INTERNATIONAL JOURNAL OF AGRICULTURE & BIOLOGY
ISSN Print: 1560–8530; ISSN Online: 1814–9596
18F–071/201x/00–0–000–000
DOI: 10.17957/IJAB/15.0778
http://www.fspublishers.org

Review Article

Gastrointestinal Metagenomics of Fish: Methods, Research Advances and Applications

Bo Dong[1,3], Deng Deng[5], Yunhai Yi[2,3], Xiaomeng Zhao[2,3,4], Xinxin You[3,4] and Qiong Shi[2,3,4*]
[1]*Agro-Biological Gene Research Center, Guangdong Academy of Agricultural Sciences, Guangzhou 510006, China*
[2]*BGI Education Center, University of Chinese Academy of Sciences, Shenzhen 518083, China*
[3]*Shenzhen Key Lab of Marine Genomics, Guangdong Provincial Key Lab of Molecular Breeding in Marine Economic Animals, BGI, Shenzhen 518083, China*
[4]*BGI Academy of Marine Sciences, BGI Marine, BGI, Shenzhen 518083, China*
[5]*Shenzhen Alphafeed Co., Ltd, Shenzhen 518000, China*
[*]For correspondence: shiqiong@genomics.cn

Abstract

Fish microbiota function in fish nutrition and health, but research has been hindered by difficulties in culturing these microorganisms. New molecular techniques, like DDGE (Denaturation gradient gel electrophoresis) and FISH (Fluorescence in situ Hybridization), have produced limited detailed quantitative results. Next-generation sequencing based metagenomics and microarray offers more promise. These high throughput methods can obtain the overall genetic information within a microorganism community and there is no need to cultivate the individual microbes in advance. Metagenomics combines the sequencing of 16S rRNA genes and genomes of the sampled microbiota. We provide an overview of recent research advances in fish metagenomics and related applications. Many studies have already been done on individual fish species, but it is necessary to obtain a comprehensive profile of the microbiota of all fish species using metagenomics sequencing. © 2018 Friends Science Publishers

Keywords: Antimicrobial peptide; Fish; Gastrointestinal microbiota; Metagenomics; Next-generation sequencing; Probiotics

Introduction

Microorganisms are widespread within living organisms. However, most of the microorganisms cannot be cultured and are difficult to access and understand. Next-generation sequencing (NGS) and microarray techniques now make it easier to study the full range of microbial diversity. With the rapid development of metagenomic sequencing, we are now able to evaluate microbial communities, functional genes and their natural products.

Introduction to Metagenomics

The microbiota residing in an organism, especially in the gastro- and intestinal tract, are often viewed as equivalent to an integral organ. The gastrointestinal (GI) microbiota of fishes and vertebrates have been studied using various methods (culture independent or dependent). However, it is currently impossible to characterize over 70% of GI microbiota (Ringø and Olsen, 1999). This is mainly due to the impossibility of microbial culture using routine laboratory methods (Wu *et al*., 2012). Usually, only the predominant microorganisms are specified and the majority of the microbes remain unknown (Cardenas and Tiedje, 2008). Compared with the fish GI microbiome studies using a culture system, studies using metagenomics and 16S rRNA gene amplicon sequencing technologies are more likely to reflect overall community diversity (Hess *et al*., 2011; Wrighton *et al*., 2012). The phylum Fusobacteria occupy more than a half of the GI microbiota metagenomic data in captive carp, which could not be cultivated on synthetic media until recently (Sakata *et al*., 1981; Van Kessel *et al*., 2011).

Metagenomics is the study of genetic material recovered directly from environmental samples by molecular and bioinformatic techniques (Fig. 1, Thomas *et al*., 2012). These approaches avoid the prolonged procedures of cloning in expression vectors (DeSantis *et al*., 2006) by harvesting thousands of reads for one microbial sample in one run cycle. This allows the discovery of new microorganisms especially those unculturable on synthetic media (Fakruddin *et al*., 2013). Thus we can now conduct in-depth analysis of microbial communities (Xing *et al*., 2013). With the rapid development of NGS sequencing, a large amount of metagenomic data is now available to researchers (Wang and Jia, 2016).

To cite this paper: Dong, B., D. Deng, Y. Yi, X. Zhao, X. You and Q. Shi, 201x. Gastrointestinal metagenomics of fish: methods, research advances and applications. *Int. J. Agric. Biol*. 00: 000-000

Metagenomics combines sequencing of the 16S rRNA genes and genomes of sampled microbiota to generate taxa diversity and species structure within the examined microbiome (Chen and Pachter, 2005). Unlike genomics dealing with the genome sequencing of individual species, metagenomics studies the overall 16S rDNA and genomic sequences of microorganisms in samples.

The metagenomic approach by NGS sequencing aims to solve problems using integrated data analysis of multiple bacteria strains (Chen and Pachter, 2005). The main characteristic of metagenomics by NGS is that it typically does not require existing sequence information from the community of interest (Roh *et al*., 2010), with which we can uncover new genes, pathways, taxa, and encoded functionality further. However, there are some challenges that require consideration, including the sampling choice, sequencing methods, assembly and coverage. Also, many microorganisms are still unknown and many host genomes are unavailable. Metatranscriptomics was developed to compensate for the shortcomings of metagenomics by NGS in detection of the expression status of microbial genes, microbial community activities and functions, as well as discovery of novel genes and regulatory elements (Wu *et al*., 2015).

Microarray analysis is a type of metadata analysis whose potential experimental outcome is defined in a specific range before analysis. The experimental results of microbial community from samples originate from the predefined probes fixed on array plates (Roh *et al*., 2010). The main feature of metagenomics by microarray is that it requires existing sequence information and does not produce novel sequence data. This is because all sequence tags for the query are predesigned (He *et al*., 2010). DNA arrays, protein arrays and the classic quantitative PCR, are closely formatted methods.

NGS sequencing and microarray detection are two widely used representative metagenomic technologies. However, each category possesses advantages and deficiencies in operation. An attractive feature of NGS is that it is useful for novel gene discovery and bacteria exploitation (Hess *et al*., 2011; Qin *et al*., 2012; Wrighton *et al*., 2012). However, contamination from the host and the environment is frequent in sample preparation, resulting in a low utilization rate of sequencing data and a waste of sequencing effort in NGS analysis.

In DNA microarray, microbial detection and microbiome community analyses are occasionally implemented (He *et al*., 2011). rRNA genes are usually the targets of phylogenetic gene arrays and these are useful for distinguishing specific taxa and studying the phylogeny of microorganisms. The representative phylogenetic gene arrays are PhyloChip (Paliy *et al*., 2009; Hazen *et al*., 2010), which can detect many known microbial groups. The functional gene array, GeoChip, has recently been developed (Fig. 2). It targets functional gene categories for biogeochemical, ecological and environmental analyses (He *et al*., 2010; Lu *et al.*, 2012). It is also a potentially useful tool for fishery projects.

GeoChip studies have been applied without greatly varying the DNA amplification. Pure cultures, mixed cultures, and environmental samples are identified by hybridization signal intensities (Wu *et al*., 2006). In addition, technical reproducibility of microarrays is less affected by inadequate random sampling than in NGS. One main defect of the microarray technologies is that it is not able to discover novel genes, taxa, and regulatory elements (Zhou *et al*., 2015).

In this review, we mainly focus on metagenomic studies of the fish GI tract with NGS sequencing since this has been extensively reported. The GeoChip-based DNA array has also been employed in our labs for a Chinese program (Fish-M1K), which aims at establishing a comprehensive microbiota gene set from a metagenomic study on > 1,000 fish species.

Research Advances in Fish Metagenomics

Teleost fishes possess the largest taxonomic and ecological diversity among vertebrates but research on their GI microbiota and functional metagenomics has been delayed compared to studies on terrestrial vertebrates (Banerjee *et al*., 2013). In contrast to the utilization of metagenomics on the GI microbiota in humans (Qin *et al*., 2012) and other vertebrates (Kostic *et al*., 2013), fish metagenomics studies have already been applied to microorganisms in gills (Kostic *et al*., 2013), skin (Lokesh and Kiron, 2016) and mucosa (Gatesoupe *et al*., 2016). However, the microorganisms in the digestive tract, which is also called the GI microbiota, still constitutes the majority of microbiota residing in fish and have a special influence on the health and growth of fish.

The intestinal morphologies of fishes show great variation (Clements and Raubenheimer, 2006). Some species have a delineated true stomach or hindgut chamber, while other species lack a delineated stomach or intestine. There are distinct microorganism populations with different metabolic functions in defined regions of fish alimentary tracts (Ye *et al*., 2013). Among the different sections of the fish GI tract, the hindgut is often used in analyses of the fish gut microbiome. This is because it is more likely that there are targeted bacterial symbionts related to digestion and fewer environmental bacteria compared to the anterior region of the intestine (Zhou *et al.*, 1998).

