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Analysis of Bacterial Population in Water, Sediment and the fish *Mystus vittatus* Collected from Lower Anicut, Thanjavur District, Tamil Nadu

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Abstract

Even though India is presently ranked second in aquaculture production, the outbreak of infectious diseases has resulted in heavy losses to the aquaculture industry. Among the various groups of pathogens affecting fishes, bacteria appear to be the most common pathogen. Hence the present study was attempted to find the bacteria that occur in water, sediment and the common fish *Mystus vittatus* collected from Lower Anicut area in Tamil Nadu. A total of 20 bacteria were identified in both sediment and water samples. The skin of *Mystus vittatus* recorded 11 bacteria while the foregut 12, midgut 9 and hindgut, 17 bacteria. Out of these, eight bacteria were common to gut. During this study, bacteria that could pose a threat to human beings were also isolated. This warrants immediate action as well as dissipation of information to the fishermen and handlers.

Keywords

Fresh water, Sediment, Bacteria, *Mystus vittatus*, Skin, Digestive system

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INTRODUCTION

With increasing demand for food, aquaculture is rapidly developing throughout the world and today in many countries fish farming has already become an important economic activity. India with its exploding human population will now have to use all its avenues for increasing its food production. India is now presently ranked second in aquaculture production (Saraswathi *et al*., 2015). However, the outbreak of infectious diseases in farm fishes has brought about a significant setback for successful aquaculture as it has resulted in losses to the farmers. Among the various groups of pathogens that cause diseases, bacterial diseases appear to be the most common fish pathogen.

Only recently has attention been given to microbiological studies focussing on isolation and establishing causes of fish disease and their medications (Saraswathi *et al*., 2015). Ogbondeminu and Okoeme (1989) reported that 50% of

microorganisms recorded from fishes in ponds fertilized with annual faecal waste had members of the family Enterobacteriaceae. Recently, Saraswathi *et al*. (2015) while analysing carps reared in a fresh water pond in Tamil Nadu, recorded enteric bacteria belonging to 10 genera involving a total of 13 species. Many scientists working on various farm fishes have been able to recover a wide range of potent bacteria that can cause diseases to man (Sakata *et al.*, 1980; Hejkal *et al*., 1983; Buras *et al*., 1987; Ogbendeminu, 1993; Saraswathi *et al.*, 2015). Hence the present study was attempted to identify the various bacteria in *Mystus vittatus* collected from Lower Anicut, Thiruppanandal Block, Tanjavur District, Tamil Nadu, India.

MATERIALS AND METHODS

Water samples for microbiological analyses were collected, put aseptically into sterile 500 ml sampling bottles and examined within 1-2 hours of collection in the laboratory. All water samples were analysed for the presence of total and faecal coliform bacteria, faecal Streptococci and pathogenic *Salmonella* by the most probable number (MPN) method following the American Public Health Association (APHA2000) procedures. The total viable count (TVC) of all heterotrophic bacteria was done on nutrient agar plates incubated at 28°C for 48 hours.

Ten specimens from each fish species were examined on the day of harvest. Swab samples of about 4-5cm^{2}fish skin area were collected and inoculated onto media as those used for the water samples to estimate the MPN values. Pieces of fish skin, muscle and digestive tracts were collected separately under aseptic conditions and put into sterile petridishes. Corresponding organs from the same fish species were pooled, weighed and homogenized with a sterile warring blender with 10 ml of 0.1% phosphate buffer saline of pH 7.5 per gram of fish tissue. A volume of 0.1ml of the homogenate was plated subsequently onto nutrient agar and MacConkey agar and incubated at 37°C for 24-48 hrs. For qualitative identification of various bacteria from water and fish samples, fresh solid media of modified fecal coliform (M-FC) agar were inoculated in duplicate and incubated at 37°C for 24 h. After distinct coloured colonies of various bacteria developed on the plates, the identification of the bacterial colonies were done according to Edwards and Ewing (1972), Cowan (1974), Martin and Washington (1980), Brenner (1984) and Cheesbrough (1989).

RESULTS

The Table-1 records the various bacteria that were identified from water, sediments, skin and gut of *Mystus vittatus*. As evident from the table, a total of 20 bacteria belonging to 15 genera were identified. Of these, the genus *Vibrio* was represented by three species while *Bacillus* and *Proteus* were represented by two species each. The remaining genera were all represented by a single species each.

