Comparative Analysis of Pathogenic Bacterial Prevalence in *Cyprinus Carpio* and *Shizothorax plagiostomus*

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ABSTRACT

The possibility of risk of pathogenic bacterial contamination to fish and fish products is a growing concern that is taking a heavy toll economically across the globe. This study was designed to have some insights on comparative bacterial infestation levels from the gills, buccal cavities, and skin surfaces of *Cyprinus Carpio* and *Shizothorax plagiostomus* respectively. The cultural, morphological, and biochemical characteristics of the bacterial isolates were investigated. Our observations arising out of experimental setup revealed the bacteria count ranged from 2.0×10^3 -2.90×10^4,1.64×10^4 -2.99×10^4, 1.1×10^3 -2.56×10^4cfu/ml, and 1.6×10^3 -2.78×10^4,1.5×10^3 -2.95×10^4, 1.1×10^3 -2.71×10^4cfu/ml in the skin, buccal cavity, and gill of Cultured fish and Wild fish respectively. Bacteria counts in the skin of cultured fish were considerably higher (2.0×10^3 -2.90×10^4). Our findings from the study further revealed the presence of, *Pseudomonas aeruginosa, Escherichia coli, Enterobacter cloacae, Bacillus spp, Klebsiella spp, Proteus spp, Salmonella spp, Streptococcus spp, Bacillus spp, Staphylococcus sp., and Enterobacter aeruginosa* from two fish species.In view of the above findings, it is anticipated that bacterial contamination potentially will add a risk for fish food safety in aquaculture.

Keywords: Bacteria, *Cyprinus carpio*,Pollution indicator, *Shizothorax plagiostomus*

INTRODUCTION

Global fish output has expanded considerably over the last 60 years, reaching around 179 million tonnes in 2018 with a value of $401 billion (FAO 2020). Global fish consumption grew as well, rising from 9.0 kg per capita in 1961 to 20.5 kg in 2018. Aquaculture production accounts for 46% of overall production and 62% of total sale value among different growing animal-food sectors. Global aquaculture production is anticipated to tripleby 2050 as a result of rising demand for high-quality protein, reduced wild fish capture, and advancements in fish farming technologies (Ibrahim *et al.*,2020).

India is the world's second-largest producer of fish, and the world's second-largest producer of freshwater fish. Fishing is the primary source of income for many communities in India, with a total population of 2,80,63,537 fishermen (1,56,65,630 males and 1,23,97,907 females) and fish production reached 141.64 lactonnes(37.27 lactonnes for

marine and 104.37 lactonnes for inland fisheries) in 2019-20, up from 107.62 lactonnes (36 lactonnes for marine and 71.62 lactonnes for inland fisheries) in 2015-2016 (Department of Fisheries, Govt. of India, 2020). India's share of global fish output has risen steadily, from around 11.4 percent in 2016 to 13.5 percent in 2018. (Department of Fisheries, Govt. of India, 2020).It has been observed that this sector in India as of 2018 employs 59.51 million people wherein women account for 14% of the total.Fisheries and aquaculture output contribute nearly 1% of India's GDP and more than 5% of agricultural GDP. Fisheries is a thriving industry in Jammu and Kashmir, with constant growthover the last few decadeswith inland fish production of 0.2 lac tonnes in 2015 -16 to 0.21 lac tonnes in 2019-20 (FAO, 2020). In Jammu and Kashmir (J&K), the fishing industry is regarded as an emerging endeavor with the potential to contribute to the state's economy as the estimated growth rate in Gross State Domestic ProductGSDP "Agriculture, Forestry & Fisheries" had the second-highest growth rate of 6.07 percent over 2016-17. Its contribution is 2.07 Lakh Quintals of total fish production in 2017-18. J&K fisheries generate up to 31% of total cold-water fish produced in the country (DCFR 2010). displays J&K state's contribution to the overall fish basket of the country, which is less than 1% (DoF 2010). The primary sector's 23 percent contribution to GSDP includes the contribution of fisheries as well (PHDCCI 2012). The fisheries sector has been emphasized as an important agriculturally related activity. It generates self-employment and provides a significant output base for the agricultural economy. Its importance in replenishing nutrients and meeting food demand, as well as creating jobs, cannot be overlooked. Modernization and the rising economic level of the people, together with changes in social structures, have had a significant positive impact on the state's fisheries structure (Baba, *et al.,* 2019).

