Dr. Mona Saleh

Senior Researcher

Molecular Genetics and molecular host pathogen interactions are my fields of expertise. I have been involved in the establishment of new molecular genetic tools and act as the molecular genetics advisor for the accredited Fish laboratories in our clinic. Application of Nanotechnology in Medical Science such as diagnostic, therapy and delivery is important part of my research activities. We developed and established in-vitro and in-vivo models for our research and are using siRNA/gene silencing approaches to knockdown expression and study the function of genes, and applied quantitative proteomics approach for identifying novel proteins after infection.

Mona Saleh also investigates the immune response of fish during single and co-infections with parasites, bacteria and virus, focusing on selected genes of SOCS/ JAK/STAT signalling pathway. She reported that balanced and effective local and systemic immune reactions and proper activation of B cells, T cells and myeloid cells are critical for host resistance during infection of fish. She also is using CRISPR-Cas9 technology to edit the DNA of organisms and particularly virulence genes for understanding gene function in different disease models. Using proteomic approaches, she recently identified regulatory proteins among several proteins and proteases produced extracellularly by pathogens.

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Project:

Exploring how *Myxobolus cerebralis* and *Tetracapsuloides bryosalmonae* determine the outcome of rainbow trout, *Oncorhrynchus mykiss*, co-infection

Abstract

Myxobolus cerebralis and *Tetracapsuloides bryosalmonae* are widespread myxozoan parasites that infect rainbow trout and are responsible for trout declines in wild populations and hatchery in USA, Canada and Europe.

There is little knowledge on the host proteins whose levels are up-or down-regulated during co-infection with *Myxobolus cerebralis* and *Tetracapsuloides bryosalmonae.* This project aims at identifying differential protein profiles of rainbow trout infected with *M. cerebralis* and *T. bryosalmonae* in the gills as a portal of entry, and posterior kidney and cranial cartilages as target tissues of proliferative kidney disease or whirling disease pathogenesis at different time points and at elucidating the proteomic background for proteins involved in host recognition and invasion of the infective stages of both parasites. Virulence factors of both parasites that are involved in host recognition and invasion of *M.*

cerebralis and *T. bryosalmonae* will be identified at the post-transcriptional and post-translational level. We shall also explore the differential modulation of host response and analyse the effect of the proteins whose levels differ after single and co-infection with the two myxozoan parasites. After experimental infection of rainbow trout with *M. cerebralis* and *T. bryosalmonae*, samples of the gills, posterior kidney and cranial cartilages will be collected at different time points. Proteomic approaches will be used to identify proteins of both parasites and fish tissues that are present at different levels. In addition, the levels of the mRNA encoding the proteins will be measured by q-RT PCR. The biological functions and networks of the proteins will be investigated. This study will give rise to the first proteomic profiles of rainbow trout in response to co-infection with two myxozoan parasites. It will help explain the observed differences in proteins in rainbow trout in response to *M. cerebralis* and *T. bryosalmonae*. The dynamic information will help us understand the biological processes and pathways activated by infection, such as signal transduction and proteasome activity. The results will be used to develop markers for the identification of fish disease and to develop novel approaches for disease management.