Abstracts

TriNation 2026

Belfast

Viral heart diseases in salmonids in Norway

Presenter: Torfinn Moldal

Affiliation: Norwegian Veterinary Institute

Co-authors: Hege Løkslett, Julie Christine Svendsen, Johanna Hol Fosse, Maria Dahle and Hilde Sindre

Summary: The Norwegian Fish Health Report has been published annually by the Norwegian Veterinary Institute (NVI) since 2003. All cases of notifiable diseases are reported to the Norwegian Food Safety Authorities and publicly available, but this does not apply to the non-notifiable diseases. However, since 2020, NVI has gained access to data at site level shared on a voluntary basis from a subset of aquaculture producers for several non-notifiable diseases diagnosed at private laboratories. With these data, the occurrence and geographical distribution of important diseases, such as cardiomyopathy syndrome (CMS) and heart and skeletal muscle inflammation (HSMI), are reported in a representative way. NVI has also been given access to registrations of mortality causes for Atlantic salmon at sea sites through the industry initiative AquaCloud, and fish health personnel as well as inspectors and advisors in the Norwegian Food Safety Authority add valuable information by completing an annual survey. The reports are published on https://www.vetinst.no/rapporter-og-publikasjoner/rapporter.

Among the notifiable diseases, infectious salmon anaemia (ISA) has been confirmed at ten to 25 sites per year during the last decade. In 2024, ISA was confirmed at 13 sites, while ISA was confirmed at 18 sites in 2025. Additionally, ISA was suspected at nine sites in 2024 and three sites in 2025. Several of the outbreaks in 2025 may be linked to ISAV HPR0 in hatcheries, and additional cases likely involve horizontal transmission from nearby sites. There has been a growing interest in vaccination towards ISA in recent years. However, a substantial proportion of the outbreaks in 2025 occurred in vaccinated populations. Pancreas disease (PD) is listed nationally in Category F in Norway. There has been a notable decline in cases of PD in recent years. In 2024 and 2025, there were 48 and 44 cases, respectively, compared to 58 cases in 2023 and 98 cases in 2022. All cases were within the endemic area. Several cases of PD in production area eight (outside the endemic area) were reported during the autumn 2023, but with no further outbreaks, all restrictions were lifted in late 2025. According to compiled data for analysis at NVI and private laboratories, there were fewer detections of CMS and HSMI in 2024 compared to previous years. However, there was an increase in the number of detections for both diseases from 2024 to 2025. These numbers are supported by data from AquaCloud where CMS and HSMI accounts for a bigger proportion of mortality caused by infectious diseases in 2025 compared 2024, as well as the survey where both diseases are ranked higher as important health challenges in 2025 compared to 2024.

Relevance to the industry: Viral heart diseases have a huge impact on Norwegian aquaculture. A good overview of the occurrence of these diseases is important, and data from several sources is crucial for estimating the real prevalence of non-notifiable diseases.

Situation update – Ireland

Presenter: Susie Mitchell

Affiliation: Stim, Ireland

Summary: Ireland has had a long history of SAV infection, with the disease being present since the early 1990's. The situation has been improved by multiple strategies, most recently widespread use of DNA vaccines has had a significant impact. CMS was first diagnosed in Ireland in 2012 and has been endemic ever since, affecting mostly larger fish close to harvest. Some selective breeding of CMS – resistant stock has helped to reduce the impacts, but it is still a significant challenge to the industry. Piscine reovirus is widespread in Ireland in the marine environment, however only one case of HSMI has ever been diagnosed in 2015.

Situation update on PD, CMS and HSMI from the Faroe Islands

Presenter: Debes Hammershaimb Christiansen

Affiliation: Faroese Food and Veterinary Authority (FFVA)

Co-authors: Petra Elisabeth Petersen PhD, Faroese Food and Veverinary Authority
Maria Marjunardóttir Dahl, PhD stud., Faroese Food and Veverinary Authority

Summary: Cardiomyopathy Syndrome (CMS), Hearth and Skeletal Muscle Inflammation (HSMI) and Pancreas Disease (PD) are some of the most important diseases in the three North Atlantic salmon farming countries Ireland, Norway, and Scotland.
As the production of farmed Atlantic salmon in the Faroe Islands increased fast in the 90'ies the industry faced increasing challenges with sea lice and several infectious diseases including CMS. In 2000 a devastating ISA epidemic hit the Faroes which caused an almost complete stand-still in production in 2006. During this period new legislation was implementing which significantly improved biosecurity measures and the aquaculture industry faced a complete reorganization. Although the production increased fast the following years, CMS and several other diseases disappeared and seemed to be eliminated for several years. However, CMS re-emerged in 2013 in one marine farm and spread to a few new sites the following years. This picture changed in 2017 as CMS was identified in several new farms concomitantly with the introduction of large-scale mechanical thermolicer treatments for sea lice. Within the last couple of years termolicer treatments has mainly been substituted with prolonged treatments in fresh water without any effect on the prevalence of PMCV or CMS.
The causative agent for HSMI, PRV-1, has been detected in all three production stages of

Atlantic salmon i.e. brood fish, freshwater smolts and marine fish since we started screening in 2010. Although very high viral loads were observed in several farms these cases were not associated with clinical signs of HSMI or increased mortality. One likely explanation was that only the low-virulent subtype of PRV-1 was circulating in Faroese aquaculture (Dhamotharan et al 2019). However, within the last couple of years this picture has changed as several cases of HSMI with increased mortality have been observed.
Whereas CMS and now also HSMI are important diseases in Faroese aquaculture PD or the causative agent Salmon Pancreas Disease Virus (SPDV) has never been detected in the Faroe Islands.
Here I will give an update on the status of CMS and HSMI in the Faroe Islands.

Industry relevance: The knowledge from the Faroe Islands suggests that one of the likely drivers for the spread of PMCV and CMS (and most likely several other pathogens as well) is the frequent movement of large treatment vessels between farming sites which are extremely complicated to clean and disinfect properly.

Post-meeting PDF permission: Maybe (Dont know yet)

Effect of biosecurity measures on pathogen persistence in RAS facilities: experimental trials and on-farm surveillance

Presenter: Sonal Patel

Affiliation: Norwegian Veterinary Institute, Norway

Co-authors: Sonal Patel1*, Duncan Colquhoun1, Sondre Veberg Larsen2, Elisabeth Midtbø Vik3, Paulo Mira Fernandes4, Hanne Nilsen1, Simon Weli1, Miriam Furne1, Merete Gåsvær Sture1, Erik Sterud5, Melanie Andrews6, Reidar Handegaard6, Håkon Dale7, Ole-Kristian Hess-Erga4
Affiliation: 1. Norwegian Veterinary Institute 2. Akvaplan-niva; 3. Patogen AS; 4. NIVA; 5. Pure Salmon Tech; 6. Marineholmen RASlab; 7. University of Bergen
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Summary: The presence of pathogenic microorganisms in RAS (Recirculating Aquaculture Systems) can result in both acute and delayed fish mortality and reduced fish welfare. There are many uncertainties regarding the role of biofilters in either outcompeting or maintaining viable pathogenic agents during commercial fish production.
Experiments were performed in controlled RAS facilities to investigate the establishment, survival, and inactivation of fish pathogenic agents. The effect of biosecurity measures such as fallowing, cleaning, and disinfection of biofilters on bacterial and viral pathogens including infectious salmon anemia virus (ISAV), IPNV and PRV was studied. Swabs from RAS unit surfaces, biofilter chips, tank, and water were sampled regularly and analysed for pathogens. After three weeks, the fish were removed and the effects of fallowing were examined further by introducing healthy naïve fish into the tanks at three different time points. Additionally, the effect of various

biosecurity measures such as changing the water and ozonation were tested in mini-scale RAS bioreactors.
We also investigated the effect of different biosecurity measures applied in commercial RAS facilities producing smolt and post-smolt Atlantic salmon. These RAS facilities had documented disease histories and conducted pathogen screening using real time rt-PCR both before and after implementation of biosecurity measures to evaluate intervention efficacy. Samples screened included swabs from risk assessed surfaces, biomedia, water and fish.
In summary, replacing all water in the system and a fallowing period between two fish generations showed reduction of most of the pathogens that were assessed in this study. There were some areas in the system where we could detect viral RNA for specific agents post implementation of biosecurity measures. The results are based on detection of RNA and do not necessarily reflect viability or infectivity of the agent detected. Subclinical infections in naïve fish introduced to the same RAS post biosecurity measures indicate that eradication of pathogens may be complex, and results from controlled trials may not be as effective in a commercial setting. Efforts to reduce pathogen persistence in smolt phase will be a huge contributing factor to reduce disease outbreaks during sea phase.

Industry relevance: REducing infectious agents in early life stages is improtant to reduce disease in later phase. The presentation will give an understanding on effect of fallowing and various biosecurity measures on viral agents in RAS facilities. This helps the industry in choosing the right strategy.

