

**Program of the workshop "Molecular tracing of viral diseases in aquaculture"
UM2, Montpellier, January 26-29, 2015**

| Monday 26 | Tuesday 27 | Wednesday 28 | Thursday 29 |
|--------------------------------|---|--|--|
| <i>Arrival of participants</i> | Stakeholder meeting 8.30-9:00 Registration 9:00-9:30 Welcome address Britt Bang Jensen, NVI: <i>MOLTRAQ - Molecular tracing of viral pathogens in aquaculture, an EMIDA-ERA net project: Background, outline and aims.</i> 9:30-10:00 Heike Schuetze, FLI: <i>Viral phylogeny and molecular tracing – Infectious hematopoietic necrosis virus as a model.</i> 10:00-10:30 Susie S. Mikkelsen, DTU: <i>Molecular tracing of viral hemorrhagic septicemia outbreaks in Denmark.</i> | Workshop day 1 8:30-8:45 Welcome and Introduction Jean-Christophe Avarre, Tatiana Vallaey 8:45 -9:25 Denis Fargette, IRD: <i>The biography of viral emergence: Rice yellow mottle virus as a case study.</i> 9:25-10:00 Samuel Alizon, CNRS <i>Clinical applications of pathogen phylogenies.</i> 10:00-10:30 Laurent Bigarré, ANSES / Niels Jørgen Olesen, DTU: <i>Virus evolution in aquaculture.</i> | Workshop day 2 8:45-9:30 Olivier Gascuel, CNRS: <i>Searching for virus phylotypes</i> 9:30-10:00 Gaël Thébaud, INRA: <i>On the origin and tracing of genetic polymorphisms for Picorna-like viruses.</i> 10:00-10:30 Britt Bang Jensen, NVI: <i>How to collate good epidemiological data for molecular tracing.</i> |
| | Coffee Break 10:30-11:00 | Coffee Break 10:30-11:00 | Coffee Break 10:30-11:00 |
| | 11:00-11:30 Sven Bergmann, FLI: <i>Cyprinid herpesviruses in European aquaculture.</i> 11:30-12:00 Jean-Christophe Avarre, IRD : <i>Input of next generation sequencing into viral genome comparisons and analyses: example of Cyprinid herpesvirus-3.</i> 12:00-12:30 Tristan Renault, IFREMER: <i>Describing genetic diversity of Ostreid herpesvirus 1 infecting Pacific oysters.</i> | 11:00-12:30 Michael Cieslak, FLI: <i>Phylogeny of viruses – practical applications in the context of the epidemiology.</i> | 11:00-12:30 Anja B. Kristoffersen, NVI: <i>Use of sequence data in epidemiological analysis.</i> |
| | Lunch 12:30 -14:00 | Lunch 12:30 -14:00 | Lunch 12:30 -14:00 |
| | 14:00-14:30 Laurent Bigarré, ANSES: <i>Tracing fish betanodaviruses.</i> 14:30-15:00 Tatiana Vallaey, UM2: <i>Development of variable number of tandem repeats (VNTR) based methods to track evolving aquatic herpesviruses.</i> 15:00-15:30 Michael Cieslak, Friedrich-Loeffler-Institut: <i>Intraspecific phylogeny and evolution of the European VHSV lineage Ia".</i> | 14:00-15:30 Jean-Christophe Avarre, IRD: <i>How may next-generation sequencing help identifying potential virulence factors ?</i> | 14:00-15:30 Valentina Panzarin, ISZVE: <i>Phylogeography.</i> |
| | Coffee Break 15:30-15:45 | Coffee Break 15:30-15:45 | Coffee Break 15:30-15:45 |
| | 15:45-16:15 Britt Bang Jensen, NVI: <i>Scenario simulation models for control options'</i> 16:15-16.45 Anja B. Kristoffersen, NVI: <i>Modelling the spread of pancreas disease (PD) in Norwegian marine salmonid farms</i> 16:45-17:15 Niels J. Olesen , DTU: <i>Outreach, perspectives and recommendations for future research</i> | 15:45-17:15 Alice Fusaro and Valentina Panzarin, ISZVE: <i>Practicals in BEAST</i> | 15:45-16:45 Anja B. Kristoffersen, NVI: <i>Practicals in epidemiological modelling</i> 16:45-17:15 Wrapping up, discussions and evaluation |