AN OUTBREAK OF VIRAL HAEMORRHAGIC SEPTICAEMIA (VHS) IN WRASSE COHABITING WITH ATLANTIC SALMON IN THE SHETLAND ISLES, SCOTLAND

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Viral Haemorrhagic Septicaemia

Viral haemorrhagic septicaemia (VHS) is an infectious disease of farmed and wild fish and has an extensive host range in both freshwater and marine environments

Widespread geographical distribution of VHSV across various marine species in the northern hemisphere

The causative virus (VHSV) is an enveloped negative-strand RNA virus belonging to the genus *Novirhabdovirus*, within the *Rhabdoviridae* family

Listed as a non-exotic disease within the European Union (Council Directive 2006/88/EC)

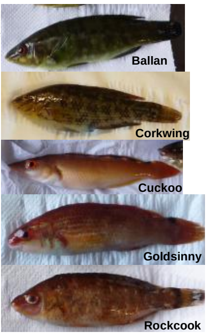
Viral Haemorrhagic Septicaemia - Wrasse

December 2012 suspicion of VHS at a SW hatchery site in Shetland

Mortality in wrasse population (5 species). ~ 10 000 wrasse on site.

Samples sent to a third party and reported as VHSV +ve by qRT-PCR

Movement restrictions (IDN) and statutory testing:
a) suspect site
b) supplying site
c) sites with cohorts to those at the suspect site



Photographs – Paul McKay and Andrea Warwick, FHI

Suspected Site

Site of initial suspicion confirmed VHSV +ve
    27/30 qRT-PCR
    30/30 VI confirmed by ELISA

Clinical signs of disease?

Movement restrictions – Confirmed Designation Notice (CDN)

Wrasse not listed as a susceptible species in CD 2006/88/EC

Photograph – Andrew Mayes, FHI

Epidemiological Investigation

Supplying site – wrasse originate from wild caught populations, some cultured stocks

150 fish statutory sample susceptible species

No clinical signs of disease

16 SW cage sites also had wrasse populations (cohorts to the suspect site) from the supplier

Statutory sampling of 15 fish per site – 16 sites considered as one population

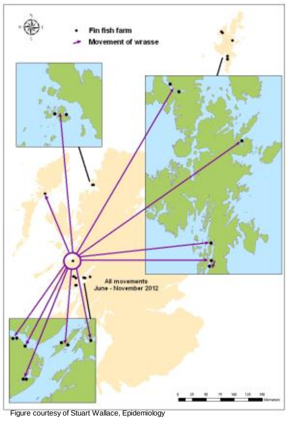


Figure courtesy of Stuart Wallace, Epidemiology

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Epidemiological Investigation

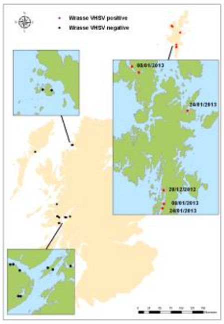
Sites that screened -ve (15 fish) were re-sampled at 150 fish level

All sites on the Scottish mainland and Western Isles screened VHSV –ve, movement restrictions revoked

Wrasse on 5 commercial marine Atlantic salmon farms in the Shetland Isles tested VHSV +ve

Co-habiting A. salmon stocks from the 5 sites tested VHSV –ve (150 fish/site)

60 mixed gadoids co-habiting with A. salmon from 1 of the VHSV infected farms were sampled. 1/60 VHSV +ve (Poor cod)



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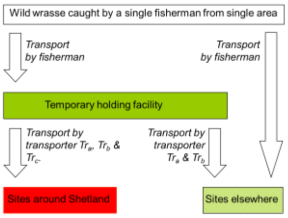
Movements of wild caught wrasse



Wild wrasse caught by a single fisherman from single area

Transport by fisherman

Transport by fisherman

Temporary holding facility

Transport by transporter Tr_a, Tr_b & Tr_c.