It is believed that each fish species possesses "core essential GI microbiota" (Shade and Handelsman, 2012). Host-derived specific pressures play an important role in determining GI bacteria in fishes and thus fishes have a local microbiota mainly dependent on the host fish (Sakata *et al*., 1981). Other studies have noted that fish GI communities are mostly occupied by indigenous organisms that are underrepresented in the environment (Cahill, 1990). Metagenomic analyses indicate that fish GI microbial communities are more similar to those of mammals,

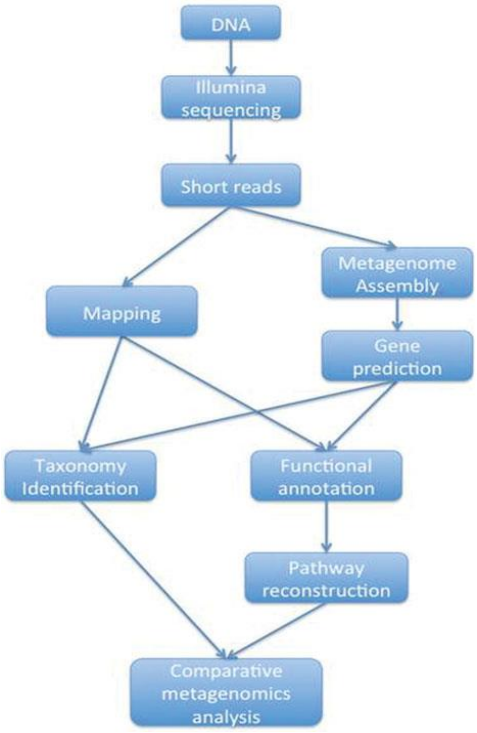

Fig. 1: Standard protocol for NGS-based metagenomics projects at BGI

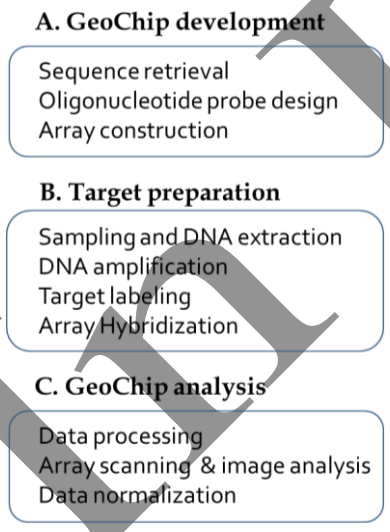

Fig. 2: Overview of the GeoChip-based DNA microarray (Zhou *et al*., 2010)

particularly in the amount of Proteobacteria, Firmicutes and Bacteroidetes (Sullam *et al*., 2012). Therefore, the GI microbiota composition of fish does not simply reflect the microorganisms in their habitat but develops from selective pressures within the gut such as species-specific behavior, immunity and metabolism (Ye *et al*., 2013; Larsen *et al*., 2014).

After long coevolution with the fish host, the fish gut microbiota assists in food digestion and provision of essential nutrients (Turnbaugh *et al*., 2006; Ley *et al*., 2008; Borsodi *et al*., 2017). The fish GI tract harbors various bacteria, archaea, viruses and eukaryotic microorganisms, which are collectively called the GI microbiota. In fish, they are primary protective barriers and occur in the gut with both beneficial and opportunistic pathogenic microorganisms. In addition to defense against pathogens, the GI microbial community facilitates the proliferation of intestinal epithelium, digestion of complex carbohydrates, modulation of the immune system, regulation of the dietary energy intake, and even the generation of secondary metabolites such as vitamins (Sugita *et al*., 1993; Flint *et al*., 2008; Dawood *et al*., 2016b). The cellulolytic bacteria in cyprinid fish intestines function in the digestion of cellulose (Wu *et al*., 2015). The GI microbiota of fish harbor many opportunistic pathogens and the GI tract is open for pathogen invasion (Kim *et al*., 2007; Roeselers *et al*., 2011). For this reason, understanding the function and the composition of GI microbial communities is crucial for health management in aquaculture fish.

The internal and external factors affecting the composition of fish GI microbial communities include developmental stage, gut structure, diet composition, health condition, habitat, water temperature and salinity, rearing conditions and host genotypes (Nayak, 2010; Sullam *et al*., 2012; Ni *et al*., 2014). Among the external factors, host diet is a well-known factor determining microbiota composition (Varma *et al*., 2014). Therefore, it is crucial to explain the relationship between host diet and the functional significance of fish intestinal communities by using the metagenomic approach.

We summarize recent research results on fish microbiome (Table 1) in which high throughput methods like 16S rDNA, metagenomics, and microarray were used. The metagenomics studies were carried out on fish species worldwide including freshwater and saltwater fishes like carp, rainbow trout, Siberian sturgeon, Atlantic salmon, catfish, Atlantic cod, reef fishes, and Antarctic notothenioids. Interestingly, the species attracting the most attention and publications are carps, including grass carp, silver carp, Prussian carp, and Jian carp. This is consistent with the large production and economic value of these cyprinid species in Asia (Tsuchiya *et al*., 2008; Han *et al*., 2010; Van Kessel *et al*., 2011; Li *et al*., 2013; Ye *et al*., 2013; Ni *et al*., 2014; Kashinskaya *et al*., 2015; Li *et al*., 2015; Wu *et al*., 2015; Zhao *et al*., 2014).

In recent studies on fish metagenomics, most microbiome samples were collected from the GI tract. The GI harbors most microorganisms in fishes and GI tract microbiomes are directly related to the metabolism and pathogens of the fish host. In some studies (Ringø *et al*., 2006; Davis *et al*., 2016), samples were obtained from larvae to determine the specific colonization processes that happen during the transition from the sterile larvae to the adult fish.

Table 1: Fish microbiome research by high throughput approaches

Species	Sample source	Method
Common carp (*Cyprinus carpio*); grass carp (*Ctenopharyngodon idellus*); transgenic common carp (*Cyprinus carpio*); grass carp (*Ctenopharyngodon idellus*); crucian carp (*Carassius cuvieri*); bighead carp (*Hypophthalmichthys nobilis*); juvenile Jian carp (*Cyprinuscarpiovar. Jian*); Prussian carp (*Carassius gibelio*); silver carp (*Hypophthalmichthys molitrix*)	GI tract pond water and sediment; ingested food (Han *et al*., 2014)	16S rDNA (Wu *et al*., 2015; Ye *et al*.,2013; Tsuchiya *et al*., 2008; Han *et al*., 2010; Van Kessel *et al*., 2011; Li *et al*., 2013; Li *et al*., 2015; Zhao *et al*., 2014; Ni *et al*., 2014; Kashinskaya *et al*., 2015); Pyrosequencing; gene fingerprinting methods (such as DGGE); Metagenomics (Ni *et al*., 2014; Kashinskaya *et al*., 2015); microarray (Ni *et al*., 2014); Metatranscriptomics (Wu *et al*., 2015)
Atlantic salmon (*Salmo salar*)	Skin mucus (Lokesh and Kiron, 2016)	16S rRNA gene
rainbow trout (*Oncorhynchus mykiss*)	GI tract (Kim *et al*., 2007; Ingerslev *et al*., 2014; Pond *et al*., 2006; Mansfield *et al*., 2010; Gonçalves and Gallardo-Escárate, 2017)	16S rRNA pyrosequencing; DGGE
zebrafish *(Danio rerio)*	GI tract (Roeselers *et al.*, 2011*;* Cantas *et al*., 2012*;* Rawls *et al.*, 2004) Larvae (Davis *et al*., 2016)	16S rDNA gene sequencing; microarray (Rawls *et al*., 2004)
Atlantic cod *(Gadus morhua)*	Larvae (Ringø *et al*., 2006)	PCR-DGGE analysis
Atlantic cod *(Gadus morhua)*	GI tract	454 sequenced 16S rRNA library (Star *et al*., 2013)
Siberian sturgeon *(Acipenser baerii)*	GI tract	454-pyrosequencing of the 16S rRNA gene (Geraylou *et al*., 2013)
catfish *(Panaque nigrolineatus)*	GI tract	16S rDNA sequence (Tsuchiya *et al*., 2008)
catfish *(Panaque nigrolineatus)*	Faeces (Di Maiuta *et al.*, 2013)	16S rRNA
reef fish *(Acanthurus nigricans, Chlorurus sordidus, Lutjanus bohar)*	Feces and distal gut contents (Smriga *et al*., 2010)	Denaturing gradient gel electrophoresis profiles of 16S rRNA-
Antarctic notothenioid	GI tract	16s cluster

The sample sources varied greatly, including wood eating catfish feces (Di Maiuta *et al*., 2013), three coral reef fish GI contents (Smriga *et al*., 2010), and salmon skin mucus during the transition from freshwater to saltwater (Lokesh and Kiron, 2016).

