still poorly understood. The aim of this study was to describe the anti-parasitic immune response of the Atlantic salmon (*Salmo salar*) against C. rogercresseyi in contrasting temperature conditions. Fish were subjected to in vivo challenge against sea lice at two temperature regimes (8 and 16°C) with 35 copepodid/fish during 25 days. Samples were collected from hosts and parasites for transcriptome sequencing using Illumina HiSeq platform. Parasitic burden was highly divergent in the two temperaturas analyzed, being the double at 16°C (38.9% of the initial parasitic load versus 19.3% at 8°C).

Furthermore, many coding genes, immune-system pathways and long non-coding RNAs (lncRNAs) were significantly up-regulated in infected fishes at the highest temperature. Meanwhile, highly-relevant biological processes were also up-regulated in the sea lice at the highest temperature, such as genes related to the secretome system and homeostasis. This study contributes with novel knowledge regarding how temperature changes, that normally take place in salmon farms, could dramatically change key molecular elements involved in the hostparasite interactions between salmon and sea lice. The discovery of novel lncRNAs involved in these interactions are also discussed.

Keywords: Temperature changes, Atlantic salmon, *Caligus rogercresseyi*, immune response

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O-071.

Embryonic incubation temperature has a long-term effect on the spleen immune transcriptome and its response to lipopolysaccharide in adult zebrafish (*Danio rerio*)

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Abstract

Temperature has a profound effect on the immune system of fish. However, little is known about the effect of temperature during early embryonic development on the immune system of adult fish. We incubated zebrafish (*Danio rerio*) embryos at low (24 °C), high (32 °C), and reference temperature (28 °C) until hatching (3-5 days post-fertilization, dpf). Afterwards, all the three groups were maintained at the reference temperature until adulthood (100 dpf). At 12 h post intraperitoneal injection with lipopolysaccharide, spleens were sampled and RNA was extracted. RNA-seq was performed and the immune transcriptomes were compared between the temperature groups, as well as between LPS-challenged and control fish injected with phosphate buffered saline.

Both low- and high embryonic incubation temperatures resulted in decreased expression of some immune transcripts related to cytokines (*tnfa*, *cxcl8a*, *ccl20a.3*), neutrophil (*serpinb1l2*, *ncf1*, *ncf4*) and T cell functions (*sema4ab*, *crtam*, *alcama*) in the adult fish spleen. In addition, high incubation temperature also resulted in lower transcript levels of genes involved in neutrophil and respiratory burst (*cebp1*, *lsp1*, *cyba*), endocytosis (*rab5ab*, *rab7*, *pikfyve*), and lysosomal activity (*atp6ap1b*, *atp6ap2*, *atp6v1h*). In the same temperature group, the expression of various immunoglobulins (*rag1*, *ciita*, *cd74a*) and complement components (*c1qa*, *c1qb*, *c1qc*) was up-regulated.

Numerous immune transcripts, including antibacterial factors, and those involved in endocytosis, lysosome formation, respiratory burst, and inflammatory signaling were up-regulated with LPS challenge in fish from the low incubation temperature group. In contrast, fish from the high temperature group showed a limited immune response to LPS. In fish from the reference temperature group, expression of diverse apolipoprotein transcripts was up-regulated, while the level of cytokine transcripts was decreased.

Taken together, our data demonstrate that early developmental temperature has a long-term effect on the spleen immune transcriptome of adult zebrafish. This is relevant to understand the molecular basis of the temperature-induced immune developmental plasticity in fish and is particularly relevant in the context of climate change.

Keywords: Temperature, immune system, transcriptome, LPS, zebrafish

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O-072.

Turbot (*Scophthalmus maximus*) Nk-Lysin induces protection against the pathogenic parasite *Philasterides dicentrarchi* via membrane disruption☆

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Abstract

P. dicentrarchi is one of the most threatening pathogens for turbot aquaculture. This protozoan ciliate is a causative agent of scuticociliatosis, which is a disease with important economic consequences for the sector. Neither vaccines nor therapeutic treatments are commercially available to combat this infection. Numerous antimicrobial peptides (AMPs) have demonstrated broad-spectrum activity against bacteria, viruses, fungi, parasites and even tumor cells; an example is Nk-lysin (Nkl), which is an AMP belonging to the saposin-like protein (SAPLIP) family with an ability to interact with biological membranes. Following the recent characterization of turbot Nkl, an expression plasmid encoding Nkl was constructed and an anti-Nkl polyclonal antibody was successfully tested. Using these tools, we demonstrated that although infection did not clearly affect nkl mRNA expression, it induced changes at the protein level. Turbot Nkl had the ability to inhibit proliferation of the *P. dicentrarchi* parasite both *in vivo* and *in vitro*. Moreover, a shortened peptide containing the active core of turbot Nkl (Nkl71-100) was synthesized and showed high antiparasitic activity with a direct effect on parasite viability that probably occurred via membrane disruption. Therefore, the *nkl* gene may be a good candidate for genetic breeding selection of fish, and either the encoded peptide or its shortened analog is a promising antiparasitic treatment in aquaculture.

Keywords: *Philasterides dicentrarchi*, turbot, Nk-lysin, antimicrobial peptide, antiparasitic.

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O-073.

Lineage/species-specific expansion of the Mx gene family in teleosts: Differential expression and modulation of nine Mx genes *in vitro* and *in vivo* in rainbow trout *Oncorhynchus mykiss*

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