



Research Progress of the Gut Microbiome in Hybrid Fish

Xinyuan Cui ¹, Qinrong Zhang ¹ , Qunde Zhang ¹, Yongyong Zhang ¹, Hua Chen ², Guoqi Liu ²
and Lifeng Zhu ^{1,*}

¹ College of Life Sciences, Nanjing Normal University, Nanjing 210046, China; cuixinyuanwj@163.com (X.C.); z1187438993@163.com (Q.Z.); qundezhang23@163.com (Q.Z.); zyy863098363@163.com (Y.Z.)

² Mingke Biotechnology, Hangzhou 310000, China; chenhua@mingkebio.com (H.C.); liuguoqi@mingkebio.com (G.L.)

* Correspondence: zhulf2020@126.com

Abstract: Fish, including hybrid species, are essential components of aquaculture, and the gut microbiome plays a vital role in fish growth, behavior, digestion, and immune health. The gut microbiome can be affected by various internal and/or external factors, such as host development, diet, and environment. We reviewed the effects of diet and dietary supplements on intestinal microorganisms in hybrid fish and the difference in the gut microbiome between the hybrid and their hybrids that originate. Then, we summarized the role of the gut microbiome in the speciation and ecological invasion of hybrid fish. Finally, we discussed possible future studies on the gut microbiome in hybrid fish, including the potential interaction with environmental microbiomes, the effects of the gut microbiome on population expansion, and fish conservation and management.

Keywords: hybrid fishes; gut microbiome; community and function; speciation; invasion; fish conservation and management



Citation: Cui, X.; Zhang, Q.; Zhang, Q.; Zhang, Y.; Chen, H.; Liu, G.; Zhu, L. Research Progress of the Gut Microbiome in Hybrid Fish. *Microorganisms* **2022**, *10*, 891. <https://doi.org/10.3390/microorganisms10050891>

Academic Editor: Konstantinos Ar. Kormas

Received: 4 April 2022
Accepted: 21 April 2022
Published: 24 April 2022

Publisher's Note: MDPI stays neutral with regard to jurisdictional claims in published maps and institutional affiliations.



Copyright: © 2022 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).

1. Introduction

The host and its microbiome are regarded as a unique biological entity holobiont, including the genome, which is called the hologenome [1]. The combination of complex microbiota and genes in the intestine are collectively referred to as the gut microbiome [2]. Animal hosts maintain a long, close, and complex relationship with their gut microbiome [3]. The gut microbiome plays a vital role in the nervous system development [4], behavior [5], immunity [6], food digestion, and metabolism [7] of the host. Gut microbiota are highly specialized microbial communities with a complex composition that is affected by many interactions among microorganisms, host, diet, and the environment [8]. Host phylogeny and diet are the two main factors shaping the animal gut microbiome [9–14].

Fish comprise nearly 50% of the total vertebrate diversity, and more than 34,000 species have been described to date, constituting a crucial part of the aquatic ecosystem [15,16]. Microorganisms exist in almost every fish organ, including the skin, digestive tract, internal organs, and luminous organs [17]. The fish gut is a complex ecosystem, composed of highly diverse microbiota. The microbiota is influenced by various factors, such as habitat environmental factors, season, host genetics, developmental stage, nutrition level, and diet composition, with the potential major determinant being the habitat environment [16].

Overall, bacteria are the primary microbial colonizers in the gastrointestinal tract of fish [18–21]. The gastrointestinal microbiota of fish mainly consist of aerobic or facultative anaerobic microorganisms and facultative and obligate anaerobes [20,22–24]. Among them, Proteobacteria, Firmicutes, and Bacteroidetes constitute 90% of the gut microbiome of most fish [15]. In addition, Actinobacteria, Fusobacteria, Bacilli, Clostridia, and Verrucomicrobia are the dominant bacterial phyla in fish gut microorganisms [15,25–29]. The gut microbiota of fish participate in various physiological functions. There are several beneficial effects on the host, such as reproduction, development, nutrition, immunity, and stress responses, and

the gut microbiota are often referred to as an ‘extra organ’ [15,30]. Nayak has described the role of fish gastrointestinal microbiota in nutrition, immunity, and health management [20].

Early research on fish gut microflora employed culture-dependent techniques. The emergence of metagenomics and next-generation sequencing techniques has entirely changed fish gut microbiome research by presenting a method that directly analyzes the microbial genome from environmental samples [31,32]. These new research methods have led to a better understanding of the connections between the microorganisms and their respective hosts. The Illumina system, Roche 454 system, and Ion Torrent Personal Genome Machine (PGM) are the primary next-generation sequencing (NGS) platforms used in fish gut microbiome research, and the Illumina system is the most commonly used [15].

The influencing factors and physiological functions of fish intestinal microbiota are two critical issues in NGS analyses [33]. Most studies have explored the effects of various host and environmental factors on the bacterial community composition of gut microbiota. Limited studies have analyzed the beneficial and harmful effects of the gut microbiota on the host [15]. However, there are many valuable bacterial species in the intestines of fish, including *Cetobacterium* spp. and *Lactobacillus* spp. [34]. Hybrid fish are indispensable components of fish species and are essential in aquaculture. We review recent research on the gut microbiome and ecological problems in hybrid fishes and discuss possible future research to improve our understanding of the gut microbiome in fish.

2. The Gut Microbiome in Hybrid Fish

2.1. Effects of Diet and Dietary Supplements on the Gut Microbiome and Immune Health of Hybrid Fish

Hybridization is a basic step in the long-term evolution of organisms, which may lead to the production of new species. Heterosis is a complex biological phenomenon where the hybrid offspring show superior natural characteristics, when compared with their parents [35,36]. Heterosis occurs in fish, and hybrid fish have advantages of faster growth performance, higher immunity, improved ecological adaptability, and an enhanced tolerance for transportation. Therefore, as wild catch fisheries can no longer support the world consumption of seafood, fish heterosis has been widely assisting aquaculture since the 1980s [37–41]. However, even the improvements made by heterosis may not be enough for the growing world consumption rate of fish [35].

In addition, different fish species inhabiting the same waters may also naturally hybridize in the wild. Hybrid fish may possess improved ecological adaptability compared to their parents and be more widely distributed in the natural environment with heterosis, due to the survival of the fittest theory [42–44]. In reality, the microbiota in hybrids may provide new favorable physiological functions and promote the utilization of new ecological niches, and the hybrid microbiota may also shape reproductive barriers, which may influence the ecological speciation or the expansion of the population range [45–48]. It has been shown that greater than 30,000 variations of hybrid fish species have formed in the wild, and these large fish populations can produce high diversity in the dietary niches. Therefore, exploring the microbiota of wild hybrid fish is of great significance for understanding the basic biological and ecological processes of speciation, population expansion, and invasion ecology [39].

We, firstly, aimed to provide a whole picture of the diet or dietary supplement effects on the fish gut microbiome (Table 1) [15,20,49,50]. Then, we focused on the relationship between the diet and the hybrid fish gut microbiome. We found that many studies have explored changing the diet or dietary additives on the composition and function of the hybrid fish gut microbiome and their promotion of the growth and health of mixed fish (Table 2), but rare in the comparison between the hybrid and their hybrids’ origin.

Table 1. The application of diet and dietary supplements in fish.

Species	Class	Order	Family	Ingredients	Intervention Type	16s rRNA Sequencing	References
<i>Oreochromis niloticus</i>	Actinopteri	Cichliformes	Cichlidae	<i>Rummeliibacillus stabekisii</i>	Probiotic	Illumina MiSeq, Amplicon: V3–V4	[51]
<i>Oreochromis niloticus</i>	Actinopteri	Cichliformes	Cichlidae	<i>Bacillus subtilis</i>	Probiotic	Illumina HiSeq, Amplicon: V4	[52]
<i>Acipenser baerii</i>	Actinopteri	Acipenseriformes	Acipenseridae	Arabinoxylan-oligosaccharides (A.X.O.S.) + <i>Lactococcus lactis</i> spp. <i>lactis</i> or <i>Bacillus circulans</i>	Synbiotic	454 GS FLX Titanium, Amplicon	[53]
<i>Ctenopharyngodon idellus</i>	Actinopteri	Cypriniformes	Xenocyprididae	Xylo-oligosaccharide	Prebiotic	Illumina MiSeq	[54]
<i>Oreochromis niloticus</i>	Actinopteri	Cichliformes	Cichlidae	<i>Lactobacillus rhamnosus</i> JCM1136 and <i>Lactococcus lactis</i> subsp. <i>lactis</i> JCM5805	Probiotic	Illumina MiSeq, Amplicon: V3–V4	[55]
<i>Dicentrarchus labrax</i>	Actinopteri	Perciformes	Moronidae	Calcium carbonate	Prebiotic	Illumina MiSeq, Amplicon: V3–V4	[56]
<i>Ctenopharyngodon idellus</i>	Actinopteri	Cypriniformes	Xenocyprididae	<i>Bacillus subtilis</i>	Probiotic	No	[57]
<i>Ctenopharyngodon idellus</i>	Actinopteri	Cypriniformes	Xenocyprididae	<i>Bacillus coagulans</i> , <i>Rhodospseudomonas palustris</i> and <i>Lactobacillus acidophilus</i>	Probiotic	No	[58]
<i>Ctenopharyngodon idellus</i>	Actinopteri	Cypriniformes	Xenocyprididae	<i>Bacillus subtilis</i> Ch9	Probiotic	No	[59]
<i>Ctenopharyngodon idellus</i>	Actinopteri	Cypriniformes	Xenocyprididae	Exogenous cellulase	Prebiotic	Amplicon: V3	[60]
<i>Ctenopharyngodon idellus</i>	Actinopteri	Cypriniformes	Xenocyprididae	Glutathione	Prebiotic	No	[61]
<i>Ctenopharyngodon idellus</i>	Actinopteri	Cypriniformes	Xenocyprididae	<i>B. licheniformis</i> + xylo-oligosaccharide	Synbiotic	No	[62]
<i>Danio rerio</i>	Actinopteri	Cypriniformes	Danionidae	Gluten formulated diet	Protein	Illumina Miseq, Amplicon: V4	[63]
<i>Danio rerio</i>	Actinopteri	Cypriniformes	Danionidae	Protein meal of animal origin (<i>ragworm Nereis virens</i>)	Protein	454 GS FLX Titanium, Amplicon	[64]
<i>Danio rerio</i>	Actinopteri	Cypriniformes	Danionidae	Chitosan silver nanocomposites (CAGNCs)	Composites	454 GS FLX Titanium, Amplicon	[65]
<i>Gambusia affinis</i>	Actinopteri	Cyprinodontiformes	Poeciliidae	Rifampicin	Antibiotic	Illumina HiSeq, Amplicon: V4	[66]
<i>Oncorhynchus mykiss</i>	Actinopteri	Salmoniformes	Salmonidae	Dietary plant proteins	Protein	Illumina Miseq, Amplicon: V6–V8	[67]
<i>Oncorhynchus mykiss</i>	Actinopteri	Salmoniformes	Salmonidae	<i>Wickerhamomyces anomalus</i> + <i>Saccharomyces cerevisiae</i>	Synbiotic	Illumina HiSeq, Amplicon	[68]
<i>Oncorhynchus mykiss</i>	Actinopteri	Salmoniformes	Salmonidae	Microalgae meal (<i>Schizochytrium limacinum</i>)	Prebiotic	Illumina HiSeq, Amplicon	[69]
<i>Oreochromis niloticus</i>	Actinopteri	Cichliformes	Cichlidae	<i>Lactobacillus plantarum</i> CCFM8610	Probiotic	Illumina MiSeq, Amplicon: V4–V5	[70]
<i>Oreochromis niloticus</i>	Actinopteri	Cichliformes	Cichlidae	<i>Lactobacillus plantarum</i> CCFM639	Probiotic	Illumina MiSeq, Amplicon	[71]
<i>Oreochromis niloticus</i>	Actinopteri	Cichliformes	Cichlidae	<i>Vibrio</i> sp. CC8 and <i>Bacillus cereus</i> CC27,	Probiotic	No	[72]
<i>Oreochromis niloticus</i>	Actinopteri	Cichliformes	Cichlidae	<i>Clostridium butyricum</i>	Probiotic	Illumina HiSeq, Amplicon-	[73]
<i>Oreochromis niloticus</i>	Actinopteri	Cichliformes	Cichlidae	<i>Allium sativum</i>	Plant	Illumina MiSeq, Amplicon: V4–V5	[74]
<i>Oreochromis niloticus</i>	Actinopteri	Cichliformes	Cichlidae	<i>Bacillus subtilis</i> and <i>Bacillus licheniformis</i>	Probiotic	No	[75]
<i>Oreochromis niloticus</i>	Actinopteri	Cichliformes	Cichlidae	<i>Metschnikowia</i> sp. GXUS03	Probiotic	No	[76]
<i>Sparus aurata</i>	Actinopteri	Spariformes	Sparidae	Sodium butyrate	Butyrate	455 GS FLX Titanium, Amplicon: V1–V3	[77]
<i>Seriola lalandi</i>	Actinopteri	Carangiformes	Carangidae	Oxytetracycline, erythromycin and metronidazole	Antibiotic	Illumina MiSeq, Amplicon: V1–V2	[78]
<i>Piaractus mesopotamicus</i>	Actinopteri	Characiformes	Serrasalmididae	Florfenicol	Antibiotic	Illumina MiSeq, Shotgun metagenome	[79]
<i>Channa striata</i>	Actinopteri	Anabantiformes	Channidae	β -glucan, galactooligosaccharides, mannan-oligosaccharide	Prebiotic	T-RFLP fragment sequencing, Amplicon	[80]
<i>Channa striata</i>	Actinopteri	Anabantiformes	Channidae	<i>Saccharomyces cerevisiae</i> and <i>Lactobacillus acidophilus</i>	Probiotic	T-RFLP fragment sequencing, Amplicon	[80]
<i>Cyprinus carpio</i>	Actinopteri	Cypriniformes	Cyprinidae	Chinese yam peel	Plant	Illumina MiSeq, Amplicon: V3–V4	[81]

Table 1. Cont.

