Fish & Shellfish Immunology 31 (2011) 1259–1267

Contents lists available at SciVerse ScienceDirect

Fish & Shellfish Immunology

journal homepage: www.elsevier.com/locate/fsi

Short communication

Bioinformatic characterization and gene expression pattern of apoptosis inhibitor from *Macrobrachium rosenbergii* challenged with infectious hypodermal and hematopoietic necrosis virus

Jesu Arockiaraj[a], Puganeshwaran Vanaraja[a], Sarasvathi Easwvaran[a], Arun Singh[b], Rofina Yasmin Othman[a], Subha Bhassu[a,*]

[a] *Centre for Biotechnology in Agriculture Research, Division of Genetics & Molecular Biology, Institute of Biological Sciences, Faculty of Science, University of Malaya, 50603 Kuala Lumpur, Malaysia*
[b] *Centre for Aquaculture Research and Extension, St. Xavier's College (Autonomous), Palayamkottai, Tamil Nadu 627002, India*

ARTICLE INFO

Article history:
Received 6 July 2011
Received in revised form
23 August 2011
Accepted 9 September 2011
Available online 18 September 2011

Keywords:
Apoptosis
Macrobrachium rosenbergii
IHHNV
Characterization
Gene expression

ABSTRACT

Apoptosis is genetically programmed cellular killing processes that execute unnecessary or infected cells. It plays an important role in embryogenesis, homeostasis, insect metamorphosis and immunity. Apoptosis inhibitor (*Mr*IAP) was sequenced from the freshwater giant prawn *Macrobrachium rosenbergii* using Illumina Solexa Genome Analyzer Technique. *Mr*IAP consisted of 1753 base pair nucleotides encoded 535 polypeptide with an estimated molecular mass of 60 kDa. *Mr*IAP amino acid sequence contains IAP superfamily domain between 5 and 490. The deduced amino acid sequences of the *Mr*IAP were aligned with the other IAP family members. The highest sequence similarity was observed in IAP-5 from ant *Camponotus floridanus* (67%) followed by IAP from body louse *Pediculus humanus corporis* (66%) and the lowest (62%) in IAP-5 isoform-5 from common chimpanzee *Pan troglodytes* and IAP-5 from *Aedes aegypti*. The IAP phylogenetic tree showed that *Mr*IAP closely related to other arthropod blacklegged tick *Ixodes scapularis*, formed a sister group with IAP from a hemichordate acorn worm *Saccoglossus kowalevskii* and finally clustered together with IAPs from fish groups. The quantitative real time PCR analysis revealed that significantly ($P < 0.05$) highest expression was noticed in hepatopancreas and significantly ($P < 0.05$) lowest expression in pleopods. Based on the results of gene expression analysis, *Mr*IAP mRNA transcription in *M. rosenbergii* challenged to infectious hypodermal and hematopoietic necrosis virus (IHHNV) was highly induced in hepatopancreas. The collective results of this study indicate that the *Mr*IAP is an essential immune gene and influences the immune response against IHHNV infection in *M. rosenbergii*.

1. Introduction

Apoptosis or programmed cell death is a cellular killing process in which impaired or damaged cells are eradicated from multicellular organisms [1]. This concept was first introduced by Kerr in 1972 [2]. From then on, numerous genes have been identified in different species which control apoptosis [3–5]. The exclusive morphological changes observed during apoptosis include cell shrinkage, membrane bleeding, DNA fragmentation and apoptotic body formation [6]. This genetically maintained mechanism plays an important role in development, tissue homeostasis and removal of redundant cells during embryogenesis. It also causes cell atrophy upon endocrine withdrawal or reduction of necessary growth factor or cytokines, tissue remodeling and repair and disposal of cells that have undergone genotoxic damage [7].

Inhibitor of apoptosis proteins (IAPs) which regulate apoptosis in both vertebrates and invertebrates is a conserved group of protein [3]. A close relationship observed between baculoviral IAPs and insect IAPs indicates that baculoviral IAPs may have been formed through gene transfer from host insect cells. Recently, IAPs have been listed out in several multicellular species from *Drosophila* to mammals. However IAPs are absent in plants, yeast and protozoans [8].

IAP protein has unique structure that contains 1–3 copies of baculoviral IAP repeat (BIR) domain [1]. It comprises almost 70 peptides and has a conserved arrangement of Cys/His which is formed in a particular pattern of 'stable fold structure' that can chelate zinc [9,10]. This BIR domain attaches to caspases and prevent the anti-apoptotic qualities of IAPs, which is important for the biological process [10]. The relationship between BIR domains and caspases is negatively maintained by proteins which contain an

* Corresponding author. Tel.: +60 3 79675829; fax: +60 3 79675908.
E-mail address: subhabhassu2010@gmail.com (S. Bhassu).

