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Molecular cloning and expression analysis of small ubiquitin-like modifier (SUMO) genes from grouper (*Epinephelus coioides*)

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ABSTRACT

Small ubiquitin-like modifier (SUMO) is a group of proteins binding to lysine residues of target proteins and thereby modifying their stability, activity and subcellular localization. In the present study, two SUMO homolog genes (EcSUMO1 and EcSUMO2) from grouper (Epinephelus coioides) were cloned and characterized. The full-length sequence of EcSUMO1 was 749 bp in length and contained a predicted open reading frame of 306 bp encoding 101 amino acids with a molecular mass of 11.34 kDa. The fulllength sequence of EcSUMO2 was 822 bp in length and contained a predicted open reading frame of 291 bp encoding 96 amino acids with a molecular mass of 10.88 kDa EcSUMO1 shares 44.55% identity with EcSUMO2. EcSUMO1 shares 99%, 90%, and 88% identity with those from Oreochromis niloticus, Danio rerio, and Homo sapiens, respectively. EcSUMO2 shares 98%, 93%, and 96% identity with those from Anoplopoma fimbria, D.rerio, and H. sapiens, respectively. Quantitative real-time PCR analysis indicated that EcSUMO1 and EcSUMO2 were constitutively expressed in all of the analyzed tissues in healthy grouper, but the expression of EcSUMO2 was higher than that of EcSUMO1. EcSUMO1 and EcSUMO2 were identified as a remarkably ($P < 0.01$) up-regulated responding to poly(I:C) and Singapore grouper iridovirus (SGIV) stimulation in head kidney of groupers. EcSUMO1 and EcSUMO2 were distributed in both cytoplasm and nucleus in GS cells. Over-expressed EcSUMO1 and EcSUMO2 enhanced SGIV and Red-spotted grouper nervous necrosis virus (RGNNV) replication during viral infection in vitro. Our study was an important attempt to understand the SUMO pathway in fish, which may provide insights into the regulatory mechanism of viral infection in E.coioides under farmed conditions.

KEYWORDS

Epinephelus coioides; SUMO1; SUMO2; SGIV; Cellular localization

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