Research projects @ FIWI Bern

Irene Adrian-Kalchhauser

Contact for all projects: irene.adrian-kalchhauser@unibe.ch

FIWI Institute for Fish and Wildlife Health

Departement of Infectious Diseases and Pathobiology, Vetsuisse Faculty, University of Bern, Switzerland

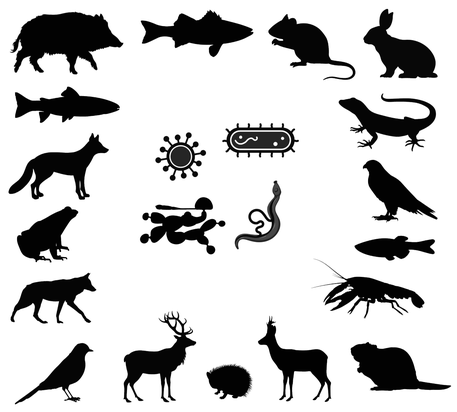
The host institute

The Institute for Fish and Wildlife Health (FIWI) works on infectious and non-infectious diseases of fish and wildlife. Our research resides at the interface of veterinary medicine, epidemiology, ecology and evolutionary biology. We also offer diagnostic services and work on the improvement and further development of methods for rapid pathogen detection.

Defining features of bioinformatics projects at FIWI are:

- Most often, we work on non-model species
- Often, we are the first ones to get this kind of data for this species

Three projects are described below, but many other ongoing projects are available (see info box to the right) - we would be happy to design one with you based on your interests!



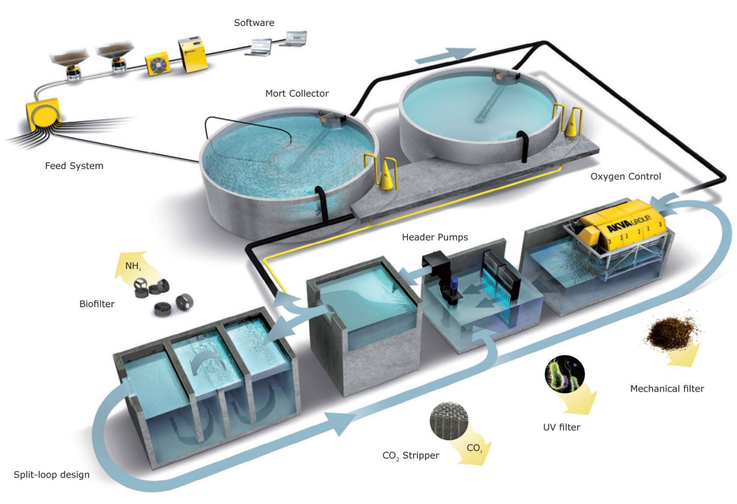
Further information

Other FIWI projects (see homepage):

- Crayfish host-pathogenomics
- Trout immune system scSeq
- Aquaculture microbiomics
- Trypanosome genomics
- Fish virus discovery
- Stickleback epigenomics
- Zebrafish evolution
- ...

FIWI homepage

Phage metagenomics



Recirculating aquaculture system raise fish for consumption. They depend on a stable and healthy microbiome to maintain optimal water parameters and fish health. This microbiome includes bacteria, archaea, phages, viruses, algae, and fungi.

We offer a project on the discovery, description and quantification of known and novel bacteriophages in recirculating aquaculture facilities. This project is embedded in the SNSF-funded project "MiCo4Sys".

Project MiCo4Sys

Data

We have generated metagenomics data for more than 500 samples collected from 6 facilities over the course of a year. Reads have been quality-controlled, and were subjected to a de-novo assembly. Currently, we are starting to identify phage-related signatures in the assembled contigs.

The student will generate count tables, and analyze the spatio-temporal dynamics, of one or several phages of interest in the data.