Species	Class	Order	Family	Ingredients	Intervention Type	16s rRNA Sequencing	References
<i>Lates calcarifer</i>	Actinopteri	Perciformes	Centropomidae	Sodium diformate	Formate	No	[82]
<i>Oreochromis niloticus</i>	Actinopteri	Cichliformes	Cichlidae	<i>Bacillus subtilis</i> and <i>Lactobacillus plantarum</i>	Probiotic	ABI PRISM 377 sequencer (Perkin-Elmer), Amplicon: V6–V8	[83]
<i>Sparus aurata</i>	Actinopteri	Spariformes	Sparidae	Poultry by-product meal and Hydrolyzed feather meal	Protein	455 GS FLX Titanium, Amplicon: V3–V4	[84]
<i>Sparus aurata</i>	Actinopteri	Spariformes	Sparidae	Fish protein hydrolysate or Autolysed dried yeast	Protein	Illumina MiSeq, Amplicon: V3–V4	[85]
<i>Dicentrarchus labrax</i>	Actinopteri	Perciformes	Moronidae	Galactomannan oligosaccharides and A mixture of garlic and labiatae-plants oils	Prebiotic	Illumina MiSeq, Amplicon: V3–V4	[86]
<i>Salmo salar</i>	Actinopteri	Salmoniformes	Salmonidae	<i>Pediococcus acidilactici</i> MA18/5M and Short chain fructooligosaccharides	Synbiotic	Amplicon: V3	[87]
<i>Arapaima gigas</i>	Actinopteri	Osteoglossiformes	Osteoglossidae	<i>Lactococcus lactis</i> subsp. <i>lactis</i> and <i>Enterococcus faecium</i>	Probiotic	Amplicon: V1–V2	[88]
<i>Cyprinus carpio</i>	Actinopteri	Cypriniformes	Cyprinidae	Dietary plant proteins	Protein	Illumina HiSeq, Amplicon: V3–V4	[89]
<i>Carassius auratus</i>	Actinopteri	Cypriniformes	Cyprinidae	<i>Bacillus subtilis</i> and <i>Enterococcus faecium</i>	Probiotic	Amplicon: V3–V4	[90]
<i>Totoaba macdonaldi</i>	Actinopteri	Perciformes	Sciaenidae	Commercial dietary prebiotic and probiotic	Synbiotic	Illumina MiSeq, Amplicon: V3–V4	[91]
<i>Totoaba macdonaldi</i>	Actinopteri	Perciformes	Sciaenidae	Soy protein concentrate	Protein	Illumina MiSeq, Amplicon: V3–V4	[92]

Table 2. The studies on the gut microbiome of hybrid fish.

Host/Parents	Class	Order	Family	NGS Platform	Amplicon Sequencing	Reference
<i>Culter alburnus</i> ♀ × <i>Megalobrama amblycephala</i> ♂	Actinopteri	Cypriniformes	Xenocyprididae	Illumina MiSeq	Amplicon: V3–V4	[39]
<i>Parachondrostoma toxostoma</i> / <i>Chondrostoma nasus</i>	Actinopteri	Cypriniformes	Leuciscidae	Illumina MiSeq	Amplicon: V4	[48]
<i>Epinephelus fuscoguttatus</i> ♀ × <i>E. lanceolatus</i> ♂	Actinopteri	Perciformes	Serranidae	Illumina NovaSeq	Amplicon: V3–V4	[93]
<i>Epinephelus fuscoguttatus</i> ♀ × <i>E. lanceolatus</i> ♂	Actinopteri	Perciformes	Serranidae	Unknown	Unknown	[94]
<i>Oreochromis niloticus</i> ♀ × <i>O. aureus</i> ♂	Actinopteri	Cichliformes	Cichlidae	Unknown	Amplicon: V3	[95]
<i>Acipenser baerii</i> × <i>A. schrenckii</i>	Actinopteri	Acipenseriformes	Acipenseridae	Illumina HiSeq	Amplicon: V3–V4	[96]
<i>Pangasianodon gigas</i> × <i>Pangasianodon hypophthalmus</i>	Actinopteri	Siluriformes	Pangasiidae	Unknown	Unknown	[97]
<i>Epinephelus fuscoguttatus</i> ♀ × <i>E. lanceolatus</i> ♂	Actinopteri	Perciformes	Serranidae	Illumina HiSeq	Amplicon: V3–V4	[98]
<i>Acipenser baeri</i> Brandt ♀ × <i>A. schrenckii</i> Brandt ♂	Actinopteri	Acipenseriformes	Acipenseridae	Illumina MiSeq	Amplicon: V3–V4	[99]
<i>Epinephelus fuscoguttatus</i> ♀ × <i>E. lanceolatus</i> ♂	Actinopteri	Perciformes	Serranidae	Illumina HiSeq	Amplicon: V3–V4	[100]
<i>Epinephelus fuscoguttatus</i> ♀ × <i>E. lanceolatus</i> ♂	Actinopteri	Perciformes	Serranidae	Lon GeneStudio S5™	Amplicon: V4	[101]
<i>Epinephelus fuscoguttatus</i> ♀ × <i>E. lanceolatus</i> ♂	Actinopteri	Perciformes	Serranidae	Illumina	Amplicon: V3–V4	[102]
<i>Epinephelus fuscoguttatus</i> ♀ × <i>E. lanceolatus</i> ♂	Actinopteri	Perciformes	Serranidae	Illumina	Amplicon: V3–V4	[103]
<i>Epinephelus fuscoguttatus</i> ♀ × <i>E. lanceolatus</i> ♂	Actinopteri	Perciformes	Serranidae	Illumina MiSeq	Amplicon: V3–V4	[104]
<i>Morone chrysops</i> × <i>M. saxatilis</i>	Actinopteri	Perciformes	Moronidae	Illumina MiSeq	Amplicon: V1–V3	[105]
<i>Coregonus</i>	Actinopteri	Salmoniformes	Salmonidae	Illumina MiSeq	Amplicon: V3–V4	[106]
<i>Hypophthalmichthys nobilis</i> × <i>H. molitrix</i>	Actinopteri	Cypriniformes	Xenocyprididae	Illumina MiSeq	Amplicon: V4	[107]

Table 2. Cont.

Host/Parents	Class	Order	Family	NGS Platform	Amplicon Sequencing	Reference
<i>Epinephelus fuscoguttatus</i> ♀ × <i>E. lanceolatus</i> ♂	Actinopteri	Perciformes	Serranidae	Illumina MiSeq	Amplicon: V3–V4	[108]
<i>Epinephelus fuscoguttatus</i> ♀ × <i>E. lanceolatus</i> ♂	Actinopteri	Perciformes	Serranidae	Unknown	Amplicon	[109]
<i>Epinephelus fuscoguttatus</i> ♀ × <i>E. lanceolatus</i> ♂	Actinopteri	Perciformes	Serranidae	Illumina MiSeq	Amplicon	[110]
<i>Morone Chrysops</i> × <i>M. Saxatilis</i>	Actinopteri	Perciformes	Moronidae	Illumina MiSeq	Amplicon: V1–V3	[111]
<i>Oreochromis niloticus</i> ♀ × <i>O. aureus</i> ♂	Actinopteri	Cichliformes	Cichlidae	454 Sequencer F.L.X.	Amplicon: V6–V8	[112]
<i>Oreochromis niloticus</i> ♀ × <i>O. aureus</i> ♂	Actinopteri	Cichliformes	Cichlidae	Unknown	Amplicon: V4	[113]
<i>Tachysurus fulvidraco</i> ♀ × <i>Pseudobagrus vachellii</i> ♂	Actinopteri	Siluriformes	Bagridae	Illumina MiSeq	Amplicon	[114]
<i>Epinephelus fuscoguttatus</i> ♀ × <i>E. lanceolatus</i> ♂	Actinopteri	Perciformes	Serranidae	Illumina	Amplicon: V3–V4	[115]
<i>Acipenser baerii</i> × <i>A. schrenckii</i>	Actinopteri	Acipenseriformes	Acipenseridae	Illumina HiSeq	Amplicon: V3–V4	[116]
<i>Epinephelus moara</i> ♀ × <i>E. lanceolatus</i> ♂	Actinopteri	Perciformes	Serranidae	Illumina HiSeq	Amplicon: V3–V4	[117]
<i>Epinephelus fuscoguttatus</i> ♀ × <i>E. lanceolatus</i> ♂	Actinopteri	Perciformes	Serranidae	Illumina MiSeq	Amplicon: V3–V4	[118]
<i>Acipenser baerii</i> × <i>A. schrenckii</i>	Actinopteri	Acipenseriformes	Acipenseridae	Illumina MiSeq	Amplicon: V3–V4	[119]
<i>Epinephelus fuscoguttatus</i> ♀ × <i>E. lanceolatus</i> ♂	Actinopteri	Perciformes	Serranidae	Illumina HiSeq	Amplicon: V3–V4	[120]
<i>Epinephelus fuscoguttatus</i> ♀ × <i>E. lanceolatus</i> ♂	Actinopteri	Perciformes	Serranidae	Illumina HiSeq	Amplicon	[121]
<i>Epinephelus fuscoguttatus</i> ♀ × <i>E. lanceolatus</i> ♂	Actinopteri	Perciformes	Serranidae	Unknown	Amplicon	[122]
<i>Epinephelus fuscoguttatus</i> ♀ × <i>E. lanceolatus</i> ♂	Actinopteri	Perciformes	Serranidae	Illumina HiSeq	Amplicon	[123]
<i>Acipenser baerii</i> × <i>A. schrenckii</i>	Actinopteri	Acipenseriformes	Acipenseridae	Illumina HiSeq	Amplicon: V3–V4	[124]

Unknown, the information is unclear in the reference.

2.1.1. Antibiotics

Infectious diseases caused by various pathogens have severely harmed the health of aquatic organisms around the world [125]. Antibiotics have been widely used as feed supplements to treat intestinal diseases in fish and have become indispensable in human health [33,126,127]. A short-term (6 days) dietary antibiotic mixture (vancomycin, neomycin sulfate, and metronidazole) can improve the lipid metabolism in hybrid groupers (*Epinephelus fuscoguttatus* ♀ × *E. lanceolatus* ♂) fed medium- and high-lipid diets. However, antibiotic treatments can also strongly alter intestinal microbiota by reducing the relative abundance and diversity of hybrid grouper gut microbiota, resulting in a significant increase in the proportion of Bacteroidetes and a decrease in the proportion of Firmicutes [93]. Long-term antibiotic supplementation can cause several side effects on fish health [127–129]. Presently, the pollution and spread of antibiotic-resistant genes caused by the long-term abuse of antibiotics have become a global problem [130]. Recently, probiotics and prebiotics are an emerging strategic approach for sustainable aquaculture, as they do not cause environmental pollution or public health hazards [51,131,132].

2.1.2. Probiotics

Probiotics are beneficial microorganisms that can modulate intestinal microbial composition and improve the host health status [133,134]. Probiotics are commonly used in the aquaculture industry as feed or water additives [20]. The essential probiotic microorganisms employed in aquaculture are lactic acid bacteria (LAB) species [135,136] and *Bacillus spp.* [52,137]. The other general probiotic species used in fish are *Saccharomyces*, *Clostridium*, *Enterococcus*, *Shewanella*, *Leuconostoc*, *Lactococcus*, *Carnobacterium*, and *Aeromonas* [20]. Fish are vulnerable to various pathogenic microorganisms, and innate immunity provides an initial line of defense [138]. The addition of probiotics to the diet plays a vital role in stimulating fish immune responses, and further promotes the innate and adaptive immune system [139]. For an example, *Bacillus subtilis* strain 7k, isolated from the gastrointestinal tract of hybrid hulong grouper (*Epinephelus fuscoguttatus* × *E. lanceolatus*), could be used in grouper culture to stimulate growth, enhance immunity and promote health in the fishes [94]. Studies reveal that *O. mykiss* fed different types of probiotics increased the expression of the TGF-β gene, which regulates fish immunity [140–142]. TGF-β levels increased in juvenile hybrid tilapia (*O. niloticus* ♀ × *Oreochromis aureus* ♂), after consuming a diet supplemented with *Bacillus subtilis* C-3102 [95], and the same occurred in Koi carp (*Cyprinus carpio*) [143]. HWF™ is a paraprobiotic and postbiotic supplementary diet using inactive and beneficial bacteria, and is considered an efficient therapeutic agent in fish. Feeding hybrid sturgeons (*Acipenser baerii* × *Acipensers chrenckii*) with HWF™ improved their growth and immunity by changing the composition and diversity of the gut bacteria, developing their healthy gut microbiota [96].

2.1.3. Prebiotics

Prebiotics are an innovative strategy, providing a dietary supplement to improve growth development and the immune system by regulating gut microbiota [144]. Prebiotics are generally non-digestible oligosaccharides added to fish feed as dietary components to promote the proliferation of specific beneficial microorganisms in the intestine and, thus, enhance host health [145]. Previous research has shown that prebiotics can decrease the adherence and colonization of pathogenic microorganisms in the intestinal tract to improve the general immunity of the host by increasing the number of lactic acid bacteria, especially *Bifidobacterium* [20,146,147]. Fructo-oligosaccharides, galactooligosaccharides, mannan-oligosaccharides (MOS), xylooligosaccharides (XOS), inulin, lactulose, and lactosucrose are common prebiotics used in various animals, including humans [20]. The level of gut lactic acid bacteria was significantly increased in hybrid catfish (*Pangasianodon gigas* × *Pangasianodon hypophthalmus*) fed with diets containing 0.6% xylooligosaccharides (XOS) [97]. In addition, several studies have reported that inulin, fructooligosaccharides, xylooligosaccharides, galactooligosaccharides, and arabinoxylan-oligosaccharides can affect growth

development, immune health, and the composition and/or diversity of the gut microbiota in different fish species [53,97,148–151]. Indeed, many researchers have reported the effect of prebiotics on the gut microbiota in fish, such as grass carp [54], Siberian sturgeon [53], Nile tilapia [55], and European sea bass [152].

The prebiotic Grobiotic™AE and dietary brewer's yeast can improve the growth performance, immune response, and resistance to *Streptococcus iniae* infection in hybrid striped bass (*Morone chrysops* × *M. saxatilis*) [153]. Dietary supplementation of 4% ESTAQUA® yeast culture (YC) for hybrid grouper (*Epinephelus fuscoguttatus* ♀ × *E. lanceolatus* ♂) could improve the alpha diversity of gut microbiota, growth performance and serum immune responses against *V. harveyi* attacks [98]. N.B.T. is an excellent indicator of the health status and/or immunization effectiveness in fish [56]. Supplementing the diet with raffinose in hybrid sturgeons (*Acipenser baeri* Brandt ♀ × *A. schrenckii* Brandt ♂) improved the growth performance and intestinal morphology, modifying the gut microbiota composition and increasing the level of N.B.T. activity [99]. Chitosan oligosaccharide (COS) is a new prebiotic, dietary COS supplementation, which improves the growth performance and health status of *Scophthalmus maximus* [154], *Cyprinus carpio koi* [155], and *Oncorhynchus mykiss* [156]. Dietary COS supplementation improved the intestinal health and immune responses of hybrid groupers (*Epinephelus fuscoguttatus* ♀ × *E. lanceolatus* ♂) when fed a low-fish meal diet [100].

It is worth noting that prebiotic supplementation is only beneficial when a moderate volume is provided; prebiotics at a high concentration can be harmful to the host. Excessive prebiotics may cause an imbalance in the gut microenvironment, which decreases the digestive capacity in fish intestines. A previous study revealed that a high concentration of inulin could damage the enterocytes of *Salvelinus alpinus* [157]. This may explain why 0.4–0.6% COS supplementation was optimum in hybrid groupers [100].

2.1.4. Fishmeal Protein Substitutes

Fishmeal (F.M.) is the most widely utilized high-quality protein source in aquatic feed and has many advantages [158]. However, fishmeal production cannot meet the growing needs of the aquaculture industry due to its rapid development, which is causing a severe impediment to industry development [101,159]. Therefore, using plant proteins is an innovative solution for sustainable aquaculture [160,161].

