higher number of GRP78/BiP transcripts in cells inoculated with the pathogenic VHSVs suggests a role of the unfolded protein response in the VHSV immune evasion.

Keywords: Rainbow trout, VHSV, transcriptome, RNA-Seq, immune evasion, host-pathogen interaction

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O-035.

Studies into B-glucan recognition in fish suggests a key role for the C-type lectin pathway

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Abstract

Immune-modulatory effects of β-glucans are generally considered beneficial to fish health. Despite the frequent application of β-glucans in aquaculture practice, the exact receptors and downstream signalling remains to be described for fish. In mammals, Dectin-1 is a member of the C-type lectin receptor (CLR) family and the best-described receptor for β-glucans. In fish genomes, no clear homologue of Dectin-1 could be identified so far. Yet, in previous studies we could activate carp macrophages with curdlan, considered a Dectin-1-specific β-(1,3)-glucan ligand in mammals. It was therefore proposed that immune-modulatory effects of β-glucan in carp macrophages could be triggered by a member of the CLR family activating the classical CLR signalling pathway, different from Dectin-1. In the current study, we used primary macrophages of common carp to examine immune modulation by β-glucans using transcriptome analysis of RNA isolated 6 h after stimulation with two different β-glucan preparations. Pathway analysis of differentially expressed genes (DEGs) showed that both β-glucans regulate a comparable signalling pathway typical of CLR activation. Carp genome analysis identified 239 genes encoding for proteins with at least one C-type Lectin Domains (CTLD). Narrowing the search for candidate β-glucan receptors, based on the presence of a conserved glucan-binding motif, identified 13 genes encoding a WxH sugar-binding motif in their CTLD. These genes, however, were not expressed in macrophages. Instead, among the β-glucan-stimulated DEGs, a total of six CTLD-encoding genes were significantly regulated, all of which were down-regulated in carp macrophages. Several candidates had a protein architecture similar to Dectin-1, therefore potential conservation of synteny of the mammalian Dectin-1 region was investigated by mining the zebrafish genome. Partial conservation of synteny with a region on the zebrafish chromosome 16 highlighted two genes as candidate β-glucan receptor. Altogether, the regulation of a gene expression profile typical of a signalling pathway associated with CLR activation and, the identification of several candidate β-glucan receptors, suggest that immune-modulatory effects of β-glucan in carp macrophages.

Keywords: β-glucan, primary macrophage, transcriptome analysis, C-type lectin-like domain, cyprinidae

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O-036.

The immune proteome of the zebra mussel deciphered by deep proteogenomics

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Abstract

Bivalve immune system modulation appears to be a relevant strategy in environmental risk assessment. Indeed, immune system is known to be sensitive to different environmental and anthropogenic stresses. To date, the immune system of marine bivalves is well documented in comparison to continental bivalves. Among them, the freshwater mussel *Dreissena polymorpha*, a non-model organism, represents the counterpart of the marine mussel in ecotoxicological studies. While cellular responses of hemocytes are well characterized for *D. polymorpha*, the molecular immune mechanisms remain relatively scared. In order to get insights into the immune proteome of the zebra mussel, proteogenomics was conducted on both hemocytes and plasma compartment of this non-model species. This strategy, combining transcriptomic sequences with mass spectrometry data acquired on proteins was relevant since 3,227 proteins were identified, which represent the largest protein inventory for this sentinel organism. Functional annotation and gene ontology (GO) analysis performed on the identified proteins described the main molecular players of hemocytes and plasma in the immune response of *D. polymorpha*. The GO analysis carried out on immune proteins showed that these two hemolymphatic compartments perform closely related and complementary immune functions: in signal transduction, adhesion and cellular mobility but also related to the recognition and elimination of microorganisms. Functional annotation revealed new mechanisms into the immune defence of the zebra mussel. Proteins rarely observed in the hemolymph of bivalves were pinpointed such as natterin-like proteins and thaumatin-like proteins. Furthermore, the high abundance of complement-related proteins observed in plasma suggested a strong implication of the complement system in the immune defence of *D. polymorpha*. This study contributes to a better understanding of the molecular mechanisms involved in immunity of bivalves and paves the way for their use as biomarkers in aquatic ecotoxicology.

Keywords: Hemolymph, bivalve, immunity, non-model organism, proteogenomics

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O-037.

Salmonid IGH genes: From genomics to repertoire sequencing

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