Fish has the advantage of being easily digestible and having a high nutritional value as a food. It has been suggested that the type of microorganisms found in any group of fish in an environment is determined by its habitat (Clucas and Ward 1996). However, the expansion of aquaculture has resulted in a number of issues, including the destruction of natural ecosystems, water pollution, biological contamination, and the emergence of a variety of fish diseases (Luis *et al.,*2017). Several works on fish bacterial flora have been conducted in the past years and are continuously going on. Virulent bacterial

spp. namely,*Aeromonas hydrophila*, *A. veronii, Pseudomonas fluorescens and P. aeruginosa* that were isolated from *Nile tilapia* (*Oreochromis niloticus*) and grey mullet (*Mugil cephalus*) were collected from freshwater fish farms (Sherif *et al.*, 2021). However, the expansion of aquaculture has resulted in a number of issues, including the destruction of natural ecosystems, water pollution, biological contamination, and the emergence of a variety of fish diseases (Luis *et al.,* 2017). Microorganisms are typically found on fish surfaces such as skin and gills, as well as inside the fish in locations such as the digestive tract and internal organs such as the kidney, liver, and spleen. Fish and fish products, particularly raw or undercooked seafood, have been linked to outbreaks of bacterial infections, biotoxins, histamine, viruses, and/or parasites (Galaviz-Silva *et al.,* 2009). Water has been shown to shape the fish microbiome (Wu *et al.,* 2012; Giatsis *et al.,* 2015; Webster *et al.,* 2018).

Aeromonas species is a common, natural member of freshwater environments, and the bacterium is found in between 33 and 100 percent of water samples (Palumbo *et al.*,2000). The *A. hydrophila* group is commonly found in fish and fish products at concentrations ranging from 102 to 106 cfu/g, but it is also easily isolated from meat, milk, poultry, and vegetable products (Palumbo *et al.,*2000). Both vacuum and modified atmosphere-packed products allow the organisms to grow (Palumbo *et al.,* 2000). The Entero-bacteriaceae family includes the genus *Salmonella.* Salmonellosis is one of the most common causes of bacterial enteric disease in both humans and animals (Brenner *et al.,*2000). Salmonellae are typically mesophilic bacteria with a global distribution that are found in fish and fishery products. Salmonella can also be found in environments contaminated with human or animal excreta, such as water reservoirs. Shellfish growing in contaminated waters, in particular, can accumulate *Salmonella,* and raw oysters have been linked to salmonellosis outbreaks (Ahmed, 1991). *Salmonella* has been reported in 15% of fish samples from India and Mexico apart from infecting several crustacean and molluscan products from India and Malaysia (D'Aoust, 2000). There is evidence that certain *Salmonella* serotypes are common in fish farms and become part of the indigenous microflora (Feldhusen, 2000). Staphylococci can be isolated from freshly caught fish, particularly in warm waters (Gram and Huss, 2000). Enterotoxigenic strains, on the other hand, are typically transmitted by food handlers who have

hand infections, a cold, or a sore throat. *S. aureus* has been isolated at levels ranging from 2-10% in fish and bivalves (Jablonski and Bohach, 1997). Several of these diseases are zoonotic, as infected animals are the primary source of human illness. Kvenberg (1991) and Rodricks (1991) discriminated between native and non-native bacterial infections in fish. Non-indigenous bacteria including *E. coli, Clostridium botulinum, Shigella dynteriae, Staphylococcusaureus, Listeria mono-cytogens, and Salmonella* affect the fish and ecology in some way. Vibrio and Aeromonas species, for example, are indigenous bacterial diseases found naturally thriving in fish habitats.

Only when fish are physiologically imbalanced, nutritionally deficient, or when other stresses, such as poor water quality or overstocking, allow opportunistic bacterial infections to proliferate, do bacteria become pathogens (Rodricks, 1991).Freshwater or rivers and lakes, on the other hand, may have a complex flora of microorganisms, including genuinely aquatic diseases and other components introduced from human, animal, and plant sources (Adams and Tobias 1999; Gisain *et al*.,2013).

These microorganisms may harm fish health, they are classified as conditionally pathogenic. The presence of enteric bacterial species in fish, such as *E. coli*, showed that the water is contaminated or polluted. The presence of *S. aureus* implies that the water was contaminated by direct human activity. Pathogen transmission in fish may also occur as a result of transferring fingerlings, without using protective gloves, netting, handling fish ponds in tropical climates, preparing fish dishes, and processing fish in food businesses (Notermans and Hoornstra, 2000). Fish has been identified as a carrier of *Salmonella* bacterial spp. with no obvious signs and symptoms of infection (Novotny *et al.*,2004). *Salmonella* spp. contamination can occur in the terrestrial environment, and fish can act as a vector for these bacterial species (Novotny *et al.*,2004).

