RELATIONSHIP BETWEEN INTESTINAL FLORA AND CYTOKAINE GENE EXPRESSION IN INTESTINE OF TILAPIA ADMINISTERED WITH PROBIOTICS

Takashi Aoki[1]*, Urara Watanabe[2], Haruko Takeyama[2], Masahira Hattori[2], Wataru Suda[3], Jun-ichi Hikima[4], Masahiro Sakai[4], Sasimanas Unajak[5] Mavichak Rapeepat [6]

[1] Research Organization for Nano & Life Innovation, Waseda University, Tokyo 162-0041, Japan
[2] Department of Life Science and Medical Bioscience, Waseda University, Tokyo 162-8480, Japan
[3] Department of Microbiology and Immunology, Keio University School of Medicine, Tokyo 160-8582, Japan
[4] Department of Biochemistry and Applied Biosciences, Faculty of Agriculture, University of Miyazaki, Miyazaki 889-2192, Japan
[5] Department of Biochemistry, Faculty of Science, Kasetsart University, Bangkok 10930, Thailand
[6] Aquatic Animal Health Research Center, Charoen Pokphand Co. Ltd., Samutsakorn 74000, Thailand

Probiotics is used frequently for prevention of an infection with microorganism in tilapia farm. Analysis of an effect on the bacteria flora in intestinal tract of tilapia administered with probiotics has not been elucidated, and the immunological relationship between the bacteria flora and mucosal cytokines are also important to understand the immunological roles in intestinal flora. In this study, genomic DNAs were extracted from the intestinal contents of cultured tilapia. Bacteria 16S rDNA V1-2 region was amplified from the extracted DNAs using the universal primers set and the amplicon was analyzed by using 454 GS-FLX platform. On the basis of the bacterial 16S rDNA diversity analysis, the operational taxonomic units (OTUs) numbers attained from intestinal contents of cultured tilapia. Six typical genuses, *Clostridium*, *Cetobacterium*, *Mycobacterium*, *Bacteroides*, *Sediminibacterium* and *Nordella* were observed from the tilapia intestinal flora. Six typical species of *Cellulomonas parahominis*, *Dechloromonas* sp. MissR, *Arthrobacter* sp. Rue61a, *Cellulomonas parahominis*, *Thioflavicoccus mobilis* and *Chthoniobacter flavus* were observed from the intestinal flora of tilapia which administered with the probiotics. *Cellulomonas parahominis* was dominant in the intestinal flora of the probiotics-administered tilapia. The expression pattern of cytokine genes including IL-1β, IL-10, IL-12, IL-17A/F, IFN-γ and TNF-α of were analyzed after probiotics administration, and suggesting an interaction between microbiota and cytokine gene expression in the intestine of tilapia treated with probiotics.

Keywords: Intestinal flora; Tilapia, OTU, cytokine gene, microbiota

*Corresponding author.
E-mail address: takashi.aoki65@gmail.com (T. Aoki)