academic publishers
INTERNATIONAL JOURNAL OF ARTIFICIAL INTELLIGENCE (ISSN: 2692-5206)
Volume 04, Issue 07, 2024
Published Date: 27-09-2024

MICROFLORA OF FISH, REVISED

Jumabayeva Sapura Narkhon kizi
+998975602001
Sapurajumabayeva@gmail.com
2nd year Master's student of the Faculty of Biology Karakalpak State University

Abstract. The results of numerous studies indicate that fish possess bacterial populations on or in their skin, gills, digestive tract, and light-emitting organs. In addition, the internal organs (kidney, liver, and spleen) of healthy fish may contain bacteria, but there is debate about whether or not muscle is actually sterile. Using traditional culture-dependent techniques, the numbers and taxonomic composition of the bacterial populations generally reflect those of the surrounding water.

Keywords: bacteria, fish, microflora, methods, digestive tract, gills, skin, population size, taxonomy, biodiversity.

INTRODUCTION

Traditionally, studies on fish-associated microorganisms involved culture-dependent techniques of dubious sensitivity, which highlighted only the bacteria (typically the aerobic heterotrophic bacterial component[1]) to the exclusion of eukaryotes. Anaerobic bacteria have been comparatively neglected[2,3,4,5] by culturists, possibly reflecting the need for more exacting techniques, although there is increasing evidence that such organisms occur in large numbers especially within the digestive tract of freshwater and marine fish[2]. More recently and in line with other studies of microbial biodiversity, emphasis has been placed on molecular-based culture-independent techniques, which have been generating some exciting data, and have revealed the presence of uncultured organisms including anaerobes[6].

MATERIALS AND METHODS

It is apparent that fish are continuously exposed to the microorganisms present in water and in sediment including the contaminants in sewage/faeces[1]. These organisms will undoubtedly influence the microflora on external surfaces, including the gills, of fish. Similarly, the digestive tract will receive water and food that is populated with microorganisms. Certainly, colonisation may well start at the egg and/or larval stage, and continue with the development of the fish[2]. Thus, the numbers and range of microorganisms present in the eggs, on food, and in the water, will influence the microflora of the developing fish. Also, it is recognised that, to some extent, it is possible to manipulate the microflora of the developing fish by use of prebiotics, i.e., nondigestible food ingredients that beneficially affect the host by stimulating growth[3] and probiotics, i.e., live microbial food supplements, which may colonise the digestive tract for short or prolonged periods[4]. This action may have benefit for the host, such as the moderation of fish diseases[5].

RESULTS AND DISCUSSION

Fishing enterprises use only gill nets and do not use other technologies and fishing gear, such as seines, trawls, etc. The technology used has very low productivity. Enterprises are still poorly equipped with boats and motors.

The main factors hindering development:

- Poor equipment for fisheries;

- The water level in lowland reservoirs is determined by irrigation needs, which prevents the successful breeding of commercial fish species;
- Insufficient conditions for storing and processing fish;
- Economic obstacles, i.e. lack of government funding and private investment in the industry. Lack of specialized credit lines.
- Poaching. As a rule, the fish catch is not registered in any way. Carp, asp, catfish, pike perch make up a significant part of poached catches. Poaching underestimates the fish resources of natural reservoirs;
- Lack of material and technical resources to increase the profitability of production.

From the published literature, it may be deduced that there are three likely scenarios for the fate of bacteria coming into contact with fish:

1. The organisms from the environment around the fish may become closely associated with andeven colonise the external surfaces of the fish. There may be accumulation of the organisms atsites of damage, such as missing scales or abrasions[6].
2. The organisms may enter the mouth with water[1] or food and pass through and/or colonise thedigestive tract[2].
3. The organisms coming into contact with fish surfaces may be inhibited by the resident microfloraor by natural inhibitory compounds present on or in the fish[3].

The overriding problem concerns whether or not it is possible to differentiate members of the indigenous (fish) microflora from transients, which could be in the water film around fish or in water/food within the digestive tract. This is a problem particularly with the culture-dependent approaches. Unfortunately, most publications do not address this issue. Yet this is not so unusual insofar as similar arguments have centred on the nature of the true microflora of other habitats, e.g., the distinction between microbial populations of the rhizoplane (root surface) vs. the rhizosphere (habitat around roots), and of the phylloplane (leaf surface) vs. the phyllosphere (habitat around leaves).

It is recognised that extraneous bacteria are capable of surviving in fish. For example, the faecal indicator organism, Escherichia coli, has been found to survive and even multiply in the digestive tract of rainbow trout (Oncorhynchus mykiss) after ingestion via contaminated food[4].

Research has focused on six principal aspects of the microbiology of fish:

- The microbiology of the surface (including gills)
- The populations in the digestive tract (an area of current interest particularly involving use ofmodern molecular-based culture-independent techniques)
- The possible presence of bacteria in muscle and the internal organs of healthy fish
- The microflora of eggs
- The presence and role of bacteria associated with the light-emitting organs, particularly of deep-sea fish
- The bacterial populations in food

As a simplification, publications have tended to emphasise either quantitative or qualitative aspects orthe supposed role of the organisms on/in fish. It is unusual for research articles to address more than one of these aspects.

CONCLUSION

Fish possess a diverse array of bacterial taxa, often reflecting the composition of the microflora of the surrounding water. It is argued that the role of many of these fish-associated bacteria is unclear, and future work should be directed at this aspect.

REFERENCES:

1. Montes, M., Perez, M.J., and Nieto, T.P. (1999) Numerical taxonomy of gram-negative, facultative anaerobic bacteria isolated from skin of turbot (Scophthalmus maximus) and surrounding water. Syst. Appl. Microbiol. **22**, 604–618.
2. Sakata, T., Sugita, H., Mitsuoka, T., Kakimoto, D., and Kadota, H. (1981) Microflora in the gastrointestinal tracts of fresh-water fish. 2. Characteristics of obligate anaerobic-bacteria in the intestines of fresh-water fish. Bull. Jpn. Soc. Sci. Fish. **47,** 421–427.
3. Kamei, Y., Sakata, T., and Kakimoto, D. (1985) Microflora in the alimentary tract of the

Tilapia: characteristics and distribution of anaerobic bacteria. J. Gen. Appl. Microbiol**.** **31**, 115–124.

4. Lee, S. and Lee, Y. (1995) Identification of intestinal microflora in rainbow trout. J. Microbiol. **33**, 273–277.
5. Gonzalez, C.J., Lopez-Diaz, T.M., Garcia-Lopez, M.L., Prieto, M., and Otero, A. (1999) Bacterial microflora of wild brown trout (Salmo trutta), wild pike (Esox lucius), and aquacultured rainbow trout (Oncorhynchus mykiss). J. Food Protect. **62**, 1270–1277.
6. Moran, D., Turner, S.J., and Clements, J.D. (2005) Ontogenetic development of the gastrointestinal microbiota in the marine herbivorous fish Kyphosus sydneyanus. Microb. Ecol. **49**, 590–597.