stimulation with flagellin. Hence, the stimulation assay in HKLs corroborated the previous predictions, and also showed a relative expression kinetic of genes concordant with a positive feedback mechanism between TLR5M/MyD88/TLR5S. Finally, the assays of RII effector mechanisms demonstrated that flagellin stimulates ROS production (extracellular and intracellular) and that these processes also depend on MyD88. In conclusion, we demonstrate that the activation of flagellin-mediated TLR5 (M and S) signaling, as well as the activation of final effector functions, depend on MyD88.

keywords: Toll-like Receptor, salmonids, MyD88, flagellin, system biology.

Corresponding author. Biotechnology and Biopharmaceutical Laboratory, Pathophysiology Department, School of Biological Sciences, University of Concepción, Victor Lamas, 1290, P.O. Box 160-C, Concepción, Chile
E-mail address: jotoledo@udec.cl (J.R. Toledo).
* These authors have contributed equally to this work.

P-011.

Differential immune responses of European sea bass (*Dicentrarchus labrax*) upon nodavirus infection by bath or intramuscular injection

Inês Ferreira [1,2], Janina Z. Costa [3], Kim D. Thompson [3], Yulema Valero [2], Alberto Cuesta [2], Teresa Baptista [1], M. Ángeles Esteban [2], Francisco A. Guardiola [2,4,#].

[1] MARE - Marine and Environmental Sciences Centre, ESTM, Polytechnic Institute of Leiria, Peniche, Portugal
[2] Department of Cell Biology and Histology. Faculty of Biology, Campus Regional de Excelencia Internacional "Campus Mare Nostrum", University of Murcia, 30100 Murcia, Spain
[3] Moredun Research Institute, Pentlands Science Park, Penicuik, EH26 0PZ, UK
[4] Centro Interdisciplinar de Investigação Marinha e Ambiental (CIIMAR), University of Porto, Terminal de Cruzeiros do Porto de Leixões, Av. General Norton de Matos s/n, 4450-208, Porto, Portugal

Abstract
Viral nervous necrosis virus (VNNV) produces the viral encephalopathy and retinopathy (VER) disease causing great mortalities in aquaculture fish. As is known, the innate system of teleost fish plays an important role in the defence against viral infection. Therefore, the aim of this study was to evaluate several immune-related enzymes (i.e. lysozyme, peroxidase and proteases) in serum, as well as the expression of immune-related genes (i.e. lysozyme, IgM, MHC I, TCR β, CD8α, IL-1β, IFNα, IL-10, IL-8, MAVS and Mx) in European sea bass (Dicentrarchus labrax) infected with VNNV by two methods with demonstrating effectiveness. In order to do this, European sea bass juveniles were infected with VNNV by either bath (1 hour, 106 TCID50 mL-1) or intramuscular injection (10^6 TCID50 mL-1). After 7, 15 and 30 days post-infection (dpi), fish serum was collected to measure innate immune parameters whilst the brain (tissue target of VNNV), spleen and intestine (as lethal samples), caudal fin, gills and skin (as low-invasive samples) were collected into RNA-later for the analysis of relative gene expression using Real-Time PCR (qPCR). The results demonstrated that serum peroxidase activity decreased in both infected groups at 15 dpi respect to the values found in control groups whilst this activity remained unchanged. In the case of protease activity, the results showed an increase in the serum of fish infected by bath method at the end of the trial (30 dpi) compare to unchallenged fish. The rest of immune-related enzymes measured not showed significant variations. Regarding to gene expression, the results revealed a modulation dependent on the type of infection and the organ studied (invasive or minimally invasive sample), which could be of great interest for the detection and treatment of this viral disease in aquaculture industry.
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keywords: Viral Encephalopathy and Retinopathy (VER), nodavirus (VNNV), innate immune system, RT-qPCR, European sea bass (*Dicentrarchus labrax*).

Corresponding author.
E-mail address: faguardiola@um.es (F.A. Guardiola).

P-012.

Identification of peritrophins as potential vaccine candidates against sea lice: A reverse vaccinology approach

A. Casuso [1,2,#,], G. Núñez-Acuña [1,*], V. Valenzuela-Muñoz [1,*], Y. Leal [1,2,*], C. Gallardo-Escárate [1,*].*

[1] Laboratory of Biotechnology and Aquatic Genomics, Interdisciplinary Center for Aquaculture Research (INCAR), Universidad de Concepción, P.O. Box160-C, Concepción, Chile
[2] Doctorate Program in Management of Aquatic Living Resources, Universidad de Concepción, Concepción, Chile

Abstract
Peritrophins are structural proteins of the peritrophic membrane (PM). This protein has been described in arthropods and have been described in some species of crustaceans. Peritrophins contribute to the maintenance of structural characteristics, including strength, elasticity and, permeability of the PM, and are capable to affect homeostatic regulation at intestinal level. In some copepod species of commercial interest such as *Caligus rogercresseyi* and *Lepeophtheirus salmonis* have not been characterized. These species are ectoparasite pathogens known as sea lice. The development of vaccine-based control strategies for sea lice control in salmonid aquaculture has been desired. The aim of this study was to use a reverse vaccinology approach to identify the *C. rogercresseyi* and *L. salmonis* peritrophins isoforms and identified by *in silico* analysis linear epitopes. We analyzed databases obtained by Illumina sequencing of the different stages of sea lice development. The contigs were compared against crustacean peritrophic membrane proteins database using BLAST and UniProt. Expression levels of different isoforms were evaluated by RNA-Seq and validated by RT-qPCR. *In silico* prediction tests of linear T and B epitopes were performed by the online software BepiPred and TEPITOPE, respectively. As results, in both sea lice species was identified different peritrophin isoforms, with differences in the number of chitin-binding domains. Furthermore, these proteins were differently expressed among sea lice developmental stages. In addition, linear epitopes of B lymphocytes were identified. These results demonstrate the antigenic potential of the peritrophins of both species. Further subsequent research will demonstrate the immunogenic action of perithrophins through *in vivo* tests against sea lice in farmed salmons.
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keywords: Peritrophins; sea lice; reverse vaccinology; *Caligus rogercresseyi*; *Lepeophtheirus salmonis.*

Corresponding author.
E-mail address: acasuso@udec.cl (A. Casuso).
* These authors have contributed equally to this work.

P-013.

Are related GABA and acetylcholine with the synthesis of IL-1β, TNF-α and TGF-β in the immune system organs of the Nile tilapia?

B.P. López-Tapia [*], M. Nájera-Martínez [*], R.L. Madera-Sandoval [*], A. Vega-López [#,].*

Instituto Politécnico Nacional, Escuela Nacional de Ciencias Biológicas, Laboratorio deToxicología Ambiental, Ciudad de México, México