Cottonseed protein concentrate (CPC) is a new experimental fishmeal (FM) replacement [162]. However, fishmeal replaced with CPC in an inappropriate proportion can have adverse effects on the intestinal health of groupers and leads to intestinal inflammation [163]. A study on pearl gentian groupers (*Epinephelus fuscoguttatus* ♀ × *Epinephelus lanceolatus* ♂) revealed that 24% CPC was considered the most appropriate volume for F.M. replacement and growth performance, digestive proteinase activity, intestinal morphology, and intestinal microflora in the pearl gentian grouper reached maximum levels with 24% CPC replacement levels. Subsequently, many physiological parameters are reduced with increasing CPC replacement levels [101]. The substitution of FM with peanut meal (PNM) of up to 50% or CPC up to 60% obviously changed the intestinal microbiota of juvenile hybrid groupers (*E. fuscoguttatus* ♀ × *E. lanceolatus* ♂), which increased intestinal pathogenic bacteria and decreased intestinal beneficial bacteria [102,103]. Similarly, replacing FM with peptides from swine blood (PSB) up to 75% could reduce growth performance for hybrid groupers (*Epinephelus fuscoguttatus* ♀ × *E. lanceolatus* ♂), and increase the abundance of the potentially pathogenic *Pseudomonas* and *Arcobacter* in the gut [104].

Another fishmeal replacement protein is soybean meal (SBM). SBM has been widely considered an inexpensive FM replacement [164]. Nevertheless, anti-nutritional factors in SBM can negatively affect the intestinal morphology of fish [165]. Research reveals that bioprocesses (such as soybean meal ingredients) can reduce the intestinal microorganism diversity in hybrid striped bass (*Morone chrysops* × *M. saxatilis*) [105]. It is challenging to find a suitable fish meal substitute for various fish, and protein substitutes have excellent potential and are important future research topics.

2.2. Hybrid Speciation and Gut Microbiome

No living organisms exist in isolation from the microbial world, and microbial symbiosis and speciation profoundly shape the biodiversity composition. Animal hosts and microbiomes are closely interconnected and interact over long evolutionary timeframes. They can even be regarded as a unique biological entity-holobiont and include their entire genome, called the hologenome [1]. Diverse and complex interactions exist between hosts and microorganisms. Microorganisms play essential roles in host physiology, health, and survival. Microorganisms can even alter host reproduction [166], resulting in host embryo death [167–170] and affect the host gametic integrity and embryonic viability, which may be closely related to the formation of new species [45,171]. The microorganisms and their interactions with hosts are potentially important factors in stimulating the formation of new species [172].

Species are reproductively isolated groups composed of potentially interbreeding individuals, and hybrids can suffer from post-mating isolation barriers, such as sterility and/or unviability [173]. The composition and functional effects of animal microbiota are closely related to host evolution, and the survival rate and performance of microorganisms can be reduced when interspecific microbiota transplantation occurs between closely related and different host species pairs. The microbiome compositional relationships (i.e., beta diversity) reflect the evolutionary relationships of the host species [173,174]. Thus, natural selection can drive phylosymbiotic changes within the parental species, which may lead to the evolution of deleterious interactions between hybrids and their microbiomes [173].

Based on the holobiont concept, host-genome–microbiome associations and their role in host adaptability demonstrate that microorganisms may participate in the process of speciation, and symbiotic microorganisms may hinder speciation through isolation, including behavioral isolation, geographical isolation, and reproductive isolation [45]. Microbial symbionts can add new functional genes to the host genome, which assists the host in expanding its dietary niche and obtaining new nutritional opportunities. Unfortunately, hybridization can inhibit symbiotic relationships by destroying the vertical transmission of some microorganisms between the host parents and offspring, which are hybridization disadvantages and hinder species formation, as observed in *Acyrtosiphon pisum* [175], *Sitophilus* [176] and the family *Plataspidae* [177]. In hybrid species, microorganisms can hinder speciation by assisting reproductive isolation. *Wolbachia* is a bacterium that widely exists in the reproductive system of arthropods and may cause hybrid male sterility in *Drosophila paulistorum* [178]. In the two-spotted mite (*Tetranychus urticae*), *Wolbachia* can also cause cytoplasmic incompatibility (CI) in the F1 generation and F2 male offspring deaths from the surviving F1 females in the CI cross [178]. Similarly, different CI *Wolbachia* in *Nasonia* wasp species can cause high levels of F1 hybrid lethality and the reproductive isolation induced by CI has evolutionary potential in the early stages of the speciation process [179,180].

Similarly, a close interaction exists between the gut microbiome and host, and plays an important role in the speciation of hybrid species. For example, the host gut microbiome may hinder the formation of new species by participating in the death of hybrids in *Nasonia* wasp species [181]. Vertebrates are a vital group for interactions in reproductive isolation and speciation research. Alterations in gut microbiota communities and increases in gut pathology exist in hybrid mice (*Mus musculus* × *Mus domesticus*) [46]. The gut microbiome does not always play negative roles in hybrid species. For example, the hybrid offspring of sika deer (*Cervus nippon*) and elk (*Cervus elaphus*) harbor a high abundance of *Acetivomaculum* bacterial species, which may assist in the absorption and metabolism of nutrients [182,183]. A similar phenomenon was identified in the hybrid offspring of ponies and donkeys, which render a completely different gut microbiota from their parents [184].

In the gut microbiome in hybrid fish research, differences in the gut microbiome between hybrid offspring and parents have been observed. In lake whitefish (*Coregonus clupeaformis*), the gut microbiome is significantly different between the F1 hybrids and their parents, especially the abundance difference between Firmicutes and Proteobacteria [106]. The research also found the interactions of the host-microbiota-environment

demonstrated three different evolutionary paths in the gut microbiome [106]. Similarly, the gut characteristics of hybrid fish from herbivorous blunt snout bream (*Megalobrama amblycephala*) and carnivorous topmouth culter (*Culter alburnus*) differ from their parents. The microbial community in the hybrid topmouth culters was markedly distinct from their parents, and varied in the cellulose content in the gut [39]. One study found that the evolutionary characteristics of hybrid fish progeny from *Megalobrama amblycephala* and *Culter alburnus* may be manifested in dietary adaptation and choice; the interactions between gut microbiota and host genetics contributed to hybrid fishes adapting to herbivorous diets more than carnivorous diets [185]. Compared to the parents, the hybrid offspring of two invasive North American carp, *Hypophthalmichthys nobilis* and *Hypophthalmichthys molitrix*, harbor different gut microbiome compositions and display higher alpha diversity than their parents [107].

2.3. The Differences in the Gut Microbiome of the Hybrid Fish and Their Hybrids Origin

There are still few studies directly comparing gut microbiome between parental and hybrid progeny. However, it has been shown that existing differences in intestinal microbiota between captive parents and hybrid fishes' offspring exist under a controlled environment [106]. There is no doubt that diet will affect the gut microbiome composition and growth performance of the host, and under the same dietary conditions (Artemia and mixed diet), the taxonomic composition of transient gut microbiota between both whitefish (*Coregonus clupeaformis*) parental species and their reciprocal hybrids showed a slight pattern of differentiation, which, within the Artemia diet group, meant a higher abundance for Firmicutes, but lower for Proteobacteria, was observed in hybrids in comparison with their parents' whitefish, while the opposite result was found in the mixed diet group, where there was a higher abundance of Proteobacteria but it was lower for Firmicutes. In addition, in the abundance composition of some specific bacterial genera, the two reciprocal hybrids, and their parents also showed the opposite pattern, that F1 D♀N♂ has more specific bacterial genera than its parents, while F1 N♀D♂ with fewer specific bacterial genera than its parents. In the hybridization experiment between whitefish and omul (*Coregonus migratorius*), the researchers found that the hybrid progeny had a lower alpha diversity (e.g., Shannon index) in hindgut microbiota than the parents [186].

Host genetics can strongly affect the gut microbial composition of the hybrid offspring [39]. Compared with carnivorous topmouth culter (*Culter alburnus*, TC) parents, the gut microbiome structure of their two-hybrid progenies is more similar to that of herbivorous blunt snout bream (*Megalobrama amblycephala*, BSB) parents, as the alpha diversity of the two types of hybrids and BSB parent is higher than that of a TC parent, as well as beta diversity analysis, which also showed that there was no significant difference between the two hybrids and the BSB parent. Interestingly, in the composition of gut microbiota, Fusobacteria and Proteobacteria are the most abundant intestinal flora in hybrid fishes, and the proportion of Fusobacteria and Proteobacteria in hybrid offspring is similar to the BSB parent but significantly different from the TC parent. Again, the shared bacterial taxa at the phylum level showed different results; the hybrids of the two types share higher proportions of gut bacterial communities with the BSB parent than the TC parent.

Recently, our study reported a direct comparison of the similarities and differences in gut microbiome (composition and potential function) among bighead carps (*Hypophthalmichthys nobilis*, B), silver carps (*Hypophthalmichthys molitrix*, S) and their hybrid offspring (SB and BS) in ponding experiments [107]. The hybrid gut microbiome displays the admixed pattern at the community level and harbors the relatively high alpha diversity (e.g., phylogenetic diversity). For example, the hybrid fish had intermediate abundances of Cyanobacteria and Bacteroidetes in the foregut, while Fusobacteria are significantly enriched in parents in the hindgut. Moreover, the hybrid gut microbiome's predicted function shows the enrichment in the genes coding for putative enzymes involved the diet utilization, which suggests the potential benefits to their local adaptation.

2.4. Gut Microbiome Might Promote Ecological Invasion by Hybrid Fish

Gut microbiota can enhance the adaptability of the host to the environment and improve the successful invasion rate of some invasive species [187]. For invasion success, the species requires a dispersal ability, environmental tolerance, phenotypic plasticity, and associated epigenetics [188,189]. Host shifts can lead to phytophagous insects becoming invasive species [190]. It has already been demonstrated that the gut microbiome plays a vital role in phytophagous insect invasion success [191], and gut bacteria can assist in the successful invasion of insect species by regulating epigenetic factors related to the host [192]. Similarly, some biological mechanisms can enhance the success rate of invasive species, such as genetic diversity [193], reproductive rate [194], food resources [195], and hybridization [44,196].

Therefore, there are complex and close relationships between hybridization, the gut microbiome, and bio-invasion. Bighead carp and silver carp are invasive species, characterized by various hybridization in the Mississippi River Basin [107]. There is higher alpha diversity in the foregut microbiota in the hybrid offspring, and an increasing discrepancy also occurs between the foregut and hindgut. Similarly, the hybrids had a higher proportion of putative genes coding for putative enzymes related to the digestion of filter-feeding phytoplankton (Cyanobacteria, cellulose, and chitin) than their parents. The improved putative enzymes could encourage the utilization of new food resources by the gut microbiota and, therefore, improve survival, environmental adaptation, and invasion by hybrid fish. Therefore, the gut microbiome and host genome may synergistically promote bigheaded carp invasion in the United States [107].

3. The Potential Impact of Environmental Microbiota

The current research focuses on fish, not hybrid fish. However, environmental microbiota impacts may also occur in hybrid fish.

3.1. Habitat Environmental Microbiome Shapes the Early Gut Microbiome of Juvenile Fish

The main determinant of fish gut microbiota is the natural environment, and fish intestinal microbiota symbionts are generally obtained from the environment [197] by neutral processes, such as drift and diffusion, which produce most of the microbial diversity [198]. The microorganisms transmitted from the environment to the fish intestine are mainly derived from two paths: the foodborne microorganisms carried by prey and the microorganisms in the water, and most of the environmental microbiota remain temporarily in the fish gut [199]. In most fish species, the ontogeny and colonization of gut microbiota in the early stages of life rely on the horizontal transmission of environmental microbiota [200]. Juvenile zebrafish (*Danio rerio*) acquire gut symbiotic bacteria from the water environment after hatching, which may promote the development and function of their intestines [201]. Similar patterns are observed in wild Atlantic salmon (*Salmo salar*), discus (*Symphysodon aequifasciata*) [200], grass carp (*Ctenopharyngodon idellus*), Mucha perch (*Siniperca chuatsi*), and southern catfish (*Silurus meridionalis*). The composition of the gut microbiota community of juvenile fish was more similar to the habitat water environment than the adults [197,200]. However, fish gut microbiota often differ from their surrounding environment after becoming adults [202]. Therefore, environmental microorganisms play an important role in shaping the gut microbiota in the early juvenile fish stages and, as fish mature, the environmental factors are less influential because the gut microbiota gradually differentiate from the environmental microbiota, showing individual variations [197,203].

3.2. Do Fish Specifically Select *Proteus* from the Water Environment?

The gut microbiota of fish are mainly Proteobacteria and Firmicutes, whereas amphibians, reptiles, birds, and mammals contain mainly Firmicutes and Bacteroidetes. The excessive reproduction and presence of *Proteus* may be a sign of ecological imbalance in the gut microbial community of mammals [204], as many symbiotic *Proteus* bacteria can translate into pathogens, and infect and promote inflammation in the host under

specific conditions. Many studies have demonstrated that, regardless of the fish living environment, the gut microbiome is composed of a common core microbiome [205]. Major environmental microorganisms are rarely observed in fish intestines [49]. *Proteus* dominate the gut microbiota of most fish species [206]. The *Proteus* abundance can increase with the growth and nutritional level of the fish (from herbivorous to carnivorous). Conversely, the abundance of Firmicutes usually decreases with increasing nutritional levels [202]. The gut microbiome not only reflects the microorganisms in its surrounding environment but also characterizes the specific selection of the environmental microbiome by the host in grass carp (*Ctenopharyngodon idellus*) [207], silver Prussian carp (*Carassius auratus gibelio*) [208], and zebrafish (*Danio rerio*) [209]. Notably, the higher proportion of *Proteus* in the fish intestines indicates the fish host has specifically selected *Proteus* from the habitat water or *Proteus* has outperformed the other environmental bacterial taxa in the water. This discrepancy is an urgent problem needing to be explored [16].

4. Future Perspectives

The gut microbiome can promote the successful ecological invasion of hybrid fish, which makes them occupy favorable ecological niches and further improves the potential for population expansion. Following Darwin’s theory of evolution, this process greatly improves the potential of hybrid fish to evolve into new species in the future (Figure 1). The gut microbiome plays a role in speciation, but its degree of impact remains unclear. Furthermore, the high genomic similarity between bighead and silver carp, and an over 90% embryonic viability in all crosses, indicate that interspecific hybridization between the carps might have promoted their range expansion [44]. In the future, the role of the gut microbiome in population expansion of hybrid species should not be ignored. It is highly significant for us to better combine the genome and metagenome to improve our understanding of the ecological problems of hybrid fish. The fish gut flora and fecal materials discharged into the water may reflect their diet preferences, physiological behaviors, and presence in the river [210], allowing gut microbiota to potentially monitor fish invasion and population expansion, which is an important research issue in fish conservation and management in the future (Figure 1).