Post-meeting PDF permission: Maybe (Dont know yet)

PRV-1 Prevalence in Norwegian Salmon Hatcheries

Presenter: Marit Stormoen

Affiliation: Norwegian University of Life Science, Faculty of Veterinary Medicine (Norway)

Co-authors: S. W. Larsen (NMBU), J. Brunet (Patogen ASA), F. N. Formo (Patogen), Ø. Wessel (NMBU)

Summary: Piscine orthoreovirus-1 (PRV-1) is widespread in Norwegian salmon aquaculture and is recognized as the causative agent of heart and skeletal muscle inflammation (HSMB). Efforts to control this disease have been hindered by the lack of effective vaccines and challenges associated with cultivating the virus. Importantly, observed differences in virulence among PRV-1 variants highlight the potential for targeted disease interventions provided that the distribution and virulence of these variants are better understood.
To address a key knowledge gap, this study aims to determine the prevalence of PRV-1 in Norwegian salmon hatcheries, where prevalence has not previously been documented. Preliminary data indicate an overall prevalence of approximately 20%, with an expected geographical variation: higher prevalence is anticipated in the northern and central regions of

Norway compared to the south, as for salmon in the sea phase.
For this investigation, we divided Norway into three geographical areas based on production areas (PO): “South” (PO 1–4), “Mid” (PO 5–7), and “North” (PO 8–13), and the Norwegian Veterinary Institute provided the number of active salmon hatcheries for each production area for 2024. PatoGen As provided an anonymized list of hatcheries that submitted suitable sample material to their bio-bank between 2021 and the end of 2025. Based on this a total of 80 hatcheries were randomly selected using R, the selection was stratified according to the number of active salmon hatcheries in each region to ensure representativity.
This prevalence investigation forms part of a larger project, “PRVariant” (FHF 900082), in which we aim to sequence all positive samples to characterize the PRV-1 variants and determine their virulence. However, for the purposes of this presentation, only results relating to PRV-1 prevalence in hatcheries will be presented.

Industry relevance: PRV-1 is an ubiquitous virus, with no vaccine available. All available measures is thus biosecurity at the moment. New knowledge has shown a variation in virulence between different variants, but we have no/limited knowledge about the status in Norwegian hatcheries and their role in the spread of virus to sea sites, this is important knowledge to take informed decisions about biosecurity. This is the first prevalence study from hatcheries.

Post-meeting PDF permission: Maybe (Dont know yet)

Proximity-Based PD Risk Insights in Norwegian Salmon Production Areas 3 & 4

Presenter: Joel Ellis

Affiliation: MSD Animal Health

Co-authors: Tony Chen, Manolin

Summary: This observational, retrospective study examined PD outbreak patterns in Norwegian Production Areas 3 & 4 (2020-2024), analysing spatial relationships between Atlantic salmon farms and neighbouring Rainbow trout sites. Using t-tests and spatial correlation analysis, we found Atlantic salmon farms experiencing PD outbreaks were located significantly closer (mean 2.87 km) to Rainbow trout farms compared to non-outbreak sites. Notably, Atlantic salmon farms located within closer proximity to Rainbow trout sites without documented PD preventative measures showed higher PD occurrence rates. Spatial risk modelling using 10-20km buffer zones revealed consistent patterns across production cycles. These findings underscore the value of shared health intelligence as an important factor in developing comprehensive area-based disease management strategies for Atlantic salmon farmers. The methodology offers a measurable approach for identifying exposure risk to inform future strategies for disease prevention in areas where species are co-farmed.

Industry relevance: This research offers practical insights for the salmon farming industry by quantifying spatial risk factors for PD outbreaks. The findings support implications for site & stock selection decisions, informing risks for Veterinary Health Plans, and improving coordinated area-based disease management - particularly relevant for regions where Atlantic salmon and Rainbow trout are co-farmed.

Post-meeting PDF permission: Maybe (Dont know yet)

Collective action under shared biological risk: Evidence from pancreas disease control in salmonid aquaculture in Norway

Presenter: Aklilu Tilahun Tadesse

Affiliation: Norwegian Veterinary Institute

Co-authors: Cecilie Sviland Walde1, Lars Qviller1, Wilma Steeneveld2, William Gilbert3, Mona Dverdal Jansen4

1Norwegian Veterinary Institute, Norway, 2University of Utrecht, Netherlands, 3University of Liverpool, UK, 4Norwegian Food Safety Authority, Norway

Summary: Collective action dilemmas arise when individual rational decisions produce collectively harmful outcomes. This research examines such a dilemma in the management of pancreas disease (PD) in Norwegian salmonid aquaculture.
PD is a highly contagious viral disease with serious consequences for fish welfare, production efficiency, and market access. PD is endemic in specific parts of Norway. Outside the endemic border PD is controlled by compulsory depopulation. Rapid depopulation of infected farms can reduce the risk of disease spread and protect neighboring farms, yet it may impose substantial short-term economic losses on individual producers, depending on the stage of production at which infection occurs. Farmers who incur this cost are not compensated by the government. The extent of the losses depend on the stage of production at which infection occurs.
The work presents a case study of multiple PD outbreaks in a non-endemic production area in 2023, where several farms were required to depopulate. To examine the implications of alternative responses (rapid vs. delayed depopulation), we apply an integrated epidemiological–economic modelling framework. Disease spread is simulated under different depopulation strategies, and subsequent shifts in profit are assessed using a partial-budget approach at both farm and area levels.
Preliminary findings show that rapid depopulation is economically beneficial for the production area, but the private costs can be substantial. This may create economic incentives to delay depopulation, thereby shifting risk onto others. Delaying depopulation, however, decreases the benefit for the area, and depending on how long depopulation is delayed the benefit eventually becomes negative. These findings highlight private incentives may conflict with collective

disease control objectives. In the conference, we further discuss how to manage unevenly distributed costs in managing shared biological risks.

Industry relevance: This presentation addresses a key operational challenge facing salmon aquaculture: balancing rapid disease control with farm-level economic sustainability. By examining how depopulation strategies influence both regional biosecurity and individual farm profitability, the research provides insights that can support more effective and practically feasible disease management policies. The findings may help industry stakeholders better understand trade-offs between short-term losses and long-term production stability

Post-meeting PDF permission: Maybe (Dont know yet)

The Impact of Sea Lice Infestation on PRV-1 and PMCV Infection Dynamics in Atlantic Salmon

Presenter: Fabio Sabbadin Zanuzzo

Affiliation: Onda, Canada

Co-authors: Donnie Sonier1,2, Brian Dixon2

1 Onda, Victoria, PE, Canada
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Summary: Viral infections associated with severe cardiac pathologies represent one of the top health challenges in Atlantic salmon aquaculture in the North Atlantic. Piscine orthoreovirus-1 (PRV-1) and Piscine myocarditis virus (PMCV) induce distinct patterns of cardiac inflammation (HSMI – Heart and Skeletal Muscle Inflammation and CMS – Cardiomyopathy Syndrome) that result in compromised animal welfare and substantial production losses at sea. At the same time, sea lice (Lepeophtheirus salmonis) infestations represent a persistent threat to growth performance and susceptibility to secondary pathogens due to extensive scale loss and skin degradation. Despite the prevalence of viral pathogens and sea lice in Atlantic salmon aquaculture, little is known about the influence of coinfection on the progression of viral diseases and clinical outcomes.
This presentation summarizes the results of controlled coinfection experiments designed to examine how infections with sea lice, and either PRV-1a (non-virulent), PRV-1b (virulent), or PMCV, influences the development of clinical HSMI and CMS, and also the susceptibility of Atlantic salmon to sea lice infection. Experimental challenges were conducted to standardized lice infestations, and the dose of PRV-1 or PMCV administered through IP-injection. Post-smolt salmon were allocated to treatment groups experiencing a sham challenge (negative control), single pathogen challenge (positive controls), PRV-1a + Sea lice (SL), PRV-1b + SL, PMCV + SL, SL + PRV-1a, or SL + PRV-1b challenges. Sampling was conducted biweekly for 14 weeks to monitor

trends in viral kinetics, cardiac lesions, and sea lice burden in respective infection groups. In addition, the immune response in the heart and spleen of fish was investigated at molecular and protein levels.
Our results indicate that sea lice infestation significantly influenced PRV-1 replication in red blood cells at early infection stages; however, this effect was specific to the virulent PRV-1b strain and absent in the non-virulent PRV-1a strain. When fish challenged with PRV-1 strains and PMCV were infested with sea lice after 6 weeks post viral challenge, the PRV-1a group had significantly fewer sea lice attached at 22 and 36 days post infection (dpi) with sea lice. The positive control (sea lice only), PRV-1b, and PMCV groups, showed similar sea lice counts at 3, 8, 22, and 36 dpi. Heart samples from SL + PRV-1 groups, PRV-1 + SL, and PMCV + SL groups were submitted for histopathological evaluation to assess the severity of lesions associated with HSMI and CMS respectively.
Proteins were extracted from heart and spleen tissues to quantify levels of IL-1β, IL-2, and IFNγ, which are key cytokines involved in early pro-inflammatory responses, the development of T cell differentiation and activation of the adaptive immune response. Gene expression was also assessed to evaluate how markers of the innate anti-viral response, and the adaptive immune response are impacted by coinfection.
Our results to date demonstrate that parasite-viral coinfection can significantly influence viral replication at early infection timepoints, and may affect subsequent disease progression. Collectively, this work highlights the importance of considering how coinfection scenarios impact animal welfare and immune responses when considering health management strategies.

Industry relevance: Sea lice infestation in combination with CMS and HSMI infections represents one of the most relevant co-infection scenarios observed in the field. However, very little information is currently available regarding the dynamics of this co-infection and its effects on fish health. From both an industry and research perspective, it is critical to understand whether—and through which mechanisms—sea lice infestation may increase susceptibility to viral infections, and conversely, how viral infections may influence parasite outcomes.

This study addresses these knowledge gaps, and the findings are highly relevant to both academic research and commercial aquaculture. In summary, our results to date demonstrate that parasite–viral co-infection can significantly influence viral replication at early stages of infection and may subsequently affect disease progression. Collectively, this work highlights the importance of considering co-infection scenarios when evaluating animal welfare, immune responses, and the development of effective fish health management strategies.

