ISAV analyses of wild and farmed Atlantic salmon in Troms, Norway.

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Infectious salmon anaemia (ISA), caused by Infectious salmon anaemia virus (ISAV), is a disease causing major losses in farmed Atlantic salmon (*Salmo salar* L.). An avirulent variant of the virus (HPR0) is found in wild salmon which virulent isolates possibly have derived from (Markussen *et al* 2008). In Norway several ISA outbreaks have been registered in aquaculture farms in the Astafjord basin in South Troms 2007-2010. Six/10 ISA outbreaks in Norway in 2009 and 3/7 in 2010 were registered in this area (Fig. 1). Nearby, several salmon rivers have their outlets, including Målselv which is the largest based on annual fish catch. The reservoirs of ISAV are not known, but a possibility exists that wild fish can be carriers of virulent virus or that highly virulent viruses can be transmitted between farmed and wild fish. Epidemiological studies suggest that horizontal transmission is the main route for spread of ISAV, which underpins the risk of spreading infection between wild and farmed fish (Scheel *et al* 2007, Lyngstad *et al* 2008).

Objective

Study the prevalence of ISAV in wild salmon from a river in close proximity to an area with repeated ISA outbreaks in farmed salmon.

Material and methods

- Five head kidney (HK) samples from moribund salmon from farm 1 (2009) and 5 from farm 2 (2010), Astafjord basin, both with verified ISA.
- 28 HK samples from wild salmon (1.3-11.5 kg's, 16♀ and 13 ♂) caught in the river Målselv 17/6-15/8 2010.

All samples were analysed by real-time PCR both by Nofima (SYBRGreen, specific primers for ISAV segment 8) and by Patogen Analyse (TaqMan assays ISAV and HPR0), a company offering analysis for ISAV (http://www.patogen.no/).

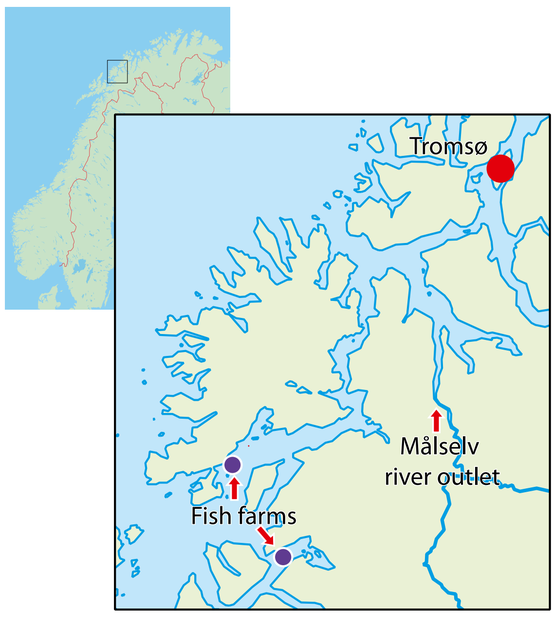


Figure 1: Overview of study area in Troms, Norway

Results

Figure 2.

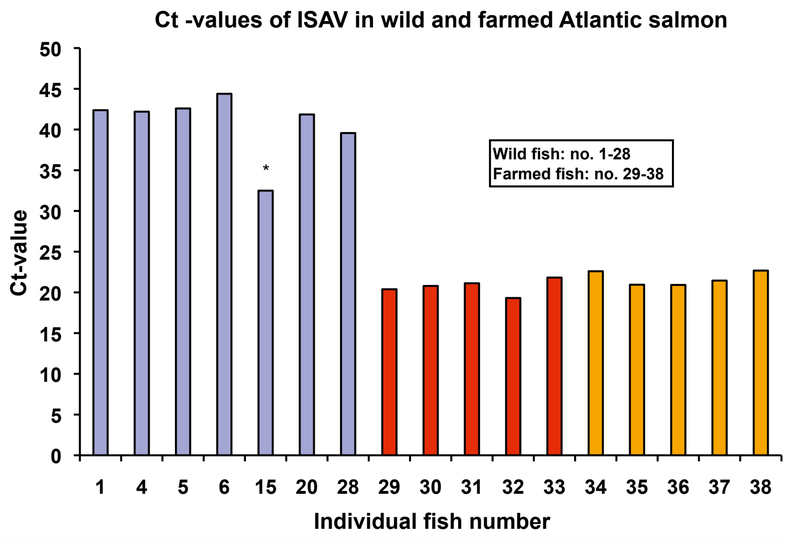


Figure 3.