However, the expansion of aquaculture has resulted in a number of issues, including the destruction of natural ecosystems, water pollution, biological contamination, and the emergence of a variety of fish diseases (Luis *et al.*,2017).Microorganisms are typically found on fish surfaces such as skin and gills, as well as inside the fish in locations such as the digestive tract and internal organs such as the kidney, liver, and spleen. Fish and fish products, particularly raw or undercooked seafood, have been linked to outbreaks of bacterial infections, biotoxins, histamine, viruses,

and/or parasites (Silva *et al.*,2009).Water has been shown to shape the fish microbiome (Wu *et al.*,2012; Giatsis *et al.*,2015; Webster *et al.*,2018;).

In general, fish and fish products have been regularly linked to foodborne disease outbreaks. This is higher than the rate of foodborne illness outbreaks linked to poultry and beef, which contributed 3.6 percent and 1.9 percent of all verified foodborne outbreaks, respectively, from 2011 to 2017. CDC (2018).Thus, bacterial detection in fish reflects the condition and safety of environments. The purpose of this study was focused on isolating and identifying pathogenic bacteria from selected diseased native fish of the Jhelum River and hatchery-cultured fish tohave some idea about the comparative microbial infestation in various tissues of wild and cultured fish species.

Materials and Methodology

Collection and Examination of fish samples

The specimens were collected twice in the month for bacterial investigations of Common carp (*Cyprinus carpio,* one of the most widely grown carps) from the Manasbalhatchery and Qazigund Local fish farm. The bacterial flora of the indigenous cold-water species *Schizothoraxplagiostomum*, which belongs to the family Cyprinidae and the order Cypriniformes, was estimated in this study. *S. plagiostomum* samples were obtained with the assistance of fishermen from twostations of Central Kashmir (Near Lasjan Bridge and Amira Kadal, Srinagar) along the Jhelum River and were identified with the help of standard taxonomic keys (Tilak, 1987; Jhingram, 2007). The fish samples were collected from 2019-2020,wherein70 and 35 samples of cultured fish and wild fish respectively were taken based on clinical symptoms. These fish were aseptically labeled and immediately transported in a sterile container to the Laboratory where they were processed within 2-4 hours of being collected. After weighing the sample in grams (g), the standard length (cm), head length (cm), gill length (cm), and buccal depression in centimeters (cm).

Assessment of Morphological/clinical obsessive indications

Stomach distension, skin blisters, wounds on the different parts of body parts, superficial ulcers, hemorrhages, and, in rare cases, intramuscular cavities filled with blood-tinged caseous or necrotic material were all signs of bacterial infection in Common carp and *S. plagiostomus*. Infected fish were examined thoroughly, and any macroscopic or gross lesions seen were noted.Clinically, collected samples were examined for

indications with an unusual center toward lesions on the skin and gills (Austin and Austin 2012; Noor El-Deen 2014).

Isolation and identification of bacterial flora:

A culture-dependent methodology and the spread plating method were used to separate fish pathogenic microorganisms (Nabeel *et al.*,2017). The infected zone's surface was swabbed in Fig. 1. (A and B) and the inoculum was disseminated throughout the surface of inoculated on Nutrient Agar, TSA, MacConkey agar and Blood agar,etc (Spanggaard*et al.*,2000; Dar *et al.*,2013; Dar *et al.*,2015), with incubation at 25°C -37°C for 24-72 hours (Whirlpool and Jones, 2002; Al-Harbi and Uddin 2004 and 2005). Purified isolates were used as stocks for morphological and biochemical analysis.