Post-meeting PDF permission: Yes

Selective breeding for CMS-resistance reduces PMCV viral loads and alters host response

Presenter: Thomas Moen

Affiliation: AquaGen, Norway

Co-authors: Thomas Moen, AquaGen
Fabian Grammes, AquaGen

Summary: AquaGen implemented selective breeding for increased CMS-resistance from 2012, initially using marker-assisted selection targeting two Quantitative Trait Loci (QTL) with large effects. In 2018, genomic selection (GS) was introduced. The GS model is trained on genotypes (70k SNP chip) and phenotypes (qPCR measurements of PMCV), such that broodfish candidates are selected based on genetic similarity to fish showing low PMCV levels after challenge tests. Selective breeding has resulted in a shift in the distribution of PMCV cycle threshold (Ct) values, with an increasing proportion of fish being PMCV-negative at the end of challenge tests. A QTL with a very large effect on chromosome 23 has been a major driver of this development; in a group homozygous for the resistance allele at this locus, 75% of individuals were PMCV-negative. PMCV levels measured in challenge tests are correlated with PMCV levels and survival in the field.
Earlier studies have classified PMCV-infected fish as low-responders or high-responders based on cardiac histopathology and viral load following infection. We find that fish with unfavourable genomic breeding values (GBVs) for CMS-resistance show gene expression profiles similar to high-responders, whereas fish with favourable GBVs resemble low-responders, indicating an improved ability to reduce viral loads.
Increased resistance to CMS benefits all eggs sold by AquaGen. In a recently introduced product, CMS-Edge, CMS resistance is further enhanced through targeted selection on CMS-associated genes in both male and female broodfish candidates.

Industry relevance: Selective breeding leads to increased CMS-resistance.

Post-meeting PDF permission: Yes

Is elimination of PMCV in brood stock maintained under closed containment achievable?

Presenter: Maria Marjunardóttir Dahl

Affiliation: Faroese Food and Veterinay Authority, Faroe Islands

Co-authors: Petra Elisabeth Petersen - Faroese Food and Veterinay Authority, Faroe Islands
Debes Hammershaimb Christiansen - Faroese Food and Veterinay Authority, Faroe Islands

Summary: Piscine myocarditis virus (PMCV), the causative agent of cardiomyopathy syndrome (CMS), poses a persistent challenge to Atlantic salmon aquaculture. High-resolution genomic analyses have demonstrated that PMCV circulating in Faroese marine farming sites forms a distinct, monophyletic Faroese clade, consistent with a single historical introduction. Despite this common origin, PMCV spreads horizontally within the marine production system, and ongoing viral evolution has resulted in extensive genetic admixture and co-circulation of multiple variants within and between farming sites. As a consequence, farm-to-farm transmission events can no longer be resolved using single viral genomes, as infections are typically characterised by genetically heterogeneous viral populations.

The Faroese Atlantic salmon brood stock was re-established in 2017 and transferred from marine cages to land-based closed containment facilities – one of which has intake of filtered and UV-disinfected seawater in a flowthrough system. At the time of transfer, all brood fish were PMCV positive with low to medium viral loads and no clinical signs of CMS. During the first spawning season, viral loads increased and CMS was observed in a subset of individuals. However, in subsequent brood fish generations maintained exclusively under closed containment, PMCV prevalence and viral load declined progressively, and all brood fish stripped in 2024 and 2025 tested PMCV negative.

Following first-time exposure to seawater, PMCV was again detected in a brood stock batch intended for stripping in 2026. The PMCV variant originally present in the brood stock was previously well characterised and represented a single variant; however, this variant is now part of the genetically admixed PMCV population circulating at Faroese marine sites. Consequently, determining the origin of PMCV detected in brood stock requires sequencing of multiple individuals to assess whether viral detection reflects persistence of the original brood stock variant or reintroduction from the marine environment. Importantly, the extensive genomic characterisation of PMCV in the Faroe Islands provides a robust framework for resolving these alternative scenarios.

Whole-genome sequencing of spatiotemporally selected brood stock samples is ongoing and will be used to evaluate viral relatedness and elucidate mechanisms underlying PMCV re-emergence following seawater exposure.

Conclusion

Although Faroese PMCV originates from a single introduction, extensive horizontal transmission and genetic admixture at marine sites limit the resolution of transmission tracing. Closed containment facilitates gradual loss of PMCV in brood stock, but seawater exposure represents a clear risk for viral re-emergence. Comprehensive, multi-sample genomic surveillance enables discrimination between viral persistence and reintroduction and is essential for informed brood stock biosecurity management.

Industry relevance: PMCV/CMS leads to welfare issues and economic losses in Atlantic salmon farming. Our results indicate that long-term closed containment of brood stock can reduce PMCV to undetectable levels, highlighting its value as a biosecurity measure. However, renewed PMCV detection following seawater exposure demonstrates the continued risk of viral

persistence or reintroduction. These findings emphasise the importance of strict biosecurity at the brood stock level and the use of genomic tools to inform management decisions and reduce disease risk in commercial aquaculture.

Post-meeting PDF permission: Maybe (Dont know yet)

Effects of combining selective breeding and vaccination on resistance to Cardiomyopathy syndrome in Atlantic salmon (Salmo salar L)

Presenter: Marius Karlsen

Affiliation: Pharmaq AS

Co-authors: Ane Sandtrø, Pharmaq AS
Ingunn Thorland, Øyvind Breivik, Grazyella Yoshida, Serap Gonen and Ross Houston, Benchmark Genetics

Summary: Cardiomyopathy syndrome (CMS) caused by Piscine myocarditis virus (PMCV) is one of the main viral diseases of farmed Atlantic salmon in Norway, Scotland and the Faroes. The disease progresses slowly, with inflammation of the heart atrium as the main histological finding. In late stage disease, the atrium may rupture, resulting in sudden death. Two main lines of mitigating measures are now emerging in the industry, one being breeding of fish with high levels of genetic resistance to PMCV, using genomic selection (Benchmark Genetics), and the other is the ongoing development of a DNA-vaccine against CMS (PHARMAQ). Here we report a laboratory trial comparing these two strategies, and examining the combined effect of both approaches. Fish originating from families with either high or low genetic resistance towards PMCV were PIT-tagged and vaccinated with the DNA-vaccine or mock vaccinated with PBS, resulting in four groups (HighVac, LowVac, HighPBS, LowPBS). Following seven weeks of immunization, the groups were intraperitoneally injected with a tissue homogenate containing infectious PMCV. The fish were then sampled three and seven weeks post challenge, and the development of CMS was assessed in each group by real-time PCR for detection of PMCV in heart and kidney samples, and by histological examination of the heart atrium. Examination of hearts from 20 fish per group at the end-point revealed that 20/20 fish had developed CMS in the LowPBS negative control group. The prevalence in the HighPBS group was reduced to 6/20 fish, indicating a major effect of genetic selection alone on reducing CMS incidence. The vaccinated groups had prevalences of 4/20 fish (LowVac) and 1/20 fish (HighVac), suggesting that the combination of the line with high genetic resistance and the DNA-vaccine was capable of almost complete protection against CMS in this model.

Industry relevance: First study where selective breeding and vaccine against PMCV/CMS are combined and tested in a challenge model

Post-meeting PDF permission: Maybe (Dont know yet)

SalmoStrong: Drivers of Salmon Robustness

Presenter: Nick Wade

Affiliation: The Roslin Institute, UK

Co-author: Herve Migaud

A new £8.5 million project named SalmoStrong, funded through the BBSRC Business and Academia Prosperity Partnership program, will be led by the Roslin Institute partnered with the UK's largest salmon farmer Mowi Scotland. This Program is aimed to solve big problems through long-term research partnerships, in this case the respective strength of the business and academic partners. The scale and duration of the SalmoStrong partnership represents one of the largest funding investments into UK aquaculture. The research is co-designed and co-delivered to ensure that world-leading science innovations are developed for relevant industry challenges and able to deliver immediate benefit to salmon production to the Scottish, UK and global salmon farming sectors.

This five-year partnership with industry will focus on the major diseases impacting farmed Atlantic salmon in Scotland (focussed on cardiac health, gill health and emerging diseases), with the overall aim to deliver breakthrough science that reduces seawater mortality levels and improves the welfare and productivity of the sector.

The research covers 4 broad Pillars and 9 new full time researchers and PhD students, which are co-led by teams of over 30 industry and academic experts, to generate knowledge that will support animal welfare, profitability, sustainability, and societal acceptance. Pillar 1: Integrated Genetics – seeks to advance the current state-of-the-art for selective breeding, capturing and exploiting causal genetic variants and incorporating novel disease phenotypes. Pillar 2: Rearing History - plans to elucidate how embryonic temperature impacts life-long robustness traits, including disease resistance, immune responses, vaccination outcomes and cardiac health across multiple stages of production, dissecting mechanisms at the cellular and epigenetic levels. Pillar 3: Robustness Phenotypes – aims to dissect and accurately measure robustness using pathogen agnostic statistical, morphological, biochemical and molecular phenotypes, and apply statistical models to disentangle host robustness traits (resistance, infectivity and tolerance). Pillar 4: Talent and People - is dedicated to developing the current and next generation of aquaculture specialists, building local skills, capacity and vibrant regional communities

This presentation will provide an outline of the approaches, and a brief project update since the work began in earnest in late 2025. With specific reference to cardiac health, one PhD student will apply advanced whole genome sequencing strategies (including pangenomics) to reveal genetic factors and genomic regions underlying susceptibility of Atlantic salmon to cardiomyopathy syndrome (CMS) and possibly reveal causal variants. A second PhD student will focus on heart cellular development, in combination with the impacts of embryonic rearing temperature, and linking cellular composition and gene expression with CMS quantitative trait loci (QTLs). A third PhD topic will apply newly developed statistical tools to separate CMS resistance and tolerance as discrete traits that can be used for selecting the best fish. Further project work will develop new CMS biomarkers that will be applied at scale across Mowi breeding populations.

