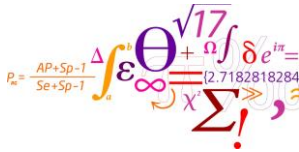


MOLTRAQ

Evolution of VHS in Denmark
 Susie Sommer Mikkelsen
 Annual Workshop 2015



DTU Vet
 National Veterinary Institute

VHS disease description

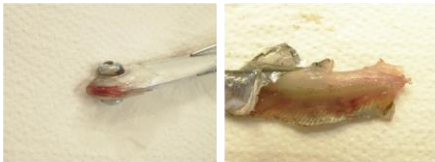
- Notifiable disease in Europe
- Typically occurs spring/autumn at low temperatures (10-14 ° C)
- Only been found in the Northern hemisphere

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VHS symptoms

- Signs of infection include hemorrhaging of skin, muscles and internal organs
- Other symptoms: Pale gills, exophthalmos and listless behaviour
- Est. Mortality: 80-100% in fry and fingerling
 – 50% in large adults



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Susceptible species



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Danish Fish farm description

Size distribution of fish farms in Denmark

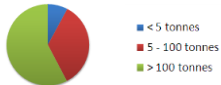


Image courtesy of <http://www.hvillstedt.dk/dambrugDK.htm>

No. Of fishfarms according to size (2013):

< 5 tonnes	5 - 100 tonnes	> 100 tonnes	all in all
19	84	140	243

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VHS Denmark history

- First discovered in 1963
- Economical losses of up to nearly 40 mill. Euro/year
- Eradication programme started in 1965
- Mainly conducted by emptying and draining fish farms removing all fish and water
- This was followed by extensive cleaning and disinfection of the whole farm
- Restocking only with fish from approved disease free farms
- Electrofishing of wild fish from streams

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VHS Denmark history

- No cases since early 2009
- Denmark officially free of VHS in 2013, but:
- Still VHSV in marine fish in the surrounding marine environment

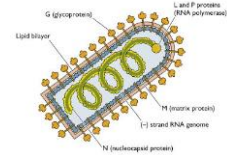


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VHS Virus description

- Belongs to the genus Novirhabdovirus and the Rhabdoviridae family
- Closely related to IHNV
- Bullet-shaped virus



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VHS Virus description

- Non-segmented negative-sense single-stranded RNA genome
- Genome is 11-12 kb in size
- Encodes five structural proteins and one non-structural protein



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Dataset description

Species: Mainly rainbow trout

Time-period: 1962-2009

Epidemiological information includes:

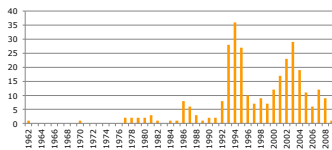


- Sampling date
- Clinical status
- Geographical information incl.
 - Coordinates
 - River systems
 - Farms positioning relative to each other and to the top of the river
- Historical knowledge about the different outbreaks and farms

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Distribution of isolates



Distribution of isolates

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Dataset description - sequences

- Full-length G-gene sequenced
- 309 isolates in dataset
- 221 isolates sequenced in the MOLTRAQ project, 10 isolates not sequenced
- 136 unique sequences
- 173 sequences with at least 1 identical sequence
- 0-4,6% difference between isolates

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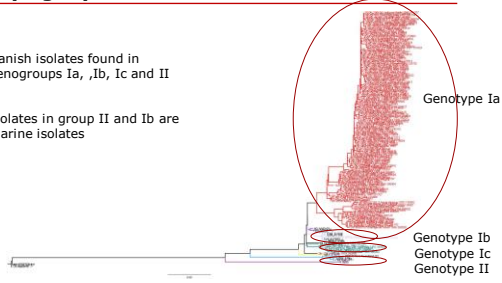
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Phylogeny – Maximum Likelihood



Danish isolates found in genogroups Ia, Ib, Ic and II

Isolates in group II and Ib are marine isolates



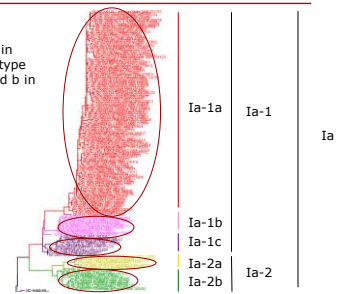
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Phylogeny – Maximum Likelihood



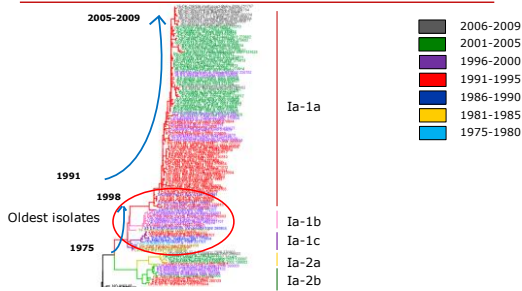
* Danish isolates found in cluster a,b and c in subtype Ia-1 and in cluster a and b in subtype Ia-2