Most previous microbiome studies on fish involved a high throughput metagenomic approach, especially 16S rDNA sequencing (Table 1). Many of these studies were combined with culture independent techniques, such as DDGE (Denaturation gradient gel electrophoresis) and FISH (Fluorescence in situ Hybridization). Only a few whole metagenomic studies have been reported. One of these was used to decipher the biosynthesis and metabolism pathways of carbohydrates, amino acids and lipids in ryegrass fed grass carp (Ni *et al*., 2014). In this research, the microarray method was also applied to detect the changing mode of metabolic products. Another study dealt with the role of the GI microbiome on metabolizing cellulose using metatranscriptomics (Wu *et al*., 2015). A comparison study was done on Prussian carp using both metagenomics and 16S sequencing. This study indicated that metagenomics is more accurate in taxonomic assignment than 16S analysis only (Kashinskaya *et al*., 2015). Microarray, including GeoChip and PhyloChip, are additional high throughput approaches but they have not been used in previous studies of fish metagenomics. However, their merits would be useful in future fish microbiome studies. Microarray will complement the 16S and NGS-based metagenomic approaches with its beneficial aspects for microbiome research.

Factors Shaping GI Microbiota and Core Microbiome

The gut microbiome of fish varies considerably from the microbiome of other vertebrates and the microflora in water and soil (Sullam *et al*., 2012). Both trophic level and salinity have great impact on its composition (Wong and Rawls, 2012; Li *et al*., 2015). In addition, animal feed, which is the direct source of animal gut microorganisms, plays a vital role in the genesis of GI microbiota, but it has variable effects on different animals (Geraylou *et al.*, 2013; Wong *et al*., 2013; Baldo *et al.*, 2015). The bacteria identified in gut microbiome can reflect the food preference of the host (Ye *et al*., 2013). Prey items of the three-spined stickleback carry microbiota that can influence the host gut microbiome, but the host genotype has a relatively greater impact (Smith *et al*., 2015). In two freshwater fish species, the relationship of gut microbiome diversity and dietary diversity was inversely correlated (Bolnick *et al*., 2014); even in Trinidadian guppies, the effect of diet on GI microbiota was so small to be ignored (Sullam *et al*., 2015a).

Other important factors determining fish GI microbiota include physiological condition of the fish and environmental components. In silver carp, components of the gut microbiome were geographically and temporally dependent (Ye *et al*., 2013). Dramatic changes of the fish GI microbiota can occur when habitats change including shifts from natural to man-made environments (Cantas *et al*., 2012; Clements *et al*., 2014; Sullam *et al*., 2015b).

Although the composition and structure of fish GI microbiomes are now better understood, the factors shaping these GI microbiomes require further study. Many factors have substantial influence on the composition of GI microbiota in vertebrates, including host genetics, environment and nutrition, but the host genetic background and the house keeping physiological function of GI microbiota play decisive roles in selecting for the essential

(core) microbial taxa. As core GI microbiota are present in all GI communities with individuals of one species, it has been an interesting goal in this realm (Turnbaugh *et al*., 2007). In research on zebrafish, a core microbiome was determined by comparing laboratory raised and wild fish. The data indicated that this species of fish harbors a core GI microbiome as do other vertebrates (Roeselers *et al.,* 2011). This finding was supported by a reciprocal microbiota transplant experiment between zebrafish and mice (Rawls *et al*., 2006).

However, there are many teleost species and the ecology within the fish GI community can be more complex (Shade and Handelsman, 2012). It is more difficult to find a common core microbiome in fishes than in mammals (Tap *et al*., 2009; Turnbaugh and Gordon, 2009). In a study on teleost GI microbiota (Roeselers *et al*., 2011), comparisons of GI microbiome between wild and domestic zebrafish populations revealed significant differences. A total of 21 shared operational taxonomic units (OTUs) are considered to be the core community present in all fish. In invasive carp species (Eichmiller *et al*., 2016), the core GI microbiome shared by laboratory-reared and wild individuals comprised up to 40% OTU abundance, while there were merely five shared OTUs, thus interpreting their critical role. Some researches suggested that the genetic background of the fish host plays a decisive role in determining GI microbial communities (Roeselers *et al*., 2011). Other studies revealed that the living environment is the primary driver for construction of GI microbiota population structure (Eichmiller *et al*., 2016), and some authors indicate that the main influence on GI microbiome of species is nutrition or trophic level (Liu *et al*., 2016). In fish-associated microbiomes, there are more similarities among freshwater fishes, regardless of their phylogenetic relationship to fish in marine environments (Sullam *et al*., 2012). *Aeromonas sp.* was predominant in the GI microbiota of freshwater fishes, while *Vibrio* spp. was the largest group in the GI microbiota of marine fish species. The evolutionary origin of the GI microbiota was not likely relevant to their roles in the gut (Sullam *et al*., 2012).

If a core microbiome does exist among fish species across distinct environments and distant phylogenetic relationship (Roeselers *et al*., 2011; Hennersdorf *et al*., 2016), the factors shaping the GI microbiota needs further investigation. Studies should include evolutionary forces dedictated by host genetics, gut physiology and bacterial symbionts. If this hypothesis is true, it would be easier to manipulate the GI bacterial communities, and this would be helpful to promote fish health and yields in aquaculture operations. Members of the phyla Proteobacteria, Firmicutes, Bacteroidetes, Actinobacteria, Verrucomicrobia and Fusobacteria have been shown to occupy the fish GI microbiome (Sullam *et al*., 2012; Llewellyn *et al*., 2014). Proteobacteria, Fusobacteria and Firmicutes had the greatest abundance in the GI microbiome of most fish species (Hennersdorf *et al*., 2016; Eichmiller *et al*., 2016).

Applications of Metagenomics: Antimicrobial Peptides (AMPs) and Probiotics

The fish GI microbiota has probably coevolved with the host for millions of years. The microbiota competes with the host for common resources, but it is an integral component of the host. The GI tract also harbors opportunistic pathogens within the gut microbiota and so it is a potential pathway for pathogen invasion (Wu *et al*., 2010; Roeselers *et al*., 2011).

The autochthonous bacteria among the gut microbiota are more likely to confer health benefits, like robust temporal stability, than allochthonous or non-fish bacteria (Fjellheim *et al*., 2010; Sun *et al*., 2010, 2015). Therefore, the beneficial autochthonous GI microbiota or their bacteriocin products warrant further investigation in farmed fish because of the potential significance of GI microbiota for disease control in aquaculture (Ringø *et al*., 1995; Ray *et al.,* 2012; Llewellyn *et al*., 2014; Ringø and Song, 2016). Diverse probiotic strains of bacteria within the genera *Lactobacillus, Bacillus, Citrobacter, Enterobacter, Streptococcus* (Ghosh *et al.,* 2010; Ray *et al*., 2010; Khan and Ghosh, 2012; Ray *et al.,* 2012) and yeasts (*Pichia kudriavzevii*, *Candida tropicalis, C. parapsilosis and C. rugosa*) (Mandal and Ghosh, 2013; Banerjee and Ghosh, 2014; Das and Ghosh, 2014) have been identified or characterized from the GI tracts of Indian major carp, exotic carp species and other teleosts. *Lactobacillus* comprises over 50 species of lactic acid bacteria, which is reported to stimulate the host immune system and fight against intestinal pathogens with their antimicrobial activity (Kemgang *et al.,* 2014). *Pediococcus acidilactici* can balance microecology by acid production (Zacharof and Lovitt, 2012). *Bacillus subtilis* is widely accepted in agriculture and food products as a form of microecologics (Field *et al*., 2015).

Bacteria are the most predominant members of the probiotic strains of gut microbiota. They use different mechanisms to modulate the microbial community and improve the microbial balance and maintain the robust temporal stability (Mohapatra *et al.,* 2013). One such mechanism is the production of bacteriocins to antagonize closely related competing bacteria *in vivo*. Bacteriocins are AMPs ribosomally synthesized both in Gram-negative and Gram-positive bacteria (Nes *et al.,* 2007). There are two kinds of bacteriocins with different antimicrobial spectra. One has relatively narrow spectra, including most bacteriocins targeting species only related to their producers. Another type, with a wider spectrum, includes the lactococcal bacteriocin nisin, which has inhibitory activity on pathogenic or problematic species of *Staphylococcus* and *Listeria* (Jack *et al*., 1995; Nes and Johnsborg, 2004; Arqués *et al.,* 2015). Bacteriocins have no effects on their producers with protection mechanisms or on other beneficial cells and eukaryotic cells, while they are active against pathogenic bacterial strains (Cotter *et al*., 2013).

