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Biological characterization, expression, and functional analysis of tumor necrosis factor receptor-associated factor 6 in nile tilapia (*Oreochromis niloticus*)

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Abstract

Nile tilapia (Oreochromis niloticus) is a pivotal economic fish that has been plagued by Streptococcus agalactiae infections for many years. Tumor necrosis factor receptor-associated factor 6 (TRAF6) is a crucial adaptor molecule of the interleukin-1 receptor/Toll-like receptor (IL-1/TLR) superfamily, which can trigger downstream signaling cascades involved in innate immunity. In this study, the full-length cDNA of TRAF6 was cloned from O. niloticus (named On-TRAF6), which has an open reading frame of 1716 bp, and encode a polypeptide of 571 amino acids. The predicted amino acid sequence of On-TRAF6 contained the characteristic motifs of TRAF proteins, including a Zinc finger of RING-type, two Zinc fingers of TRAF-type, and a MATH (meprin and TRAF homology) domain. Multiple sequence alignment revealed that On-TRAF6 shares a relatively high level of identity with those of other fishes (64-98%). In healthy tilapia, mRNA expression of On-TRAF6 could be detected in all the examined tissues and the highest expression occurred in the spleen. Moreover, we found that *On-TRAF6* was involved immune response of Nile tilapia following the stimulation with Streptococcus agalactiae and polyinosinic: polycytidylic acid (Poly I:C) when determined by using qPCR. The result of subcellular localization showed that On-TRAF6 distributed in the cytoplasm, and over-expression of On-TRAF6 could strongly activated NF-κB pathway in HEK293T cells. These findings indicated that On-TRAF6 may play an important role in the immune response to intracellular bacteria in Nile tilapia.

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Key words: Oreochromis niloticus; TRAF6; Infection; mRNA expression

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