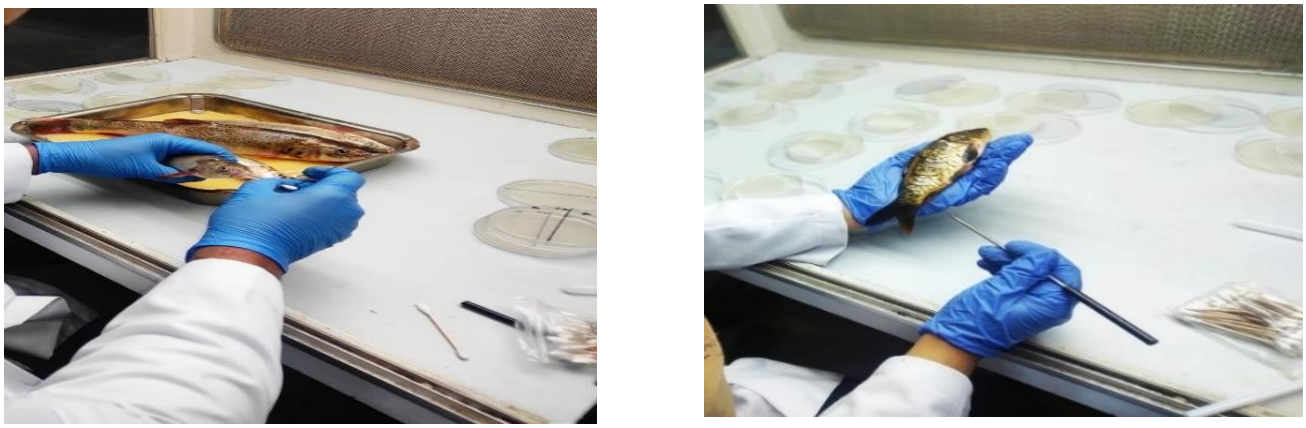
Gills of fish were cut using sterile scissors under aseptic conditions and then processed individually. The cut samples were kept in 0.85% sodium chloride (saline water) solution and 1gram of gill sample was crushed with the help of a homogenizer with about 10 ml of sterilized pre-chilled saline water and the stock solution were serially diluted. The gills homogenate was used as inoculum, samples were separately analyzed by ensuring homogeneity of the samples using a sterile pipette. The 1 mL of each sample was suspended into 9 mL sterile saline water aseptically which was then shaken together in a vortex shaker. Further serial dilution of 10-folds was carried out. 100µl of serially diluted homogenized samples were spread on duplicate sterilized culture media Nutrient Agar, TSA, MacConkey agar, Blood agar plates, etc., and incubated at 25ºC - 37ºC for 24-72 hours. Colonies with various morphological characteristics were isolated. By streaking the isolates individually on culture medium plates, the purity of the isolates was assessed. The cultures were kept and stored at 4°C (Ghosh *et al.*, 2002).

Bacterial colonies were counted using the Digital Colony Counter. The formula was used to figure out how many colony formation units (CFU) =

$$\frac{\text{Number of colonies}}{\text{Volume of sample}} \text{ X dilution factor}$$

Pure cultures of the isolates were identified using biochemical characterization using the criteria outlined in Bergey's Manual of Determinative Bacteriology (Garrity, 2001). The analytical profile index of the API20-E

system was used to confirm each strain (Buller, 2004).



A B

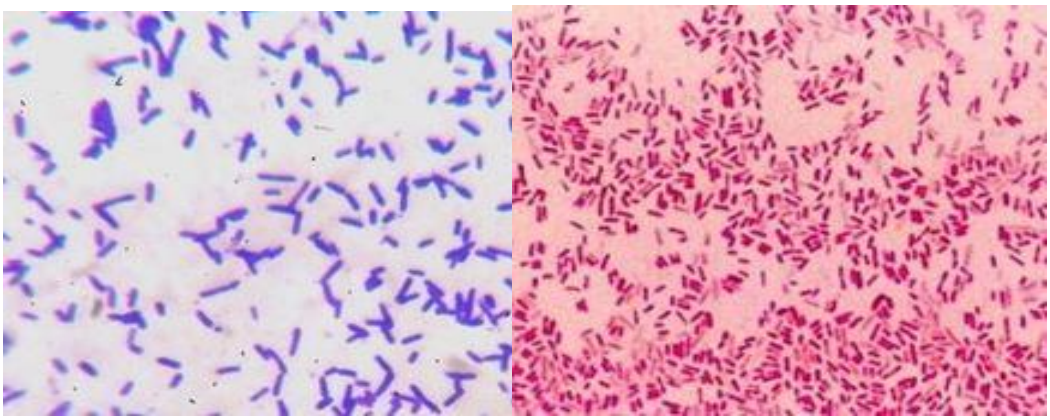
Fig. 1. Isolation of bacteria by swabbing method from A (wild fish) and B (cultured fish).