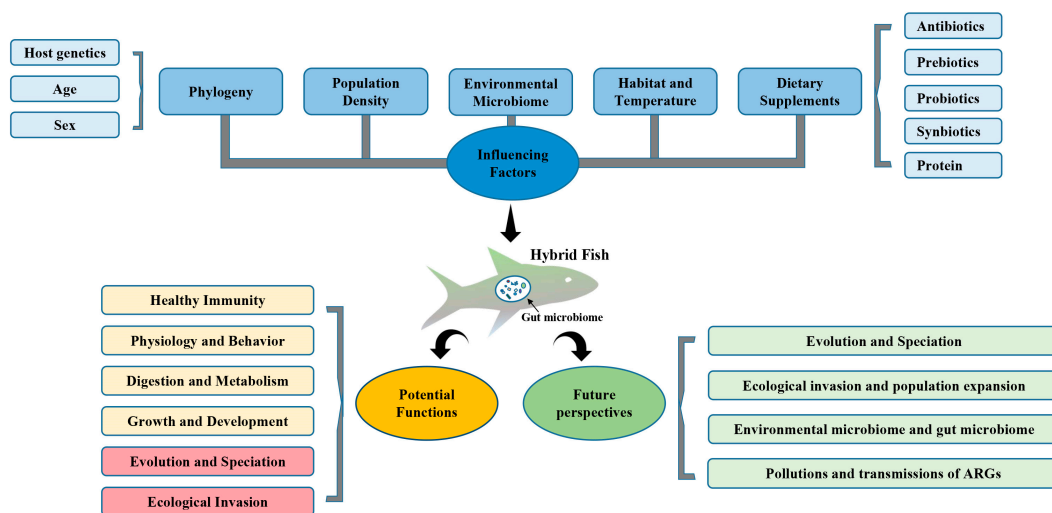


Figure 1. Major research progress and future perspectives on hybrid fish gut microbiome.

For a long time, the source of gut microbiota has been an attractive research topic. Environmental microbiome transmission plays an important role in animal gut microbiota, and the differences between terrestrial and aquatic environments cause the gut of aquatic animals to be very different from that of terrestrial organisms, including fish and aquatic mammals. Research shows 13% of the gut microbiota of threespine stickleback (*Gasterosteus aculeatus*) comes from the surrounding water environment and 73% from prey [199]. In

addition, in most fish species, the ontogeny and colonization by gut microbiota in the early stages of life mainly occur through the horizontal transmission of environmental microbiota [200]. Juvenile zebrafish (*Danio rerio*) acquire gut symbiotic bacteria from the water environment after hatching, potentially promoting the development and function of the intestines [201]. Similar patterns are observed in wild Atlantic salmon (*Salmo salar*), discus (*Symphysodon aequifasciata*) [200], grass carp (*Ctenopharyngodon idellus*), Mucha perch (*Siniperca chuatsi*), and southern catfish (*Silurus meridionalis*), and the composition of the gut microbiota community of juvenile fish was more similar to the habitat water than the adults [197,200]. In addition, different fish tissue types, such as skin, gills, and intestines, may also be the main determinants of microbiota diversity and composition [48]. Successful hybrid fish invasion depends on the relationships and interactions between an individual's characteristics (age and gender), gut microbiome, environmental microbiome, and post-mating reproductive isolation, associated with environmental microbial transmission. Future research is required to assist our understanding of these interactions (Figure 1). In addition, the aquatic environment can become a reservoir of antibiotic-resistant genes (ARGs), providing an ideal path for the acquisition and dissemination of ARGs [211]. Aquatic animals, such as fish, are direct witnesses and victims of ARG-water pollution. Therefore, wild fish can be recipients and disseminators of ARGs in aquatic environments [130]. At present, there are few studies assessing ARG pollution and transmission in wild hybrid fish, providing great research potential in the future (Figure 1).

Author Contributions: L.Z. conceived the ideas and methodology. X.C., Q.Z. (Qinrong Zhang), Q.Z. (Qunde Zhang), Y.Z., H.C. and G.L. collected the data. X.C. and L.Z. wrote the manuscript. All authors have read and agreed to the published version of the manuscript.

Funding: Financial support was provided by the Priority Academic Program Development of Jiangsu Higher Education Institutions (PAPD).

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Acknowledgments: We thank the team members for the help during literature collection.

Conflicts of Interest: The authors declare no conflict of interest.

References

1. Bordenstein, S.R.; Theis, K.R. Host Biology in Light of the Microbiome: Ten Principles of Holobionts and Hologenomes. *PLoS Biol.* **2015**, *13*, e1002226. [[CrossRef](#)] [[PubMed](#)]
2. Rosenberg, E.; Zilber-Rosenberg, I. The hologenome concept of evolution after 10 years. *Microbiome* **2018**, *6*, 78. [[CrossRef](#)] [[PubMed](#)]
3. McFall-Ngai, M.; Hadfield, M.G.; Bosch, T.C.G.; Carey, H.V.; Domazet-Lošo, T.; Douglas, A.E.; Dubilier, N.; Eberl, G.; Fukami, T.; Gilbert, S.F.; et al. Animals in a bacterial world, a new imperative for the life sciences. *Proc. Natl. Acad. Sci. USA* **2013**, *110*, 3229–3236. [[CrossRef](#)] [[PubMed](#)]
4. Carlson, A.; Xia, K.; Azcarate-Peril, M.A.; Goldman, B.D.; Ahn, M.; Styner, M.A.; Thompson, A.L.; Geng, X.; Gilmore, J.H.; Knickmeyer, R.C. Infant Gut Microbiome Associated With Cognitive Development. *Biol. Psychiatry* **2018**, *83*, 148–159. [[CrossRef](#)] [[PubMed](#)]
5. Archie, E.A.; Tung, J. Social behavior and the microbiome. *Curr. Opin. Behav. Sci.* **2015**, *6*, 28–34. [[CrossRef](#)]
6. Levy, M.; Blacher, E.; Elinav, E. Microbiome, metabolites and host immunity. *Curr. Opin. Microbiol.* **2017**, *35*, 8–15. [[CrossRef](#)]
7. Hollister, E.B.; Gao, C.; Versalovic, J. Compositional and functional features of the gastrointestinal microbiome and their effects on human health. *Gastroenterology* **2014**, *146*, 1449–1458. [[CrossRef](#)]
8. Kers, J.G.; Velkers, F.; Fischer, E.A.J.; Hermes, G.D.A.; Lamot, D.M.; Stegeman, J.A.; Smidt, H. Take care of the environment: Housing conditions affect the interplay of nutritional interventions and intestinal microbiota in broiler chickens. *Anim. Microbiome* **2019**, *1*, 10. [[CrossRef](#)]
9. Youngblut, N.D.; Reischer, G.H.; Walters, W.; Schuster, N.; Walzer, C.; Stalder, G.; Ley, R.E.; Farnleitner, A.H. Host diet and evolutionary history explain different aspects of gut microbiome diversity among vertebrate clades. *Nat. Commun.* **2019**, *10*, 2200. [[CrossRef](#)]
10. Ley, R.E.; Lozupone, C.A.; Hamady, M.; Knight, R.; Gordon, J.I. Worlds within worlds: Evolution of the vertebrate gut microbiota. *Nat. Rev. Microbiol.* **2008**, *6*, 776–788. [[CrossRef](#)]
11. Sharpton, T.J. Role of the Gut Microbiome in Vertebrate Evolution. *Msystems* **2018**, *3*, e00174-17. [[CrossRef](#)] [[PubMed](#)]

12. Zhu, L.; Zhang, Y.; Cui, X.; Zhu, Y.; Dai, Q.; Chen, H.; Liu, G.; Yao, R.; Yang, Z. Host Bias in Diet-Source Microbiome Transmission in Wild Cohabiting Herbivores: New Knowledge for the Evolution of Herbivory and Plant Defense. *Microbiol. Spectr.* **2021**, *9*, e0075621. [[CrossRef](#)] [[PubMed](#)]
13. Wei, F.; Wu, Q.; Hu, Y.; Huang, G.; Nie, Y.; Yan, L. Conservation metagenomics: A new branch of conservation biology. *Sci. China Life Sci.* **2019**, *62*, 168–178. [[CrossRef](#)] [[PubMed](#)]
14. Ley, R.E.; Hamady, M.; Lozupone, C.; Turnbaugh, P.J.; Ramey, R.R.; Bircher, J.S.; Schlegel, M.L.; Tucker, T.A.; Schrenzel, M.D.; Knight, R.; et al. Evolution of mammals and their gut microbes. *Science* **2008**, *320*, 1647–1651. [[CrossRef](#)] [[PubMed](#)]
15. Johnny, T.K.; Puthusseri, R.M.; Bhat, S.G. A primer on metagenomics and next-generation sequencing in fish gut microbiome research. *Aquac. Res.* **2021**, *52*, 4574–4600. [[CrossRef](#)]
16. Kim, P.S.; Shin, N.R.; Lee, J.B.; Kim, M.S.; Whon, T.W.; Hyun, D.W.; Yun, J.H.; Jung, M.J.; Kim, J.Y.; Bae, J.W. Host habitat is the major determinant of the gut microbiome of fish. *Microbiome* **2021**, *9*, 166. [[CrossRef](#)]
17. Austin, B. The bacterial microflora of fish. *Sci. World J.* **2002**, *2*, 558–572. [[CrossRef](#)]
18. Spanggaard, B.; Huber, I.; Nielsen, J.; Nielsen, T.; Appel, K.F.; Gram, L.J.A. The microflora of rainbow trout intestine: A comparison of traditional and molecular identification. *Aquaculture* **2000**, *182*, 1–15. [[CrossRef](#)]
19. Pond, M.J.; Stone, D.M.; Alderman, D.J. Comparison of conventional and molecular techniques to investigate the intestinal microflora of rainbow trout (*Oncorhynchus mykiss*). *Aquaculture* **2006**, *261*, 194–203. [[CrossRef](#)]
20. Nayak, S.K. Role of gastrointestinal microbiota in fish. *Aquac. Res.* **2010**, *41*, 1553–1573. [[CrossRef](#)]
21. Molinari, L.M.; Scoaris, D.; Pedroso, R.B.; Bittencourt, N.D.L.R.; Filho, B. Bacterial microflora in the gastrointestinal tract of Nile tilapia, *Oreochromis niloticus*, cultured in a semi-intensive system. *Acta Sci. Biol. Sci.* **2003**, *25*, 267–271.
22. Saha, S.; Roy, R.N.; Sen, S.K.; Ray, A.K. Characterization of cellulase-producing bacteria from the digestive tract of tilapia, *Oreochromis mossambica* (Peters) and grass carp, *Ctenopharyngodon idella* (Valenciennes). *Aquac. Res.* **2010**, *37*, 380–388. [[CrossRef](#)]
23. Bairagi, A.; Ghosh, K.S.; Sen, S.K.; Ray, A.K. Enzyme producing bacterial flora isolated from fish digestive tracts. *Aquac. Int.* **2002**, *10*, 109–121. [[CrossRef](#)]
24. Clements, K.D. *Gastrointestinal Microbiology: Volume 1 Gastrointestinal Ecosystems and Fermentations*; Mackie, B.A., White, B., Eds.; Springer: Boston, MA, USA, 1997; pp. 156–198.
25. Carda-Diéguez, M.; Mira, A.; Fouz, B. Pyrosequencing survey of intestinal microbiota diversity in cultured sea bass (*Dicentrarchus labrax*) fed functional diets. *FEMS Microbiol. Ecol.* **2014**, *87*, 451–459. [[CrossRef](#)]
26. Desai, A.R.; Links, M.G.; Collins, S.A.; Mansfield, G.S.; Hill, J. Effects of plant-based diets on the distal gut microbiome of rainbow trout (*Oncorhynchus mykiss*). *Aquaculture* **2012**, *350–353*, 134–142. [[CrossRef](#)]
27. Ghanbari, M.W.; Kneifel, J.A.; Domig, K.J. A new view of the fish gut microbiome: Advances from next-generation sequencing. *Aquaculture* **2015**, *448*, 464–475. [[CrossRef](#)]
28. Givens, C.E.; Ransom, B.; Bano, N.; Hollibaugh, J. Comparison of the gut microbiomes of 12 bony fish and 3 shark species. *Mar. Ecol. Prog. Ser.* **2015**, *518*, 209–223. [[CrossRef](#)]
29. Ringø, E.; Sperstad, S.; Myklebust, R.; Refstie, S.; Krogdahl, Å. 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* **2006**, *261*, 829–841. [[CrossRef](#)]
30. Butt, R.L.; Volkoff, H. Gut Microbiota and Energy Homeostasis in Fish. *Front. Endocrinol.* **2019**, *10*, 9. [[CrossRef](#)]
31. Handelsman, J.; Rondon, M.R.; Brady, S.F.; Clardy, J.; Goodman, R.M. Molecular biological access to the chemistry of unknown soil microbes: A new frontier for natural products. *Chem. Biol.* **1998**, *5*, R245–R249. [[CrossRef](#)]
32. Riesenfeld, C.S.; Schloss, P.D.; Handelsman, J. Metagenomics: Genomic analysis of microbial communities. *Annu. Rev. Genet.* **2004**, *38*, 525–552. [[CrossRef](#)] [[PubMed](#)]
33. Yukgehnaish, K.; Kumar, P.; Sivachandran, P.; Marimuthu, K.; Arshad, A.; Paray, B.A.; Arockiaraj, J. Gut microbiota metagenomics in aquaculture: Factors influencing gut microbiome and its physiological role in fish. *Rev. Aquac.* **2020**, *12*, 1903–1927. [[CrossRef](#)]
34. Méndez-Pérez, R.; García-López, R.; Bautista-López, J.S.; Vázquez-Castellanos, J.F.; Peña-Marín, E.S.; Martínez-García, R.; Domínguez-Rodríguez, V.I.; Adams-Schroeder, R.H.; Baltierra-Trejo, E.; Valdés, C.M.; et al. Gut Microbiome Analysis In Adult Tropical Gars (*Atractosteus tropicus*). *bioRxiv* **2019**. [[CrossRef](#)]
35. Zhang, G.; Li, J.; Zhang, J.; Liang, X.; Zhang, X.; Wang, T.; Yin, S. Integrated Analysis of Transcriptomic, miRNA and Proteomic Changes of a Novel Hybrid Yellow Catfish Uncovers Key Roles for miRNAs in Heterosis. *Mol. Cell. Proteom. MCP* **2019**, *18*, 1437–1453. [[CrossRef](#)]
36. Liu, S.; Luo, J.; Chai, J.; Ren, L.; Zhou, Y.; Huang, F.; Liu, X.; Chen, Y.; Zhang, C.; Tao, M.; et al. Genomic incompatibilities in the diploid and tetraploid offspring of the goldfish × common carp cross. *Proc. Natl. Acad. Sci. USA* **2016**, *113*, 1327–1332. [[CrossRef](#)]
37. Zhang, G.; Tao, P.; Chen, J.; Wang, R.; Zang, X.; Yin, S. The complete mitochondrial genome of the hybrid of *Pelteobagrus fulvidraco* (♀) × *Pelteobagrus vachelli* (♂). *Mitochondrial DNA Part A DNA Mapp. Seq. Anal.* **2016**, *27*, 4191–4192. [[CrossRef](#)]
38. Gui, J. Scientific frontiers and hot issues in hydrobiology. *Chin. Sci. Bull.* **2015**, *60*, 2051–2057. [[CrossRef](#)]
39. Li, W.; Liu, J.; Tan, H.; Yang, C.; Ren, L.; Liu, Q.; Wang, S.; Hu, F.; Xiao, J.; Zhao, R.; et al. Genetic Effects on the Gut Microbiota Assemblages of Hybrid Fish From Parents With Different Feeding Habits. *Front. Microbiol.* **2018**, *9*, 2972. [[CrossRef](#)]
40. Li, X.; Yu, Y.; Li, C.; Yan, Q. Comparative study on the gut microbiotas of four economically important Asian carp species. *Sci. China Life Sci.* **2018**, *61*, 696–705. [[CrossRef](#)]