Transport by transporter Tr_a & Tr_b

Sites around Shetland

Sites elsewhere

🟩 Site tested VHS negative
🟩 All sites tested are VHS negative
🟥 Site tested VHS positive

Figure courtesy of Dr Malcolm Hall, Epidemiology

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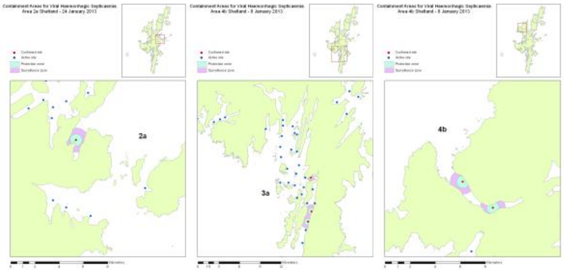
Protection and Surveillance Zones



Figures courtesy of Andrea Warwick, FHI

Protection and surveillance zones surrounding marine cage sites - 500m and 1Km, respectively and 250m and 500m around the Marine Hatchery.

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Wild Fish Survey – Shetland

Wild marine species were sampled following demersal trawling (April 2013)

Fish sampled in proportion to the number of species caught and screened for VHSV in pools of 10 by VI & ELISA

11/140 VHSV +ve

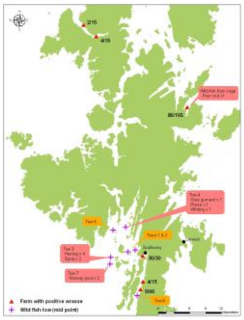


Figure courtesy of Stuart Wallace, Epidemiology

Grey gurnard (1/3)

Herring (4/22)

Plaice (1/40)

Norway Pout (2/4)

Sprat (2/5)

Whiting (1/24)

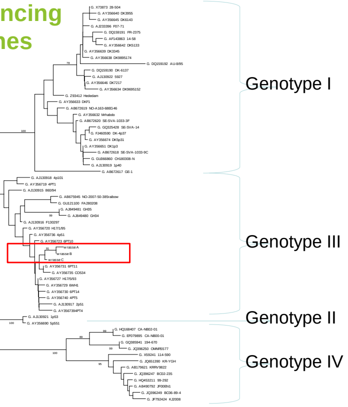
Nucleic acid sequencing of the N- and G-genes

All isolates group within VHSV genotype III

Wrasse isolates >99% similar at the nt level

10/11 wild fish isolates identical

Comparable variation between wild fish isolates and wrasse isolates as between wrasse isolates



Phylogenetic tree courtesy of Dr Iveta Matejosova, Aquaculture and Environment Group

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Withdrawal of wrasse from infected sites

Wrasse at the marine hatchery culled (19/12/2012)

Wrasse removal programme commenced (20/12/2012) on the 5 remaining sites

Creels; dead socks; removal during therapeutic treatment

Photographs – Paul McKay and Andrea Warwick, FHI

2 sites are now depopulated, farm records and statistical analysis indicates that ≥99% of wrasse have been removed from the 3 other sites

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Listonella anguillarum

Lumpsucker held as part of sea lice control Strategy on VHS +ve site

Heavy mortality – up to 6% per day

Clinical signs – 630 fish tested, VHSV –ve

Isolated consistent heavy pure growth identified as *Listonella anguillarum* the causative agent of vibriosis.

Histology – internal widespread bacterial infection severe septicaemia due to Gram negative bacteria

Controlled through antibiotic treatment

Photographs – Andrea Warwick and Sonia Duguid, FHI

Origin of the outbreak?

- Hypothesis one: that the outbreak originated with wrasse which were infected with VHSV before or during harvesting Low
- Hypothesis two: that the outbreak originated with wrasse which were infected with VHSV during transport to the temporary holding site Low
- Hypothesis three: that the outbreak originated with wrasse infected with VHSV at the temporary holding site Low

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Origins of outbreak?

- Hypothesis four: that the outbreak originated with wrasse which were infected with VHSV during transport from the temporary holding site to Shetland Negligible
- Hypothesis five: that the outbreak originated with wrasse which were infected with VHSV at the first-reported site Low
- Hypothesis six: that the outbreak originated from wild fish around Shetland Moderate

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Summary of VHSV Outbreak

- 6 sites stocked with wrasse species within Shetland infected with VHSV genotype III. Statistical analysis demonstrating that Shetland represents a distinct cluster
- Protection and surveillance zones established around infected sites in accordance with Council Directive 2006/88/EC
- Over 99% of wrasse removed from infected sites. Three sites depopulated.
- Qualitative risk assessment - origin of the outbreak most likely from wild fish around Shetland

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Acknowledgements

- MSS Diagnostic Group
- MSS Epidemiology Group
- MSS Fish Health Inspectors
- MSS Aquaculture and Environment Group

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