RESULTS AND DISCUSSION

The morphometric parameters of *Cyprinus carpio* and *S. plagiostomus* are summarized in Table 1. A keen look over the data revealed that*Cyprinus carpio*recorded the highest mean body weight (364±6.23) g while*S. plagiostomus* recorded the lowest mean body weight (275±5.45) g. *Cyprinus carpio* recorded the lowest mean standard length (20.05±5.40) cm while *S. plagiostomus*recorded the highest mean standard length (25.60 ± 6.25) cm.*Cyprinus carpio*recorded the highest mean head length (3.24±0.68) cm while *S. plagiostomus*recorded the lowest mean head length (2.57 ± 0.40) cm. *Cyprinus carpio* recorded the highest mean gill length (2.79±0.52) cm. *S. plagiostomus*recorded the lowest mean gill length(2.20±0.24) cm. *Cyprinus carpio*recorded the highest mean buccal depth (3.25 ± 0.20) cm while *S. plagiostomus*recorded the lowest mean buccal depth (1.45 ± 0.12) cm.*Cyprinus carpio* had the highest mean weight (grams), buccal depth (cm), head length (cm), and gill length (cm). The standard length of *S. plagiostomus* was the longest.

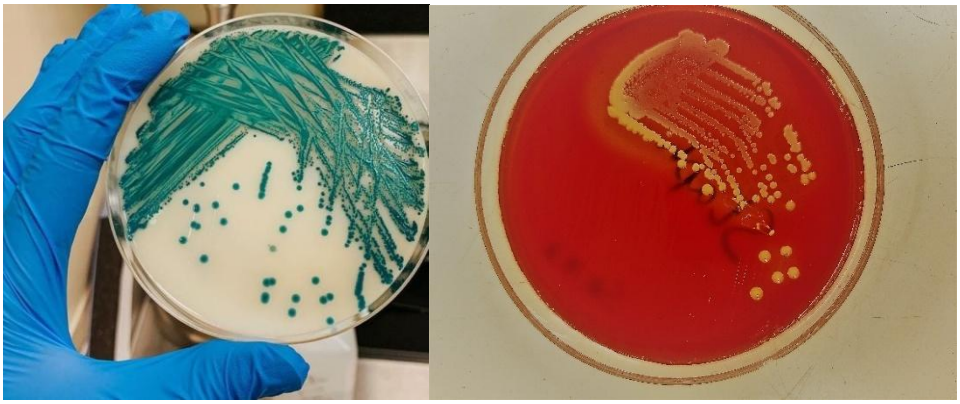
Table 1. Summary of morphometric characteristics of two fish species

Morphometrics	*Cyprinus carpio*	*S. plagiostomus*
Weight (g)	364.52±6.23	275±5.45
Standard length (cm)	20.05±5.40	25.60±6.25
Head Length (cm)	3.24±0.68	2.57±0.40
Gill length (cm)	2.79±0.52	2.20±0.24
Buccal depth (cm)	3.25±0.20	1.45±0.12
Viable bacteria count (cfu/ml).		
Skin	2.0×10^3 -2.90×10^4	1.6×10^3 -2.78×10^4
Buccal cavity	1.64×10^4 -2.99×10^4	1.5×10^3 -2.95×10^4
Gill	1.1×10^3 -2.56×10^4	1.1×10^3 -2.71×10^4



A: Gram-positive bacteria B: Gram-negative bacteria

Fig 2. Represented A (Gram-positive bacteria) and B: (Gram-negative bacteria)



A **B**

C **D**

E **F**

Fig. 3. Pure culture of bacterial species on different media **(A)** *Salmonella*, **(B)***Staphylococcus*, **(C**) *Pseudomonas***, (D)** *E.coli*, **(E)** *Proteus*, **(F)** *Klebsiella*,

Table 2: Screening of Biochemical tests for the identification of fish-associated bacterial flora.