41. Zhong, X.; Wang, X.; Zhou, T.; Jin, Y.; Tan, S.; Jiang, C.; Geng, X.; Li, N.; Shi, H.; Zeng, Q.; et al. Genome-Wide Association Study Reveals Multiple Novel QTL Associated with Low Oxygen Tolerance in Hybrid Catfish. *Mar. Biotechnol.* **2017**, *19*, 379–390. [[CrossRef](#)]
42. McGinnity, P.; Prodöhl, P.; Ferguson, A.; Hynes, R.; Maoiléidigh, N.O.; Baker, N.; Cotter, D.; O’Hea, B.; Cooke, D.; Rogan, G.; et al. Fitness reduction and potential extinction of wild populations of Atlantic salmon, *Salmo salar*, as a result of interactions with escaped farm salmon. *Proc. Biol. Sci.* **2003**, *270*, 2443–2450. [[CrossRef](#)] [[PubMed](#)]
43. Solberg, M.F.; Kvamme, B.O.; Nilsen, F.; Glover, K.A. Effects of environmental stress on mRNA expression levels of seven genes related to oxidative stress and growth in Atlantic salmon *Salmo salar* L. of farmed, hybrid and wild origin. *BMC Res. Notes* **2012**, *5*, 672. [[CrossRef](#)] [[PubMed](#)]
44. Wang, J.; Gaughan, S.; Lamer, J.T.; Deng, C.; Hu, W.; Wachholtz, M.; Qin, S.; Nie, H.; Liao, X.; Ling, Q.; et al. Resolving the genetic paradox of invasions: Preadapted genomes and postintroduction hybridization of bigheaded carps in the Mississippi River Basin. *Evol. Appl.* **2020**, *13*, 263–277. [[CrossRef](#)] [[PubMed](#)]
45. Brucker, R.M.; Bordenstein, S.R. Speciation by symbiosis. *Trends Ecol. Evol.* **2012**, *27*, 443–451. [[CrossRef](#)]
46. Wang, J.; Kalyan, S.; Steck, N.; Turner, L.M.; Harr, B.; Künzel, S.; Vallier, M.; Häsler, R.; Franke, A.; Oberg, H.H.; et al. Analysis of intestinal microbiota in hybrid house mice reveals evolutionary divergence in a vertebrate hologenome. *Nat. Commun.* **2015**, *6*, 6440. [[CrossRef](#)]
47. Janson, E.M.; Stireman, J.O., 3rd; Singer, M.S.; Abbot, P. Phytophagous insect-microbe mutualisms and adaptive evolutionary diversification. *Evol. Int. J. Org. Evol.* **2008**, *62*, 997–1012. [[CrossRef](#)]
48. Guivier, E.; Martin, J.-F.; Pech, N.; Ungaro, A.; Chappaz, R.; Gilles, A. Microbiota Diversity within and between the Tissues of Two Wild Interbreeding Species. *Microb. Ecol.* **2018**, *75*, 799–810. [[CrossRef](#)]
49. Talwar, C.; Nagar, S.; Lal, R.; Negi, R.K. Fish Gut Microbiome: Current Approaches and Future Perspectives. *Indian J. Microbiol.* **2018**, *58*, 397–414. [[CrossRef](#)]
50. Tran, N.T.; Wang, G.-T.; Wu, S.-G. A review of intestinal microbes in grass carp *Ctenopharyngodon idellus* (Valenciennes). *Aquac. Res.* **2017**, *48*, 3287–3297. [[CrossRef](#)]
51. Tan, H.Y.; Chen, S.W.; Hu, S.Y. Improvements in the growth performance, immunity, disease resistance, and gut microbiota by the probiotic *Rummeliibacillus stabekisii* in Nile tilapia (*Oreochromis niloticus*). *Fish Shellfish Immunol.* **2019**, *92*, 265–275. [[CrossRef](#)]
52. Giatsis, C.; Sipkema, D.; Ramiro-Garcia, J.; Bacanu, G.M.; Abernathy, J.; Verreth, J.; Smidt, H.; Verdegem, M. Probiotic legacy effects on gut microbial assembly in tilapia larvae. *Sci. Rep.* **2016**, *6*, 33965. [[CrossRef](#)] [[PubMed](#)]
53. Geraylou, Z.; Souffreau, C.; Rurangwa, E.; De Meester, L.; Courtin, C.M.; Delcour, J.A.; Buyse, J.; Ollevier, F. Effects of dietary arabinoxylan-oligosaccharides (AXOS) and endogenous probiotics on the growth performance, non-specific immunity and gut microbiota of juvenile Siberian sturgeon (*Acipenser baerii*). *Fish Shellfish Immunol.* **2013**, *35*, 766–775. [[CrossRef](#)] [[PubMed](#)]
54. Xiong, J.; Wu, Z.; Zhang, P.; Qu, Y.; Fu, S.; Liu, J.; Chen, X. Effects of dietary xylo-oligosaccharide on intestinal microflora of grass carp (*Ctenopharyngodon idellus*). *Microbiology* **2011**, *38*, 317–321.
55. Xia, Y.; Lu, M.; Chen, G.; Cao, J.; Gao, F.; Wang, M.; Liu, Z.; Zhang, G.; Zhu, H.; Yi, M. Effects of dietary *Lactobacillus rhamnosus* JCM1136 and *Lactococcus lactis* subsp. *lactis* JCM5805 on the growth, intestinal microbiota, morphology, immune response and disease resistance of juvenile Nile tilapia, *Oreochromis niloticus*. *Fish Shellfish Immunol.* **2018**, *76*, 368–379. [[CrossRef](#)]
56. Anderson, D.P.; Moritomo, T.; de Grooth, R. Neutrophil, glass-adherent, nitroblue tetrazolium assay gives early indication of immunization effectiveness in rainbow trout. *Veter Immunol. Immunopathol.* **1992**, *30*, 419–429. [[CrossRef](#)]
57. Li, W.; Shen, T.; Chen, N.; Deng, B.; Fu, L.; Zhou, X. Effects of dietary *Bacillus subtilis* on digestive enzyme activity and intestinal microflora in grass carp *Ctenopharyngodon idellus*. *J. Dalian Ocean Univ.* **2012**, *27*, 221–225.
58. Wang, Y. Use of probiotics *Bacillus coagulans*, *Rhodopseudomonas palustris* and *Lactobacillus acidophilus* as growth promoters in grass carp (*Ctenopharyngodon idella*) fingerlings. *Aquac. Nutr.* **2011**, *17*, E372–E378. [[CrossRef](#)]
59. Wu, Z.X.; Feng, X.; Xie, L.L.; Peng, X.Y.; Yuan, J.; Chen, X.X. Effect of probiotic *Bacillus subtilis* Ch9 for grass carp, *Ctenopharyngodon idella* (Valenciennes, 1844), on growth performance, digestive enzyme activities and intestinal microflora. *J. Appl. Ichthyol.* **2012**, *28*, 721–727. [[CrossRef](#)]
60. Zhou, Y.; Yuan, X.C.; Liang, X.F.; Fang, L.; Li, J.; Guo, X.Z.; Bai, X.L.; He, S. Enhancement of growth and intestinal flora in grass carp: The effect of exogenous cellulase. *Aquaculture* **2013**, *416*, 1–7. [[CrossRef](#)]
61. Yuan, X.; Zhou, Y.; Liang, X.F.; Guo, X.; Fang, L.; Li, J.; Liu, L.; Li, B. Effect of dietary glutathione supplementation on the biological value of rapeseed meal to juvenile grass carp, *Ctenopharyngodon idellus*. *Aquac. Nutr.* **2015**, *21*, 73–84. [[CrossRef](#)]
62. Yao, D.; Zou, Q.; Liu, W.; Xie, S.; Zhou, A.; Chen, J.; Zou, J. Effects of *Bacillus licheniformis* and xylo-oligosaccharide on growth performance, intestinal microflora and enzyme activities in grass carp *Ctenopharyngodon idella*. *J. Dalian Ocean Univ.* **2014**, *29*, 136–140.
63. Koo, H.; Hakim, J.A.; Powell, M.L.; Kumar, R.; Eipers, P.G.; Morrow, C.D.; Crowley, M.; Lefkowitz, E.J.; Watts, S.A.; Bej, A.K. Metagenomics approach to the study of the gut microbiome structure and function in zebrafish *Danio rerio* fed with gluten formulated diet. *J. Microbiol. Methods* **2017**, *135*, 69–76. [[CrossRef](#)] [[PubMed](#)]
64. Rurangwa, E.; Sipkema, D.; Kals, J.; Ter Veld, M.; Forlenza, M.; Bacanu, G.M.; Smidt, H.; Palstra, A.P. Impact of a novel protein meal on the gastrointestinal microbiota and the host transcriptome of larval zebrafish *Danio rerio*. *Front. Physiol.* **2015**, *6*, 133. [[CrossRef](#)] [[PubMed](#)]

65. Udayangani, R.M.C.; Dananjaya, S.H.S.; Nikapitiya, C.; Heo, G.-J.; Lee, J.; De Zoysa, M. Metagenomics analysis of gut microbiota and immune modulation in zebrafish (*Danio rerio*) fed chitosan silver nanocomposites. *Fish Shellfish Immunol.* **2017**, *66*, 173–184. [CrossRef]
66. Carlson, J.M.; Leonard, A.B.; Hyde, E.R.; Petrosino, J.F.; Primm, T.P. Microbiome disruption and recovery in the fish *Gambusia affinis* following exposure to broad-spectrum antibiotic. *Infect. Drug Resist.* **2017**, *10*, 143–154. [CrossRef]
67. Michl, S.C.; Ratten, J.M.; Beyer, M.; Hasler, M.; LaRoche, J.; Schulz, C. The malleable gut microbiome of juvenile rainbow trout (*Oncorhynchus mykiss*): Diet-dependent shifts of bacterial community structures. *PLoS ONE* **2017**, *12*, e0177735. [CrossRef]
68. Huyben, D.; Nyman, A.; Vidaković, A.; Passoth, V.; Moccia, R.; Kiessling, A.; Dicksved, J.; Lundh, T. Effects of dietary inclusion of the yeasts *Saccharomyces cerevisiae* and *Wickerhamomyces anomalus* on gut microbiota of rainbow trout. *Aquaculture* **2017**, *473*, 528–537. [CrossRef]
69. Lyons, P.P.; Turnbull, J.F.; Dawson, K.A.; Crumlish, M. Effects of low-level dietary microalgae supplementation on the distal intestinal microbiome of farmed rainbow trout *Oncorhynchus mykiss* (Walbaum). *Aquac. Res.* **2017**, *48*, 2438–2452. [CrossRef]
70. Zhai, Q.; Yu, L.; Li, T.; Zhu, J.; Zhang, C.; Zhao, J.; Zhang, H.; Chen, W. Effect of dietary probiotic supplementation on intestinal microbiota and physiological conditions of Nile tilapia (*Oreochromis niloticus*) under waterborne cadmium exposure. *Antonie Van Leeuwenhoek* **2017**, *110*, 501–513. [CrossRef]
71. Yu, L.; Qiao, N.; Li, T.; Yu, R.; Chen, W.J.P. Dietary supplementation with probiotics regulates gut microbiota structure and function in Nile tilapia exposed to aluminum. *PeerJ* **2019**, *7*, e6963. [CrossRef]
72. Hortillosa, E.; Amar, M.; Nuñal, S.; Pedroso, F.; Ferriols, V.M.E. Effects of putative dietary probiotics from the gut of milkfish (*Chanos chanos*) on the growth performance and intestinal enzymatic activities of juvenile Nile tilapia (*Oreochromis niloticus*). *Aquac. Res.* **2021**, *53*, 98–108. [CrossRef]
73. Zhang, M.; Dong, B.; Lai, X.; Chen, Z.; Hou, L.; Shu, R.; Huang, Y.; Shu, H. Effects of *Clostridium butyricum* on growth, digestive enzyme activity, antioxidant capacity and gut microbiota in farmed tilapia (*Oreochromis niloticus*). *Aquac. Res.* **2021**, *52*, 1573–1584. [CrossRef]
74. Foysal, J.; Alam, M.; Momtaz, F.; Chaklader, M.R.; Siddik, M.A.B.; Rahman, M. Dietary supplementation of garlic (*Allium sativum*) modulates gut microbiota and health status of tilapia (*Oreochromis niloticus*) against *Streptococcus iniae* infection. *Aquac. Res.* **2019**, *50*, 2107–2116. [CrossRef]
75. Tachibana, L.; Telli, G.S.; Dias, D.d.C.; Gonçalves, G.S.; Guimarães, M.C.; Ishikawa, C.M.; Cavalcante, R.B.; Natori, M.M.; Fernandez Alarcon, M.F.; Tapia-Paniagua, S.; et al. *Bacillus subtilis* and *Bacillus licheniformis* in diets for Nile tilapia (*Oreochromis niloticus*): Effects on growth performance, gut microbiota modulation and innate immunology. *Aquac. Res.* **2021**, *52*, 1630–1642. [CrossRef]
76. Liao, Q.; Zhen, Y.; Qin, Y.; Jiang, Q.; Lan, T.; Huang, L.; and Shen, P. Effects of dietary *Metschnikowia* sp. GXUS03 on growth, immunity, gut microbiota and *Streptococcus agalactiae* resistance of Nile tilapia (*Oreochromis niloticus*). *Aquac. Res.* **2022**, *53*, 1918–1927. [CrossRef]
77. Piazzon, M.C.; Caldúch-Giner, J.A.; Fouz, B.; Estensoro, I.; Simó-Mirabet, P.; Puyalto, M.; Karalazos, V.; Palenzuela, O.; Sitjà-Bobadilla, A.; Pérez-Sánchez, J. Under control: How a dietary additive can restore the gut microbiome and proteomic profile, and improve disease resilience in a marine teleostean fish fed vegetable diets. *Microbiome* **2017**, *5*, 164. [CrossRef] [PubMed]
78. Legrand, T.; Catalano, S.R.; Wos-Oxley, M.L.; Wynne, J.W.; Weyrich, L.S.; Oxley, A.P.A. Antibiotic-induced alterations and repopulation dynamics of yellowtail kingfish microbiota. *Anim. Microbiome* **2020**, *2*, 26. [CrossRef] [PubMed]
79. Sáenz, J.S.; Marques, T.V.; Barone, R.S.C.; Cyrino, J.E.P.; Kublik, S.; Nesme, J.; Schloter, M.; Rath, S.; Vestergaard, G. Oral administration of antibiotics increased the potential mobility of bacterial resistance genes in the gut of the fish *Piaractus mesopotamicus*. *Microbiome* **2019**, *7*, 24. [CrossRef]
80. Munir, M.B.; Marsh, T.L.; Blaud, A.; Hashim, R.; Janti Anak Joshua, W.; Mohd Nor, S.A. Analysing the effect of dietary prebiotics and probiotics on gut bacterial richness and diversity of Asian snakehead fingerlings using T-RFLP method. *Aquac. Res.* **2018**, *49*, 3350–3361. [CrossRef]
81. Meng, X.; Hu, W.; Wu, S.; Zhu, Z.; Lu, R.; Yang, G.; Qin, C.; Yang, L.; Nie, G. Chinese yam peel enhances the immunity of the common carp (*Cyprinus carpio* L.) by improving the gut defence barrier and modulating the intestinal microflora. *Fish Shellfish Immunol.* **2019**, *95*, 528–537. [CrossRef]
82. Reyshari, A.; Mohammadiarm, H.; Mohammadian, T.; Mozanzadeh, M.T. Effects of sodium diformate on growth performance, gut microflora, digestive enzymes and innate immunological parameters of Asian sea bass (*Lates calcarifer*) juveniles. *Aquac. Nutr.* **2019**, *25*, 1135–1144. [CrossRef]
83. Guimarães, M.C.; Moriñigo, M.Á.; Moyano, F.J.; Tachibana, L. Oral administration of *Bacillus subtilis* and *Lactobacillus plantarum* modulates the gut microbiota and increases the amylase activity of Nile tilapia (*Oreochromis niloticus*). *Aquac. Int.* **2021**, *29*, 91–104. [CrossRef]
84. Psafakis, P.; Meziti, A.; Berillis, P.; Mente, E.; Kormas, K.A.; Karapanagiotidis, I.T. Effects of Dietary Fishmeal Replacement by Poultry By-Product Meal and Hydrolyzed Feather Meal on Liver and Intestinal Histomorphology and on Intestinal Microbiota of Gilthead Seabream (*Sparus aurata*). *Appl. Sci.* **2021**, *11*, 8806. [CrossRef]
85. Rimoldi, S.; Gini, E.; Koch, J.F.A.; Iannini, F.; Brambilla, F.; Terova, G. Effects of hydrolyzed fish protein and autolyzed yeast as substitutes of fishmeal in the gilthead sea bream (*Sparus aurata*) diet, on fish intestinal microbiome. *BMC Vet. Res.* **2020**, *16*, 118.