Industry relevance: Outcomes of this research will establish a world-leading framework to identify regions of the genome associated with complex diseases, develop new ways to measure and improve immune system performance and define novel phenotypes to select the most resilient fish.

Essential fatty acids (EPA+DHA) enhance resistance to viral disease in in Atlantic Salmon (*Salmo salar*): Evidence from both controlled and large-scale farming studies

Presenter: Jinni Gu

Affiliation: BioMar AS; Norway

Co-authors: Trygve Sigholt, Ida-Kathrin Gjerstad Nerbøvik, Torunn Forberg, Elisabeth Aasum

Summary: Viral diseases represent a major health and economic challenge in global salmonid aquaculture. Diseases such as cardiomyopathy syndrome (CMS), heart and skeletal muscle inflammation (HSMI), jaundice syndrome, and pancreas disease (PD) contribute to significant economic losses and compromised fish welfare. Numerous studies have demonstrated that eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA) are essential for both optimal salmonid growth and resilience to viral infections.
From 2023 to 2025 we conducted studies to evaluate whether increasing dietary EPA+DHA beyond requirement for growth can enhance resistance to viral infections under both controlled and standard farming conditions.
Atlantic salmon (initial weight ~25 g) underwent a 9-week prefeeding period including smoltification, followed by a 10-week SAV3 cohabitation challenge. Fish were sampled biweekly to assess the challenge effect by evaluating heart viral load, plasma biomarkers (e.g., creatine kinase (CK), alanine transaminase (ALT), and aspartate transaminase (AST)), and

histopathological lesions in the pancreas, heart, and skeletal muscle. Statistical analysis revealed that salmon fed elevated dietary EPA+DHA had significantly lower SAV3 loads, reduced plasma CK, ALT, AST levels, and milder tissue lesions associated with PD.
A large-scale field trial was conducted with two smolt groups (spring and autumn) at two farm sites, Havstein S (13284) and Slapøy N (14676), in Norway. During the period with a natural HSMI outbreak, both spring and autumn smolt (approximately 2 kg and 1 kg, respectively) fed diets with higher EPA+DHA showed improved blood biomarkers associated with immunity and tissue integrity, including higher albumin and lower creatine kinase (CK) and cardiac creatine kinase (CK-MB) across farm sites.
Together, results from both controlled viral challenge and farming conditions consistently demonstrate that increasing dietary essential EPA+DHA enhances Atlantic salmon resistance to viral infections. These findings support nutritional strategies that optimize EPA+DHA levels prior to the high-risk period to promote health, welfare, and robustness in salmon aquaculture.

Industry relevance: Numerous studies have demonstrated that eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA) are essential for both optimal salmonid growth and resilience to viral infections. Our findings support nutritional strategies that optimize EPA+DHA levels prior to the high-risk period to enhance the resistance to viral disease, promote health, welfare, and robustness in salmon aquaculture.

Post-meeting PDF permission: Yes

Practical use of clinical nutrition during viral disease outbreaks in Atlantic salmon (*Salmo salar*)

Presenter: Torunn Forberg

Affiliation: BioMar AS; Norway

Co-authors: Marte Hauge, Jonny Nordheim, Eirik Jakobsen, Ida-Kathrin Gjerstad Nerbøvik, Iselin Lillevik Møllerstuen, Pål Anders Wang, Vegard Denstadli

Summary: It is well established that specific nutritional components such as marine omega3 fatty acids EPA and DHA contribute to improved robustness and modulation of inflammatory responses in Atlantic salmon during viral disease. However, continuous use of high-cost, high-marine diets throughout the full production cycle is neither practical, sustainable, nor economically justified under commercial farming conditions. The key challenge is therefore not whether nutrition can influence disease robustness, but how limited nutritional resources can be applied in a targeted and effective way.

This work summarizes practical field experience from customer trials using a clinical nutrition feed, Qardio HP. Across multiple sites, Qardio HP was applied during naturally occurring outbreaks of cardiomyopathy syndrome (CMS) and heart and skeletal muscle inflammation (HSMI/HSMB). Data collection focused on disease development and fish performance before and after initiation

of clinical nutrition and was conducted in close collaboration with farmers and fish health personnel.

Across locations, feeding Qardio HP during active disease phases was consistently followed by stabilization or reduction in observed mortality and increased robustness. Fatty acid analyses confirmed rapid enrichment of EPA and DHA in heart tissue after 6–8 weeks of feeding. Supporting diagnostic data from selected sites indicated improvements in physiological biomarkers and trends toward reduced severity of cardiac pathology over time.

Industry relevance: These field experiences demonstrate that the value of clinical nutrition lies in strategic application during periods of elevated disease risk. When used deliberately and in collaboration with farmers, targeted clinical nutrition represents an effective way to translate established nutritional mechanisms into measurable benefits under commercial farming conditions.

Characterization of recent IHNV strains with focus on diagnostics in the field and in vivo virulence testing

Presenter: Niccoló Vendramin

Affiliation: DTU Aqua - National institute of aquatic resources / EU reference laboratory for fish diseases

Co-authors: Argelia Cuenca DTU AQUA, Niels Lorenzen DTU AQUA, Dagoberto Sepulveda DTU AQUA, Britt Bang Jensen DTU AQUA

Summary: In 2021, infectious haematopoietic necrosis virus (IHNV) was detected in farmed rainbow trout in Denmark for the first time. Given epidemiological situation and implementation of control measures Denmark relinquished official freedom of IHNV later in the year. Apart from the impact on Danish rainbow trout production, there was also a potential risk of the virus being accidentally transmitted to Atlantic salmon in Denmark and/or in neighboring countries. Earlier outbreaks of IHN among farmed Atlantic salmon in Canada stressed the importance of controlling the Danish epidemics and of determining whether the Danish IHNV variant was virulent to this species.
Point mutation of the isolate genome reduced sensitivity of recommended diagnostic method at the time and prompted re-validation of updated tools.
A first experimental challenge in rainbow trout and Atlantic salmon was conducted to assess virulence of the new virus variant. The fish were exposed to the virus both by immersion and intraperitoneal injection. Later, a series of cohabitation challenge trials were conducted in Atlantic salmon.
The initial infection trials confirmed that the new IHNV isolate was highly virulent to rainbow trout, while limited clinical disease occurred among exposed Atlantic salmon. However, co-habitation trials, where naïve fish were kept together with fish injected with the virus, demonstrated that the virus could adapt to Atlantic salmon within a few in vivo passages and that efforts should be made to prevent transmission to farms rearing this species.

Industry relevance: Infection with infectious haematopoietic necrosis virus (IHNV) has historically been endemic in continental Europe. in recent years firstly IHN occurred in Finland in 2018 and then in 2021 in Denmark. Rainbow trout and Atlantic salmon are susceptible to the infection and increased awareness is pivotal to early detect emergence of disease and control of it.

Post-meeting PDF permission: Maybe (Dont know yet)

Third party bio security challenges

Presenter: Marcus Darler

Affiliation: O'Three Ltd, United Kingdom

Summary: We have been supplying diving dry suits to the Aquaculture industry for over 20 years and during this time we have gained an good understanding that in the majority of cases this activity is carried out by sub contractors. When dry suits that have been used in this environment are returned for repair it is very apparent from the smell that there are issues with the level of cleanliness. We are unsure from a bio security point of view how bad the contamination needs to be on these suits to create an issue but would like to make the industry aware of this, share best practice of one Aquaculture company and additional solutions that could be implemented.

Industry relevance: Unwanted in pen contamination and cross contamination to other pens and sites. Any opportunity to minimise this and the bad public image, reduce losses and increase profitability.

Post-meeting PDF permission: Maybe (Dont know yet)

Automated Deep Learning Detection and Quantification of Myocardial Inflammation in Salmon Heart Whole Slide Images

Presenter: Kai-Inge Lie

Affiliation: Pharmaq Analytiq, Norway

Co-authors: Marianne Kraugerud, Pharmaq Analytiq

Summary: Inflammation of the myocardium is a central feature of both heart and skeletal muscle inflammation (HSMI) and cardiomyopathy syndrome (CMS), two significant diseases affecting salmon. Traditionally, semi-quantitative scoring of the myocardial inflammation severity has been widely applied in both experimental and observational studies of these conditions. To reduce turnaround times and to provide a more robust and reproducible method for scoring myocardial inflammation in large studies, we trained artificial intelligence (AI) deep

learning models to quantify the relative extent of myocardial inflammation in histopathological heart samples. The models were trained utilizing Python with open-source libraries in Jupyter notebooks in a cloud computing environment (Azure Machine Learning Studio). The training of the myocarditis detection model included a total of 206,000 jpeg images obtained from 443 different heart whole slide images, while the myocardium detection model was trained on a dataset of 70,000 jpeg images obtained from 208 different whole slide images.

