

EADGENE European Animal Disease Genomics Network of Excellence for Animal Health and Food Safety

Animal Disease Genomics: Opportunities and Applications
 10th - 11th June 2008, Edinburgh, UK



**The EADGENE FISH Pathogen Working Group:
 Genomics of pathogen - salmonid interactions
 and genetic resistance**

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Partners


- INRA (France)
- DJF (Denmark)
- ROSLIN (UK)
- RIBFA/FLI (Germany)
- NSVS (Norway)
- Leaders Bjørn Høyheim, NSVS and Pierre Boudinot, INRA

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Hosts/Pathogens

- Host:
 Atlantic salmon
 Rainbow trout
- Pathogens:
 Infectious Salmon Anaemia Virus (ISAV)
 Infectious Pancreatic Necrosis Virus (IPNV)
- General objective: study the host response to viruses
- Approach: Integrate genetics, transcriptomics and dedicated functional studies to prepare the best use of the salmon:trout genome in a collaborative framework



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Salmonids

- Important commercial species
- Genomics:
 - Genetic maps
 - ESTs (salmon: 430 000, trout: 250 000)
 - BAC libraries; partial physical maps
 - Microarray chips
- NO GENOMIC SEQUENCE
- Immune system of salmonids one of the best known among teleosts

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Viruses

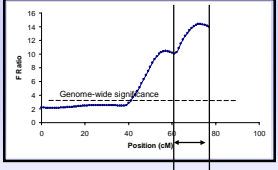
- ISAV: Infectious salmon anaemia virus, an orthomyxovirus, a model for influenza.
 - subversion strategies of ISAV
 - Susceptible species.
- IPNV: Infectious pancreatic necrosis virus, an *Aquabimavirus*, the economically most important disease for Atlantic salmon.
 - high degree of antigenic heterogeneity and variation in infectivity and pathogenicity
 - good models for the analysis of the mechanisms responsible for genetic resistance and viral pathogenesis.

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Work in progress

- Collect data from genome scans
 - 3 QTLs identified in salmon challenged with IPNV (LG 21, 26, 19)



Houston et al (2008) Genetics 178:1109-1115

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Work in progress

- Collect data from transcriptome analysis (ISAV, IPNV, salmon and trout)
- A set of genes in salmon that are either up- or down-regulated after challenging salmon with ISAV has been identified
 - 566 unique sequences identified
 - 63% assigned putative function

Expression studies has been performed after challenging rainbow trout with viral hemorrhagic septicaemia (VHS) virus

Hagen-Larsen et al (2008) submitted

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Work in progress

- ISAV has been fully sequenced
- Several mini-genomes have been constructed

ISAV Recovery from cDNA by Reverse Genetics

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Work in progress

- Factors contributing to the TLR-mediated signal transduction has been structurally characterised
- Basal and infection induced expression of these factors has been analysed in trout after infection with VHSV
- A reconstitution system of TLR-mediated pathogen dependent signal transduction has been established

	three Toll-like receptors	
trout-	TLR22	(AM233509)
trout-	TLR22L	(AJ878915)
salmon-	TLR22	(AJ628348)
	one adaptor molecule	
trout-	MyD88	(AJ878919)
	four regulatory molecules	
trout-	Tollip I	(AJ878916)
trout-	Tollip II	(AJ878917)
salmon-	Tollip I	(AM691828, AM691829)
salmon-	Tollip II	(AM691830, AM691831)
	one effector molecule	
trout-	SAA	(AM422446, AM422447)

Rebi et al (2007) Dev. Comp. Immunol., 37, 499-510
 Rebi et al (2008) Fish Shellfish Immunol. Epub ahead of print

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Work in progress

- Working towards a standard micro-array used in both species (salmon/trout), first steps towards a comparative analysis of induced/repressed genes
- Work on new microarray chip for salmon started
 - existing slide 17 000 (TRAITS/SGP)
 - new slide 20 000
 - Developing an Agilent oligo-array
- A system for direct typing of IPNV strains is being optimized
 - RT-PCR up to now
 - Microarray based system started

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Presentations from the FISH package

- Mette Hansen: Tackling the disease viral hemorrhagic septicaemia (VHS) in rainbow trout (*Onchorynchus mykiss*) by identifying genes for resistance using gene-expression analysis
- Stéphane Biacchesi: First steps of ISAV Recovery from cDNA by Reverse Genetics

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