in rivers. Particularly, the change of dietary lipid composition from around 20% to 10% drastically impacts fry physiology. Indeed, lipids play a key role in fry development and some polyunsaturated fatty acids (PUFA) such as eicosapentanoid acid (EPA) are involved in immune defenses. In addition, the use of dry "germ-limited" food in a controlled environment probably reduces the exposure of fry to environmental bacteria known to shape the immune system and that could later lead to weak immune responses to fight pathogens present in the environment.
In this study, we aimed to optimize the diets of fry to improve their immune defenses and thus their ability to survive in the wild. For this, fry were fed six experimental or commercial diets: experimental diets with 12.7% lipids enriched either with EPA (1) or ALA (2), experimental diets with 20% lipids enriched either with EPA (3) or ALA (4), commercial diet (5), commercial diet (70% of energy supply) supplemented by living chironomids (30% of energy supply) containing complex microbiota (6). After 6 weeks of nutritional conditioning, fry were challenged with the pathogen *Aeromonas salmonicida salmonicida* by bathing. The body part of fry was sampled before and 24h after infection and was used for immune gene expression analyses involved in innate immune responses (*mpo*, *mcsfra*, *lysozyme*). Before bacterial infection, the expression of *mpo* and *igm* genes was lower in fry fed chironomids (F) diets compared to all other diets. This suggested that the supplementation of chironomids in diet could differentially modulate the immune system compared to dry diet. The results of immune gene expression after bacterial challenge, still under analysis, should provide information on how this living preys influence immune defense when fry are exposed to a pathogen. In addition, despite no differences were observed before infection between fry fed EPA- or ALA-enriched diets at different lipid percentage, we could expect some differences in immune responses after bacterial challenge as EPA is a direct precursor of leukotriene and prostaglandins production.
Keywords: Living prey diet; PUFA; bacterial challenge; restocking program; *Salmo salar*

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O-100.

Meta analyses of transcriptome responses to infections and stress in Atlantic salmon

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Abstract
Transcriptomics provides comprehensive information on host responses to pathogens, PAMP, antigens and treatments affecting the immune system. The main goal and challenge in data analyses is finding of consistent trends. Identification of transcription signatures (TS) – gene sets with reproducible expression profiles – is of high value. TS are instrumental for functional annotations of genes, interpretation and classification of transcriptome profiles. We have accumulated a large volume of data for Atlantic salmon produced with DNA microarrays, studies included multiple challenges with viruses, bacteria and parasites and various treatments stimulating immune and stress responses, totally 125 experiments and 4464 microarrays. Meta analyses started with selection of representative controlled experiments with large scale transcriptome responses, finding and ranking of genes with expression changes in at least two related experimental series followed with analyses of expression profiles in the entire database. Three large functional groups with several TS in each are presented, gene numbers and five genes with top ranks are indicated. **Virus responsive genes – VRG** (123 genes, *receptor transporting protein 3, viperin, isg15, ifit5, sacsin*) were identified in multiple trials with four viruses (IPNV, PRV, SAV and salmon poxvirus). These genes are equally activated with viruses and PAMPs (poly-IC, CpG, gardiquimod and bacterial DNA) *in vitro* and *in vivo*. In addition to specialized immune genes, VRG include many members with versatile or unknown functions and genes that most likely have changed their roles in higher vertebrates. While viral infection and exposure to PAMP induce the entire group, VRG fall into subgroups under different conditions suggesting a complex regulatory network. Systemic suppression of VRG was observed in fish infected with *Moritella viscosa* and sea lice. **Markers of inflammation** (105 genes, *C-C motif chemokine 4, serum amyloid, mmp 9, neutrophil cytosolic factor 1 and cathelicidin*) were selected by responses to PAMP and wounds. Multiple functional groups and pathways represent different aspects of immune responses, while several transcription signatures correspond to different scenarios of inflammation. **Stress markers** (31 genes, *mmp 9*, *immediate early response 2, junb, c/ebp-b* and *natterin*) were identified in studies of wound healing and exhausting physical load. These genes respond to various stressors in different tissues of Atlantic salmon. Stress component is manifested in various diseases with different magnitude.
Keywords: Atlantic salmon, transcriptome, antiviral response, inflammation, stress

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O-101.

Genomic and biological characterization of inhibitors and activators of the NF-kB pathway in rainbow trout (*Oncorhynchus mykiss*)

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Abstract
Bacterial infection on aquaculture facilities are a major problem for productivity and quality of fish production. One of the most common and important pathogens is Aeromonas salmonicida. This Gram-negative bacterium is the causative agent of the disease furunculosis, which had a devastating impact on salmonid aquaculture up until the late 1980's. An efficient vaccination against this pathogen would represent a decisive improvement of healthcare concepts in aquaculture systems. The NF-kB pathway is considered an important target of vaccinations as it is the responsible for the expression of cytokines and other pro-inflammatory molecules. We profiled the expression of several genes involved in the NF-kB pathway and NF-kB-dependent effector genes in rainbow trout after immunization. using multiplex RT-qPCR. NKIRAS1/NKIRAS2, RelA/NFKB1 and PIAS1 were selected as interesting indicator genes. Using CHSE-214 cell line derived from a Chinook salmon (*Oncorhynchus tshawytscha*) embryo, as in vitro model, we transfected these three factors in order to analyze the subcellular localization
of these proteins. Additional luciferase reporter assays showed that NKIRAS1 inhibits the activation of the NFkappa-β pathway following stimulation with different PAMPs. Surprisingly, NKIRAS2 showed the opposite effect as reported in literature for mammals. On trout cells it rather acts as pro-inflammatory molecule which drives the overexpression of cytokines. Furthermore, a panel of genes, related to the immune response, was selected to determine the modulation of gene expression during the immunization and transfections and analyzed with
Fluidigm technology. Results will contribute to better understanding of the role of inhibitors during inflammatory stimuli.
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