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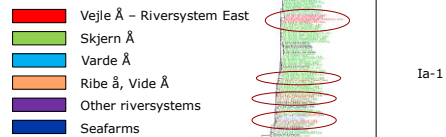
Phylogeny – temporal distribution



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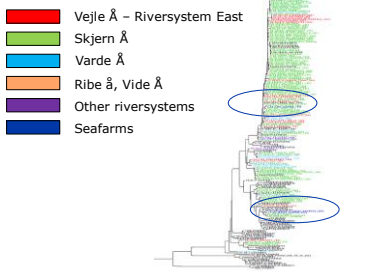
Geographical distribution



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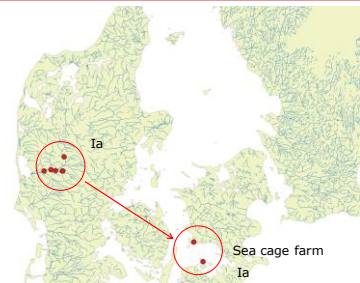
Geographical distribution



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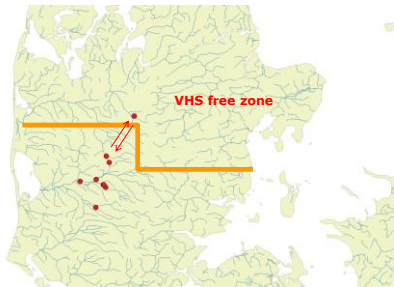
Infection of sea cage farms



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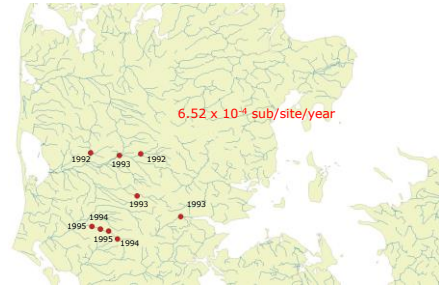
Illegal movement of fish



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Slow evolution conditions?

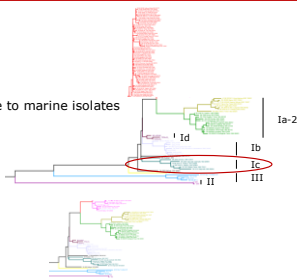


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Genotype 1c

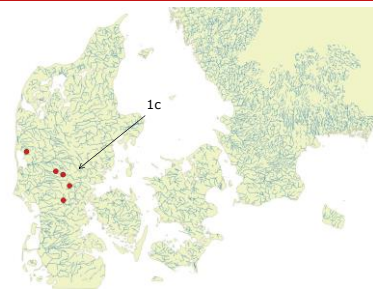
- Freshwater farms
- Old isolates (1980's)
- Phylogenetically close to marine isolates



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Genotype 1c



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Fishpathogens.eu

Fish Pathogens Database

FishPathogens.eu offers a platform for sharing of available information on isolates of fish pathogens and their relationship to fish diseases. Research on fish pathogens, the database can be used for research, education, and epidemiological surveillance of diseases. The database contains data on almost the entire range of fish pathogens isolated in fish laboratories worldwide. The database is available as a public website for all researchers in the field. It is a requirement to register to the website and to agree to the conditions of use.

For more information on using the database, please see [FishPathogens.eu](#) or contact the database administrator, Dr. Niels Jørgen Olsen, at njo@vet.dtu.dk.

The website also contains: For more information about what a database is, see [this](#). To see what makes the website easy to use, see [this](#). For more information on how to use the website, see [this](#).

European Union Reference Laboratory for Fish Diseases

EPIZ ONE

The development of FishPathogens.eu was funded by the DTU-DFP Project (to project 013712). Further maintenance and development is funded by the European Commission through the European Reference Laboratory for Fish Diseases.

SAV database to be created

All IHNV, VHSV and betanoda data to be put in

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Workshop: Molecular tracing of viral diseases in aquaculture

at the EAFP Conference, Canary Islands, Spain September 2015

Organisers: Prof. Niels Jørgen Olsen (njo@vet.dtu.dk) from the EURL for Fish Diseases, DTU Vet, Denmark, Dr. Bitt Bang Jensen (bitt.bang.jensen@vetinst.no) from NVI, Norway, and Dr. Jean-Christophe Avariz, IRD, France

This workshop will focus on 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 discuss improved methods for risk analysis and prevention of spread of serious diseases in aquaculture. The workshop will last 1.45 hours

Preliminary program: 1) *Molecular tracing of viral pathogens in aquaculture - a review*; 2) B. B. Jensen, NVI: *Scenario simulation models for control options*; 3) A. B. Kristoffersen, NVI: *Use of sequence data in epidemiological analysis*; 4) V. Panzerin, IZSV: *Evolution for VHSV and IHNV in Italy*; 5) N.J. Olsen, DTU: *facilitator: Round table discussions.*

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Thank you

- Henrik Korsholm, Danish Veterinary and Food Administration

- My colleagues at DTU:
 - Morten S. Bruun
 - Niccoló Vendramin
 - Torsten Boutrup
 - Niels-Jørgen Olesen



EMIDA era net/Aniwha