As first validation step of the myocarditis model an external independent test dataset of 78,200 jpeg images was used. This test dataset was obtained from multiple slides from hearts with either HSMI, CMS or no myocardial pathology in addition to various non myocardial salmon tissues. Prediction using this model on this dataset indicated a sensitivity of 0.962, specificity of 0.983 and accuracy of 0.973 at the chosen decision threshold. A second validation step assessed the performance of the combined models on whole slide images that were also scored by veterinary pathologists using established semi-quantitative protocols. This evaluation included two joint datasets: one comprising fish from HSMI challenge studies (n = 1,014) with HSMI lesions scored from 0 to 4, and another containing sea-caged salmon (n = 244) with general (non-disease-specific) myocarditis scores, including both HSMI and CMS cases. For both these validations, the veterinary pathologist's semiquantitative scores showed strong positive correlation with the AI-estimated extent of myocardial inflammation. Specifically, for the HSMI challenge group, the fish Spearman correlation coefficient was 0.64 ($p < 0.0001$), while for the sea-caged group, it was 0.68 ($p < 0.0001$). The validation of the model demonstrates its effectiveness in detecting and quantifying inflammation in salmon hearts affected by HSMI and CMS. This approach improves reproducibility of scoring, minimizing both intra- and interobserver variability commonly encountered in manual histopathological assessments. At the slide level, the model reports the relative proportion of sectors with inflamed myocardium out of the total sectors of detected myocardium in the slide, resulting in a continuous numerical variable. This provides advantages over traditional ordinal scoring systems in terms of versatility for statistical analysis. For large-scale studies, the method also significantly reduces turnaround time.

Industry relevance: Semi-quantitative scoring of myocardial inflammation severity has been widely applied in both experimental and observational studies of both heart and skeletal muscle inflammation (HSMI) and cardiomyopathy syndrome (CMS). We will present the development and performance of artificial intelligence (AI) deep learning models that enables an automated detection and quantification of myocardial inflammation with high reproducibility. This method can be used by industry doing experimental or observational research on HSMI and CMS.

Post-meeting PDF permission: Yes

TRINATION

A dual-readout approach to understand heart healing after PMCV infection in Atlantic salmon: collagen remodeling and cardiomyocyte gene signatures

Presenter: Øystein Evensen

Affiliation: Norweigan University of Life Sciences, Faculty of Veterinary Medicine

Co-authors: A. Gamil, H.K. Karlsen, M. Austad, T. Hjemsæter, M. Finnbråten, Norwegian University of Life Sciences

Summary: Cardiomyopathy syndrome (CMS) caused by piscine myocarditis virus (PMCV) is characterized by a necrotizing myocarditis of the spongy ventricular myocardium and atrium. It is clinically associated with poor resolution of cardiac lesions. A central unresolved question is whether the post-PMCV heart primarily undergoes repair (persistent extracellular matrix deposition/fibrosis) rather than regeneration (restoration of cardiomyocyte mass and contractile architecture). To address this, we adopt a two-sided approach that combines collagen-focused histology with targeted transcriptional readouts of cardiomyocyte homeostasis (phospholamban; pln) and regenerative signaling (Notch).

We first evaluated CMS-affected field material using routine histopathology and then applied collagen- and matrix-oriented special stains, including Van Gieson/EVG, Masson's trichrome, reticulin, and Picrosirius red. In a dataset of PMCV-positive hearts from a confirmed CMS outbreak (n=50; qPCR-confirmed), the dominant lesion pattern involved substantial inflammatory and necrotizing changes in the spongiosa and atrium. Picrosirius red with polarized light microscopy (12 selected slides) demonstrated that total collagen was generally sparse across large areas, but with focal regions of increased collagen in damaged myocardium. Both collagen type I and III were detected; however, collagen type I tended to predominate in areas with higher collagen abundance, consistent with a shift toward mature, potentially persistent scar-like matrix rather than a transient, remodelled matrix.

In parallel, hearts from an experimental PMCV challenge were sampled at 4 and 10 weeks post challenge (wpc). Targeted qPCR showed reduced expression of pln and Notch in infected fish compared with controls at both time points. These shifts are compatible with persistent cardiomyocyte stress/dedifferentiation and/or dilution of cardiomyocyte transcripts by inflammatory infiltrates, together with limited engagement of Notch-linked regenerative signaling at these stages; importantly, bulk-tissue qPCR cannot resolve compartment-specific activation. Combined with collagen I/III mapping, the results motivate time-course studies integrating spatial analyses and direct cell-cycle readouts (e.g., PCNA/BrdU) to test regenerative cardiomyogenesis after infection.

The take-home message is methodological and biological: (i) collagen subtype readouts (Picrosirius/reticulin) provide an interpretable map of matrix remodeling in CMS lesions, (ii) targeted transcriptional markers (pln and Notch) add a complementary window into cardiomyocyte homeostasis and candidate regenerative signaling after experimental infection, and (iii) together these readouts suggest a tendency toward dominant repair in focal lesions and persistent remodeling at 4-10 wpc. These early-stage studies motivate the next step, which will include spatial analyses and in situ proliferation and immune-resolution markers (e.g., PCNA/BrdU, macrophage phenotyping) and time-course sampling, to directly test whether and when regenerative cardiomyogenesis occurs after PMCV infection.

Industry relevance: CMS is a major welfare and loss-driver in salmon farming. An ability to distinguish reversible/regenerative/healing from persistent fibrotic repair in PMCV-affected hearts would strengthen prognosis, inform management decisions and provide measurable endpoints for evaluating interventions like selective breeding, vaccination, and mitigation strategies.

Post-meeting PDF permission: Maybe (Dont know yet)

Trialling the use of a portable PCR machine for onsite rapid detection of pathogens in Atlantic salmon aquaculture.

Presenter: Sarah McEvoy, Fish Health Biologist

Affilation: Mannin Bay Salmon Co. Ltd, Ireland

Summary:
This study was an appraisal on the use of the Genesig q16 Real-Time PCR instrument in combination with the genesig Easy Kits in aquaculture as a portable PCR machine for pathogen screening in Atlantic salmon.
Methods for sampling, sampling preparation and extraction were adapted and refined for purpose in order to provide reproduceable and validated detections/quantitative results for *Piscirickettsia salmonis* and salmonid alphavirus.
A turnaround time of 12 hours from sampling to results, allows for an independent screening of pathogens with rapid results providing crucial and instant information directly to site managers who can then make decisions on fish husbandry practices while prioritising the health and welfare of fish.

PMCV in skin and mucus

Presenter: Espen Rimstad

Affiliation: Norwegian University of Life Sciences

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Wessel, Øystein, NMBU, Norway

Summary: Introduction:
Control of cardiomyopathy syndrome (CMS) in Atlantic salmon relies on an understanding of the etiology and pathogenesis of the disease. CMS was characterized histologically as a separate entity already in the 1980s, but its transmissible nature and association with Piscine myocarditis virus (PMCV) were not established until more than two decades later. PMCV particles consists of a single-layered icosahedral capsid and a double-stranded RNA (dsRNA) genome containing two open reading frames (ORFs), as well as a third unique ORF and has recently been put in the Pistolviridae family. Experimental and field observations indicate that PMCV spreads at a relatively slow rate. The aim of this study is to improve our understanding of fundamental aspects of viral biology, pathogenesis, and transmission of PMCV.

Methodology:
We assessed the presence of PMCV in field samples by testing for PMCV RNA in fish tissues and the surrounding environment and investigated the cellular localization of genomic and transcribed PMCV RNA across multiple internal organs.
Results:
Notably, the skin was the most frequently PMCV RNA–positive tissue sampled, and several fish tested positive in skin samples despite negative results in internal organs. RNAscope in situ hybridization revealed strong, localized PMCV RNA signals both in the skin cells and mucus. Additional sampling of external sites, including surrounding water, was conducted, and the virus can be present in large amounts in the surrounding aquatic environment such as sedation tanks. In fish with heart lesion a strong, localized PMCV RNA signals was present within myocardial cells of the spongiosum layer of the heart, with minimal detection in the compactum. Among all organs examined, the heart harbored the highest viral RNA load, particularly during clinical disease. Transcription of viral single-stranded RNA (ssRNA; viral mRNA) was largely confined to the spongiosum, while no comparable transcriptional activity was detected in the kidneys or

other internal organs.
Conclusion:
Our findings indicate that PMCV infection colonization of the fish surface and is not restricted to internal tissues. PMCV presence in the surrounding aquatic environment, including sedation tanks used during de-lousing procedures strongly indicates potential transmission through such equipment. Future studies should investigate possible external reservoirs or vectors, as well as sources of environmental contamination such as equipment surfaces and biofilms.

Funding: FHF – Norwegian Seafood Research Fund, # 901671.

Industry relevance: It has been approximately 35 years since CMS was recognized as a disease in farmed salmon and 15 years since the first characterization of PMCV. Despite this, it has not been possible to significantly reduce the prevalence of CMS. One important reason for this is that effective biosecurity measures require a reasonably good understanding of transmission routes, the effects of disinfectants on viral infectivity etc. This project is a contribution to knowledge base necessary for control, routines, and related practices to reduce the PMCV prevalence.

Post-meeting PDF permission: Yes

Gill swabs reveal early PRV-1 infection

Presenter: May Linn Buberg

Affiliation: Salmax Research AS, Norway

Co-authors: Jakob Mo, Salmax Research AS
Øystein Wessel, Norwegian University of Life Sciences

Summary: Piscine orthoreovirus (PRV-1) is highly prevalent in Atlantic salmon (Salmo salar), where it causes heart and skeletal muscle inflammation (HSMI) and impaired production performance. While horizontal transmission of PRV-1 is well documented under field conditions, the routes of viral shedding and entry, including fecal–oral transmission remain unclear. In addition, reliable and non-invasive diagnostic tools are increasingly needed to reduce stress and improve welfare during both experimental and commercial monitoring.