86. Rimoldi, S.; Torrecillas, S.; Montero, D.; Gini, E.; Makol, A.; Valdenegro, V.V.; Izquierdo, M.; Terova, G. Assessment of dietary supplementation with galactomannan oligosaccharides and phytogenics on gut microbiota of European sea bass (*Dicentrarchus Labrax*) fed low fishmeal and fish oil based diet. *PLoS ONE* **2020**, *15*, e0231494. [[CrossRef](#)]
87. Abid, A.; Davies, S.J.; Waines, P.; Emery, M.; Castex, M.; Gioacchini, G.; Carnevali, O.; Bickerdike, R.; Romero, J.; Merrifield, D.L. Dietary synbiotic application modulates Atlantic salmon (*Salmo salar*) intestinal microbial communities and intestinal immunity. *Fish Shellfish Immunol.* **2013**, *35*, 1948–1956. [[CrossRef](#)]
88. Pereira, G.d.V.; Pereira, S.A.; Soares, A.; Mourinho, J.L.P.; Merrifield, D. Autochthonous probiotic bacteria modulate intestinal microbiota of Pirarucu, *Arapaima gigas*. *J. World Aquac. Soc.* **2019**, *50*, 1152–1167. [[CrossRef](#)]
89. Xie, M.; Zhou, W.; Xie, Y.; Li, Y.; Zhang, Z.; Yang, Y.; Olsen, R.E.; Ran, C.; Zhou, Z. Effects of *Cetobacterium somerae* fermentation product on gut and liver health of common carp (*Cyprinus carpio*) fed diet supplemented with ultra-micro ground mixed plant proteins. *Aquaculture* **2021**, *543*, 736943. [[CrossRef](#)]
90. Xu, Q.; Yang, Z.; Chen, S.; Zhu, W.; Xiao, S.; Liu, J.; Wang, H.; Lan, S. Effects of Replacing Dietary Fish Meal by Soybean Meal Co-Fermented Using *Bacillus subtilis* and *Enterococcus faecium* on Serum Antioxidant Indices and Gut Microbiota of Crucian Carp *Carassius auratus*. *Fishes* **2022**, *7*, 54. [[CrossRef](#)]
91. González-Félix, M.L.; Gatlin, D.M.; Urquidez-Bejarano, P.; de la Reé-Rodríguez, C.; Duarte-Rodríguez, L.; Sánchez, F.; Casas-Reyes, A.; Yamamoto, F.Y.; Ochoa-Leyva, A.; Perez-Velazquez, M. Effects of commercial dietary prebiotic and probiotic supplements on growth, innate immune responses, and intestinal microbiota and histology of *Totoaba macdonaldi*. *Aquaculture* **2018**, *491*, 239–251. [[CrossRef](#)]
92. Larios-Soriano, E.; Zavala, R.C.; López, L.M.; Gómez-Gil, B.; Ramírez, D.T.; Sanchez, S.; Canales, K.; Galaviz, M.A. Soy protein concentrate effects on gut microbiota structure and digestive physiology of *Totoaba macdonaldi*. *J. Appl. Microbiol.* **2022**, *132*, 1384–1396. [[CrossRef](#)] [[PubMed](#)]
93. Xu, J.; Xie, S.; Chi, S.; Zhang, S.; Cao, J.; Tan, B. Short-term dietary antibiotics altered the intestinal microbiota and improved the lipid metabolism in hybrid grouper fed medium and high-lipid diets. *Aquaculture* **2022**, *547*, 737453. [[CrossRef](#)]
94. Zhou, S.; Song, D.; Zhou, X.; Mao, X.; Zhou, X.; Wang, S.; Wei, J.; Huang, Y.; Wang, W.; Xiao, S.-M.; et al. Characterization of *Bacillus subtilis* from gastrointestinal tract of hybrid Hulong grouper (*Epinephelus fuscoguttatus* × *E. lanceolatus*) and its effects as probiotic additives. *Fish Shellfish Immunol.* **2019**, *84*, 1115–1124. [[CrossRef](#)] [[PubMed](#)]
95. Liu, W.; Wang, X.; Chen, D.; Wang, Y.; Zhang, A.; Zhou, H. Comparison of adhesive gut bacteria composition, immunity, and disease resistance in juvenile hybrid tilapia fed two different *Lactobacillus* strains. *Fish Shellfish Immunol.* **2013**, *35*, 54–62. [[CrossRef](#)]
96. Wu, X.; Teame, T.; Hao, Q.; Ding, Q.; Liu, H.; Ran, C.; Yang, Y.; Zhang, Y.; Zhou, Z.; Duan, M.; et al. Use of a paraprobiotic and postbiotic feed supplement (HWF™) improves the growth performance, composition and function of gut microbiota in hybrid sturgeon (*Acipenser baerii* × *Acipenser schrenckii*). *Fish Shellfish Immunol.* **2020**, *104*, 36–45. [[CrossRef](#)]
97. Hahor, W.; Thongprajukaew, K.; Suanyuk, N. Effects of dietary supplementation of oligosaccharides on growth performance, gut health and immune response of hybrid catfish (*Pangasianodon gigas* × *Pangasianodon hypophthalmus*). *Aquaculture* **2019**, *507*, 97–107. [[CrossRef](#)]
98. Wang, Q.; Ayiku, S.; Liu, H.; Tan, B.; Dong, X.; Chi, S.; Yang, Q.; Zhang, S.; Zhou, W. Effects of dietary ESTAQUA® yeast culture supplementation on growth, immunity, intestinal microbiota and disease-resistance against *Vibrio harveyi* in hybrid grouper (♀*Epinephelus fuscoguttatus* × ♂*E. lanceolatus*). *Aquac. Rep.* **2022**, *22*, 100922. [[CrossRef](#)]
99. Xu, G.; Xing, W.; Li, T.; Ma, Z.; Liu, C.; Jiang, N.; Luo, L. Effects of dietary raffinose on growth, non-specific immunity, intestinal morphology and microbiome of juvenile hybrid sturgeon (*Acipenser baeri* Brandt ♀ × *A. schrenckii* Brandt ♂). *Fish Shellfish Immunol.* **2018**, *72*, 237–246. [[CrossRef](#)]
100. Chen, G.; Yin, B.; Liu, H.; Tan, B.; Dong, X.; Yang, Q.; Chi, S.; Zhang, S. Supplementing Chitosan Oligosaccharide Positively Affects Hybrid Grouper (*Epinephelus fuscoguttatus* & FEMALE; × *E. lanceolatus* & MALE;) Fed Dietary Fish Meal Replacement With Cottonseed Protein Concentrate: Effects on Growth, Gut Microbiota, Antioxidant Function and Immune Response. *Front. Mar. Sci.* **2021**, *8*, 707627. [[CrossRef](#)]
101. Chen, G.; Yin, B.; Liu, H.; Tan, B.; Dong, X.; Yang, Q.; Chi, S.; Zhang, S. Effects of fishmeal replacement with cottonseed protein concentrate on growth, digestive proteinase, intestinal morphology and microflora in pearl gentian grouper (♀*Epinephelus fuscoguttatus* × ♂*Epinephelus lanceolatus*). *Aquac. Res.* **2020**, *51*, 2870–2884. [[CrossRef](#)]
102. Ye, G.; Dong, X.; Yang, Q.; Chi, S.; Liu, H.; Zhang, H.; Tan, B.; Zhang, S. Dietary replacement of fish meal with peanut meal in juvenile hybrid grouper (*Epinephelus fuscoguttatus* ♀ × *Epinephelus lanceolatus* ♂): Growth performance, immune response and intestinal microbiota. *Aquac. Rep.* **2020**, *17*, 100327. [[CrossRef](#)]
103. Ye, G.; Dong, X.; Yang, Q.; Chi, S.; Liu, H.; Zhang, H.; Tan, B.; Zhang, S. Low-gossypol cottonseed protein concentrate used as a replacement of fish meal for juvenile hybrid grouper (*Epinephelus fuscoguttatus* ♀ × *Epinephelus lanceolatus* ♂): Effects on growth performance, immune responses and intestinal microbiota. *Aquaculture* **2020**, *524*, 735309. [[CrossRef](#)]
104. He, Y.; Guo, X.; Tan, B.; Dong, X.; Yang, Q.; Liu, H.; Zhang, S.; Chi, S. Partial fishmeal protein replacement with peptides from swine blood modulates the nutritional status, immune response, and intestinal microbiota of hybrid groupers (female *Epinephelus fuscoguttatus* × male *E. lanceolatus*). *Aquaculture* **2021**, *533*, 736154. [[CrossRef](#)]
105. Fowler, E.C.; Poudel, P.; White, B.; St-Pierre, B.; Brown, M. Effects of a Bioprocessed Soybean Meal Ingredient on the Intestinal Microbiota of Hybrid Striped Bass, *Morone chrysops* × *M. saxatilis*. *Microorganisms* **2021**, *9*, 1032. [[CrossRef](#)]

106. Sevellec, M.; Laporte, M.; Bernatchez, A.; Derome, N.; Bernatchez, L. Evidence for host effect on the intestinal microbiota of whitefish (*Coregonus* sp.) species pairs and their hybrids. *Ecol. Evol.* **2019**, *9*, 11762–11774. [[CrossRef](#)]
107. Zhu, L.; Zhang, Z.; Chen, H.; Lamer, J.T.; Wang, J.; Wei, W.; Fu, L.; Tang, M.; Wang, C.; Lu, G. Gut microbiomes of bigheaded carps and hybrids provide insights into invasion: A hologenome perspective. *Evol. Appl.* **2021**, *14*, 735–745. [[CrossRef](#)]
108. Deng, Y.; Zhang, Y.; Chen, H.; Xu, L.; Wang, Q.; Feng, J. Gut-Liver Immune Response and Gut Microbiota Profiling Reveal the Pathogenic Mechanisms of *Vibrio harveyi* in Pearl Gentian Grouper (*Epinephelus lanceolatus* ♂ × *E. fuscoguttatus* ♀). *Front. Immunol.* **2020**, *11*, 607754. [[CrossRef](#)]
109. He, Y.; Liang, J.; Dong, X.; Yang, Q.; Liu, H.; Zhang, S.; Chi, S.; Tan, B. Glutamine alleviates β-conglycinin-induced enteritis in juvenile hybrid groupers *Epinephelus fuscoguttatus*♀ × *Epinephelus lanceolatus*♂ by suppressing the MyD88/NF-κB pathway. *Aquaculture* **2022**, *549*, 737735. [[CrossRef](#)]
110. Liu, X.; Shi, H.; He, Q.; Lin, F.; Wang, Q.; Xiao, S.; Dai, Y.; Zhang, Y.; Yang, H.; Zhao, H. Effect of starvation and refeeding on growth, gut microbiota and non-specific immunity in hybrid grouper (*Epinephelus fuscoguttatus*♀ × *E. lanceolatus*♂). *Fish Shellfish Immunol.* **2020**, *97*, 182–193. [[CrossRef](#)]
111. Fowler, E.; St-Pierre, B.; Poudel, P.; White, B.; Brown, M. 183 Effects of Protein Supplementation on the Gut Bacterial Community Composition of Hybrid Striped Bass, Morone Chrysops X M. Saxatilis. *J. Anim. Sci.* **2021**, *99*, 88–89. [[CrossRef](#)]
112. Ran, C.; Hu, J.; Liu, W.; Liu, Z.; He, S.; Bui Chau Truc, D.; Nguyen Ngoc, D.; Ooi, E.L.; Zhou, Z. Thymol and Carvacrol Affect Hybrid Tilapia through the Combination of Direct Stimulation and an Intestinal Microbiota-Mediated Effect: Insights from a Germ-Free Zebrafish Model. *J. Nutr.* **2016**, *146*, 1132–1140. [[CrossRef](#)] [[PubMed](#)]
113. Qin, C.; Zhang, Y.; Liu, W.; Xu, L.; Yang, Y.; Zhou, Z. Effects of chito-oligosaccharides supplementation on growth performance, intestinal cytokine expression, autochthonous gut bacteria and disease resistance in hybrid tilapia *Oreochromis niloticus* ♀ × *Oreochromis aureus* ♂. *Fish Shellfish Immunol.* **2014**, *40*, 267–274. [[CrossRef](#)] [[PubMed](#)]
114. Zhu, H.; Qiang, J.; He, J.; Tao, Y.; Bao, J.; Xu, P. Physiological parameters and gut microbiome associated with different dietary lipid levels in hybrid yellow catfish (*Tachysurus fulvidraco*♀ × *Pseudobagrus vachellii*♂). *Comp. Biochem. Physiol. Part D Genom. Proteom.* **2021**, *37*, 100777. [[CrossRef](#)] [[PubMed](#)]
115. Ye, G.; Dong, X.; Yang, Q.; Chi, S.; Liu, H.; Zhang, H.; Tan, B.; Zhang, S. A formulated diet improved digestive capacity, immune function and intestinal microbiota structure of juvenile hybrid grouper (*Epinephelus fuscoguttatus* ♀ × *Epinephelus lanceolatus* ♂) when compared with chilled trash fish. *Aquaculture* **2020**, *523*, 735230. [[CrossRef](#)]
116. Hao, Q.; Teame, T.; Wu, X.; Ding, Q.; Ran, C.; Yang, Y.; Xing, Y.; Zhang, Z.; Zhou, Z. Influence of diet shift from bloodworm to formulated feed on growth performance, gut microbiota structure and function in early juvenile stages of hybrid sturgeon (*Acipenser baerii* × *Acipenser schrenckii*). *Aquaculture* **2021**, *533*, 736165. [[CrossRef](#)]
117. Wang, L.; Tian, Y.; Li, Z.; Li, Z.; Chen, S.; Li, L.; Li, W.; Wang, Q.; Lin, H.; Li, B. Comparison of the gut microbiota composition between asymptomatic and diseased *Epinephelus moara* ♀ × *Epinephelus lanceolatus* ♂ with nervous necrosis virus infection. *Aquac. Res.* **2022**, *53*, 633–641. [[CrossRef](#)]
118. Hlordzi, V.; Wang, J.; Li, T.; Cui, Z.; Tan, B.; Liu, H.; Yang, Q.; Dong, X.; Zhang, S.; Chi, S. Effects of Lower Fishmeal with Hydrolyzed Fish Protein Powder on the Growth Performance and Intestinal Development of Juvenile Pearl Gentian Grouper (*Epinephelus fuscoguttatus* ♀ and *Epinephelus lanceolatus* ♂). *Front. Mar. Sci.* **2022**, *9*, 398. [[CrossRef](#)]
119. Huang, X.; Zhong, L.; Fan, W.; Feng, Y.; Xiong, G.; Liu, S.; Wang, K.; Geng, Y.; Ouyang, P.; Chen, D.; et al. Enteritis in hybrid sturgeon (*Acipenser schrenckii*♂ × *Acipenser baeri*♀) caused by intestinal microbiota disorder. *Aquac. Rep.* **2020**, *18*, 100456. [[CrossRef](#)]
120. Long, S.; You, Y.; Dong, X.; Tan, B.; Zhang, S.; Chi, S.; Yang, Q.; Liu, H.; Xie, S.; Yang, Y.; et al. Effect of dietary oxidized fish oil on growth performance, physiological homeostasis and intestinal microbiome in hybrid grouper (♀*Epinephelus fuscoguttatus* × ♂*Epinephelus lanceolatus*). *Aquac. Rep.* **2022**, *24*, 101130. [[CrossRef](#)]
121. Long, S.; Dong, X.; Yan, X.; Liu, H.; Tan, B.; Zhang, S.; Chi, S.; Yang, Q.; Liu, H.; Yang, Y.; et al. The effect of oxidized fish oil on antioxidant ability, histology and transcriptome in intestine of the juvenile hybrid grouper (♀*Epinephelus fuscoguttatus* × ♂*Epinephelus lanceolatus*). *Aquac. Rep.* **2022**, *22*, 100921. [[CrossRef](#)]
122. Yan, X.; Chen, Y.; Dong, X.; Tan, B.; Liu, H.; Zhang, S.; Chi, S.; Yang, Q.; Liu, H.; Yang, Y. Ammonia Toxicity Induces Oxidative Stress, Inflammatory Response and Apoptosis in Hybrid Grouper (♀*Epinephelus fuscoguttatus* × ♂*E. lanceolatus*). *Front. Mar. Sci.* **2021**, *8*, 100880. [[CrossRef](#)]
123. Wei, H.; Li, R.; Yang, Q.; Tan, B.; Ray, G.W.; Dong, X.; Chi, S.; Liu, H.; Zhang, S. Effects of Zn on growth performance, immune enzyme activities, resistance to disease and intestinal flora for juvenile pearl gentian grouper (*Epinephelus lanceolatus* ♂ × *Epinephelus fuscoguttatus* ♀) under low fishmeal diet. *Aquac. Rep.* **2021**, *21*, 100880. [[CrossRef](#)]
124. Wu, X.; Hao, Q.; Teame, T.; Ding, Q.; Liu, H.; Ran, C.; Yang, Y.; Xia, L.; Wei, S.; Zhou, Z.; et al. Gut microbiota induced by dietary GWF contributes to growth promotion, immune regulation and disease resistance in hybrid sturgeon (*Acipenser baerii* × *Acipenser schrenckii*): Insights from a germ-free zebrafish model. *Aquaculture* **2020**, *520*, 734966. [[CrossRef](#)]
125. Limbu, S.M.; Chen, L.-Q.; Zhang, M.-L.; Du, Z.-Y. A global analysis on the systemic effects of antibiotics in cultured fish and their potential human health risk: A review. *Rev. Aquac.* **2021**, *13*, 1015–1059. [[CrossRef](#)]
126. Sx, A.; Yin, P.; Tian, L.; Liu, Y.; Tan, B.; Niu, J. Interactions between dietary lipid levels and chronic exposure of legal aquaculture dose of sulfamethoxazole in juvenile largemouth bass *Micropterus salmoides*. *Aquat. Toxicol.* **2020**, *229*, 105670.