A comparison of the bacteria flora in water and sediment reveals that all the 20 bacteria that were identified were found in both the water as well as sediment. Examination of the skin of *Mystus vittatus* reveals that a total of 11 bacteria could be isolated which were recorded in the water and sediment. However, bacteria like *B. cereus,C. perfringens, F. johnsoniae, P. vulgaris, S. marcescens, S. sonnei, S. faecalis* and *V.parahaemolyticus* which were recorded in both sediment and water could not be found in the skin of *Mystus vittatus*.

Examination of the gut of *Mystus vittatus* reveals that the foregut recorded a total of 12 bacteria while the midgut recorded nine bacteria and the hindgut recorded 17 bacteria. A closer examination reveals that the foregut recorded two unique bacteria (*E. aerogenes* and *S. typhi*), which were not found in the midgut and hindgut while the hindgut recorded six unique bacteria (*A. aerogenes, B. cereus, C. pefrogens, F. johnsoniae, S. marcescens* and *V. alginolyticus*) which were not found in the midgut and foregut. However, the midgut did not record the presence of any unique bacteria. Further, the midgut and hindgut recorded two species (*V. cholerae* and *V. parahaemolyticus*) which was not recorded in the midgut while the midgut and hindgut recorded *S. faecalis* which was not recorded in the foregut. However, *P. mirabilis* was the only species which was not recorded in the gut even though there were eight bacteria that were common to all regions of the gut (*A. hydrophila, B. subtilis, E. coli, K. pneumoniae, P. vulgaris, P. aerugimosa, S. sonnei* and *S. aureus*). Thus, it appears that bacteria can survive in all parts of the gut even though the hindgut is the most preferred habitat of these organisms.

A perusal of the bacterial load in water and the different regions of *Mystus vittatus* suggest that the bacteria are similar. No new species of bacteria could be identified from the *Mystus vittatus* suggesting that there is a close correlation between the bacteria present in water and the *Mystus vittatus*. Similar observations have also been reported by a number of workers (Hejkal *et al*., 1983; Buras *et al*., 1987; Ogbendiminu, 1993; Zmyslowska *et al*., 2001; Saraswathi *et al*., 2015).

An analysis of the bacteria flora recorded in the gut of various fishes reveals that bacteria isolated in the present study was also documented by others. Thus, the presence of genera like *Enterobacter, Salmonella, Pseudomonas, Proteus* and *Shigella* were all reported by Souter *et al.* (1976), Ogbondeminu (1993), Surendraja *et al*. (2009) and Saraswathi *et al*. (2015).

The present study has recorded the presence of several bacteria that can pose a threat to human beings (*E. coli* and *S. typhi*). This necessitates immediate action and also dissipation of information to the fishermen to be vigilant when coming in contact with these fishes.

Table-1: Existence of bacterial population in various samples of *Mystus vittatus* collected from Lower Anicut area

Name of the Bacteria	Name of the Samples					
	Sediments	Water	Epidermis	Foregut	Midgut	Hindgut
Aerobacter aerogenes	+	+	+	–	–	+
Aeromonas hydrophila	+	+	+	+	+	+
Bacillus cereus	+	+	–	–	–	+
Bacillus subtilis	+	+	+	+	+	+
Clostridium perfringens	+	+	–	–	–	+
Enterobacter aerogenes	+	+	+	+	–	–
Escherichia coli	+	+	+	+	+	+
Flavobacterium johnsoniae	+	–	–	–	–	+
Klebsiella pneumoniae	+	+	+	+	+	+
Proteus mirabilis	+	+	+	–	–	–
Proteus vulgaris	+	+	–	+	+	+
Pseudomonas aeruginosa	+	+	+	+	+	+
Salmonella typhi	+	+	+	+	–	–
Serratia marcescens	+	+	–	–	–	+
Shigella sonnei	+	+	–	+	+	+
Staphylococcus aureus	+	+	+	+	+	+
Streptococcus faecalis	+	+	–	–	+	+
Vibrio alginolyticus	+	+	–	–	–	+
Vibrio cholerae	+	+	+	+	–	+
Vibrio parahaemolyticus	+	–	–	+	–	+

+ denotes present; –denotes absent.

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