This collaborative project between Salmax Research AS and NMBU, conducted at VESO Vikan aimed to establish an experimental infection model to evaluate the use of non-invasive swab sampling for detection and monitoring and to investigate routes of entry and exit during PRV transmission. Atlantic salmon were challenged with PRV-1 by intraperitoneal injection and placed with naïve cohabitants. Fish were monitored and sampled weekly for a period of 16 weeks. Sampling included blood and tissue, but also mucus, gill and fecal swabs, to evaluate diagnostic sensitivity and practicality. Feces from the cohabitants were collected and a separate

naïve fishgroup were exposed fecally contaminated water, enabling evaluation of feces as the potential infectious route.

Gill swab sampling proved to be highly sensitive for early detection of PRV infection. PRV-1 RNA was detected in gill swabs from cohabitants as early as 1 week post-cohabitation (wpc), with all gill swab samples testing positive by 3 wpc. This preceded or coincided with detection in blood, where all samples were positive by 3 wpc. Gill swabs consistently showed high diagnostic sensitivity and reliable detection across the infection period. Contrary to the initial hypothesis, fecal–oral transmission could not be confirmed under the experimental conditions applied. Only low levels of PRV-1 RNA were detected in the fecally exposed group, and these fish did not develop infection dynamics comparable to those observed in cohabitant fish.

The results strongly indicate the gills as a primary portal of entry for PRV-1 infection and potentially also as an early site of viral shedding. The high sensitivity of gill swab sampling, particularly during the early phase of infection, supports its use as a non-invasive and welfare-friendly diagnostic approach for early detection and longitudinal monitoring of PRV-1. Further these findings suggest that fecal–oral transmission is unlikely to represent a dominant infection route for PRV-1 under the tested conditions. This study refines the experimental infection model for PRV-1 and provides practical implications for surveillance, research, and disease management in Atlantic salmon aquaculture.

Industry relevance: The demonstration that gill swabs provide highly sensitive early detection of PRV-1 enables earlier identification of infected populations than is typically possible with blood or tissue sampling. Earlier detection improves the timing and precision of management decisions, including cohort separation, site-level risk assessment, and production planning. Gill swab sampling is non-invasive and can be performed without euthanasia, reducing handling stress, mortality, and ethical concerns associated with repeated sampling. This is particularly valuable for longitudinal monitoring in broodstock, smolt production, and research trials.

Post-meeting PDF permission: Maybe (Dont know yet)

Comparison of virulence across recent ISAV-HPR deleted strains in Atlantic salmon infected by bath challenge

Presenter: Sonal Patel

Affiliation: Norwegian Veterinary Institute, Norway

Co-authors: Authors: Sonal Patel, Ole Bendik Dale, Johanna Hol Fosse, Torfinn Moldal, Bjørn Spilsberg, and Simon Weli

Summary: Infectious salmon anaemia (ISA) is a serious infectious disease of Atlantic salmon caused by the orthomyxovirus Isavirus salaris (ISAV). ISA outbreak mortality varies widely, with a

range of environmental and host factors obscuring potential virus-specific contributions to this variability. Experimental challenge studies are few but indicate that ISAV-HPR deleted strains may vary considerably in virulence. The aim of this study was to compare the virulence of a panel of recent Norwegian ISAV isolates and generate material for future in-depth studies of the mechanistic basis of ISAV virulence, using synchronized bath challenge.
Atlantic salmon (50-80 g) were challenged with ten different ISAV isolates. Two sets of ten tanks each was designated as sampling group and observational groups for each isolate, respectively. The trial was performed in a freshwater flow-through aquaculture system at 12°C, and mortality was monitored. Possible differences in mortality and pathology were investigated and used as criteria for defining virulence. The cumulative mortality in fish groups infected with different isolates ranged from 15 to 100%, suggesting considerable variability in virulence. Even isolates originating from farms with no clinical signs of ISA caused mortality, but in the lower range. Virus shedding and viral load in heart also varied between groups but did not correlate with mortality.

Industry relevance: Understanding the variation in ISAV isoaltes would support testing of vaccine efficacy. Additionally, the information will help in control strategies and management.

Post-meeting PDF permission: Maybe (Dont know yet)

Validation of water-sampling to tissue-sampling for surveillance of ISAV

Presenter: Britt Bang Jensen

Affiliation: Technical University of Denmark (DTU AQUA)

Co-authors: Argelia Cuenca, DTU AQUA
Manuel Alejandro Perez Maldonado, DTU AQUA

Summary: In the last decade, research have shown that DNA/RNA of different fish pathogens can be detected from water samples, as a supplement to samples from fish tissue. The drive for investigating methods to detect pathogens in water is that it could be a cost-effective and non-lethal method for surveillance and control of pathogens. eDNA is thus seen as a promising and complimentary tool that can support surveillance and early detection. The World Organization for Animal Health encourages guidelines on the appropriate applications and limitations of eDNA methods, as diagnostic performance data for eDNA assays are not yet sufficient for use in surveillance. In Norway, eDNA methods have been developed for several important pathogens, like SAV, ISAV, PRV and Aphanomyces astaci.

Using ISAV as an example, we have performed an experimental study with the aim of validating eDNA from water samples to the traditional tissue sampling, by means of a modified diagnostic test evaluation.

In this study, we made an experimental setup of replicate tanks with Atlantic salmon. Infected fish were added to 180 l tanks with non-infected fish at different proportions, thus creating a dilution series of 10%, 20%, 30%, 50% and 100% infection prevalence, respectively. Water samples were taken from each tank twice a day for a 7-day period, and fish were sampled on days 5 and 7. This sampling scheme was selected as to explore the ability of water samples to detect ISAV at early stages of infection, and before fish present any clinics.

At every sampling point, we sampled both small aliquots of water, and larger volumes (1 l) that were passed through a filter to concentrate the virus. Nucleic acids were extracted from water aliquots (200 µl), filters, fish mucus, gills, hearth and kidney samples. All samples were tested for detection of ISAV using standard diagnostic test (RT-qPCR), including a gene targeting fish RNA. Samples were binary coded (positive/negative) targeting Bayesian latent-class analyses for statistical calculation of the sensitivity and specificity of the different sampling methods, in the absence of a gold standard.

Studies like these is an important step towards validating the eDNA methods. The ultimate goal is to identify in what situations it could be recommended to use water sampling as a substitute for fish sampling, or even sometimes as the preferred approach.

Industry relevance: Use of water samples for surveillance would be a very attractive alternative to the traditional sampling of fish. Water samples do not incur the sacrifice of fish that could be used in production, and there is also considerable less handling associated with sampling of water, as compared to the catching, sedating, killing and necropsy of the fish. Studies like these are important in order to validate the use of eDNA methods with a systematic, statistically sound approach.

Post-meeting PDF permission: Maybe (Dont know yet)

Tracing the Spread of SAV2 to the Helgeland Coast in 2023

Presenter: Jan Inge Øvrebø

Affiliation: Norwegian Veterinary Institute, Norway

Co-authors: Jan Inge Øvrebø1, Hilde Sindre1, Hege Løkslett1, Torfinn Moldal1, Monika Hjortaas1
1 Norwegian Veterinary Institute, Norway

Summary: Salmonid alphavirus (SAV) causes pancreas disease (PD) in Atlantic salmon (Salmo salar) and represents a major challenge for salmon aquaculture in Northern Europe due to its impact on fish welfare and production. In Norway, PD outbreaks are associated with two SAV subtypes, SAV2 and SAV3, which exhibit distinct geographic distributions. While SAV3 predominates along the southwestern coast, SAV2 has been restricted to Mid-Norway. After several years without PD cases north of the established PD zone, SAV2 was detected in 2023 at

four aquaculture sites along the Helgeland coast.

Advances in whole-genome sequencing have improved resolution of SAV transmission dynamics and enable discrimination between local viral persistence and new introductions. Although long-distance spread is largely attributed to industry-related activities such as fish movements, the relative roles of environmental transmission and local reservoirs remain unclear. The introduction of SAV2 in the Helgeland region therefore provides an opportunity to investigate the spread of PD at the northern limit of its known distribution.

Industry relevance: This work is relevant to the fish industry because it directly informs how SAV spreads, why it is appearing in new regions, and how salmon producers can reduce disease risk, protect fish welfare, and avoid major economic losses.