127. Limbu, S.M.; Ma, Q.; Zhang, M.-L.; Du, Z.-Y. High fat diet worsens the adverse effects of antibiotic on intestinal health in juvenile Nile tilapia (*Oreochromis niloticus*). *Sci. Total Environ.* **2019**, *680*, 169–180. [CrossRef]
128. Zhou, L.; Limbu, S.M.; Qiao, F.; Du, Z.Y.; Zhang, M.J.Z. Influence of Long-Term Feeding Antibiotics on the Gut Health of Zebrafish. *Zebrafish* **2018**, *15*, 340–348. [CrossRef]
129. Nakano, T.; Hayashi, S.; Nagamine, N. Effect of excessive doses of oxytetracycline on stress-related biomarker expression in coho salmon. *Environ. Sci. Pollut. Res. Int.* **2018**, *25*, 7121–7128. [CrossRef]
130. Zhou, Z.C.; Lin, Z.J.; Shuai, X.Y.; Zheng, J.; Meng, L.X.; Zhu, L.; Sun, Y.J.; Shang, W.C.; Chen, H. Temporal variation and sharing of antibiotic resistance genes between water and wild fish gut in a peri-urban river. *J. Environ. Sci.* **2021**, *103*, 12–19. [CrossRef]
131. Carbone, D.; Faggio, C. Importance of prebiotics in aquaculture as immunostimulants. Effects on immune system of *Sparus aurata* and *Dicentrarchus labrax*. *Fish Shellfish Immunol.* **2016**, *54*, 172–178. [CrossRef]
132. Song, S.K.; Beck, B.R.; Kim, D.; Park, J.; Kim, J.; Kim, H.D.; Ringø, E. Prebiotics as immunostimulants in aquaculture: A review. *Fish Shellfish Immunol.* **2014**, *40*, 40–48. [CrossRef]
133. Taverniti, V.; Guglielmetti, S. The immunomodulatory properties of probiotic microorganisms beyond their viability (ghost probiotics: Proposal of paraprobiotic concept). *Genes Nutr.* **2011**, *6*, 261–274. [CrossRef]
134. Xia, Y.; Wang, M.; Gao, F.; Lu, M.; Chen, G. Effects of dietary probiotic supplementation on the growth, gut health and disease resistance of juvenile Nile tilapia (*Oreochromis niloticus*). *Anim. Nutr.* **2020**, *6*, 69–79. [CrossRef]
135. Beck, B.R.; Kim, D.; Jeon, J.; Lee, S.M.; Kim, H.K.; Kim, O.J.; Lee, J.I.; Suh, B.S.; Do, H.K.; Lee, K.H.J.F.; et al. The effects of combined dietary probiotics *Lactococcus lactis* BFE920 and *Lactobacillus plantarum* FGL0001 on innate immunity and disease resistance in olive flounder (*Paralichthys olivaceus*). *Fish Shellfish Immunol.* **2015**, *42*, 177–183. [CrossRef]
136. Liu, L.; Wu, R.; Zhang, J.; Shang, N.; Li, P. D-Ribose Interferes with Quorum Sensing to Inhibit Biofilm Formation of *Lactobacillus paraplantarum* L-ZS9. *Front. Microbiol.* **2017**, *8*, 1860. [CrossRef]
137. Chai, P.C.; Song, X.L.; Chen, G.F.; Xu, H.; Huang, J. Dietary supplementation of probiotic Bacillus PC465 isolated from the gut of *Fenneropenaeus chinensis* improves the health status and resistance of *Litopenaeus vannamei* against white spot syndrome virus. *Fish Shellfish Immunol.* **2016**, *54*, 602–611. [CrossRef]
138. Staykov, Y.; Spring, P.; Denev, S.; Sweetman, J.W. Effect of a mannan oligosaccharide on the growth performance and immune status of rainbow trout (*Oncorhynchus mykiss*). *Aquac. Int.* **2007**, *15*, 153–161. [CrossRef]
139. Folligné, B.; Dewulf, J.; Breton, J.; Claisse, O.; Lonvaud-Funel, A.; Pot, B. Probiotic properties of non-conventional lactic acid bacteria: Immunomodulation by *Oenococcus oeni*. *Int. J. Food Microbiol.* **2010**, *140*, 136–145. [CrossRef]
140. Panigrahi, A.; Kiron, V.; Satoh, S.; Hirono, I.; Kobayashi, T.; Sugita, H.; Puangkaew, J.; Aoki, T. Immune modulation and expression of cytokine genes in rainbow trout *Oncorhynchus mykiss* upon probiotic feeding. *Dev. Comp. Immunol.* **2007**, *31*, 372–382. [CrossRef]
141. Yang, M.; Wang, X.; Chen, D.; Wang, Y.; Zhang, A.; Zhou, H. TGF- β 1 exerts opposing effects on grass carp leukocytes: Implication in teleost immunity, receptor signaling and potential self-regulatory mechanisms. *PLoS ONE* **2012**, *7*, e35011. [CrossRef]
142. Kadowaki, T.; Yasui, Y.; Takahashi, Y.; Kohchi, C.; Soma, G.; Inagawa, H. Comparative immunological analysis of innate immunity activation after oral administration of wheat fermented extract to teleost fish. *Anticancer Res.* **2009**, *29*, 4871–4877. [PubMed]
143. He, S.; Liu, W.; Zhou, Z. Evaluation of probiotic strain *Bacillus subtilis* C-3102 as a feed supplement for koi carp (*Cyprinus carpio*). *J. Aquac. Res. Dev.* **2011**, *51*, 005. [CrossRef]
144. Gibson, G.R.; Probert, H.M.; Loo, J.V.; Rastall, R.A.; Roberfroid, M.B. Dietary modulation of the human colonic microbiota: Updating the concept of prebiotics. *Nutr. Res. Rev.* **2004**, *17*, 259–275. [CrossRef] [PubMed]
145. Gibson, G.R.; Roberfroid, M.B. Dietary Modulation of the Human Colonic Microbiota: Introducing the Concept of Prebiotics. *J. Nutr.* **1995**, *125*, 1401–1412. [CrossRef]
146. Hoseinifar, S.H.; Zoheiri, F.; Dadar, M.; Rufchaei, R.; Ringø, E. Dietary galactooligosaccharide elicits positive effects on non-specific immune parameters and growth performance in Caspian white fish (*Rutilus frisii kutum*) fry. *Fish Shellfish Immunol.* **2016**, *56*, 467–472. [CrossRef]
147. Watzl, B.; Girrbach, S.; Roller, M. Inulin, oligofructose and immunomodulation. *Br. J. Nutr.* **2005**, *93* (Suppl. 1), S49–S55. [CrossRef]
148. Hoseinifar, S.H.; Khalili, M.; Rostami, H.K.; Esteban, M. Immunology, Dietary galactooligosaccharide affects intestinal microbiota, stress resistance, and performance of Caspian roach (*Rutilus rutilus*) fry. *Fish Shellfish Immunol.* **2013**, *35*, 1416–1420. [CrossRef]
149. Hoseinifar, S.H.; Sharifian, M.; Vesaghi, M.J.; Khalili, M.; Esteban, M. The effects of dietary xylooligosaccharide on mucosal parameters, intestinal microbiota and morphology and growth performance of Caspian white fish (*Rutilus frisii kutum*) fry—ScienceDirect. *Fish Shellfish Immunol.* **2014**, *39*, 231–236. [CrossRef]
150. Ali, S.S.R.; Ambasankar, K.; Nandakumar, S.; Praveena, P.E.; Syamadaya, J. Effect of dietary prebiotic inulin on growth, body composition and gut microbiota of Asian seabass (*Lates calcarifer*). *Anim. Feed Sci. Technol.* **2016**, *217*, 87–94.
151. Guerreiro, I.; Serra, C.R.; Enes, P.; Couto, A.; Salvador, A.; Costas, B.; Oliva-Teles, A. Effect of short chain fructooligosaccharides (scFOS) on immunological status and gut microbiota of gilthead sea bream (*Sparus aurata*) reared at two temperatures. *Fish Shellfish Immunol.* **2016**, *49*, 122–131. [CrossRef]
152. Lp, A.; Yúfera, M.; Navarro-Guillén, C.; Moyano, F.J.; Soverini, M.; D’Amico, F.; Candela, M.; Fontanillas, R.; Gatta, P.P.; Bonaldo, A. Effects of calcium carbonate inclusion in low fishmeal diets on growth, gastrointestinal pH, digestive enzyme activity and gut bacterial community of European sea bass (*Dicentrarchus labrax* L.) juveniles. *Aquaculture* **2019**, *510*, 283–292.