Tentatively Identified Bacteria	**Gram reaction**	**Catalase**	**Oxidase**	**Carbohydrate fermentation test**				**Indole**	**MR**	**VP**	**CU**	**H_2S production**	**Urease production**
				G	**F**	**L**	**S**						
Enterobacter cloacae	**GNB**	**+**	**-**	**Nil**	**Nil**	**+**		**+**	**-**	**+**	**+**	**-**	**+**
Enterobacter aerogenes	**GNB**	**+**	**-**	**Nil**	**Nil**	**+**	**Nil**	**-**	**+**	**+**	**+**	**-**	**-**
E. coli	**GNB**	**+**	**-**	**+**	**+**	**+**	**+**	**+**	**+**	**-**	**-**	**-**	**-**
Klebsiella pneumoniae	**GNB**	**+**	**-**	**+**	**+**	**-**	**+**	**-**	**-**	**+**	**+**	**-**	**+**
Proteus vulgaris	**GNB**	**+**	**-**	**Nil**	**Nil**	**-**	**Nil**	**+**	**+**	**-**	**-**	**+**	**+**
***Shigella* sp.**	**GNB**	**+**	**-**	**+**	**+**	**-**	**-**	**+**	**+**	**-**	**-**	**Nil**	**Nil**
***Salmonella* sp.**	**GNB**	**+**	**-**	**+**	**-**	**-**	**-**	**-**	**+**	**-**	**-**	**+**	**-**
Pseudomonas aeruginosa	**GNB**	**+**	**+**	**+**	**+**	**-**	**-**	**-**	**-**	**-**	**+**	**-**	**-**
Aeromonas hydrophila	**GNB**	**+**	**+**	**+**	**-**	**-**	**+**	**+**	**-**	**+**	**+**	**+**	**-**
***Bacillus* sp.**	**GPC**	**+**	**-**	**+**	**+**	**+**	**+**	**-**	**-**	**-**	**-**	**-**	**-**
***Staphylococcus* sp.**	**GPC**	**+**	**-**	**Nil**	**Nil**	**+**	**Nil**	**-**	**-**	**-**	**-**	**-**	**+**

Key: GNB= Gram negative bacilli, GPC= Gram positive cocci +ve = Positive, -ve = Negative, Indole Test, MR= Methyl Red Test, VP=Voges-Proskeur Test, H_2S= Hydrogen Sulphide Production Test, Nil= Not Present