Post-meeting PDF permission: Maybe (Dont know yet)

Using genomic data to understand viral evolution and reconstruct transmission scenarios in Atlantic salmon aquaculture

Presenter: Bertie Knight

Affiliation: The Roslin Institute, University of Edinburgh, UK

Co-authors: Svein Alexanderson (Pharmaq), Ane Sandrø (Pharmaq), Chris Matthews (Pharmaq Analytiq UK), Elise Hjelle (Pharmaq)
Marte Follesø Sønnervik (Pharmaq), Mari Solheim (Pharmaq Analytiq), Sam Lycett (The Roslin Institute, University of Edinburgh), Marius Karlsen (Pharmaq), Daniel Macqueen (The Roslin Institute, University of Edinburgh)

Summary: Viral genomic data may be useful to understand and mitigate disease spread across a range of salmonid viruses including those that cause cardiomyopathies such as salmonid alphavirus (SAV) and piscine orthoreovirus (PRV). Oxford Nanopore amplicon sequencing assays were developed to obtain viral whole genomes for these two viruses and create a database of whole-genome sequences with associated epidemiological metadata, enabling reconstructions of viral genetic diversity and transmission scenarios.
SAV is widespread within Norwegian aquaculture, with SAV2 and SAV3 subtypes present in discrete endemic zones. Of 188 SAV samples sequenced, 171 belong to SAV3. We identify four well supported SAV3 clades, with strong regional geographic signal within Norway. Using time-calibrated phylogeographic analysis, we show that all major SAV3 lineages likely originate in Hordaland. This supports a scenario where high-density salmon farming in Hordaland acts as a primary source of SAV3 with periodic transmission events responsible for outbreaks in neighbouring counties, including distinct SAV3 lineages co-circulating in Sogn og Fjordane.
We also sequenced 12 Scottish SAV2 samples from outbreaks in Orkney and Shetland. Analyses show island specific lineages of SAV2, which shared a common ancestor 30 years ago. Despite

limited sequencing, our data is consistent with minimal transmission between Orkney and Shetland.
We have also sequenced 92 PRV whole genomes from Norway. Subtype PRV1a circulates in the Pacific Ocean and PRV1b in the North Atlantic and Europe. Our analyses capture multiple additional well-supported clades, indicating the existence of further genetically distinct lineages of PRV1 beyond characterised PRV1a and PRV1b subtypes. Phylogenetic analyses of individual PRV genomic segments provides evidence that reassortment, the exchange of genomic segments during co-infection, is common. These events include the exchange of genomic segments between PRV1a and PRV1b.
Together, our data highlights the need for whole genome sequencing to fully understand PRV evolutionary history including reassortment events, alongside the need for a revised nomenclature for PRV1 genotypes.

Industry relevance: Viral disease outbreaks threaten the sustainability of salmonid aquaculture, resulting in economic losses and concerns for fish welfare. Characterising viral genetic diversity is key in identifying the emergence of novel viral strains. The genomic landscapes for these viruses are relatively unknown due to the limited number of publicly available sequences. Greater characterisation will enable the distinction between novel variants and under-sequenced circulating viral strains. This sort of data can also underpin and support updates to vaccines to emergent viral strains.
Coupling viral whole genome sequencing with epidemiological approaches helps gain a better insight into the geographical distribution of different viral subtypes and their relative contribution to regional outbreaks. More detailed and updated viral molecular epidemiology can allow for more targeted infection control measures. Standard partial sequencing approaches used for genotyping lack the resolution to be able to conduct such analyses, providing limited information on patterns of transmission.
Additionally, this approach can be used to reconstruct historical and contemporary transmission scenarios on national and regional levels. Inferences on these transmission scenarios can inform infection control decision making and the management of viral disease spread and limit future transmission.

Post-meeting PDF permission: Yes

Why whole-genome sequencing matters for segmented viruses in salmon farming: lessons from ISAV

Presenter: Mingli Zhao

Affiliation: Royal Veterinary College

Co-authors: Jack O'Brien1, Helene Duault2, Mari Aas Solheim3, Abdullah Madhun4, Silvia Soares5, Ana Da Silva Filipe6, Katherine Smollett6, Chris Matthews7, Svein Alexandersen3,

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Summary: RNA viruses with segmented genomes can evolve through reassortment, where genome segments are exchanged when multiple viruses infect the same fish. In salmon aquaculture, this complicates surveillance because routine investigations often rely on RT-qPCR and single-segment sequencing. In infectious salmon anaemia virus (ISAV), segment 6 is commonly used for typing based on the highly polymorphic region (HPR). While these methods enable rapid detection and classification, they capture only one part of the virus's evolutionary history and can mislead interpretation when other segments tell different stories.
In this talk, I explain why whole-genome sequencing (WGS) is particularly valuable for segmented viruses, using ISAV as a case study. Using multi-region datasets, I compare outbreak and transmission inferences based on a single segment with those based on all genome segments. We find that reassortment is prevalent in ISAV, meaning that relationships inferred from one segment do not always reflect genome-wide relatedness. Notably, we detect reassortment even between European and North American genotypes, showing how segment-based typing can miss key evolutionary events and lead to misleading conclusions about outbreak connectivity, shared sources, or direct transmission.
Finally, I discuss how WGS strengthens interpretation of variant emergence, including relationships between non-virulent HPR0 and virulent HPR-deleted (HPRdel) forms. Although segment 6 underpins HPR classification, genome-wide data can reveal additional markers in other segments that help clarify when and how virulent variants emerge and spread. Overall, the focus is on what WGS changes in practice: more robust outbreak linkage, clearer clues about infection sources, and stronger evidence to guide biosecurity decisions in salmon farming.

Industry relevance: This presentation translates ISAV WGS into practical value for better understanding virus spread in salmon aquaculture. Sequencing all segments provides a clearer picture of how viruses move through production systems, improving outbreak investigations and strengthening the evidence base behind control measures, especially when reassortment or mixed lineages are involved.

Post-meeting PDF permission: Maybe (Dont know yet)

Infection with SAV2 and SAV3 under equal conditions results in differences in viral loads, disease progression, severity and growth impact

Presenter: Fabian Kropp

Affiliation: Norwegian University of Life Sciences (NMBU), Norway

Co-authors: Markussen T(1), Nørstebø S(1), Lorenzini P(2), Vignuzzi M(2), Evensen Ø(1) and Mikalsen AB(1)
(1): Norwegian University of Life Sciences (NMBU), Norway, (2): A*STAR Infectious Diseases Labs, Singapore

Summary: Pancreas disease (PD) which is caused by salmonid alphavirus (SAV) poses an important challenge to the Norwegian and European aquaculture industry. Pancreas disease leads to severe lesions in the pancreas of infected fish along with lesions and inflammation of the heart and skeletal muscles. This leads to a severe impact on animal welfare as well as big economic losses for aquaculture production, due to mortality and stunted growth. In Norway, PD is caused by two genotypes of SAV, SAV2 and SAV3. Field experiences and earlier challenge studies indicate that PD cases caused by SAV3 are characterized with more severe infections compared to SAV2. However, the mechanisms behind this difference are not well understood. To understand more, we have performed a challenge experiment of Atlantic salmon to compare SAV3 and SAV2 challenged fish, when challenged under completely equal conditions.
For this, we produced SAV2 and SAV3 virus in cell culture from plasmid-based clones and used an early passage of the viruses to challenge Atlantic salmon parr. The fish were kept in separate tanks and challenged with either of the viruses under equal conditions and with equal infective dose of the virus used. The infected fish were then monitored over a total of 16 weeks, including sampling of tissue and blood from fish individuals performed weekly in the first four weeks followed by every four weeks until termination of the trial. Viral RNA in the heart was analyzed by quantitative RT-PCR and histopathological analysis was performed on samples from both heart and pancreas. Additionally, next generation sequencing and host transcriptomics were performed to investigate the host response during the early stages of infection. Blood samples were used to evaluate potential biomarkers associated with pancreas damage and to investigate regeneration mechanisms.
The in vivo challenge experiment demonstrates that SAV3 is present at higher levels than SAV2 during the first four weeks post infection (wpi). This coincides with more severe pancreas damage arising as early as 2 wpi, which impairs normal growth. SAV2 shows less severe pancreas damage with an earlier onset of regeneration, which is consistent with the lower levels of the virus. Heart lesions are also less severe and almost insignificant in individuals infected with SAV2. Analysis of the concentration of potential blood biomarkers show an increase over the same time period corresponding to the progress of the varying levels of disease characteristic lesions caused by the two SAV genotypes

Industry relevance: Pancreas disease severely impacts animal welfare as well as industry revenue due to stunted growth. Our project and results provide new knowledge and understanding of potential differences in virulence between SAV genotypes and host responses associated with these differences, which provides knowledge vital for combating the spread and

severity of infections and for public management of outbreaks caused by the different genotypes.

Post-meeting PDF permission: No

The role of cell-culture medium and viral antigens in the prevalence of spinal deformities including cross-stitch vertebrae and reduced growth in Atlantic salmon

Presenter: Rodrigo Belmonte da Silva[1*],
Affilation: MSD Animal Health Innovation AS, norway

Co-authors: Tom Hansen[2], Ann Cathrine Einen[1], Kjartan Hodneland[1], Stephane Villoing[1], Petter Frost[3] and Helene Midtbø[1] and Ragnar Thorarinsson[1]
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Summary: Several studies have demonstrated that oil-adjuvanted vaccines (OAVs) can cause a range of adverse effects in Atlantic salmon, including spinal deformities. A novel spinal pathology in salmon, termed cross-stitch vertebrae, was first noted in the Norwegian industry between 2017 and 2018 and later described in 2020. Subsequently, this vertebral pathology has been linked with the use of inactivated salmonid alphavirus (SAV) components in OAVs used to protect against Pancreas Disease. What causes cross-stitch vertebrae has, until now, remained unknown. The development of cross-stitch vertebrae in salmon can lead to serious fish-welfare challenges and substantial economic losses due to both reduced growth performance and impaired slaughter quality.

The production of vaccines based on inactivated viruses requires large-scale production of virus in cell cultures grown in nutrient-rich medium. In fish vaccinated with multivalent OAVs, we identified specific antibodies directed against one of the components traditionally included in the cell-culture medium (Fetal Bovine Serum, FBS), used for large-scale virus production. In the field study presented here, five multivalent OAV formulations, with and without FBS and SAV antigen, were tested in PIT-tagged Atlantic salmon produced under different smoltification and temperature regimes.

Fish vaccinated with formulations containing FBS showed a high prevalence of cross-stitch vertebrae at the time of slaughter, compared with fish groups immunized with vaccine formulations lacking this component in which no or only a very limited occurrence of cross-stitch vertebrae was observed. The inactivated SAV antigen in a vaccine formulation without FBS did not increase the prevalence of cross-stitch vertebrae when compared to the control group.