Hence, they are promising components of antibiotics for the prevention and control of diseases in aquaculture.

Since bacteriocins and bacteriocin-like peptides are ribosomally translated by gene regulation, they are good candidates for metagenome data mining (Donia *et al.,* 2014; Walsh *et al*., 2015). The sequencing data facilitated by NGS has enabled high throughput *in silico* mining of putative antimicrobial substance genes and probiotics that modulate the gut microbiota (Erejuwa *et al.,* 2014; Walsh *et al*., 2014), or can help moderate the increasing risk to host health caused by antibiotic resistance. Therefore, research on the abundance and categories of bacteriocins encoded in the fish GI microbiome could estimate beneficial or harmful microorganism in the GI community and identify the key organisms that help maintain the integral composition and union. Using NGS, we can study probiotic strains by homology-based searches with the antimicrobial peptide sequences obtained from the metagenome data.

In the commercial fishery industry, unfavorable conditions can decrease production and increase the rate of infectious diseases (Bondad-Reantaso *et al*., 2005). However, the resistance that has developed from the overuse of antibiotics (Romero *et al*., 2012; Lyapparaj *et al*., 2013) requires discovery of antibiotic alternatives, such as phage therapy, immunostimulants, plant extracts, pro-, pre- and symbiotic concepts, and bacteriocins (Balcázar *et al*., 2006; Ringø *et al.,* 2014; Newaj-Fyzul and Austin, 2014; Ringø *et al*., 2016). AMPs or bacteriocins isolated from the GI tracts of Japanese coastal fish (Sugita *et al.,* 1998) and Indian major carp (*Labeorohita*) (Giri *et al*., 2011), which were produced by bacilli, are possible alternative antibiotics to control intestinal pathogens in fish (Ghanbari *et al.,* 2013). The mortality of fish challenged with a virulent strain of *Aeromonas salmonicida* was reduced by oral delivery of *Lactobacillus rhamnosus* (Nikoskelainen *et al*., 2001). Because the healthy fish gut is resilient and dynamic, the microbiota composition may not be affected by bacteriocinogenic microbes, but at lower taxonomic levels, significant changes were observed.

In this post genomic era, we need greater detection of probiotics and AMPs in the reservoir of GI microbiota in fish species of economic value, and we need to integrate bioinformatics data from different levels (gene, metagenome, peptide, strain, microbiota, literature mining). We recently identified 5 AMPs in the metagenome of the grass carp GI tract (Dong *et al.,* 2017) and found lactococcin 972, pediocin, aureocin-like bacteriocins and subtilosin A. To confirm strains producing them, 16S rDNA analysis was used by bacteriocinogenic microbiota. We demonstrated that many commensal microorganisms in grass carp, especially three species of *Lactococcus* (*L. raffinolactis, L. lactis, L. garvieae*), and many members of *Streptococcus, Bacillus, Lactobacillus* and *Enterococcus*, were potential probiotics for grass carp, as they were closely related to those characterized probiotic strains already used as microecologics (Mansfield *et al.,* 2010).

NGS accelerates the discovery and development of novel AMPs and potential probiotics in the GI. Traditionally, purified bacteriocins are usually acquired in a case by case fashion (Zendo *et al.,* 2008). Now the developed genome mining bioinformatics tools, including the Bacteriocin Operon and gene block Associator (BOA; Walsh *et al*., 2017), Hidden Markov Model (HMM) (De Jong *et al.,* 2010) and BAGEL2 (Scheffler *et al*., 2013), are employed to discover functional AMPs or bacteriocin genes (Li *et al.,* 2016). The high throughput and trans-omic approach would be beneficial to determine the bacteriocins and bacteriocinogenic microbes that exist in fish GI. These are also the subjects of metagenomics studies. In order to assess the antimicrobial potency of a bacterial strain, the characterization of the bacteriocin-coding gene is indispensable. Bacteriocinogenic microbiota are a valuable resource for exploring potential probiotics (Więckowicz *et al.,* 2011).

Probiotics, containing living beneficial bacteria, have been widely used as animal feed additives. They can adhere to the intestinal epithelial cells, stimulate gut mucosal immune tissues and induce cellular or humoral immune responses (Guarner *et al.,* 2010; Neu, 2014). Fish intestinal microbiota have maintained a balance with the mucosa immunity. This protects fish health and inhibits colonization by foreign pathogenic strains. However, when external adverse factors like deterioration of the water quality or a decreased oxygen level happen, the balance will be upset and enable pathogens to rapidly grow, translocate and infect other fish organs. Hence, addition of probiotic microbiota to restrain proliferation of pathogens and adjust the immune functions of fish intestines is important to maintain healthy conditions. This should provide economic returns to the fish aquaculture industry and the side effects of using chemical products, including antibiotics and chemotherapeutics, could be minimized (Cerezuela *et al.,* 2013). Probiotic supplements consisting of multi-species components could be more efficient than those containing only one species or strain (Dawood *et al*., 2016a).

Many commercial probiotic products do not provide effective or stable results. This may be due to the inappropriate selection or application of the probiotics. Many probiotic strains are isolated from the environment or endotherm rather than from a fish digestive tract. They are thus incapable of colonizing in the fish digestive tract or only capable of colonizing for a short time. The profile and function of microbiota in the fish digestive tract have not been thoroughly studied, and the composition and distribution of beneficial and pathogenic microbiota are not well known. Hence, the successful application of probiotics in fish farming has been hindered. For example, the probiotics in use may share no identical colonization sites with the targeted pathogens, and they are therefore ineffective.

The fish gastrointestinal microbiota is an important resource for screening potential probiotics for cultured fish

species. We must determine the composition, distribution and function of microbiota in fish digestive tract. The metagenomic approach is the best way to achieve this goal. We initiated the China Fish-M1K program to sequence colonizing metagenomes from 1,000 fish species. It will be completed within 5 years with help from the Chinese Academy of Fishery Sciences using a combination of NGS, GeoChip and 16S rDNA methods. Like our previous Fish-T1K Project (Sun *et al.*, 2016) and China Aquatic 10-100-1,000 Genomics Program (Liu *et al.*, 2017), the Fish-M1K Program will involve international collaboration from both academic and commercial organizations.

Concluding Remarks

Fish metagenomics is a rapidly developing field that has been advanced by high throughput sequencing technology. Community profiles of the GI microbiota in many fish have been documented, but understanding of their functions in digestion and immunity, as well as the causation of intraspecific composition variations and interspecific differences have not been clarified.

Many studies have been performed on individual fish species to characterize the profiles of GI-related microbiota. However, describing the microbiota of the more than 25,000 teleost fish species living in many different environments will require substantially more research than what has already been performed. Prior to designing strategies to manipulate the microbiota, a more in-depth understanding of how this system is organized, how it is influenced and how it affects fish health will be required. These aspects are not clearly understood in fish. It is necessary to set up a unitary and comprehensive project to normalize the fish metagenomics searches, including sampling, shipment, sample storage, analytic pipelines and data networks. This will be useful for comparison of metadata across species and geographic locations, and building an international platform for fish metagenomics research.

Acknowledgements

This work was supported by National Natural Science Foundation of China (No. 31370047) and Shenzhen Special Program for Future Industrial Development (No. JSGG20141020113728803).

