

THREE HAMP GENES OF NILE TILAPIA WERE DIFFERENTIALLY ACTIVATED IN SPLEEN TO DEFEND AGAINST *STREPTOCOCCUS INIAE* INFECTION

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ABSTRACT

We would like to investigate the molecular mechanism of immune regulation in Nile tilapia (*Oreochromis niloticus*) against critical pathogen *Streptococcus iniae*. Firstly, we established two transcriptomes (15.6 Gb) and analyzed expression changes of 64,181 transcripts of 3-month Nile tilapia (NTOU1 strain) whole fish with no infection and 12-hour post infection by IP injection of 10^4 cfu/g of *S. iniae*. Three Nile tilapia hepatic antimicrobial peptide HAMP cDNAs, encoding 87-a.a. HAMP1, 90- a.a. HAMP2 and 83-a.a. HAMP3, were identified to be differentially regulated. Tissue distribution of three HAMP genes was analyzed in 14 tissues of Nile tilapia with no infection by quantitative RT-PCR. Three Nile tilapia HAMP genes were not only all strongly expressed in the liver but also weakly expressed in the head kidney. HAMP2 was also expressed in spleen but HAMP1 and HAMP3 were little expressed in spleen of Nile tilapia. Furthermore, Nile tilapia NT1 strain adult fish were challenged with *S. iniae* by dose of LD50 (1.5×10^5 CFU/g BW). HAMP1 and HAMP3 were strongly activated in spleen of Nile tilapia from 6 hpi and reached to maximum at 24 hpi then returned to weak expression at 48 hpi. HAMP2 was early activated at 3 hpi in spleen and reached to peak at 6 hpi then gradually decreased to weak expression level at 48 hpi. In addition to strongly expressed and further activated in the liver, three Nile tilapia HAMP genes were differentially highly activated in the spleen of Nile tilapia to contribute for defense against *S. iniae* infection.

KEYWORDS

Oreochromis niloticus, transcriptome, HAMP, hepcidin, *Streptococcus iniae*

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