

Accepted Manuscript

Gut microbiota analysis of juvenile genetically improved farmed tilapia (*Oreochromis niloticus*) by dietary supplementation of different resveratrol concentrations

Yao Zheng, Wei Wu, Gengdong Hu, Liping Qiu, Shunlong Meng, Chao Song, Limin Fan, Zhixiang Zhao, Xuwen Bing, Jiazhang Chen



PII: S1050-4648(18)30157-8

DOI: [10.1016/j.fsi.2018.03.040](https://doi.org/10.1016/j.fsi.2018.03.040)

Reference: YFSIM 5195

To appear in: *Fish and Shellfish Immunology*

Received Date: 4 July 2017

Revised Date: 5 March 2018

Accepted Date: 20 March 2018

Please cite this article as: Zheng Y, Wu W, Hu G, Qiu L, Meng S, Song C, Fan L, Zhao Z, Bing X, Chen J, Gut microbiota analysis of juvenile genetically improved farmed tilapia (*Oreochromis niloticus*) by dietary supplementation of different resveratrol concentrations, *Fish and Shellfish Immunology* (2018), doi: 10.1016/j.fsi.2018.03.040.

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

Gut microbiota analysis of juvenile genetically improved farmed tilapia (*Oreochromis niloticus*) by dietary supplementation of different resveratrol concentrations

Yao Zheng^a, Wei Wu^a, Gengdong Hu^a, Liping Qiu^a, Shunlong Meng^a, Chao Song^a, Limin Fan^a, Zhixiang Zhao^b, Xuwen Bing^{a,b}, Jiazhang Chen^{a,b,c*}

^aFreshwater Fisheries Research Center, Chinese Academy of Fishery Sciences/Fishery Eco-Environment Monitoring Center of Lower Reaches of Yangtze River, Ministry of Agriculture/Laboratory of Quality & Safety Risk Assessment for Aquatic Products on Environmental Factors(Wuxi), Ministry of Agriculture, Wuxi Jiangsu 214081;

^bWuxi Fishery College, Nanjing Agricultural University, Wuxi Jiangsu 214081

^cKey Laboratory of Control of Quality and Safety for Aquatic Products, Ministry of Agriculture, PR China

*Corresponding Author:

Freshwater Fisheries Research Center, Chinese Academy of Fishery Sciences, No. 9 Shanshui east Rd., Wuxi, Jiangsu 214081, China, Tel: +86-510-85559936, Fax: +86-510-85559936,

E-mail: chenjz@ffrc.cn (Jiazhang Chen).

ABSTRACT

The genetically improved farmed tilapia (GIFT, *Oreochromis niloticus*) is cultured widely for production of freshwater fish in China, while streptococcosis, likely related to pathogenic infections, occurs frequently in juvenile, mother, and operated GIFT. The gut microbiota plays an important role in nutrient digestibility in animals, and resveratrol (RES) has been used in feed for different freshwater fish species. Therefore, understanding changes in the tilapia gut microbiota across different concentrations of dietary RES supplementation is extremely important. The gut microbiota population in tilapia at 45 d after supplementation with different concentrations (0, 0.025, 0.05, 0.1 g/kg) of dietary RES was assessed by 16S rDNA gene sequencing. A total of 5445 operational taxonomic units were identified from all samples, and 14 phyla and 81 families were identified from all fecal samples. The bacteria of the phylum Firmicutes were significantly enriched in the 0.025 g/kg RES group when compared with the controls. Proteobacteria, Firmicutes and Cyanobacteria were the most dominant three phyla in all samples. With the increasing concentrations, the proportion of beneficial microbial taxa (Acetobacteraceae and Methylobacteriaceae) increased, whereas the proportion of harmful microbial taxa decreased, eg. Streptococcaceae except for 0.1 g/kg RES groups. RES did not affect the richness and diversity in tilapia gut microbiota. These findings provide information on the diversity and differences in GIFT gut microbiota database, and may contribute to developing strategies for management of diseases and long-term sustainability of *O. niloticus* culture.

Key words: resveratrol; GIFT; gut microbiota; 16S rDNA; disease defense

1. Introduction

The GIFT (*Oreochromis niloticus*) is sensitive to the stress of various treatments and is an ideal model for immunological experimentation^[1-2]. The total global production of tilapia reached 1.6 billion tons in 2016 in China; however, the disease streptococcosis caused by *Streptococcus iniae* leads to high losses to the tilapia market amounting to approximately 23 billion dollars per year. A high amount of feed causes tilapia to grow faster between the months of May (July in some place) and September, and an effective strategy to reduce infection and disease is dietary supplementation with functional immunopotentiators. In recent decades, cultured microorganisms were the exclusive source from which to identify antimicrobial activity through their growth in standard laboratory culture medium^[3]. A recent review showed that the gut microbiome of vertebrates plays an integral role in host health by stimulating development of the immune system, aiding in nutrient acquisition, and outcompeting opportunistic pathogens^[4]. For fish, the gut microbiota is a reliable alternative approach to reveal the potential reservoir of antimicrobial compounds in the uncultured microbial community that inhabits the environment^[5]. Researchers intent to find the relationship between gut microbiota with immune response or disease resistance, such evidences have been reported: fulvic acid (using *Paramisgurnus dabryanus* as a fish model)^[5], mixed probiotic spores (*Pangasianodon hypophthalmus*)^[6], *Shewanella putrefaciens* (*Solea senegalensis*)^[7], probiotics (*Pagrus major*)^[8], *Ocimum americanum* essential oil (*Sciaenops ocellatus*)^[9], and probiotics or autolyzed yeast (*Senegalese sole*)^[10].

Download English Version:

<https://daneshyari.com/en/article/8498447>

Download Persian Version:

<https://daneshyari.com/article/8498447>

[Daneshyari.com](https://daneshyari.com)