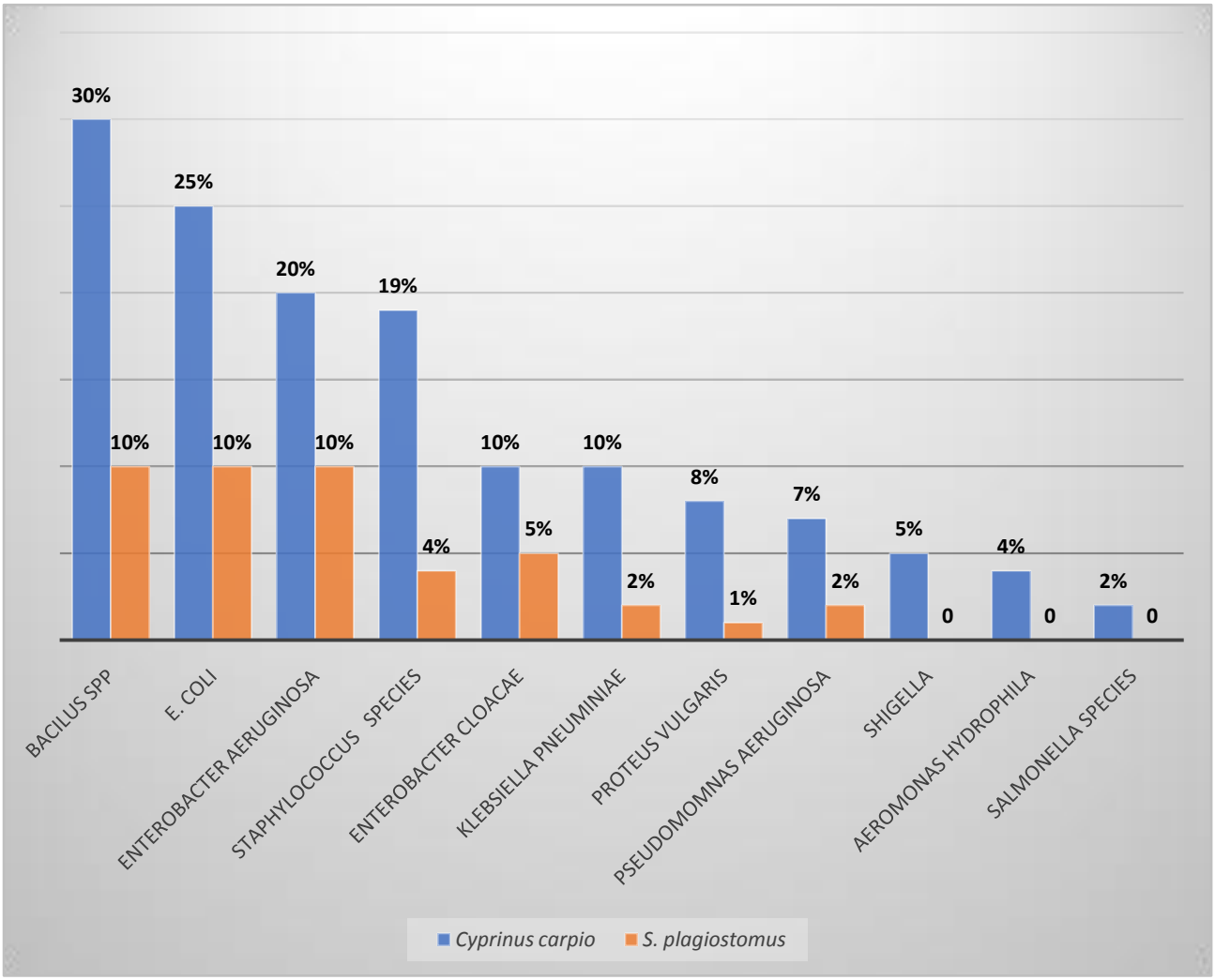


Fig. 4: Percentage distribution of bacterial isolates in both fish species

Viable bacteria count of bacteria growth isolated from three (3) spots/sections of the two different species was done for each. Table 1 also shows the data on viable bacteria count (cfu/ml) in fish samples, *Cyprinus carpio* and *S. plagiostomus* ranged 2.0×10^3 -2.90×10^4 and 1.6×10^3 -2.78×10^4 in the skin, 1.64×10^4 -2.99×10^4 and 1.5×10^3 -2.95×10^4 in the buccal cavity and 1.1×10^3 -2.56×10^4 and 1.1×10^3 -2.71×10^4 in the gills respectively. The skin of *Cyprinus carpio* had the greatest bacteria count range of 2.0×10^3 -2.90×10^4, which contradicts the premise of Akinyemi and Buoro, 2011. They reported the gill of *L. agennes* recorded the highest viable count while the skin of *P. elongatus* recorded the least viable count. Table 1 also revealed that *P. elongatus* had the highest number of growth (2.7x103-2.98x104) in general followed by *L. agennes* (3.3x103-2.48x104) and the least seen in *S. barracuda* (2.5x103 - 2.18x104).

A total of 11 bacteria species were recovered from the gills, buccal cavity, and skin of *Cyprinus carpio* and *S. plagiostomus* in this investigation. Nine of the bacteria species identified were gram-negative (-ve), whereas the other two were gram-positive (+ve). This result corroborated prior research findings by Al-Harbi and Uddin (2005), who found that the microorganisms isolated from brackish pond water were mostly gram-negative bacteria (-ve).

Prevalence of pathogens in fish samples and Percentage occurrence of bacteria isolates:

The prevalence of bacterial isolates during the current investigation is presented in Fig. 4 as (30%) *Bacillus* sp, (25%) *E. coli*, (20%) *Enterobacter aeruginosa*, (19%) *Staphylococcus* species, (10%) *Enterobacter cloacae*, (10%) *Klebsiella pneumonia*, (8%) *Proteus vulgaris*, (7%)*Pseudomonas aeruginosa*, (5%) *Shigella* sp,(4%) A*eromonas hydrophila*, and (2%) *Salmonella* species. While, as in *S. plagiostomus* fish species were (10%) *Bacillus* sp, (10%) *E. coli*, (10%) *Enterobacter aeruginosa*, (4%) *Staphylococcus* species,(5%) *Enterobacter cloacae*, (2%) *Klebsiella pneumonia*, (1%) *Proteus vulgari* and(2%)*Pseudomonas aeruginosa.*

Bacillus spp. was the most common species detected (30% in cultured fish and 10% in wild fish, respectively). Various investigations elsewhere have also reported *Bacillus cereus* more abundant in *Sidra* samples (16.7 %) than in S*ukuti* samples (11.8%). *Bacillus cereus has also been reported to be the cause* increase in food-borne illness (Yu *et al.*,2020), as it can withstand heating and pasteurization by generating spores (Kotiranta *et al.*,2000).The prevalence of *Escherichia coli* (25 % and 10%in cultured and wild fish respectively) was the second most common species discovered in this investigation. High prevalence by *E. Coli* has also been widely reported like Danba *et al.*,2014 found *E. coli* prevalence (34.62 percent),and Jatt *et al.*,2019 found E. coli prevalence (54.27 percent).

