

# Accepted Manuscript

Identification, characterization and expression analysis of MAVS in *Pelodiscus sinensis* after challenge with Poly I:C

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PII: S1050-4648(18)30178-5

DOI: [10.1016/j.fsi.2018.03.054](https://doi.org/10.1016/j.fsi.2018.03.054)

Reference: YFSIM 5209

To appear in: *Fish and Shellfish Immunology*

Received Date: 9 December 2017

Revised Date: 19 March 2018

Accepted Date: 29 March 2018

Please cite this article as: Xu H, Zhao J, Zou Y, Lu B, Chen H, Zhang W, Wu Y, Yang J, Identification, characterization and expression analysis of MAVS in *Pelodiscus sinensis* after challenge with Poly I:C, *Fish and Shellfish Immunology* (2018), doi: 10.1016/j.fsi.2018.03.054.

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15 **ABSTRACT**

16 *Pelodiscus sinensis*, which is one of the important reptile species in the  
17 aquaculture industry in China, frequently suffers from serious infectious diseases  
18 caused by viruses. However, there is a lack of biological knowledge about its antiviral  
19 innate immunity. In this study, we identified and characterized the open reading frame  
20 (ORF) of PsMAVS cDNA in *P. sinensis*. It consisted of 2691 nucleotides encoding a  
21 protein of 896 amino acid residues, which were composed of an N-terminal CARD, a  
22 central proline-rich domain and a C-terminal TM domain. Based on the amino acid  
23 sequence, phylogenetic analyses revealed a closer relationship of PsMAVS with those  
24 of Chelonia. qRT-PCR analysis indicated that PsMAVS was ubiquitously expressed in  
25 all of the examined healthy tissues with different expression levels; it was expressed  
26 at high levels in spleen, muscle and heart and at moderate levels in kidney, liver,  
27 intestine, intestinum crissum and oesophagus. PsMAVS was detected in embryos at  
28 10 days post hatching, and it gradually upregulated with the embryonic development  
29 stage. Its expression levels in the examined tissues were all upregulated significantly

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