

**O-051.****B-glucan immuno-modulation in common carp intestine: A role for microbiota and its metabolites**

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**Abstract**

Dietary supplementation of fish with  $\beta$ -glucans has been widely associated with immunomodulation and commonly accepted as beneficial for fish health. However, to date the exact mechanisms of immunomodulation by  $\beta$ -glucan supplementation in fish are still largely unknown. In mammals a clear relation has been observed between high fibre diets and immunomodulation via intestinal microbiota and its metabolites. In this study, we first described the normal microbiota of common carp intestine by 16S rRNA sequencing. Based on the abundance of the genus *Bacteroides*, well known for their capacity to degrade and ferment carbohydrates, we hypothesized that common carp intestinal microbiota could ferment dietary  $\beta$ -glucans. Indeed, two different  $\beta$ -glucan preparations (curdlan and MacroGard®) were both fermented *in vitro* albeit with distinct fermentation dynamics and significant differences in production of short chain fatty acids (SCFA). MacroGard® more than curdlan lead to production of propionate, a SCFA with immunomodulatory properties. Subsequently, *in vivo* treatment effects of a single oral gavage with MacroGard® were analysed. Intestinal microbial composition seven days post-treatment showed a significant shift towards the family *Rhodocyclaceae*, including *Propionibacterium* sp, known to synthesize propionic acid by using unusual transcarboxylase enzymes. Coinciding with the shift in microbial composition, an overall immunomodulation could be observed as inhibition of expression of several pro-inflammatory genes (*il1 $\beta$* , *il6*, *tnfa*). Based on our data, we discuss the possibility that fermentation of MacroGard® by specific bacteria part of the normal microbiota of common carp intestine can lead to a shift in microbial composition and associated production of the SCFA propionate, the increased presence of which could possibly explain (part of)  $\beta$ -glucan-induced immunomodulatory effects.

**Keywords:** Microbiota,  $\beta$ -glucan, SCFA, *Cyprinidae*, 16S rRNA sequencing

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**O-052.****Transcriptome and proteome analyses of red blood cells from rainbow trout challenged with viral haemorrhagic septicaemia virus**

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**Abstract**

Teleost red blood cells (RBCs) have gained interest due to the fact that are nucleated and possess intracellular machinery necessary to develop a response to pathogens. Several studies have lately pointed out the implication of RBCs in the immune processes against viral infections. We have recently demonstrated that rainbow trout (*Oncorhynchus mykiss*) RBCs can also mount an immune response against abortive viral hemorrhagic septicemia virus (VHSV) infection *in vitro*. In this work, rainbow trout were challenged with VHSV. After two days post-challenge, peripheral blood and head kidney tissue samples were collected. For the transcriptomic analysis, RBCs were purified from these samples using a single cell sorting technique. For the proteomic analysis, RBCs were purified by two consecutive density gradient centrifugations. Results from the transcriptomic and proteomic analyses revealed an upregulation in genes from several immune-related GO-terms categories such as type I interferon, antigen presentation, complement activation and humoral response. Clusterization of genes from RBCs of peripheral blood and head kidney indicates a complementary profile, where downregulated genes from head kidney RBCs have a higher expression in blood RBCs and vice versa. In summary, in this work we show for the first time that RBCs can develop an immune response during *in vivo* VHSV infection of rainbow trout.

**Keywords:** Transcriptomics, proteomics, red blood cells, VHSV, complement

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**O-053.****From lamb to lion: Unleashing the beast in “virulent” *Aeromonas hydrophila***

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**Abstract**

An emerging pathotype of *Aeromonas hydrophila* (vAh) has been responsible for widespread farm losses in the US catfish industry over the last decade. While our genetic and biochemical understanding of vAh has been greatly enhanced in this time frame, our ability to reliably induce the disease in the laboratory remained limited. Utilizing established protocols for Aeromonad challenges resulted in minimal mortality and inconsistent clinical symptoms. Therefore, taking cues from observed farm conditions associated with outbreaks, we perturbed iron scavenging dynamics and catfish feeding status. Addition of a xenosiderophore, deferoxamine mesylate (DFO), to vAh cultures prior to immersion challenge significantly increased virulence in several vAh isolates but not in a non-epidemic strain. DFO addition did not impact vAh growth dynamics or perturb iron-sensitive gene pathways, but did significantly enhance hemolysis of catfish blood. Furthermore, hours between last feeding and immersion challenge (postprandial status), was observed to be a critical determinant of catfish susceptibility. Fish with a full gastrointestinal tract had significantly lower survival than those in a fasted state, and this effect was cumulative with that of DFO-enhanced vAh virulence. Utilizing our more robust challenge model, we are currently examining the practical efficacy of varying protective strategies for the industry including diet modification, vaccination, genetic selection, and modulation of the pond environment. Our latest results in this vein will be presented.

**Keywords:** Host-pathogen; *Aeromonas*; catfish; iron; siderophore

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