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The Gut Microbiome of Fish - A Review

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Abstract

The importance of gut microbiome in various function of host physiology, modulation of this microbiome is a possible strategy to reduce the emerging diseases in aquaculture industry. The gut microbiome not only reinforces the immune systems in fish but is itself shaped by several host-associated factors. Unfortunately, the majority of studies have focused upon the structure of fish gut microbiome providing little knowledge of effects of these factors distinctively and the immune functional potential of the gut microbiome. In this review, we have highlighted the recently gained insight into the diversity and functions of the fish gut microbiome. The literature reviewed indicated that the future research should shifted functional microbiomics to improve the maximum sustainable yield in aquaculture.

Introduction

The complex community of microorganisms inhabiting body sites in which surfaces and cavities are open to the environment is termed the microbiome; previously this was called the microflora or microbiome. Moreover, the epithelial surfaces of fish and all other vertebrates are colonized at birth by large numbers of microorganisms (microbiome) that are commensal or mutual relationships with their host (Sakata *et al.*, 1978). The majority of these microbes reside in the digestive tract, where they influence a broad range of host biological process.

The diversity of microbiome has been determined by increased access to next generation sequencing (NGS), a tool that is not reliant upon culture-based techniques, which often require previous information of target microbes. Currently, gut microbiome communities have been analyzed in over 145 species of teleosts from 111 genera, representing a varied range of physiology and ecology, often with similarities in bacterial composition between fish species, dominated by Bacteroidetes and Firmicutes. The gut microbiome of fish has accelerated for many reasons, as not only do teleosts group represent the most varied vertebrate group, they are also of significant economic importance, including in aquaculture system. Aquaculture now provides over 45% of fish-based food products Worldwide and influence of the aquaculture industry on teleost gut microbiome research is demonstrated by the research questions tackled with a clear bias towards salmonids (genera: *Oncorhynchus* and *Salmo*), carp (genera: *Hypophthalmichthys*, *Carassius*, *Cyprinus* and *Ctenopharyngodon*) and tilapia (genus: *Oreochromis*). Rapid growth of the aquaculture industry has led to mounting pressure to make it more sustainable (Naylor *et al.*, 2000).

The studies are to provide a scientific basis for developing effective strategies for manipulating gut microbial communities to promote animal health and improve aquaculture

production. The vast majority of these studies have focused on the bacterial communities and to a lesser extent yeast; very little information is available for the viral and protozoan populations in the gut of fish.

Fish Alimentary Canal

Fish biology varies greatly with differing life history, ecology and environmental factors. The philtre feeders, parasites and predators as well as herbivorous and carnivorous fish exist and each has an appropriately adapted digestive system. All fish alimentary canals begin with the buccal and pharyngeal cavities of the head gut. The gut can be loosely divided into the fore-gut, mid-gut and hind-gut which include various digestive organs. The mid gut is where the majority of digestion activity occurs and the pyloric caeca are thought to be organs acquired to produce a greater surface area for absorption. Gut length is loosely associated with diet and as a guide is three times longer than body length in herbivorous fish, one to three times in omnivores and approximately equal in carnivores (Bone *et al.*, 1995).

Development of the Gut Microbiome in Fish

Microbial colonisation of fish larvae originates from the eggs, the surrounding water and the first fish feed. Bacteria associated with fish egg that the dominating species included *Cytophaga*, *Flavobacterium*, and *Pseudomonas*. The initial colonising bacteria are accepted as species-specific with differences controlled by variation in binding glycoproteins on the egg surface (Larsen, 2014). In addition, the microbiome of the surrounding water bodies dictates what bacteria encounter the eggs and consequently have the opportunity to colonise. Upon hatching period, sterile larvae obtain in the chorion-associated bacteria, which become the first colonisers of the developing gastrointestinal tract (GIT). Subsequent inhabiting bacteria are acquired when the fish larvae begin to drink water to control osmoregulation and the microbiome then become further diversified through feeding. To begin, the GIT of newly hatched larvae tends to contain few bacteria. Interestingly, like in humans, it appears the diversity of bacteria increases as fish develop.

Structure of the Fish Gut Microbiome

The fish microbiome can be different, including parasites, fungi, yeasts viruses, and members of the Bacteria. Bacteria are the dominant microbiome of the fish intestine. Fish hind-gut microbial communities closely resemble those of mammals much more so than their surrounding environmental microbial communities. In mammals the dominant gut microbiome are anaerobes from the phyla of Bacteroidetes whereas Proteobacteria are the prominent microbial phyla found in the fish GIT.

Proteobacteria in addition to Bacteroidetes, comprise 90% of the fish intestinal microbiome of the different fish species.

The density, composition and function of the microbiome change in the different sections of the fish GIT. Furthermore, there is a distinction between the allochthonous and autochthonous communities. Allochthonous are the free living, transient microbiome associated with the digesta, whereas, autochthonous microbiome colonises the mucosal surface of the digestive tract and make up the core community. The density of viable aerobic and anaerobic bacteria usually ranges from 10^4 - 10^9 colony forming units (CFU) g^{-1} of intestinal content, respectively. This is notably lower than that of warm-blooded animals which are generally orders of magnitude higher.

Diversity of Fish Gut Microbiome

Studies on the gut microbiome of fish have found substantial intra and inter-species diversity. Trophical position relates natural diet with evolutionary development and marine fish fill many of these levels. In terms of investigating the relationship of gut microbial composition with trophical level, early studies included flatfish and salmon; however, there was also significant interest in herbivore species. Anaerobic bacteria species, phylum of Firmicutes and class of Clostridia have been repeatedly identified in the digestive tracts of herbivorous fishes. Gut microbial communities of fish in other trophic levels have less characteristic dominance when compared to herbivore species. However, one study comparing phylogenetically similar benthivore and planktivore freshwater species showed they contained different unique intestinal bacterial communities.

Historically, seasonal trends were reported in total bacterial counts recorded from gut samples from skate, *Raja* sp., and lemon sole plated on seawater agar. This study discussed that changes in plankton availability influenced the gut bacterial community in fish. The first study to directly investigate seasonal variation in gut microbiome in marine fish was by Hovda *et al.* (2012). The gut microbiome of adult Atlantic salmon was analyzed between August and June the following year, using 16S rRNA DNA sequencing. The water temperature varied between 5.5 and 18.8 °C during the experimental study period. Although some bacterial species were only recorded at some of the sample time points, overall the variation reported was not statistically significant. Contrarily, a more recent study on salmon did find a relationship between seasonal water temperature changes and shifts in gut microbial composition. Further research is necessary to find out the effects of seasonal variation and temperature changes on the gut microbiome of marine fish.

Conclusion

Fish are affected by several pathogenic microorganisms such as bacteria, virus, parasites and Fungi. These are often treated with antibiotics. We should be aware of the microbiome in gut, its characteristics, mode of growth and factors affecting the microbiome community in the gut for treat the pathogenic microorganisms to prevent the disease. The emerging concept of “forward microbiomics” that involves manipulating the gut flora to promote fish health finds important applications in aquaculture.

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