References

Arqués, J. L., E. Rodríguez, S. Langa, J. M. Landete, and M. Medina, 2015. Antimicrobial activity of lactic acid bacteria in dairy products and gut: effect on pathogens. *BioMed Res. Int.*, 2015, 584183

Balcázar, J.L., I. de Blas, I. Ruiz-Zarzuela, D. Cunningham, D. Vendrell and J.L. Múzquiz, 2006. The role of probiotics in aquaculture. *Vet. Microbiol*., 114: 173–186

Baldo, L., J.L. Riera, A. Tooming-Klunderud, M.M. Albà and W. Salzburger, 2015. Gut microbiota dynamics during dietary shift in Eastern African cichlid fishes. *PLoS One*, 10: e0127462

Banerjee, G., A.K. Ray, F. Askarian and E. Ringø, 2013. Characterisation and identification of enzyme-producing autochthonous bacteria from the gastrointestinal tract of two Indian air-breathing fish. *Benef. Microbiol.*, 4: 277–284

Banerjee, S. and K. Ghosh, 2014. Enumeration of gut associated extracellular enzyme-producing yeasts in some freshwater fishes. *J. Appl. Ichthyol*., 30: 986–993

Bolnick, D.I., L.K. Snowberg, P.E. Hirsch, C.L. Lauber, R. Knight, J.G. Caporaso and R. Svanbäck, 2014. Individuals' diet diversity influences gut microbial diversity in two freshwater fish (threespine stickleback and Eurasian perch). *Ecol. Lett.*, 17: 979–987

Bondad-Reantaso, M.G., R.P. Subasinghe, J.R. Arthur, K. Ogawa, S. Chinabut, R. Adlard, Z. Tan and M. Shariff, 2005. Disease and health management in Asian aquaculture. *Vet. Parasitol.*, 132: 249–272

Borsodi, A.K., A. Szabó, G. Krett, T. Felföldi, A. Specziár and G.C. Boros, 2017. Gut content microbiota of introduced bigheaded carps (*Hypophthalmichthys* spp.) inhabiting the largest shallow lake in Central Europe. *Microbiol. Res.*, 195: 40–50

Cahill, M.M., 1990. Bacterial flora of fishes: a review. *Microbiol. Ecol.*, 19: 21–41

Cantas, L., J.R.T. Sørby, P. Aleström and H. Sørum, 2012. Culturable gut microbiota diversity in zebrafish. *Zebrafish*, 9: 26–37

Cardenas, E. and J.M. Tiedje, 2008. New tools for discovering and characterizing microbial diversity. *Curr. Opin. Biotech.*, 19: 544–549

Cerezuela, R., J. Meseguer and M.Á. Esteban, 2013. Effects of dietary inulin, *Bacillus subtilis* and microalgae on intestinal gene expression in gilthead seabream (*Sparus aurata* L.). *Fish Shellf. Immunol*., 234: 843–848

Chen, K. and L. Pachter, 2005. Bioinformatics for whole-genome shotgun sequencing of microbial communities. *PLoS Comput. Biol.*, 1: e24

Clements, K.D. and D. Raubenheimer, 2006. Feeding and nutrition. *In: The Physiology of Fishes*, pp: 47–82. David, H.E. and J.B. Claiborne (eds.). CRC press, New York, USA

Clements, K.D., E.R. Angert, L. Montgmery and J.H. Choat, 2014. Intestinal microbiota in fishes: what's known and what's not. *Mol. Ecol.*, 23: 1891–1898

Cotter, P.D., R.P. Ross and C. Hill, 2013. Bacteriocins-a viable alternative to antibiotics? *Nat. Rev. Microbiol*., 11: 95–105

Das, P. and K. Ghosh, 2014. The presence of phytase in yeasts isolated from the gastrointestinal tract of four major carps [*Labeo rohita* (Hamilton, 1822), *Catla catla* (Hamilton,1822), *Cirrhinus mrigala* (Hamilton, 1822), *Hypophthalmichthys molitrix* (Valenciennes,1844)], climbing perch [*Anabas testudineus* (Bloch, 1792)] and Mozambique tilapia [*Oreochromis mossambicus* (Linnaeus, 1758)]. *J. Appl. Ichthyol*., 30: 403–407

Davis, D.J., E.C. Bryda, C.H. Gillespie and A.C. Ericsson, 2016. 16S rRNA amplicon sequencing dataset for conventionalized and conventionally raised zebrafish larvae. *Data Brief*, 8: 938–943

Dawood, M.A., S. Koshio, M. Ishikawa, M. El-Sabagh, M.A. Esteban and A.I. Zaineldin, 2016a. Probiotics as an environment-friendly approach to enhance red sea bream, *Pagrus major* growth, immune response and oxidative status. *Fish Shellf. Immunol*., 57: 170–178

Dawood, M.A., S. Koshio, M. Ishikawa, S. Yokoyama, M.F. El Basuini, M.S. Hossain, T.H. Nhu, S. Dossou and A.S. Moss, 2016b. Effects of dietary supplementation of *Lactobacillus rhamnosus* or/and *Lactococcus lactis* on the growth, gut microbiota and immune responses of red sea bream, *Pagrus major*. *Fish Shellf. Immunol.*, 49: 275–285

De Jong, A., A.J. van Heel, J. Kok and O.P. Kuipers, 2010. BAGEL2: mining for bacteriocins in genomic data. *Nucl. Acids Res*., 38: 647–651

DeSantis, T.Z., P. Hugenholtz, N. Larsen, M. Rojas, E.L. Brodie, K. Keller, T. Huber, D. Dalevi, P. Hu and G.L. Andersen, 2006. Green genes, a chimera-checked 16S rRNA gene database and workbench compatible with ARB. *Appl. Environ. Microbiol.*, 72: 5069–5072

Di Maiuta, N., P. Schwarzentruber, M. Schenker and J. Schoelkopf, 2013. Microbial population dynamics in the faeces of wood-eating loricariid catfishes. *Lett. Appl. Microbiol*., 56: 401–407

Dong, B., Y. Yi, L. Liang and Q. Shi, 2017. High throughput identification of antimicrobial peptides from fish gastrointestinal microbiota. *Toxins*, 9: 266

Donia, M.S., P. Cimermancic, C.J. Schulze, L.C.W. Brown, J. Martin, M. Mitreva, J. Clardy, R.G. Linington and M.A. Fischbach, 2014. A systematic analysis of biosynthetic gene clusters in the human microbiome reveals a common family of antibiotics. *Cell*, 158: 1402–1414

Eichmiller, J.J., M.J. Hamilton, C. Staley, M.J. Sadowsky and P.W. Sorensen, 2016. Environment shapes the fecal microbiome of invasive carp species. *Microbiome*, 4: 44

Erejuwa, O.O., S.A. Sulaiman and M.S.A. Wahab, 2014. Modulation of gut microbiota in the management of metabolic disorders: the prospects and challenges. *Int. J. Mol. Sci*., 15: 4158–4188

Fakruddin, M., K.S.B. Mannan and S. Andrews, 2013. Viable but nonculturable bacteria: food safety and public health perspective. *ISRN Microbiol*., 2013: 703813

Field, D., P.D. Cotter, R.P. Ross and C. Hill, 2015. Bioengineering of the model lantibiotic nisin. *Bioengineered*, 6: 187–192

Fjellheim, A.J., G. Klinkenberg, J. Skjermo, I.M. Aasen and O. Vadstein, 2010. Selection of candidate probionts by two different screening strategies from Atlantic cod (*Gadus morhua* L.) larvae. *Vet. Microbiol*., 144: 153–159

Flint, H.J., E.A. Bayer, M.T. Rincon, R. Lamed and B.A. White, 2008. Polysaccharide utilization by gut bacteria: potential for new insights from genomic analysis. *Nat. Rev. Microbiol.*, 6: 121–131

Gatesoupe, F.J., C. Huelvan, N. Le Bayon, H. Le Delliou, L. Madec, O. Mouchel, P. Quazuguel, D. Mazurais and J.L. Zambonino-Infante, 2016. The highly variable microbiota associated to intestinal mucosa correlates with growth and hypoxia resistance of sea bass, *Dicentrarchus labrax*, submitted to different nutritional histories. *BMC Microbiol.*, 16: 266

Geraylou, Z., C. Souffreau, E. Rurangwa, G.E. Maes, K.I. Spanier, C.M. Courtin, J.A. Delcour, J. Buyse and F. Ollevier, 2013. Prebiotic effects of arabinoxylan oligosaccharides on juvenile Siberian sturgeon (*Acipenser baerii*) with emphasis on the modulation of the gut microbiota using 454 pyrosequencing. *FEMS Microbiol. Ecol.*, 86: 357–371

Ghanbari, M., M. Jami, W. Kneifel and K.J. Domig, 2013. Antimicrobial activity and partial characterization of bacteriocins produced by lactobacilli isolated from Sturgeon fish. *Food Cont.*, 32: 379–385

Ghosh, K., M. Roy, N. Kar and E. Ringø, 2010. Gastrointestinal bacteria in rohu, *Labeorohita* (Actinopterygii: Cypriniformes: Cyprinidae): scanning electron microscopy and bacteriological study. *Acta Ichthyol. Piscat*., 40: 129–135

Giri, S.S., V. Sukumaran, S.S. Sen, J. Vinumonia, B.N. Banu and P.K. Jena, 2011. Antagonistic activity of cellular components of potential probiotic bacteria, isolated from the gut of *Labeo rohita*, against *Aeromonas hydrophila*. *Probiotics Antimicro*., 3: 214–222

