MOLTRAQ - MOLECULAR TRACING AND
EPIDEMIOLOGY OF VIRAL DISEASES IN AQUACULTURE

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17th Annual Workshop
of the National Reference Laboratories
for Fish Diseases

DTU Vet
National Veterinary Institute

Partners

- National Veterinary Institute, NVI, Norway

- National Veterinary Institute , Technical University of Denmark (DTU-VET), Denmark

- Agence Nationale de Sécurité Sanitaire (ANSES), France

- Institut Francais de Recherche pour Léxploitation de la Mer (Ifremer), France

- Institut de Recherche pour le Développement (IRD), France

- Friedrich-Loeffler Institut (FLI), Germany

- Norwegian Computing Centre (NR), Norway

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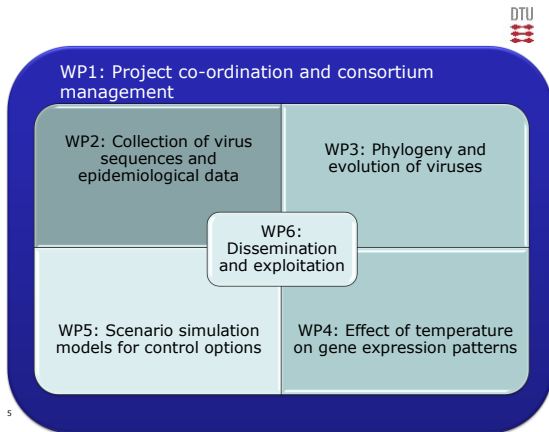

Additional partners

- Giovanni Cattoli, Valentina Panzarin, Istituto Zooprofilattico Sperimentale delle Venezie, IZSVe, Italy
  – Collaboration on phylogenetic and evolutionary analyses
  – Adding isolate and sequence information on VHSV and IHNV samples

- Tatiana Vallaeys from Université de Montpellier, France
  – Collaboration on phylogeny, evolution, tracking and tracing
  – Developing novel tools for whole genome data exploitation

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WP1: Project co-ordination and consortium management

WP2: Collection of virus sequences and epidemiological data	**WP3: Phylogeny and evolution of viruses**
	WP6: Dissemination and exploitation
WP5: Scenario simulation models for control options	**WP4: Effect of temperature on gene expression patterns**

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WP2
Collection of virus sequences and epidemiological data

- Aim: to collect high quality data on samples of representative isolates belonging to various fish and shellfish viruses, including part and whole genome sequences together with epidemiological data

- Collection of the following viruses:
  - Herpesviruses: OsHV-1, KHV/CyHV3
  - Rhabdoviruses: VHSV, IHNV , percirhabdo, HIRRV, EVEX
  - Nodaviruses
  - Salmonid alphaviruses: SAV
  - Birnaviruses: IPN

- Investigate the genetic diversity and select a sub sample for genomic approaches
- Perform genome sequencing
- Generate and collate all data necessary for conducting phylogenetic analysis and molecular epidemiological studies within the project (WP3)

OSHV-1

- Herpesvirus found in molluscs
- Genome-size 207 kb
- OsHV-1µVar presents polymorphism in ORF4 and ORFs 42/43
- OsHV-1 µVar was first reported in 2008 during mortality outbreaks among *C. gigas* in France
- Evolution, spread and differences between species will be investigated

  – Already have positive samples from France (400) and other countries (50) from 1993-2012
  – At least 15 full-genome OsHV-1 to be sequenced by IFREMER (Illumina sequencing)
  – Partial sequencing of specific regions with areas of interest
  – To be done on collection of isolates from different countries (France, Korea, Brasil, Ireland, Sweden and New Zealand)


VHSV

- Rhabdovirus
- Genome-size 11 kb
- G-gene codes for the glyco-protein

  – (DTU) 271 isolates from DTU, 171 to be sequenced by Dr. Schütze in Germany, 100 to be sequenced in Denmark. Full g-gene.
  – (DTU) Furthermore, information from another 50 full-length g-genes from another project will be included
  – (ANSES) 23 isolates from to be sequenced
  – (FLI) have about 200 isolates to be sequenced/already sequenced
  – (IZSVe) 260 isolates of which 43 has been sequenced full-length g-gene

- **Almost 600 full length g-gene sequences!**

www.fishpathogens.eu
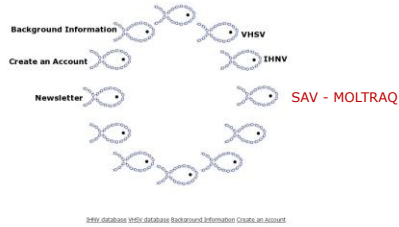
WP3
Phylogeny and evolution of viruses

- Sequences from WP2 will be collated together with already published sequences from databases (fishpathogens and GenBank)

- Isolates will be identified by phylogenetic analysis by conventional methods

- For VHSV, European spread and evolution will be analysed. Single-country analysis is also a possibility, depending on whether we have enough interesting samples

- For OsHV, the evolution of OsHV and OsHV-µVar will be examined, as well as the spread and differences between species. Here, the difference between single-gene and concatenated gene models will also be studied

WP4
Effect of temperature on gene expression patterns

- Temperature plays a key role in triggering virulence of almost all fish viruses and development of OsHV-1 infections in bivalves, and will be used to seek molecular markers of virulence and of virus spread, in the frame of comparative studies, by investigating the effect of temperature on viral gene expression.

- Still a question on whether to go for microarrays or high throughput qPCR

- OsHV: Cannot be grown in cell culture. Instead, in another experiment called Gigassat, ANR, one specimen will be injected into oysters at different temperatures.

- Studies also to be done on Nodaviruses and KHV

WP5
Scenario simulation models for control options

- It is possible to compare the genetic distance between each pair of locations with the geographic distances, thereby using this for molecular tracing. The aim is to quantify the probability of transmission based on the distance, which can then be used in the simulations on disease spread.

- Ultimately such simulations can be used as a mathematical laboratory to test intervention strategies.

- Informed idea about pathways of transmission, eg. distance, networks, genetic relationships etc

- VHSV will be used to create scenario simulation models

- Depending on the variability of genetic information, OsHV is also a candidate for these studies.

• For more information about MOLTRAQ, go to:

www.moltraq.wordpress.com

MOLTRAQ

Thank you!

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NR Norsk Regnesentral

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