

Accepted Manuscript

Molecular identification and expression analysis of a novel cyclophilin a gene in the red swamp crayfish, *Procambarus clarkii*

Junjie Zhu, Feng Lin, Fei Li, Yan Wang

PII: S1050-4648(17)30660-5

DOI: [10.1016/j.fsi.2017.10.053](https://doi.org/10.1016/j.fsi.2017.10.053)

Reference: YFSIM 4924

To appear in: *Fish and Shellfish Immunology*

Received Date: 27 April 2017

Revised Date: 17 October 2017

Accepted Date: 28 October 2017

Please cite this article as: Zhu J, Lin F, Li F, Wang Y, Molecular identification and expression analysis of a novel cyclophilin a gene in the red swamp crayfish, *Procambarus clarkii*, *Fish and Shellfish Immunology* (2017), doi: 10.1016/j.fsi.2017.10.053.

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.



Molecular Identification and Expression Analysis of a Novel Cyclophilin A Gene in the Red Swamp Crayfish, *Procambarus clarkii*

Junjie Zhu^{a,b}, Feng Lin^c, Fei Li^c, Yan Wang^{a,*}

^a College of Animal Sciences, Zhejiang University, Hangzhou, 310058, China

^b School of life sciences, Huzhou University, Huzhou, 313000, China

^c Zhejiang Institute of Freshwater Fisheries, Huzhou, 313001, China

Abstract: Cyclophilin A (Cyp A) is the main intracellular receptor of cyclosporin A (CsA) belonging to the immunophilin family, which is known as an effective immunosuppressive drug. This study aimed to gain insights into the structure and biological function of cyclophilin A in the red swamp crayfish, *Procambarus clarkii* (PcCypA). We cloned PcCypA by homology cloning and anchored polymerase chain reaction (PCR), and assessed its mRNA and protein expression levels in different tissues using quantitative real-time PCR and western blot analysis, respectively. The full-length DNA contained a 5' untranslated region (UTR) comprising 108 base pairs (bp), an open reading frame of 495 bp encoding a polypeptide of 164 amino acids with an estimated molecular mass of 17.3 kDa, and a 3' UTR of 281 bp including a significant poly(A) plus tail sequence. The predicted amino acid sequence of PcCypA shared high identity with CypA in other organisms. PcCypA transcripts were detected in the hepatopancreas, gill, heart, muscle, testis, and ovary of crayfish, with the highest expression levels in the heart. Western blot analysis found one 17-kDa band in all of the tissues examined, except for the ovary. Molecular identification and expression analysis of PcCypA will facilitate further studies of the immune defense mechanisms in red swamp crayfish, and provide new insights into freshwater invertebrate immunology.

Keywords: Cyclophilin A; *Procambarus clarkii*; Real-time PCR; Western blot; Open reading frame

1. Introduction

Cyclophilins (CyPs) comprise a family of proteins found in vertebrates and other organisms that bind to cyclosporine, which is an immunosuppressant used to inhibit rejection after internal organ transplantation [1]. Diverse CyPs have been found in organisms ranging from bacteria to humans [2-6], including five classic Cyp isoforms in mammals (CypA, B, C, D, and cyclophilin 40), with sizes ranging from 18–40 kDa [7-9]. These proteins contain a single highly-conserved peptidyl-prolyl cis-trans

* corresponding author. Tel/Fax: +86 571 86971891.
E-mail: ywang@zju.edu.cn (Yan Wang).

Download English Version:

<https://daneshyari.com/en/article/8498882>

Download Persian Version:

<https://daneshyari.com/article/8498882>

[Daneshyari.com](https://daneshyari.com)