Gonçalves, A.T. and C. Gallardo-Escárate, 2017. Microbiome dynamic modulation through functional diets based on pre- and probiotics (mannan-oligosaccharides and *Saccharomyces cerevisiae*) in juvenile rainbow trout (*Oncorhynchus mykiss*). *J. Appl. Microbiol*., 122: 1333–1347

Guarner, F., T. Requena and A. Marcos, 2010. Consensus statements from the workshop "Probiotics and health: scientific Evidence". *Nutr. Hosp.*, 25: 700–704

Han, S., Y. Liu, Z. Zhou, S. He, Y. Cao, P. Shi, B. Yao and E. Ringø, 2010. Analysis of bacterial diversity in the intestine of grass carp (*Ctenopharyngodon idellus*) based on 16S rDNA gene sequences. *Aquac. Res.*, 42: 47–56

Hazen, T.C., E.A. Dubinsky, T.Z. DeSantis, G.L. Andersen, Y.M. Piceno, N. Singh, J.K. Jansson, A. Probst, S.E. Borglin, J.L. Fortney, W.T. Stringfellow, M. Bill, M.E. Conrad, L.M. Tom, K.L. Chavarria, T.R. Alusi, R. Lamendella, D.C. Joyner, C. Spier, J. Baelum, M. Auer, M.L. Zemla, R. Chakraborty, E.L. Sonnenthal, P. D'haeseleer, H.Y.N. Holman, S. Osman, Z. Lu, J.D.V. Nostrand, Y. Deng, J. Zhou and O.U. Mason, 2010. Deep-sea oil plume enriches indigenous oil-degrading bacteria. *Science*, 330: 204–208

He, Z., Y. Deng, J.D. Van Nostrand, Q. Tu, M. Xu, C.L. Hemme, X. Li, L. Wu, T.J. Gentry, Y. Yin, J. Liebich, T.C. Hazen and J. Zhou, 2010. GeoChip 3.0 as a high-throughput tool for analyzing microbial community composition, structure and functional activity. *ISME J.*, 4: 1167–1179

He, Z., J.D. Van Nostrand, Y. Deng and J. Zhou, 2011. Development and applications of functional gene microarrays in the analysis of the functional diversity, composition, and structure of microbial communities. *Front. Environ. Sci. Eng.*, 5: 1–20

Hennersdorf, P., S. Kleinertz, S. Theisen, M.A. Abdul-Aziz, G. Mrotzek, H.W. Palm and H.P. Saluz, 2016. Microbial diversity and parasitic load in tropical fish of different environmental conditions. *PLoS One*, 11: e0151594

Hess, M., A. Sczyrba, R. Egan, T.W. Kim, H. Chokhawala, G. Schroth, S. Luo, D.S. Clark, F. Chen, T. Zhang, R.I. Mackie, L.A. Pennacchio, S.G. Tringe, A. Visel, T. Woyke, Z. Wang and E.M. Rubin, 2011. Metagenomic discovery of biomass-degrading genes and genomes from cow rumen. *Science*, 331: 463–467

Ingerslev, H.C., M.L. Strube, L. von Gersdorff Jørgensen, I. Dalsgaard, M. Boye and L. Madsen, 2014. Diet type dictates the gut microbiota and the immune response against *Yersinia ruckeri* in rainbow trout (*Oncorhynchus mykiss*). *Fish Shellf. Immunol*., 40: 624–633

Jack, R.W., J.R. Tagg and B. Ray, 1995. Bacteriocins of gram-positive bacteria. *Microbiol. Rev*., 59: 171–200

Kashinskaya, E.N., N.I. Belkova, G.I. Izvekova, E.P. Simonov, K.B. Andree, V.V. Glupov, O.A. Baturina, M.R. Kabilov and M.M. Solovyev, 2015. A comparative study on microbiota from the intestine of Prussian carp (*Carassius gibelio*) and their aquatic environmental compartments, using different molecular methods. *J. Appl. Microbiol*., 119: 948–961

Kemgang, T. S., S. Kapila, V.P. Shanmugam, and R. Kapila, 2014. Cross-talk between probiotic lactobacilli and host immune system. *J. Appl. Microbiol*., 117: 303-319

Khan, A. and K. Ghosh, 2012. Characterization and identification of gut-associated phytase-producing bacteria in some freshwater fish cultured in ponds. *Acta Ichthyol. Piscat*., 42: 37–45

Kim, D.H., J. Brunt and B. Austin, 2007. Microbial diversity of intestinal contents and mucus in rainbow trout (*Oncorhynchus mykiss*). *J. Appl. Microbiol*., 102: 1654–1664

Kostic, A.D., M.R. Howitt and W.S. Garrett, 2013. Exploring host-microbiota interactions in animal models and humans. *Gene. Dev.*, 27: 701–718

Larsen, A.M., H.H. Mohammed and C.R. Arias, 2014. Characterization of the gut microbiota of three commercially valuable warmwater fish species. *J. Appl. Microbiol.*, 116: 1396–1404

Ley, R.E., C.A. Lozupone, M. Hamady, R. Knight and J.I. Gordon, 2008. Worlds within worlds: evolution of the vertebrate gut microbiota. *Nat. Rev. Microbiol.*, 6: 776–788

Li, X., Q. Yan, S. Xie, W. Hu, Y. Yu and Z. Hu, 2013. Gut microbiota contributes to the growth of fast-growing transgenic common carp (*Cyprinus carpio* L.). *PLoS One*, 8: e64577

Li, T., M. Long, F.J. Gatesoupe, Q. Zhang, A. Li and X. Gong, 2015. Comparative analysis of the intestinal bacterial communities in different species of carp by pyrosequencing. *Microb. Ecol*., 69: 25–36

Li, D., R. Luo, C.M. Liu, C.M. Leung, H.F. Ting, K. Sadakane, H. Yamashita and T.W. Lam, 2016. MEGAHIT v1.0: A fast and scalable metagenome assembler driven by advanced methodologies and community practices. *Methods*, 102: 3–11

Liu, Y., P. Xu, J. Xu, Y. Huang, Y. Liu, H. Fang, Y. Hu, X. You, C. Bian, M. Sun, R. Gu, L. Cui, X. Zhang, P. Xu and Q. Shi, 2017. China is initiating the aquatic 10-100-1,000 genomics program. *Sci. Chin. Life Sci.* 60: 329–332

Liu, H., X. Guo, R. Gooneratne, R. Lai, C. Zeng, F. Zhan, and W. Wang, 2016. The gut microbiome and degradation enzyme activity of wild freshwater fishes influenced by their trophic levels. *Sci. Rep*. 6: 24340

Llewellyn, M.S., S. Boutin, S.H. Hoseinifar and N. Derome, 2014. Teleost microbiomes: the state of the art in their characterization, manipulation and importance in aquaculture and fisheries. *Front. Microbiol.*, 5: 207

Lokesh, J. and V. Kiron, 2016. Transition from freshwater to seawater reshapes the skin-associated microbiota of Atlantic salmon. *Sci. Rep*., 6: 19707

Lu, Z., Y. Deng, J.D. Van Nostrand, Z. He, J. Voordeckers, A. Zhou, Y.J. Lee, O.U. Mason, E.A. Dubinsky, K.L. Chavarria, L.M. Tom, J.L. Fortney, R. Lamendella, J.K. Jansson, P. D'haeseleer, T.C. Hazen and J. Zhou, 2012. Microbial gene functions enriched in the deepwater horizon deep-sea oil plume. *ISME J*., 6: 451–460

Lyapparaj, P., T. Maruthiah, R. Ramasubburayan, S. Prakash, C. Kumar, G. Immanuel and A. Palavesam, 2013. Optimization of bacteriocin production by *Lactobacillus* sp. MSU3IR against shrimp bacterial pathogens. *Aquat. Biosyst.*, 9: 1–10

Mandal, S. and K. Ghosh, 2013. Isolation of tannase-producing microbiota from the gastrointestinal tracts of some freshwater fish. *J. Appl. Ichthyol*. 29: 145–153

Mansfield, G.S., A.R. Desai, S.A. Nilson, A.G. Van Kessel, M.D. Drew and J.E. Hill, 2010. Characterization of rainbow trout (*Oncorhynchus mykiss*) intestinal microbiota and inflammatory marker gene expression in a recirculating aquaculture system. *Aquaculture*, 307: 95–104

Mohapatra, S., T. Chakraborty, V. Kumar, G. DeBoeck and K.N. Mohanta, 2013. Aquaculture and stress management: a review of probiotic intervention. *J. Anim. Physiol. Anim. Nutr.*, 97: 405–430

