Bacterial diversity in organic manured fish ponds

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Indian freshwater aquaculture is mainly based on organic fertilization with the use of raw cow manure along with inorganic fertilizers for pond fertilization (Ayyappan et al., 1990). In integrated fish farming recycled animal excreta, poultry droppings and agricultural byproducts are used as fertilizers. Processing of organic matter prior to application to fish ponds provide ready substrate would to decomposing bacterial communities which otherwise would have caused a lag period before the requisite bacterial activity (Zhu et al., 1990). Organic manuring results in composite fertilization providing nutrients on a sustained basis to the fish culture system (Wohlfarth and Schroeder, 1979). Significance of bacterial communities in the recycling of organic material in aquatic ecosystems is important as they maintain ecological balance through various microbial processes and these microbial processes increases the fertility of the ecosystems. Bacterial communities in fish pond ecosystems serve as reliable indices of the efficiencies of manurial practices, based on the concept of substrate utilization (Jha et al., 2008; Das et al., 2013). The objective of the present study was to evaluate the different bacterial genera involved in nutrient cycling of both raw and processed organic manured carp culture fish ponds.

The water and sediment samples were collected aseptically from the organic manured fish ponds with cow manure and biogas slurry and transferred to laboratory

under sterile conditions for the assessment of bacterial diversity. Standard dilution plate count method was employed for heterotrophic enumeration of aerobic bacterial populations once in a month both in water and sediment for a period of one year using nutrient glucose agar (Norris and Ribbons, 1970; Collins and Lyne, 1976) at the farm of Central Institute of Freshwater Aquaculture, Kausalyaganga, Bhubaneswar, Orissa (Lat.20⁰11'06"-20⁰11'45" N; Long. $85^{0}50'52''-85^{0}51'35''E$). The isolation of bacterial cultures was carried out using dilution technique. While 10-3 serial dilutions with sterile physiological saline (0.85% NaCl) were used for water samples, 10⁻⁵ dilutions were employed for sediment samples. Samples in sterile petridishes (15 Psi, 121°C for 20 minutes) were mixed in nutrient agar medium by the pour plate method and the plates were incubated at room temperature $(30^\circ \pm 2^\circ C)$ in a bacteriological incubator (BEC model, 1989) for 48 hours. Hundred numbers of different bacterial isolates were selected and were sub cultured in nutrient agar slants and subjected to staining procedures. For generic identification. physiological and (motility, biochemical tests catalase reduction. production. nitrate starch hydrolysis, gelatin liquefaction, H₂S production. utilization of carbohydrate sources like glucose, sucrose, lactose, mannitol, indole production, Methyl Red-Voges Proskaver test, urea hydrolysis, arginine hydrolysis, casein hydrolysis) were carried out following standard methods of

Bergey's Manual of Systematic Bacteriology (Krieg, 1984; Sneath, 1986).

The bacterial communities isolated were identified up to generic level (Table.1). The generic representations among the heterotrophic bacterial isolates comprised Methylococcus, Pseudomonas, Aquaspirillum, Bacillus. Planococcus. Micrococcus, Streptococcus, Listeria, Lactobacillus, Sporosarcina and Sporolactobacillus. The dominance of Bacillus sp. (Fig.1) along with other gram positive forms like Planococcus (Fig.2) and Micrococcus in the isolates was conspicuous. The bacterial strains isolated from pond water and sediment indicated diverse occurrence of different bacterial genera. This is typical of the shallow freshwater fish ponds with allochthonous organic enrichment and active sedimentwater nutrient interactions (Ram et al., 1982; Qin et al., 1995; Zhang et al., 2002). The occurrence of other genera among the isolates may be attributed to the sources of application of different organic manures (Wolen and Miller, 1983; Guo Xianshen et al., 1984; Gijzen et al., 1987).

CONCLUSION

In the present investigation, an attempt was made to identify the bacterial genera associated with the nutrient cycling of both raw and processed organic manured carp culture fish ponds. Eleven bacterial species isolated from water and sediment media from organic manured carp cultured ponds with cow manure and biogas slurry comprised diverse bacterial strains of Methylococcus, Pseudomonas. Aquaspirillum, Bacillus, Planococcus, Micrococcus, Streptococcus, Lactobacillus, Sporosarcina Listeria. and Sporolactobacillus. Bacillus sp. (44.1%) along with other gram-positive forms like Planococcus sp. (14.3%) and Micrococcus sp. (10.7%) were the important microbial groups and their occurrence may be attributed organic to allochthonous enrichment and active sediment-water nutrient interactions.

Sl.No.	Genus	Occurrence,%
1	Methylococcus	1.2
2	Pseudomonas	7.1
3	Aquaspirillum	1.2
4	Bacillus	44.1
5	Planococcus	14.3
6	Micrococcus	10.7
7	Streptococcus	7.1
8	Lactobacillus	5.9
9	Listeria	2.4
10	Sporosarcina	3.6
11	Sporolactobacillus	2.4

 Table 1: Generic representation among bacterial isolates from organic manured fish ponds

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