



INVITATION to Workshop and training course: Molecular tracing of viral diseases in aquaculture



Montpellier

January 26 – 30, 2015

The EMIDA project MOLTRAQ is coming to an end, and we would hereby like to share new findings and tools for molecular tracing of viral diseases in aquaculture. The primary aim of the workshop is to bring colleagues involved in molecular biology, bioinformatics and epidemiology together in order to develop strong methods for risk analysis and prevention of spread of serious diseases in aquaculture.

Location: Université de Montpellier 2, place Eugene Bataillon 34095 Montpellier, France

Registration: <http://moltraq.wordpress.com/author/moltraq/>

Organizer(s): MOLTRAQ

Contact: Tatiana Vallaeys tvallaey@univ-montp2.fr
Aurélien Livernois aurelien.livernois@gmail.com
Niels Jørgen Olesen njol@vet.dtu.dk
Britt Bang Jensen britt-bang.jensen@vetinst.no

General objectives

The workshop and course aims to provide participants knowledge on the molecular and genetic tools available for providing molecular epidemiological analysis and tracing of disease outbreaks in aquatic animals. In addition focus will be on virus evolution and on factors in the environment, the host and the virus that drive the evolution of viruses in aquatic environments.

Program:

The program is divided into a workshop and stakeholder meeting Tuesday 27.01.2015 and a training course in molecular epidemiology 28-29.01.2015.

An internal progress meeting will be held back to back Friday 30th.

The key topics of the training course are:

- **How to collect molecular data in aquatic animals for epidemiological use**
- **Phylogeny and bioinformatics of viral aquatic pathogens**

The sessions in the course will be a combination of theory and practical studies. Leading scientists within epidemiology and molecular biology are invited to present talks on molecular epidemiology and virus evolution.

Number of participants: Maximum 50 at the workshop sessions 1-2, and maximum 25 in course sessions 3-6. Application with background for participation needed.

At registration please inform us your background and reason for participating.

Project participant: Jean-Christophe Avarre IRD , Tatiana Vallaes IRD, Michael Cieslak FLI, Magne Aldrin NR, Peder Jansen NVI, Niels Jørgen Olesen DTU , Susie Sommer Mikkelsen DTU, Morten S. Bruun DTU, Britt Bang Jensen NVI, Heike Schuetze FLI, Sven Bergmann FLI, Laurent Bigarré ANSES , Saliha Haloumni IRD, Tristan Renault IFREMER, Alice Fusaro IZSve, Valentina Panzerin IZSve.

The workshop and training course itself is free of charge, but you will have to pay a fee for meals and coffees.



FRIEDRICH-LOEFFLER-INSTITUT

FLI

Bundesforschungsinstitut für Tiergesundheit
Federal Research Institute for Animal Health



Draft Program

Workshop, course and progress meeting on molecular tracing of viral diseases in aquaculture 26-30 January 2015

| Monday 26 | Tuesday 27: Workshop and stakeholder meeting | Wednesday 28: Training course d1 | Thursday 29 Training course d2 | Friday 30 Internal progress meeting |
|--|--|---|--|--|
| <p>Venue. Arrival to Montpellier</p> <p>18.30 – 20.00 Registration</p> | <p>9:00-10:30 MOLTRAQ: Molecular tracing of viral pathogens in aquaculture, an EMIDA-ERA net project: outline and results. Welcome address: Britt Bang Jensen. «MOLTRAQ –Background and aims»</p> <p>Heike Schuetze, FLI: <i>Viral phylogeny and molecular tracing – Infectious hematopoietic necrosis virus as a model</i></p> <p>Susie S. Mikkelsen, DTU: <i>“Molecular tracing of viral hemorrhagic septicemia outbreaks”</i></p> | <p>8:30-10:30 SESSION 1 Virus evolution Dr. Samuel Alizon (CNRS) <i>“Clinical applications of pathogen phylogenies”</i>, Dr. Denis Fargette (IRD) <i>“Biogeography of a viral emergence: rice yellow mottle virus as a case study”</i>, Dr. Laurent Bigarré, (ANSES) / Dr. Niels Jørgen Olesen, (DTU) <i>Virus evolution in aquaculture</i></p> | <p>8:30-10:30 – Molecular epidemiology Dr. Olivier Gascuel (CNRS) <i>“Searching for virus phylotypes”</i> Dr. Gaël Thébaud (INRA) <i>“On the origin and tracing of genetic polymorphisms for Picorna-like viruses”</i> Dr. Britt Bang Jensen (NVI) <i>How to collate good epidemiological data for molecular tracing</i></p> | <p>8:30-10:30 MOLTRAQ- Progress meeting</p> |
| | Coffee Break 10:30-11:00 | Coffee Break 10:30-11:00 | Coffee Break 10:30-11:00 | Coffee Break 10:30-11:00 |
| | <p>11:00-12:30 Laurent Bigarré, ANSES: <i>“Tracing fish betanodaviruses”</i> Sven Bergmann, FLI: <i>Cyprinid herpes viruses in Europe</i> Jean-Christophe Avarre, IRD : <i>Input of next generation sequencing into viral genome comparisons and analyses: example of Cyprinid herpesvirus-3.</i></p> | <p>11:00-12:30 Dr. Michael Cieslak, (FLI) <i>Phylogeny of viruses – practical applications in the context of the epidemiology.</i></p> | <p>11:00-12:30 (NVI) <i>Use of sequence data in epidemiological analysis</i></p> | <p>11:00-12:30 MOLTRAQ Progress meeting</p> |
| | Lunch 12.30 -14:00 | Lunch 12:30 -14:00 | Lunch 12:30 -14:00 | Lunch 12:30-14:00 |
| | <p>14:00-15:30 TBA, IFREMER: <i>tracing outbreaks Ostreid herpes virus μ-var infections in pacific oysters Tatiana Vallaeys: TBA</i></p> | <p>14:00-15:30 Dr. Jean-Christophe Avarre, IRD <i>Use of NGS/deep sequencing in molecular tracing</i></p> | <p>14:00-15:30 Valentina Panzarin (IZSve) <i>Phylogeography</i></p> | <p>14:00-15:30 Departure</p> |
| | Coffee Break 15:30-15:45 | Coffee Break 15:30-15:45 | Coffee Break 15:30-15:45 | |
| | <p>15:45-17:15 Britt Bang Jensen: <i>Scenario simulation models for control options’</i> TBA: <i>Modelling the spread of pancreas disease (PD) in Norwegian marine salmonid farms</i> Niels J. Olesen , DTU: <i>Outreach, perspectives and recommendations for future research</i></p> | <p>15:45-17:15 Alice Fusaro and Valentina Panzarin, IZSve <i>Practicals in BEAST</i></p> | <p>15:45-17:15 TBA (NVI) <i>Practicals in epidemiological modelling</i> Wrapping up, discussions and evaluation</p> | |