Nayak, S.K., 2010. Role of gastrointestinal microbiota in fish. *Aquac. Res*., 41: 1553–1573

Nes, I.F. and O. Johnsborg, 2004. Exploration of antimicrobial potential in LAB by genomics. *Curr. Opin. Biotech*., 15: 100–104

Nes, I.F., S.S. Yoon and D.B. Diep, 2007. Ribosomally synthesized antimicrobial peptides (bacteriocins) in lactic acid bacteria: a review. *Food Sci. Biotechnol*., 16: 675–690

Neu, J., 2014. The developing intestinal microbiome: probiotics and prebiotics. *In: Nutritional Care of Preterm Infants: Scientific Basis and Practical Guidelines. World Rev. Nutr. Diet*, Vol. 110, pp: 167–176. Koletzko, B., B. Poindexter and R. Uauy (eds.). Karger publishers, Basel, Switzerland

Newaj-Fyzul, A. and B. Austin, 2014. Probiotics, immune stimulants, plant products and oral vaccines, and their role as feed supplements in the control of bacterial fish diseases. *J. Fish Dis.*, 38: 937–955

Ni, J., Q. Yan, Y. Yu and T. Zhang, 2014. Factors influencing the grass carp gut microbiome and its effect on metabolism. *FEMS Microbiol. Ecol*., 87: 704–714

Nikoskelainen, S., S. Salminen, G. Bylund and A.C. Ouwehand, 2001. Characterization of the properties of human- and dairy-derived probiotics for prevention of infectious diseases in fish. *Appl. Environ. Microbiol*., 67: 2430–2435

Paliy, O., H. Kenche, F. Abernathy and S. Michail, 2009. High-throughput quantitative analysis of the human intestinal microbiota with a phylogenetic microarray. *Appl. Environ. Microbiol.*, 75: 3572–3579

Pond, M.J., D.M. Stone and D.J. Alderman, 2006. Comparison of conventional and molecular techniques to investigate the intestinal microflora of rainbow trout (*Oncorhynchus mykiss*). *Aquaculture*, 261: 194–203

Qin, J., Y. Li, Z. Cai, S. Li, J. Zhu, F. Zhang, S. Liang, W. Zhang, Y. Guan, D. Shen, Y. Peng, D. Zhang, Z. Jie, W. Wu, Y. Qin, W. Xue, J. Li, L. Han, D. Lu, P. Wu, Y. Dai, X. Sun, Z. Li, A. Tang, S. Zhong, X. Li, W. Chen, R. Xu, M. Wang, Q. Feng, M. Gong, J. Yu, Y. Zhang, M. Zhang, T. Hansen, G. Sanchez, J. Raes, G. Falony, S. Okuda, M. Almeida, E. LeChatelier, P. Renault, N. Pons, J.M. Batto, Z. Zhang, H. Chen, R. Yang, W. Zheng, S. Li, H. Yang, J. Wang, S.D. Ehrlich, R. Nielsen, O. Pedersen, K. Kristiansen and J. Wang, 2012. A metagenome-wide association study of gut microbiota in type 2 diabetes. *Nature*, 490: 55–60

Rawls, J.F., B.S. Samuel and J.I. Gordon, 2004. Gnotobiotic zebrafish reveal evolutionarily conserved responses to the gut microbiota. *P. Natl. Acad. Sci. USA*, 101: 4596–4601

Rawls, J.F., M.A. Mahowald, R.E. Ley and J.I. Gordon, 2006. Reciprocal gut microbiota transplants from zebrafish and mice to germ-free recipients reveal host habitat selection. *Cell*, 127: 423–433

Ray, A.K., T. Roy, S. Mondal and E. Ringø, 2010. Identification of gut-associated amylase, cellulose and protease-producing bacteria in three species of Indian major carps. *Aquac. Res*., 41: 1462–1469

Ray, A.K., K. Ghosh and E. Ringø, 2012. Enzyme-producing bacteria isolated from fish gut: a review. *Aquac. Nutr*., 18: 465–492

Ringø, E., E. Strøm and J.A. Tabachek, 1995. Intestinal microflora of salmonids: a review. *Aquac. Res*., 26: 773–789

Ringø, E. and R.E. Olsen, 1999. The effect of diet on aerobic bacterial flora associated with intestine of Arctic charr (*Salvelinus alpinus* L.). *J. Appl. Microbiol*., 86: 22–28

Ringø, E., S. Sperstad, R. Myklebust, S. Refstie and A. Krogdahl, 2006. Characterisation of the microbiota associated with intestine of Atlantic cod (*Gadus morhua* L.): the effect of fish meal, standard soybean meal and a bioprocessed soybean meal. *Aquaculture*, 261: 829–841

Ringø, E., R.E. Olsen, I. Jensen, J. Romero and H.L. Lauzon, 2014. Application of vaccines and dietary supplements in aquaculture: possibilities and challenges. *Rev. Fish Biol. Fish*., 4: 1005–1032

Ringø, E. and S.K. Song, 2016. Application of dietary supplements (synbiotics and probiotics in combination with plant products and β-glucans) in aquaculture. *Aquac. Nutr*., 22: 4–24

Roeselers, G., E.K. Mittge, W.Z. Stephens, D.M. Parichy, C.M. Cavanaugh, K. Guillemin and J.F. Rawls, 2011. Evidence for a core gut microbiota in the zebrafish. *ISME J*., 5: 1595–1608

Roh, S.W., G.C. Abell, K.H. Kim, Y.D. Nam and J.W. Bae, 2010. Comparing microarrays and next-generation sequencing technologies for microbial ecology research. *Trends Biotechnol*., 28: 291–299

Romero, J., C.G. Feijoó and P. Navarrete, 2012. Antibiotics in aquaculture-use, abuse and alternatives. *In: Health and Environment in Aquaculture*, pp. 159–198. E. Carvalho (ed.). IntechOpen, London, UK

Sakata, T., H. Sugita, T. Mitsuoka, D. Kakimoto and H. Kadota, 1981. Characteristics of obligate anaerobic bacteria in the intestines of freshwater fish. *Bull. Jap. Soci. Sci. Fish*, 47: 421–427

Scheffler, R.J., S. Colmer, H. Tynan, A.L. Demain and V.P. Gullo, 2013. Antimicrobials, drug discovery, and genome mining. *Appl. Microbiol. Biotechnol*., 97: 969–978

Shade, A. and J. Handelsman, 2012. Beyond the venn diagram: the hunt for the core microbiome. *Environ. Microbiol*., 14: 4–12

Smith, C.C., L.K. Snowberg, J.G. Caporaso, R. Knight and D.I. Bolnick, 2015. Dietary input of microbes and host genetic variation shape among-population differences in stickleback gut microbiota. *ISME J*., 9: 2515–2526

Smriga, S., S.A. Sandin and F. Azam, 2010. Abundance, diversity, and activity of microbial assemblages associated with coral reef fish guts and feces. *FEMS Microbiol. Ecol*., 73: 31–42

Star, B., T.H. Haverkamp, S. Jentoft and K.S. Jakobsen, 2013. Next generation sequencing shows high variation of the intestinal microbial species composition in Atlantic cod caught at a single location. *BMC Microbiol*., 13: 248

Sugita, H., S. Sasanuma, K. Tanaka and Y. Deguchi, 1993. Vitamin B12-producing ability of bacteria isolated from coastal waters. *Biosci. Biotechnol. Biochem*., 57: 138–139

Sugita, H., Y. Hirose, N. Matsuo and Y. Deguchi, 1998. Production of antibacterial substances by *Bacillus* sp. strain NM12, an intestinal bacterium of Japanese coastal fish. *Aquaculture*, 165: 269–280

Sullam, K.E., S.D. Essinger, C.A. Lozupone, M.P. O'Connor, G.L. Rosen, R. Knight, S.S. Kilham and J.A. Russell, 2012. Environmental and ecological factors that shape the gut bacterial communities of fish: a meta-analysis. *Mol. Ecol*., 21: 3363–3378

Sullam, K.E., C.M. Dalton, J.A. Russell, S.S. Kilham, R. El-Sabaawi, D.P. German and A.S. Flecker, 2015. Changes in digestive traits and body nutritional composition accommodate a trophic niche shift in Trinidadian guppies. *Oecologia*, 177: 245–257

Sullam, K.E., B.E. Rubin, C.M. Dalton, S.S. Kilham, A.S. Flecker and J.A. Russell, 2015. Divergence across diet, time and populations rules out parallel evolution in the gut microbiomes of Trinidadian guppies. *ISME J*., 9: 1508–1522

