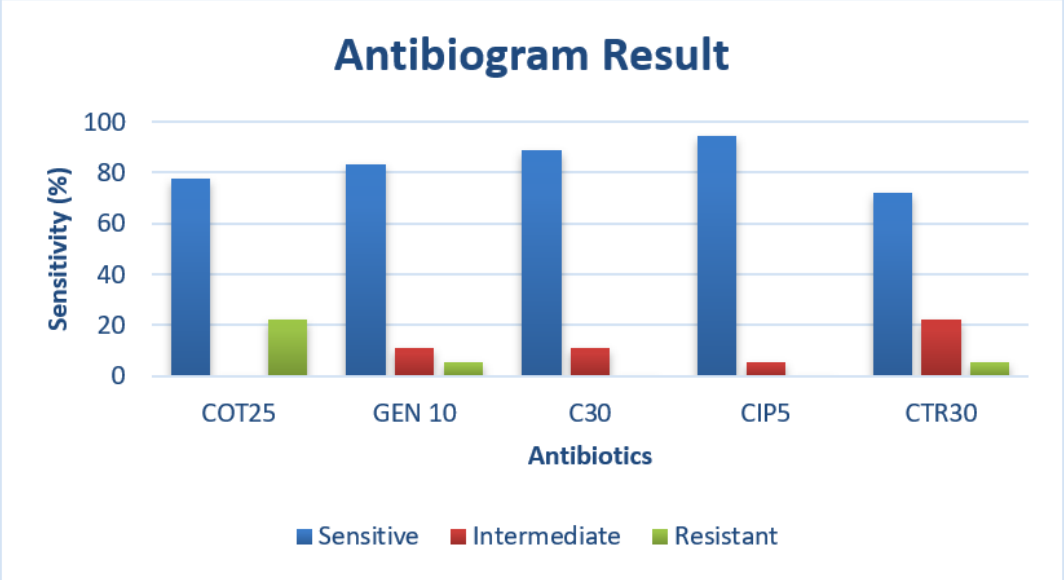

Figure 1: Percentage of resistant, intermediate and sensitive isolates against commercial antibiotics

Resistant (R) isolates: 5 of the 18 isolates (27.8%) were resistant to at least one antibiotic, with Co-trimoxazole and Ceftriaxone showing the highest resistance. Intermediate (I) isolates: four (22.2%) isolates showed intermediate susceptibility, particularly Ceftriaxone, Gentamicin, and Chloramphenicol. Sensitive (S) isolates comprise mostly 66.7% remaining tender to all the medications tested, indicating that bacterial response varied. The existence of antibiotic-resistant and intermediate isolates, most notably multiple-drug-resistant (MDR) organisms, raises alarm about the consequence of antimicrobial resistance (AMR) in the aquacultural food chain. The revelations necessitate strong regulation on antibiotic use, improvement in hygiene practices, and continuous monitoring to prevent the dissemination of resistant microorganisms.

DISCUSSION

High levels of contamination reported in the microbiological examination of *Harpadon nehereus* and *Otolithoides pama* collected from different marketplaces in Dhaka have raised serious concerns about food safety and public health. The level of total viable counts, *coliforms, Salmonella spp., Shigella spp., Vibrio spp., Staphylococcus aureus, and fungi* indicate that extensive microbial contamination has occurred, likely due to poor hygiene in terms of handling, storage, and transportation. The findings coincide with previously published results that observed significant levels of microbial contamination in fish and seafood sold in Bangladesh and other poor countries (Novoslavskij *et al.,* 2016) (Talukdar *et al.*, 2023).

The total number of bacteria counts of both the fish species exceeded the allowable limits given by the international food safety regulations, stating that they have very poor post-harvest management and exposure to unsanitary conditions in the market (Islam *et al.,* 2023). The high level of incidences associated with these two bacteria is becoming a point of concern because they are well-known organisms causing foodborne illnesses such as gastroenteritis, typhoid fever, and dysentery (Rahman *et al.,* 2016). The emergence of *Vibrio spp.* in significant quantities is alarming, having been implicated in cholera and seafood-borne gastroenteritis, bringing significant support to the prior research results carried out in Bangladesh (Faridullah *et al.,* 2022). The identification of bacteria in this study confirmed strains resistant to multiple drugs (MDR) such as *Stenotrophomonas maltophilia, Acinetobacter baumannii, and Proteus hauseri*, which are classically associated with hospital-acquired infections and with opportunistic human diseases (Sheng & Wang, 2021). These bacteria have inherent resistance to many antibiotics and are increasingly being recognized as pathogens in food and marine systems (Acharjee *et al.,* 2021). The antimicrobial susceptibility testing showed resistance to other conventional antibiotics like co-trimoxazole, ciprofloxacin, and ceftriaxone, thereby triggering great concern on the intensifying threat of antimicrobial resistance (AMR) to foodborne pathogens (Talukdar *et al.,* 2023). The fact that AMR develops through fish contaminated with such resistant bacteria can have grave consequences, considering these bacteria could be passed to people through-food chain, causing diseases that may eventually become difficult to manage (Lipi *et al.,* 2023).

Fish can acquire a high microbial load for various reasons, including contamination from dirty water sources, poor handling in the fish market, and improper refrigeration. Results from previous studies have established that poor sanitary practices and unhygienic market conditions were responsible for promoting microbial growth in fishery products (V *et al.,*

2017). The detection of *Salmonella spp.* and *Vibrio spp.* in fish indicates water contamination or cross-contamination during fish handling and processing (Nur *et al.*, 2020). In addition, the presence of antibiotic-resistant bacteria suggests antibiotic misuse in aquaculture, which is already known as a significant contributor to AMR in fish and shellfish (Md. Rokibul *et al.*, 2013).

The consequences of this study stress the pressing need for regulatory activities to safeguard food safety in fish markets. The introduction of good hygiene practices (GHP) and hazard analysis and critical control points (HACCP) in seafood handling and processing will significantly reduce bacterial contamination and ensure the microbiological safety of fish products (World Health Organization, 2011). Regular surveillance and microbiological testing should be mandatory to establish how much contamination and to tighten the food safety regulations (Sheng & Wang, 2021). Moreover, responsible use of antibiotics in aquaculture will help in preventing the spread of antimicrobial resistance in the environment and in humans (Acharjee *et al.*, 2021).

CONCLUSION

The microbiological analysis that was done on Otolithoides pama and Harpadon nehereus from the markets of Dhaka revealed alarming levels of contamination involving coliforms, Salmonella spp., Shigella spp., and multidrug-resistant pathogens such as Acinetobacter baumannii and Stenotrophomonas maltophilia. These results indicate serious deficiencies in post-harvest handling, storage, and hygiene, which further aggravates the absence of due regulatory oversight. Resistance to necessary antibiotics, such as ceftriaxone (11.1%) and co-trimoxazole (22.2%), highlights the critical issue of antimicrobial resistance (AMR) in the food chain. Therefore, urgent action is needed to enforce cleanliness maintenance through Hazard Analysis Critical Control Points (HACCP) and monitor antibiotic usage in aquaculture. Prioritizing the containment of antimicrobial resistance (AMR) in Bangladesh's fisheries industry is crucial to safeguard public health and ensure seafood safety. These concerns would resolve nutrition and economic stability.

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