

European sea bass rtp3 genes: genomic characterization and transcription analyses

Patricia Moreno Garcia¹, Juan Gemez Mata¹, Daniel Alvarez Torres², Esther Garcia Rosado¹, Julia Bejar Alvarado³, Sra M. Carmen Alonso Sanchez¹

¹Universidad de Málaga, Instituto de Biotecnología y Desarrollo Azul, IBYDA, Departamento de Microbiología, Facultad de Ciencias, Malaga, ²Universidad de Málaga, Instituto de Biotecnología y Desarrollo Azul, IBYDA, Malaga, ³Universidad de Málaga, Instituto de Biotecnología y Desarrollo Azul, IBYDA, Departamento de Biología Celular, Genética y Fisiología, Facultad de Ciencias, Malaga,

Introduction: Fish RTP3, belonging to receptor-transporting protein (RTP) family, has been described as an interferon- α (IFN- α)-responsive gene. However, little information is available about fish rtp3 gene structure and the role of RTP3 proteins during viral infections. NNV (Nodaviridae family, Betanodavirus genus) is the causative agent of the viral nervous necrosis, the main viral disease affecting European sea bass (*Dicentrarchus labrax*) culture. Betanodaviruses have been classified into four species, although RGNNV is the only one causing high mortalities in sea bass.

Aim: The aim of the study has been to analyse the genomic structure of European sea bass rtp3, and its transcription profile after injection with LPS, poly I:C, or RGNNV infection.

Methodology: A partial sequence of seabass rtp3 gene was used as alignment sequence within European sea bass genome database. The located sequences were used as templates to design primers for full-length rtp3 sequencing. In addition, rtp3 X1 and X2 transcription was analysed in brain and head kidney by relative qPCR.

Results: European sea bass displays two rtp3 genes, X1 and X2, composed of two exons and a single intron (1007-bp and 888-bp long, respectively) within the ORF sequence. The full-length cDNA is 1969 bp for rtp3 X1, and 1491 bp for rtp3 X2. Several ATTTA motifs have been detected in the intron sequence of both genes, whereas rtp3 X1 also showed this motif in both untranslated regions. Regarding transcription analysis, the results revealed a significant level of rtp3 X2 transcription in brain and head kidney after LPS and poly I:C inoculation; however, the induction caused by RGNNV infection is much higher, suggesting an essential role of this protein in controlling NNV infections.

Conclusion: The present study contributes to further characterize the European sea bass response against RGNNV, being the first step in elucidating the role of sea bass rtp3 in the course of infections.

Acknowledgment: Project PID2020-115954RB100/AEI/10.13039/501100011033 (Spanish Government) and I+D+I Project UMA20-FEDERJA103 by the Operative Program FEDER Andalucía 2014-2020. In vivo challenges were conducted in the Center for Ecology and Microbiology of Controlled Aquatic Systems (CEMSAC). Thanks to Carmar Cultivos Marinos S.L. (Grupo CUMAREX) for providing the fish. Universidad de Málaga. Campus de Excelencia Internacional Andalucía Tech.