Sun, Y.Z., H.L. Yang, R.L. Ma and W.Y. Lin, 2010. Probiotic applications of two dominant gut *Bacillus* strains with antagonistic activity improved the growth performance and immune responses of grouper *Epinephelus coioides. Fish Shellf. Immunol*., 29: 803–809

Sun, Y., Y. Huang, X. Li, C.C. Baldwin, Z. Zhou, Z. Yan, K.A. Crandall, Y. Zhang, X. Zhao, M. Wang, A. Wong, C. Fang, X. Zhang, H. Huang, J.V. Lopez, K. Kilfoyle, Y. Zhang, G. Ortí, B. Venkatesh and Q. Shi, 2016. Fish-T1K (Transcriptomes of 1,000 Fishes) project: large-scale transcriptome data for fish evolution studies. *GigaScience*, 5: 18

Sun, Z., H.M.B. Harris, A. McCann, C. Guo, S. Argimon, W. Zhang, X. Yang, I.B. Jeffery, J.C. Cooney, T.F. Kagawa, W. Liu, Y. Song, E. Salvetti, A. Wrobel, P. Rasinkangas, J. Parkhill, M.C. Rea, O. O'Sullivan, J. Ritari, F.P. Douillard, R.P. Ross, R. Yang, A.E. Briner, G.E. Felis, W.M. de Vos, R. Barrangou, T.R. Klaenhammer, P.W. Caufield, Y. Cui, H. Zhang and P.W. O'Toole, 2015. Expanding the biotechnology potential of lactobacilli through comparative genomics of 213 strains and associated genera. *Nat. Commun*., 6: 8322

Tap, J., S. Mondot, F. Levenez, E. Pelletier, C. Caron, J.P. Furet, E. Ugarte, R. Muñoz-Tamayo, D.L.E. Paslier, R. Nalin, J. Dore and M. Leclerc, 2009. Towards the human intestinal microbiome phylogenetic core. *Environ. Microbiol*., 11: 2574–2584

Thomas, T., J. Gilbert, and F. Meyer, 2012. Metagenomics - a guide from sampling to data analysis. *Microb. Inform. Exp.*, 2: 3

Tsuchiya, C., T. Sakata and H. Sugita, 2008. Novel ecological niche of *Cetobacterium somerae*, an anaerobic bacterium in the intestinal tracts of freshwater fish. *Lett. Appl. Microbiol*., 46: 43–48

Turnbaugh, P.J., R.E. Ley, M.A. Mahowald, V. Magrini, E.R. Mardis and J.I. Gordon, 2006. An obesity-associated gut microbiome with increased capacity for energy harvest. *Nature*, 444: 1027–1031

Turnbaugh, P.J., R.E. Ley, M. Hamady, C. Fraser-Liggett, R. Knight and J.I. Gordon, 2007. The human microbiome project. *Nature*, 449: 804–810

Turnbaugh, P.J. and J.I. Gordon, 2009. The core microbiome, energy balance and obesity. *J. Physiol*., 587: 4153–4158

Van Kessel, M.A., B.E. Dutilh, K. Neveling, M.P. Kwint, J.A. Veltman, G. Flik, M.S. Jetten, P.H. Klaren and H.J. Op den Camp, 2011. Pyrosequencing of 16S rRNA gene amplicons to study the microbiota in the gastrointestinal tract of carp (*Cyprinus carpio* L.). *AMB Express*, 1: 41

Walsh, C.J., C.M. Guinane, P.W. O'Toole and P.D. Cotter, 2014. Beneficial modulation of the gut microbiota. *FEBS Lett*., 588: 4120–4130

Walsh, C.J., C.M. Guinane, C. Hill, R.P. Ross, P.W. O'Toole and P.D. Cotter, 2015. *In silico* identification of bacteriocin gene clusters in the gastrointestinal tract, based on the Human Microbiome Project's reference genome database. *BMC Microbiol*., 15: 183

Walsh, C.J., C.M. Guinane, P.W. O'Toole and P.D. Cotter, 2017. A Profile Hidden Markov Model to investigate the distribution and frequency of LanB-encoding lantibiotic modification genes in the human oral and gut microbiome. *Peer J*., 5: e3254

Wang, J. and H. Jia, 2016. Metagenome-wide association studies: fine-mining the microbiome. *Nat. Rev. Microbiol*., 14: 508–522

Więckowicz, M., M. Schmidt, A. Sip and W. Grajek, 2011. Development of a PCR-based assay for rapid detection of class IIa bacteriocin genes. *Lett. Appl. Microbiol.*, 52: 281–289

Wong, S.D. and J.F. Rawls, 2012. Intestinal microbiota composition in fishes is influenced by host ecology and environment. *Mol. Ecol.*, 21: 3100–3102

Wong, S., T. Waldrop, S. Summerfelt, J. Davidson, F. Barrows, P.B. Kenney, T. Welch, G.D. Wiens, K. Snekvik, J.F. Rawls and C. Good, 2013. Aquacultured rainbow trout (*Oncorhynchus mykiss*) possess a large core intestinal microbiota that is resistant to variation in diet and rearing density. *Appl. Environ. Microbiol*., 79: 4974–4984

Wrighton, K.C., B.C. Thomas, I. Sharon, C.S. Miller, C.J. Castelle, N.C. VerBerkmoes, M.J. Wilkins, R.L. Hettich, M.S. Lipton, K.H. Williams, P.E. Long and J.F. Banfield, 2012. Fermentation, hydrogen, and sulfur metabolism in multiple uncultivated bacterial phyla. *Science*, 337: 1661–1665

Wu, L., X. Liu, C.W. Schadt and J. Zhou, 2006. Microarray-based analysis of subnanogram quantities of microbial community DNAs by using whole-community genome amplification. *Appl. Environ. Microbiol*., 72: 4931–4941

Wu, S., T. Gao, Y. Zheng, W. Wang, Y. Cheng and G. Wang, 2010. Microbial diversity of intestinal contents and mucus in yellow catfish (*Pelteobagrus fulvidraco*). *Aquaculture*, 303: 1–7

Wu, S., G. Wang, E.R. Angert, W. Wang, W. Li and H. Zou, 2012. Composition, diversity, and origin of the bacterial community in grass carp intestine. *PLoS One*, 7: e30440

Wu, S., Y. Ren, C. Peng, Y. Hao, F. Xiong, G. Wang, W. Li, H. Zou and E.R. Angert, 2015. Metatranscriptomic discovery of plant biomass-degrading capacity from grass carp intestinal microbiomes. *FEMS Microbiol. Ecol*., 91: fiv107

Xing, M., Z. Hou, J. Yuan, Y. Liu, Y. Qu and B. Liu, 2013. Taxonomic and functional metagenomic profiling of gastrointestinal tract microbiome of the farmed adult turbot (*Scophthalmus maximus*). *FEMS Microbiol*., 86: 432–443

Ye, L., J. Amberg, D. Chapman, M. Gaikowski and W.T. Liu, 2013. Fish gut microbiota analysis differentiates physiology and behavior of invasive Asian carp and indigenous American fish. *ISME J*., 8: 541–551

Zacharof, M.P. and R.W. Lovitt, 2012. Bacteriocins produced by lactic acid bacteria a review article. *APCBEE Proc*., 2: 50–56

Zendo, T., J. Nakayama, K. Fujita and K. Sonomoto, 2008. Bacteriocin detection by liquid chromatography/mass spectrometry for rapid identification. *J. Appl. Microbiol*., 104: 499–507

Zhou, J., Z. He, J.D. Van Nostrand, L. Wu and Y. Deng, 2010. Applying GeoChip analysis to disparate microbial communities. *Microb*, 5: 60–65

Zhao, J., L. Feng, Y. Liu, W. Jiang, P. Wu, J. Jiang, Y. Zhang and X. Zhou, 2014. Effect of dietary isoleucine on the immunity, antioxidant status, tight junctions and microflora in the intestine of juvenile Jian carp (*Cyprinus carpio var*. Jian). *Fish Shellf. Immunol*., 41: 663–673

Zhou, J., Z. He, Y. Yang, Y. Deng, S.G. Tringe and L. Alvarez-Cohen, 2015. High-throughput metagenomic technologies for complex microbial community analysis: open and closed formats. *mBio*, 6: e02288–14

Zhou, W.H., X. Chen, D. Zhang and C. Chen, 1998. A preliminary study on the influence of different feeding stuff on intestinal microflora of grass carp (*Ctenopharyngodon idellus*). *J. Huazhong Agric*., 17: 252–256

(Received 16 April 2018 Accepted 02 June 2018)