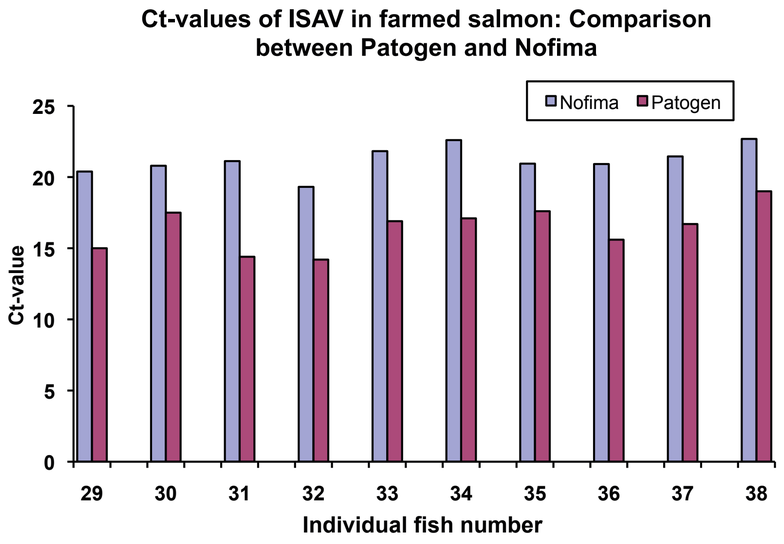
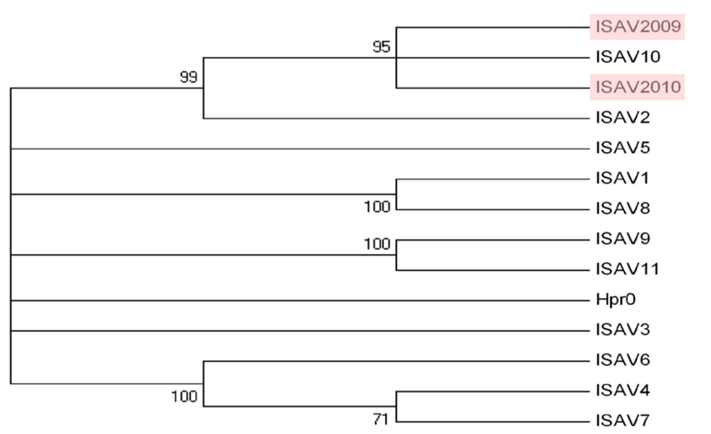


Figure 4.



Wild fish
Nofima: 27/28 wild fish were ISAV negative or had weak signal (~Ct 40) (Fig. 2: Fish 1-28, negative fish not shown). One fish (no.15) with Ct ~33 could possibly be ISAV positive, but further examination by touch-down PCR and sequencing demonstrated that it was ISAV negative.
Patogen Analyse: 28/28 fish were found to be both ISAV and HPR0 negative.

Farmed fish
All farmed fish samples from both 2009 and 2010 were ISAV positive with high ISAV transcript levels (Fig. 2: fish 29-38). Patogen Analyse confirmed this result (Fig. 3).

Standard PCR on Hemaglutinin-esterase (HE) gene (ISAV segment 6) and sequencing of PCR positive samples.
- All farmed fish were ISAV positive as shown previously and sequencing of the HE gene showed that the 2009 and 2010 isolates were practically identical.
- Both isolates had a truncated HE compared to ISAV HPR0 (results not shown).
- Sequence similarity and a phylogenetic study showed that ISAV 2009 and ISAV 2010 were most similar to reference strain ISAV10 (Fig. 4). The same was shown in another study (Lyngstad *et al* 2011). The virus is thus most likely established in the fjord system, either in farms or in a natural host in the sea.

Summary

- None of the wild salmon from the river Målselv were carriers of ISAV.
- Based on sequencing and phylogenetic studies, ISA outbreaks in two farms in Troms in 2009 and 2010 were caused by the same ISAV strain.

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