153. Li, P.; Gatlin, D.M. Dietary brewers yeast and the prebiotic Grobionic™AE influence growth performance, immune responses and resistance of hybrid striped bass (*Morone chrysops* × *M. saxatilis*) to *Streptococcus iniae* infection. *Aquaculture* **2004**, *231*, 445–456. [[CrossRef](#)]
154. Cui, L.; Xu, W.; Ai, Q.; Wang, D.; Mai, K. Effects of dietary chitosan oligosaccharide complex with rare earth on growth performance and innate immune response of turbot, *Scophthalmus maximus* L. *Aquac. Res.* **2013**, *44*, 683–690. [[CrossRef](#)]
155. Lin, S.; Mao, S.; Yong, G.; Lin, L.; Li, L.; Yu, P. Effects of dietary chitosan oligosaccharides and *Bacillus coagulans* on the growth, innate immunity and resistance of koi (*Cyprinus carpio koi*). *Aquaculture* **2012**, *342–343*, 36–41. [[CrossRef](#)]
156. Luo, L.; Cai, X.; He, C.; Xue, M.; Wu, X.; Cao, H. Immune response, stress resistance and bacterial challenge in juvenile rainbow trouts *Oncorhynchus mykiss* fed diets containing chitosan-oligosaccharides. *Curr. Zool.* **2009**, *55*, 416–422. [[CrossRef](#)]
157. Olsen, R.E.; Myklebust, R.; Kryvi, H.; Mayhew, T.M.; Ringø, E. Damaging effect of dietary inulin on intestinal enterocytes in Arctic charr (*Salvelinus alpinus* L.). *Aquac. Res.* **2001**, *32*, 931–934. [[CrossRef](#)]
158. Tacon, A.G.J.; Metianb, M. Global overview on the use of fish meal and fish oil in industrially compounded aquafeeds: Trends and future prospects. *Aquaculture* **2008**, *285*, 146–158. [[CrossRef](#)]
159. Hardy, R.W.; Tacon, A.G.J. Fish meal: Historical uses, production trends and future outlook for sustainable supplies. *Responsible Mar. Aquac.* **2002**, 311–325.
160. Hardy, R.W. Utilization of plant proteins in fish diets: Effects of global demand and supplies of fishmeal. *Aquac. Res.* **2010**, *41*, 770–776. [[CrossRef](#)]
161. Daniel, A. Studies, A review on replacing fish meal in aqua feeds using plant protein sources. *Int. J. Fish. Aquat. Stud.* **2018**, *6*, 164–179.
162. Robinson, E.H.; Li, M.H. Use of Plant Proteins in Catfish Feeds: Replacement of Soybean Meal with Cottonseed Meal and Replacement of Fish Meal with Soybean Meal and Cottonseed Meal. *J. World Aquac. Soc.* **1994**, *25*, 271–276. [[CrossRef](#)]
163. Li, Y.; Ai, Q.; Mai, K.; Xu, W.; Deng, J.; Cheng, Z. Comparison of high-protein soybean meal and commercial soybean meal partly replacing fish meal on the activities of digestive enzymes and aminotransferases in juvenile Japanese seabass, *Lateolabrax japonicus* (Cuvier, 1828). *Aquac. Res.* **2014**, *45*, 1051–1060. [[CrossRef](#)]
164. Laporte, J.; Trushenski, J. Production performance, stress tolerance and intestinal integrity of sunshine bass fed increasing levels of soybean meal. *J. Anim. Physiol. Anim. Nutr.* **2012**, *96*, 513–526. [[CrossRef](#)] [[PubMed](#)]
165. Baeverfjord, G.T.; Krogdahl, A.J. Development and regression of soybean meal induced enteritis in Atlantic salmon, *Salmo salar* L., distal intestine: A comparison with the intestines of fasted fish. *J. Fish Dis.* **2010**, *19*, 375–387. [[CrossRef](#)]
166. Theodosopoulos, A.N.; Hund, A.K.; Taylor, S.A. Parasites and Host Species Barriers in Animal Hybrid Zones. *Trends Ecol. Evol.* **2019**, *34*, 19–30. [[CrossRef](#)]
167. Dittmer, J.; Bouchon, D. Feminizing Wolbachia influence microbiota composition in the terrestrial isopod *Armadillidium vulgare*. *Sci. Rep.* **2018**, *8*, 6998. [[CrossRef](#)]
168. Zchori-Fein, E.; Faktor, O.; Zeidan, M.; Gottlieb, Y.; Czosnek, H.; Rosen, D. Parthenogenesis-inducing microorganisms in *Aphytis* (Hymenoptera: Aphelinidae). *Insect Mol. Biol.* **1995**, *4*, 173–178. [[CrossRef](#)]
169. Nadal-Jimenez, P.; Griffin, J.S.; Davies, L.; Frost, C.L.; Marcello, M.; Hurst, G.D.D. Genetic manipulation allows in vivo tracking of the life cycle of the son-killer symbiont, *Arsenophonus nasoniae*, and reveals patterns of host invasion, tropism and pathology. *Environ. Microbiol.* **2019**, *21*, 3172–3182. [[CrossRef](#)]
170. Perlmutter, J.I.; Bordenstein, S.R. Microorganisms in the reproductive tissues of arthropods. *Nat. Rev. Microbiol.* **2020**, *18*, 97–111. [[CrossRef](#)]
171. Gebiola, M.; Kelly, S.E.; Hammerstein, P.; Giorgini, M.; Hunter, M.S. Darwin's corollary and cytoplasmic incompatibility induced by *Cardinium* may contribute to speciation in *Encarsia* wasps (Hymenoptera: Aphelinidae). *Evol. Int. J. Org. Evol.* **2016**, *70*, 2447–2458. [[CrossRef](#)]
172. Gatenby, J.B. Symbioticism and the Origin of Species. *Nature* **1928**, *121*, 164–165. [[CrossRef](#)]
173. Miller, A.K.; Westlake, C.S.; Cross, K.L.; Leigh, B.A.; Bordenstein, S.R. The microbiome impacts host hybridization and speciation. *PLoS Biol.* **2021**, *19*, e3001417. [[CrossRef](#)] [[PubMed](#)]
174. Brooks, A.W.; Kohl, K.D.; Brucker, R.M.; van Opstal, E.J.; Bordenstein, S.R. Phylosymbiosis: Relationships and Functional Effects of Microbial Communities across Host Evolutionary History. *PLoS Biol.* **2016**, *14*, e2000225. [[CrossRef](#)] [[PubMed](#)]
175. Tsuchida, T.; Koga, R.; Fukatsu, T. Host plant specialization governed by facultative symbiont. *Science* **2004**, *303*, 1989. [[CrossRef](#)] [[PubMed](#)]
176. Nardon, P.; Grenier, A.M. Serial endosymbiosis theory and weevil evolution: The role of symbiosis. In *Symbiosis as a Source of Evolutionary Innovation: Speciation and Morphogenesis*; Margulis, L., Fester, R., Eds.; MIT Press: Cambridge, MA, USA, 1991; pp. 153–169.
177. Hosokawa, T.; Kikuchi, Y.; Nikoh, N.; Shimada, M.; Fukatsu, T. Strict host-symbiont cospeciation and reductive genome evolution in insect gut bacteria. *PLoS Biol.* **2006**, *4*, e337. [[CrossRef](#)] [[PubMed](#)]
178. Miller, W.J.; Ehrman, L.; Schneider, D. Infectious speciation revisited: Impact of symbiont-depletion on female fitness and mating behavior of *Drosophila paulistorum*. *PLoS Pathog.* **2010**, *6*, e1001214. [[CrossRef](#)]
179. Breeuwer, J.A.; Werren, J.H. Microorganisms associated with chromosome destruction and reproductive isolation between two insect species. *Nature* **1990**, *346*, 558–560. [[CrossRef](#)]

180. Bordenstein, S.R.; O'Hara, F.P.; Werren, J.H. Wolbachia-induced incompatibility precedes other hybrid incompatibilities in *Nasonia*. *Nature* **2001**, *409*, 707–710. [[CrossRef](#)]
181. Brucker, R.M.; Bordenstein, S.R. The hologenomic basis of speciation: Gut bacteria cause hybrid lethality in the genus *Nasonia*. *Science* **2013**, *341*, 667–669. [[CrossRef](#)]
182. Li, Z.; Wright, A.G.; Si, H.; Wang, X.; Qian, W.; Zhang, Z.; Li, G. Changes in the rumen microbiome and metabolites reveal the effect of host genetics on hybrid crosses. *Environ. Microbiol. Rep.* **2016**, *8*, 1016–1023. [[CrossRef](#)]
183. Petri, R.M.; Schwaiger, T.; Penner, G.B.; Beauchemin, K.A.; Forster, R.J.; McKinnon, J.J.; McAllister, T.A. Characterization of the core rumen microbiome in cattle during transition from forage to concentrate as well as during and after an acidotic challenge. *PLoS ONE* **2013**, *8*, e83424. [[CrossRef](#)] [[PubMed](#)]
184. Edwards, J.E.; Schennink, A.; Burden, F.; Long, S.; van Doorn, D.A.; Pellikaan, W.F.; Dijkstra, J.; Saccenti, E.; Smidt, H. Domesticated equine species and their derived hybrids differ in their fecal microbiota. *Anim. Microbiome* **2020**, *2*, 8. [[CrossRef](#)] [[PubMed](#)]
185. Li, W.; Zhou, Z.; Li, H.; Wang, S.; Ren, L.; Hu, J.; Liu, Q.; Wu, C.; Tang, C.; Hu, F.; et al. Successional Changes of Microbial Communities and Host-Microbiota Interactions Contribute to Dietary Adaptation in Allopolyploid Hybrid Fish. *Microb. Ecol.* **2022**. [[CrossRef](#)] [[PubMed](#)]
186. Belkova, N.L.; Sidorova, T.V.; Glyzina, O.Y.; Yakshchenko, V.M.; Sapozhnikova, Y.P.; Bukin, Y.S.; Baturina, O.A.; Sukhanova, L.V. Gut microbiome of juvenile coregonid fishes: Comparison of sympatric species and their F1 hybrids. *Fundam. Appl. Limnol.* **2017**, *189*, 279–290. [[CrossRef](#)]
187. Bahrndorff, S.; Alemu, T.; Alemneh, T.; Nielsen, J.L. The Microbiome of Animals: Implications for Conservation Biology. *Int. J. Genom.* **2016**, *2016*, 5304028. [[CrossRef](#)]
188. Chown, S.L.; Hodgins, K.A.; Griffin, P.C.; Oakeshott, J.G.; Byrne, M.; Hoffmann, A.A. Biological invasions, climate change and genomics. *Evol. Appl.* **2015**, *8*, 23–46. [[CrossRef](#)]
189. Simberloff, D.; Rejmánek, M. *Encyclopedia of Biological Invasions*, 1st ed.; Simberloff, D., Rejmánek, M., Eds.; University of California Press: Oakland, CA, USA, 2011. [[CrossRef](#)]
190. Lefort, M.C.; Boyer, S.; De Romans, S.; Glare, T.; Armstrong, K.; Worner, S. Invasion success of a scarab beetle within its native range: Host range expansion versus host-shift. *PeerJ* **2014**, *2*, e262. [[CrossRef](#)]
191. Lefort, M.C.; Boyer, S.; Glare, T.R. A response to Pennisi—How do gut microbiomes help herbivores, a hint into next-generation biocontrol solutions. *Rethink. Ecol.* **2017**, *1*, 9–13. [[CrossRef](#)]
192. Kim, D.; Thairu, M.W.; Hansen, A.K. Novel Insights into Insect-Microbe Interactions-Role of Epigenomics and Small RNAs. *Front. Plant Sci.* **2016**, *7*, 1164. [[CrossRef](#)]
193. Dlugosch, K.M.; Parker, I.M. Founding events in species invasions: Genetic variation, adaptive evolution, and the role of multiple introductions. *Mol. Ecol.* **2008**, *17*, 431–449. [[CrossRef](#)]
194. Clark, J.S.; Lewis, M.; Horvath, L. Invasion by extremes: Population spread with variation in dispersal and reproduction. *Am. Nat.* **2001**, *157*, 537–554. [[CrossRef](#)] [[PubMed](#)]
195. Ficetola, G.F.; Siesa, M.E.; de Bernardi, F.; Padoa-Schioppa, E. Complex impact of an invasive crayfish on freshwater food webs. *Biodivers. Conserv.* **2012**, *21*, 2641–2651. [[CrossRef](#)]
196. Figueroa, M.E.; Castillo, J.M.; Redondo, S.; Luque, T.; Castellanos, E.M.; Nieva, F.J.; Luque, C.J.; Rubio-Casal, A.E.; Davy, A.J. Facilitated invasion by hybridization of *Sarcocornia* species in a salt-marsh succession. *J. Ecol.* **2003**, *91*, 616–626. [[CrossRef](#)]
197. Llewellyn, M.S.; Boutin, S.; Hoseinifar, S.H.; Derome, N. Teleost microbiomes: The state of the art in their characterization, manipulation and importance in aquaculture and fisheries. *Front. Microbiol.* **2014**, *5*, 207. [[CrossRef](#)]
198. Burns, A.R.; Stephens, W.Z.; Stagaman, K.; Wong, S.; Rawls, J.F.; Guillemin, K.; Bohannan, B.J. Contribution of neutral processes to the assembly of gut microbial communities in the zebrafish over host development. *ISME J.* **2016**, *10*, 655–664. [[CrossRef](#)]
199. Smith, C.C.; Snowberg, L.K.; Caporaso, J.G.; Knight, R.; Bolnick, D.I. Dietary input of microbes and host genetic variation shape among-population differences in stickleback gut microbiota. *ISME J.* **2015**, *9*, 2515–2526. [[CrossRef](#)]
200. Sylvain, F.E.; Derome, N. Vertically and horizontally transmitted microbial symbionts shape the gut microbiota ontogenesis of a skin-mucus feeding discus fish progeny. *Sci. Rep.* **2017**, *7*, 5263. [[CrossRef](#)]
201. Bates, J.M.; Mittge, E.; Kuhlman, J.; Baden, K.N.; Cheesman, S.E.; Guillemin, K. Distinct signals from the microbiota promote different aspects of zebrafish gut differentiation. *Dev. Biol.* **2006**, *297*, 374–386. [[CrossRef](#)]
202. Yan, Q.; Li, J.; Yu, Y.; Wang, J.; He, Z.; Van Nostrand, J.D.; Kempfer, M.L.; Wu, L.; Wang, Y.; Liao, L.; et al. Environmental filtering decreases with fish development for the assembly of gut microbiota. *Environ. Microbiol.* **2016**, *18*, 4739–4754. [[CrossRef](#)]
203. Stephens, W.Z.; Burns, A.R.; Stagaman, K.; Wong, S.; Rawls, J.F.; Guillemin, K.; Bohannan, B.J. The composition of the zebrafish intestinal microbial community varies across development. *ISME J.* **2016**, *10*, 644–654. [[CrossRef](#)]
204. Shin, N.R.; Whon, T.W.; Bae, J.W. Proteobacteria: Microbial signature of dysbiosis in gut microbiota. *Trends Biotechnol.* **2015**, *33*, 496–503. [[CrossRef](#)] [[PubMed](#)]
205. Roeselers, G.; Mittge, E.K.; Stephens, W.Z.; Parichy, D.M.; Cavanaugh, C.M.; Guillemin, K.; Rawls, J.F. Evidence for a core gut microbiota in the zebrafish. *ISME J.* **2011**, *5*, 1595–1608. [[CrossRef](#)] [[PubMed](#)]
206. Sullam, K.E.; Essinger, S.D.; Lozupone, C.A.; O'Connor, M.P.; Rosen, G.L.; Knight, R.; Kilham, S.S.; Russell, J.A. Environmental and ecological factors that shape the gut bacterial communities of fish: A meta-analysis. *Mol. Ecol.* **2012**, *21*, 3363–3378. [[CrossRef](#)] [[PubMed](#)]

207. Wu, S.; Wang, G.; Angert, E.R.; Wang, W.; Li, W.; Zou, H. Composition, diversity, and origin of the bacterial community in grass carp intestine. *PLoS ONE* **2012**, *7*, e30440. [[CrossRef](#)]
208. Wu, S.G.; Tian, J.Y.; Gatesoupe, F.J.; Li, W.X.; Zou, H.; Yang, B.J.; Wang, G.T. Intestinal microbiota of gibel carp (*Carassius auratus gibelio*) and its origin as revealed by 454 pyrosequencing. *World J. Microbiol. Biotechnol.* **2013**, *29*, 1585–1595. [[CrossRef](#)]
209. Wong, S.; Stephens, W.Z.; Burns, A.R.; Stagaman, K.; David, L.A.; Bohannon, B.J.; Guillemin, K.; Rawls, J.F. Ontogenetic Differences in Dietary Fat Influence Microbiota Assembly in the Zebrafish Gut. *Mbio* **2015**, *6*, e00687-15. [[CrossRef](#)]
210. Ye, L.; Amberg, J.; Chapman, D.; Gaikowski, M.; Liu, W.T. Fish gut microbiota analysis differentiates physiology and behavior of invasive Asian carp and indigenous American fish. *ISME J.* **2014**, *8*, 541–551. [[CrossRef](#)]
211. Yang, Y.; Song, W.; Lin, H.; Wang, W.; Du, L.; Xing, W. Antibiotics and antibiotic resistance genes in global lakes: A review and meta-analysis. *Environ. Int.* **2018**, *116*, 60–73. [[CrossRef](#)]