1050-4648/$ – see front matter © 2011 Elsevier Ltd. All rights reserved.
doi:10.1016/j.fsi.2011.09.008

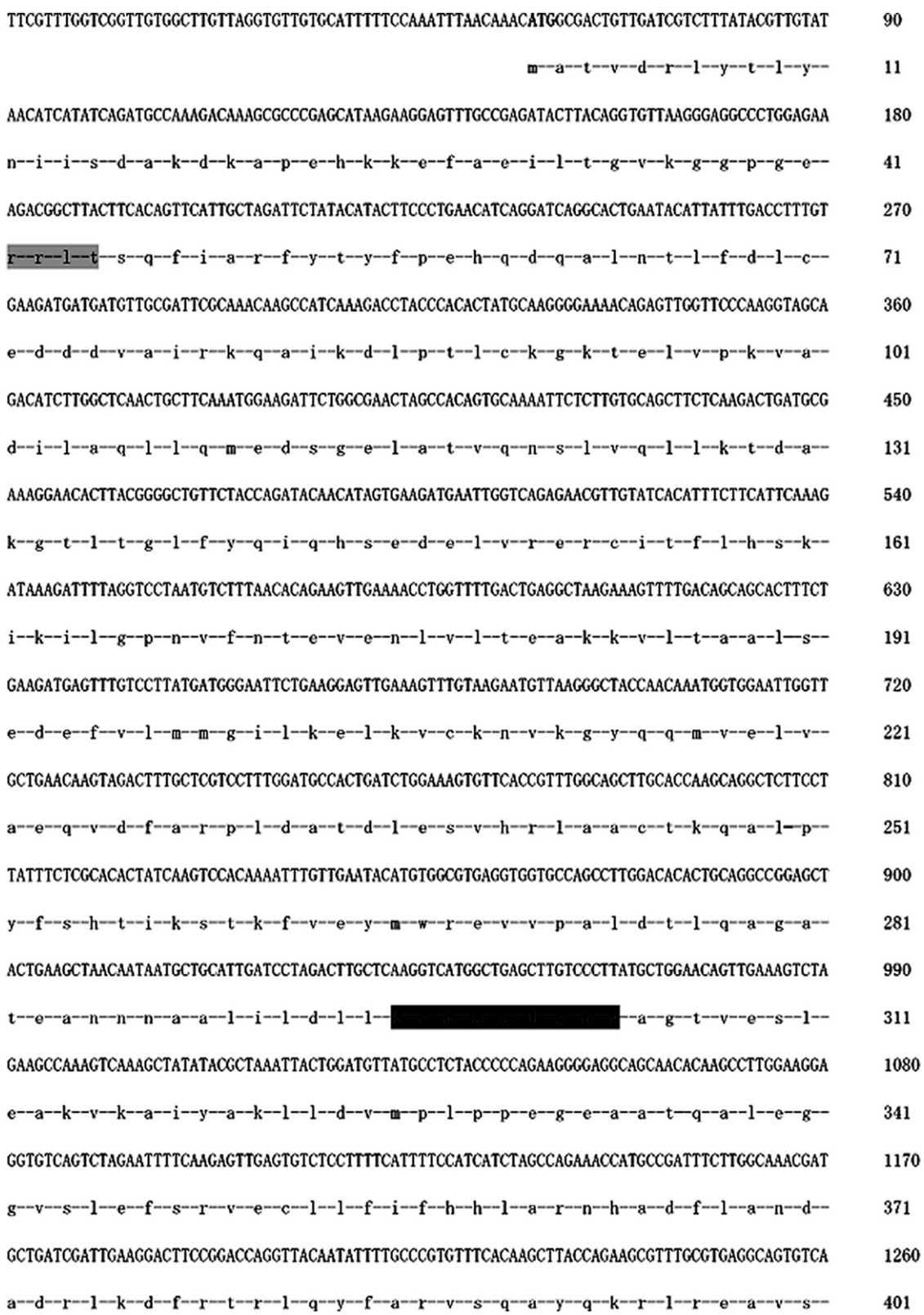

Fig. 1. Nucleotide and deduced amino acid sequences of *Mr*IAP. The nucleotide sequence is numbered from 5′ end, and the single letter amino acid code is shown below the corresponding codon. The start codon (ATG) and the end codon (TAA) are bolded. cAMP- and cGMP-dependent protein kinase phosphorylation sites are highlighted in light gray color. Tyrosine kinase phosphorylation sites are highlighted in dark gray color. And amidation site is underlined. The termination code is marked with an asterisk.