Staphylococcus species(19% and 4% in cultured and wild fish respectively) were investigated in our study. Same bacterial isolated were reported by Jatt, *et al.*,2019as *Escherichia coli*(34.62 %), *Aeromonas salmonicida* (30.77 %), *Staphylococcus aureus* (23.07%), and *Salmonella typhi* (11.54 %) in *Cirrhinusmrigala.*

Pseudomonas aeruginosa (7% and 2% in cultured and wild fish respectively) were identified in the present investigation. *Pseudomonas aeruginosa* (10.85%) were reported by Danba *et al.*,2014 and Jatt, *et al.*,2019). *Pseudomonas* spp. and many others have been identified as Antibiotic Resistant Bacteria (Hoa *et al.*, 2011; Naviner *et al.*,2011; Ranjbar, 2013, Shah *et al.*,2019; Nikuli and Sorum, 2020).

Aeromonas hydrophila (4%) was isolated from several organs of cultured fish species *Cyprinus carpio*in this study. *Aeromonas hydrophila* has been isolated from a variety of fish and fish products. The prevalence ranges from 0.8 percent in retail frozen tilapia collected in Mexico City (Castro-Escarpulli *et al.*,2003 and 2016) to 47 percent in Egyptian farmed fish (Dahdouh*et al.*,2016). Many studiesreported *Aeromonas salmonicida* (30.77 %) as by Jatt, *et al.*,2019. The pathogenicity of *A. hydrophila* for experimentally infected *O. niloticus* fish species may be linked to the generation of toxins and extracellular enzymes by *A. hydrophila* (Saavedra *et al.*,2004).

Only 2% of *Salmonella* species were identified in the cultured fish from various organs. More or less the same observations s from farm fishes have also been e reported by Klase *et al.*,2019 in China, in numerous fish products (Santos *et al.*,2019; Yu *et al.*,2020; Kotiranta *et al.*,2000). Similarly in our study, *Enterobacter cloacae* were found 10% and 5% in cultured and wild fish, *Enterobacter aeruginosa as 2*0% and 10% in cultured and wild fish, and *Proteus vulgaris*as8% and 1% in cultured and wild fish respectively. 10% and 2% of *Klebsiella pneuminiae* were found in cultured and wild fish respectively and *Shigella* sp. as 5% only in cultured fish.

It is estimated that 7% of the total annual food outbreaks are confirmed to be associated with fish (Dewey-Mattia, *et al.*,2016; 2018). The connection of opportunistic and pathogenic microbial species with fish demonstrates a severe state affecting human health (Sichew *et al.*,2014; Mhango *et al.*,2010).Due to ineffective farm management techniques, the aquaculture sectors are prone to numerous diseases, increasing susceptibility to pathogenic infections (El - Sayed 2006) and the dispersion of mobile *Aeromonas spp.* in the aquatic environment and fish has been recorded (Hatha *et al.*,2005; Hussain *et al.*,2014). Similar findings were made by (Noor El Deen *et al.*, 2014), who stated that skin ulcers could be the source of infection caused by *Aeromonas* sp. The findings

matched with those of Hazen *et al.*,2012 who stated that the color of a bacterial colony may be used to determine its genus level. *Aeromonas* sp. is an opportunistic pathogen found in freshwater ecosystems worldwide, as well as soil, water, and food. This bacterium is capable of causing foodborne and nosocomial illnesses (Cabral, 2010; Janda, 2010; Gauthier, 2015).

In the current investigation, pathogenic bacterial load was shown to be greater in cultivated fish species than in wild fish species. The presence of pathogenic bacterial species such as *Shigella*, *Aeromonas,* and *Salmonella* in cultured fish poses a greater risk to the fisheries sector and the environment, whereas these were absent in wild fish species during this study. In hatcheries, there is stagnant water and also a crowding of fish species in a specific volume, which may be the cause of these microorganisms with this environment, whereas, in rivers, there is always running water flow and the occurrences of disease-causing bacteria in the wild fish are due to anthropogenic pressures.In general, outbreaks of food poisoning linked to fish and related food products are caused by the eating of uncooked or insufficiently heat-treated fish spp., which may have been infected with harmful bacteria from water or terrestrial environmental sources.

CONCLUSIONS

From our study, we observed that bacterial infections are the most prominent microbiological agents impacting cultured fish, *Bacillus* sp. and *E. coli* were most prevalent in fish microbiota.Contamination of fish's natural environment may have an impact not only on the health of fish stocks but also on public health, as fish and fish products can be a source of human pathogens. This study offers some inputs on likely bacterial infestation of fish and fish products which can compromise public health.

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