MOLECULAR CLONING, EXPRESSION ANALYSIS AND CHARACTERIZATION OF GRASS CARP IKK-BETA

Haizhou Wang [1,2], Chengyu Hu [1§]

1. College of Life Sciences, Nanchang University, Jiangxi , P.R.China, 330031

2. College of Materials and Chemical Engineering, Pingxiang University, Jiangxi , P.R.China, 330045

ABSTRACT:

IKK-beta is a member of the IKK complex and plays an important role in the innate immune response. IKK-beta can interact with PKR to activate the NF-κB pathway in response to dsRNA in mammals. In this study, a grass carp (*Ctenopharyngodon idllus*) IKK-beta gene (*CiIKKβ*) was obtained by homology cloning and RACE technique. The full length of *Ci*IKKβ cDNA is 3428 bp, including 185 bp 5'UTR, 906 bp 3'UTR and 2337 bp open reading frame encoding 778 aa. SMART predicts that there is a serine/threonine kinase region at *Ci*IKKβ protein N-terminal, followed by a UBQ structural domain and a leucine zipper structure (LZ), then a NEMO binding domain (NBD) at C-terminal. Phylogenetic tree showed that *Ci*IKKβ is highly homologous to zebrafish IKKβ (*Dr*IKKβ). The real-time PCR result showed that the expression of *CiIKKβ* was detected in brain, intestine, liver, spleen, kidney, gill and heart tissues. For the purpose of searching for the mechanism of NF-κB activation mediated by the interaction between *CiIKKβ* and grass carp PKR (*Ci*PKR), a glutathione S-transferase(GST) pull-down assay was performed. By GST pull down, *Ci*IKKβ was shown to be physically associated with the N-terminal of *Ci*PKR.

KEYWORDS: IKKβ, Tissue expression, PKR, Interaction, GST pull down

[§]Corresponding author. Tel.: +86 79188317270; Fax: +86 79183969530.
E-mail address: hucy2008@163.com