Project team

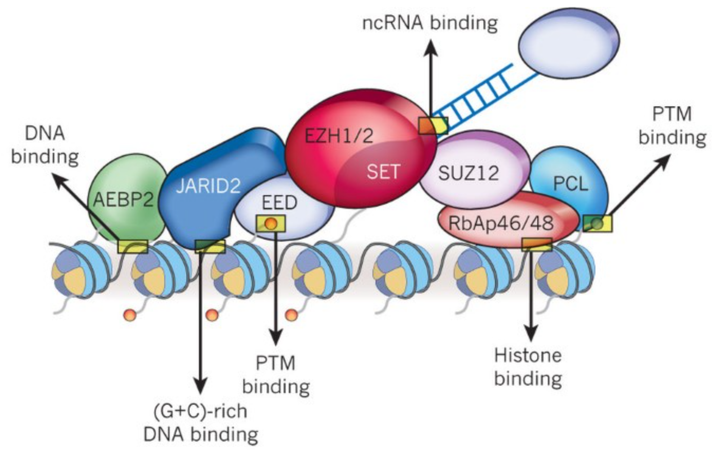
Co-PIs:
Prof. Irene Adrian-Kalchhauser, FIWI, Vetsuisse Bern
Prof. Claudia Bank, Inst. f. Ecology and Evolution

PhD:
Jessica Rieder, FIWI, Vetsuisse Bern

Bioinformatics:
Dr. Adamantia Kapopoulou, Inst. f. Ecology and Evolution

Collaborator on phages:
Dr. Vincent Somerville, University of Montreal

Epigenetic evolution



Epigenetic modifiers often work as part of large complexes. The PRC2 complex for example features 2 alternative catalytic subunits, and a wide range of obligatory and facultative cofactors. In fish, many genescoding for epigenetic machinery occur in multiple copies because fish genomes underwent multiple rounds of genome duplication during their evolution.

We offer a project on identifying signatures of evolution in epigenetic modifiers in fish. We would like to understand what happens to core components of the epigenetic machinery after duplication under (presumably) relaxed selection. Questions include:

- Where do these highly conserved proteins accumulate SNPs?
- How do the changes affect proteins?
- Can we use Alpha Fold to predict effects on structure of individual components, or to locate the SNPs on the protein?

Data

We have previously generated a pipeline to identify and locate a certain list of epigenetic modifiers, to extract their sequence and to identify regions of divergence in the stickleback genome.

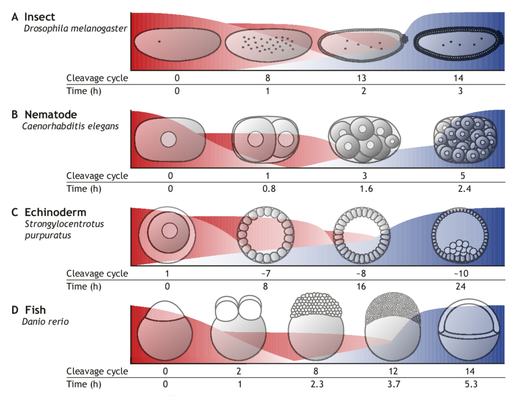
The student will download genome sequences of other species and/or other stickleback genomes from repositories, and will adapt the existing pipeline to other genomes and species. They will establish an AlphaFold pipeline for future use in the group.

Project team

PI:
Prof. Irene Adrian-Kalchhauser, FIWI, Vetsuisse Bern

Bioinformatics:
Dr. James Ord, Univ. Helsinki (existing pipeline)
Dr. Simone Oberhänsli, FIWI, Vetsuisse Bern

Maternal txomics



Maternal RNAs are deposited in the egg by the mother and govern a substantial portion of early embryonic development. Therefore, maternal RNA can potentially act as epigenetic information and transfer information from one generation to the next.

We have previously shown that the maternal rmeperature experience shapes the maternal RNA contribution in a wild fish population. We now aim to understand molecular mechanisms in greater detail, using the model organism zebrafish.

Maternal RNA publication

We offer a project exploring the response of zebrafish maternal RNA to heat stress. We would like to understand both global responses - i.e., responses that happen in every oocyte - and diversifying responses - i.e., responses characterized by increased diversity upon parental heat shock. We are particularly interested in increased within-clutch variability .

Data

Heat shock experiments will be carried out in summer 2023, and oocytes will be collected. RNAseq data is expected to be available by the autumn term.

The student will contribute to the generation of a suitable RNAseq analysis pipeline and validate it against existing zebrafish maternal RNA data.

Project Team

PI:
Prof. Irene Adrian-Kalchhauser, FIWI, Vetsuisse Bern

PhD:
Anastasiia Berezenko

Postdoc:
Dr. Dragan Stajic

Bioinformatics:
Dr. Simone Oberhänsli, FIWI, Vetsuisse Bern