The fish that developed cross-stitch vertebrae also exhibited significantly reduced growth rates compared with fish displaying normal spinal morphology, irrespective of the farming regime. As previously reported, there was a significant correlation between the severity of cross-stitch vertebrae and growth, while the condition factor was also affected, most likely due to the relatively shorter vertebral columns of the fish impacted by this pathology.

Industry relevance: This study is the first to demonstrate a direct causal relationship between a traditional component of cell-culture medium used in the production of a viral component in OAVs and the development of cross-stitch vertebrae in Atlantic salmon. The impact on animal welfare and the economic losses caused by spinal deformities are matters for concern and therefore should be focus of further studies. Nevertheless, and based on these results, it is strongly recommended that whole virus vaccine components in future OAVs do not contain any FBS.

Challenges in evaluating mRNA vaccines against ISA due to variable mortality in challenge experiments with a recent ISAV isolate

Presenter: Lars Ole Sti Dahl

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Summary: Background:
Infectious salmon anemia virus (ISAV) belongs to the family Orthomyxoviridae and occurs in two phenotypes: avirulent ISAV-HPR0 and virulent ISAV-HPRΔ. ISAV has a segmented, single-stranded, negative-sense RNA genome that is prone to antigenic drift and shift, resulting in the emergence of isolates of varying virulence. In Norway, approximately 15-20 outbreaks are still reported annually. Vaccination is used as a preventative strategy, but is not mandatory, and reports of ISA in vaccinated fish populations indicates that current vaccines do not provide sufficient protection against infection.
The success of the COVID-19 mRNA vaccines accelerated the interest in this vaccine platform for

other viral diseases and across different species. We have previously demonstrated that mRNA, encapsulated in lipid nanoparticles (LNPs), can express antigens in Atlantic salmon. Recently, two mRNA vaccines have demonstrated protective efficacy against diseases caused by rhabdoviruses in rainbow trout, highlighting that this platform is applicable in salmonids. We designed and tested an mRNA-LNP vaccine in Atlantic salmon challenged with a recent ISAV isolate. Preliminary virulence assessments of this isolate showed high mortality, while in the following vaccine challenge experiment, using similar conditions, the ISAV isolate failed to induce mortality. The same trend was observed in a repeated experiment. Consequently, we decided to use a well-characterized ISAV isolate in a subsequent vaccination study to ensure predictable viral challenge in order to conclude whether the mRNA vaccine can protect against ISA.

Methodology:
A recent ISAV isolate (70-72) from Norway was used in a series of challenge experiments in Atlantic salmon. A virulence test was done where shedder fish were injected with ISAV 70-72 isolate and then introduced to naïve cohabitant fish. and high mortality was observed in both shedder and cohabitant fish. Following the virulence experiment, an mRNA-LNP vaccine encoding HE was challenged with the ISAV 70-72 isolate, but this time it resulted in barely any mortality in shedder fish and no mortality in vaccine and control groups. Consequently, a freshly cell-culture-propagated ISAV 70-72 stock was made and re-tested in virulence and vaccine challenges. The same trend was observed, where the virulence test resulted in high mortality, however, again, during the following vaccine trial, the challenge did not take off. Therefore, a new vaccine experiment was conducted with a well-established ISAV isolate and is now ongoing.

Results and conclusion:
In the first ISAV 70-72 virulence trial, cumulative mortality reached 100% in shedders and 60% in cohabitant fish, while the cumulative mortality of the shedder fish in the first vaccine study only reached 25% with no observed mortality in vaccinated or control groups. The second virulence test with re-amplified virus reached 80% mortality, while the 2nd vaccination study resulted in 10% mortality in shedder fish. As the same virus stock was used for both the virulence and vaccination experiments, one potential explanation of the lack of challenge could have been reduction in titer due to storage. This was tested with a store batch of the virus, but we did not find any significant reduction when stored at -80 °C. Studies of potential differences in induction of cellular responses between the ISAV 70-72 isolate and a well-established ISAV isolate are ongoing.
Additionally, the results from the ongoing vaccine experiment with the well-established ISAV isolate will be presented.

Industry relevance: The ISAV regulations do not consider virulence apart from HPR0 and HPRΔ. In the experiments described, we run into complication due to unforeseen differences of

virulence between isolates. The industry experiences virulence variability between ISAV isolates, and frustration thereof. Our studies may contribute to explain the difference of virulence, and possibly also describe the efficacy of an mRNA vaccine against ISA.

Post-meeting PDF permission: Yes

Infectious salmon anemia in global salmon farming: Trends, management and vaccination

Presenter: Lars G. Jørgensen

Affiliation: Pharmaq AS, Norway

Summary: Infectious salmon anemia (ISA) continues to pose significant challenges for the global salmon farming industry, impacting fish health, production efficiency, and market stability. This presentation will provide an update on the ISA situation in different salmon-producing regions, including Norway, Chile, Canada, and the Faroe Islands. Emphasis will be placed on recent outbreak trends and differences in ISA management.
Special attention will be given to vaccination as a control strategy, drawing on field experiences and regional case examples. The presentation aims to promote knowledge exchange and discussion on future ISA mitigation.

Industry relevance: Infectious salmon anemia remains a significant challenge for the salmon farming industry. By providing updated information on ISA trends, management practices, and experiences with vaccination across different regions, this presentation delivers insights for participants both from the industry and researchers.

Post-meeting PDF permission: Maybe (Dont know yet)

From Hatchery to Sea: Understanding stocking behaviours of Norwegian salmonid farms using wellboat movements.

Presenter: Trishang Udhwani

Affiliation: Norwegian Veterinary Institute, Norway

Co-authors: Cecilia Mia Wolff, Norwegian Veterinary Institute, Victor Henrique Silva De Oliveira, Norwegian Veterinary Institute, Katharine Rose Dean, Norwegian Veterinary Institute

Summary: The intensification of salmonid production in Norway has led to conditions that favour the spread of infectious diseases. Live fish movements have been identified as an important mechanism of pathogen spread in several salmon-producing countries. For example, studies in Scotland and Chile have shown that transfers of live fish could have facilitated long-distance transmission of infectious salmon anaemia virus. In Norway, previous studies have shown that wellboat movements are associated with pancreas disease (PD) outbreaks, but not fish movements specifically. A lack of detailed data on the purpose and characteristics of wellboat movements has hindered more comprehensive assessments of this transmission pathway.

In Norway, movements of fish to marine sites follow a pyramidal structure, where most transfers originate from a relatively small number of freshwater hatcheries and are distributed to a large number of marine grow-out sites. Movements between marine sites occur less frequently. Although there are regulations on the transport of aquatic animals to reduce disease risks, management decisions can influence outbreak potential. Previous studies have shown that farms stocked from multiple hatcheries or using several marine sites during a cycle have higher odds of PD outbreaks. Additional factors, such as transfer time, distance, the increasing use of larger smolts, and the use of intermediate sites, may also influence disease risk. Despite their potential importance, these stocking behaviours have not been systematically described at a national scale.

The aim of this study was to characterize live fish movements related to stocking salmon and trout farms in Norway using production and wellboat data from 2022 and 2023. Over these two years, 807 production cycles began at 722 marine grow-out sites. Of these, 82% could be linked to at least one source, either a hatchery or another marine site, while an additional 6% had partial movement information, with some stocking months lacking identifiable connections. We could not identify stocking events in 12% of the production cycles. The percentage of missing data varied across production areas, ranging from 9% of cycles missing established sources in PO7 to 33% in PO10. We found that 50 production cycles were stocked from both hatcheries and other marine sites within the same cycle, indicating complex stocking behaviours.

Key challenges in evaluating these movements include potential aggregation errors in wellboat data from BarentsWatch and biomass data from the Directorate of Fisheries, determining realistic cutoffs for travel time between sites while moving fish, and distinguishing time spent at hatcheries or grow-out sites for fish transfer versus other purposes. Intermediate stops recorded in movement data further complicate interpretation. Addressing these data constraints is essential for improving our understanding of how live fish transfers may contribute to disease spread in Norwegian salmon aquaculture.

Industry relevance: By systematically mapping live fish movements between hatcheries and marine grow-out sites through wellboats, this study highlights where biosecurity vulnerabilities

may arise within the current production structure. Understanding patterns such as multisource stocking, the use of intermediate sites, and regional variation in fish stocking behaviours allows producers and regulators to better assess disease transmission risks. These findings can inform more targeted movement regulations, optimize wellboat movements and support farm-level strategies aimed at minimizing unnecessary contacts between sites. Ultimately, improving our understanding of live fish movements not only improves risk assessments but also contributes to more resilient production planning, reduced mortality, and better fish welfare across the value chain.

Post-meeting PDF permission: Yes

The Dilemmas of Digital PCR: Technology Transfer for Fish Health Diagnostics

Presenter: Stephanie Linehan

Affiliation: Marine Institute, Ireland and ATU Galway, Ireland

Co-authors: Dr Anita Talbot - Principal Supervisor (ATU Galway). Dr Samantha White - Co Supervisor (Marine Institute), Dr Fiona Swords - Co Supervisor (Marine Institute)

Summary: Digital PCR offers advantages for multiplex viral detection in aquaculture, but transferring established qPCR assays to a droplet digital PCR (ddPCR) platform presents technical challenges. In this study, assays targeting three myocarditis-associated RNA viruses of Atlantic salmon (SAV, PRV and PMCV) were transferred from qPCR to the Stilla Naica 3 ddPCR system. Early results showed significant limitations related to probe dye availability, quencher compatibility and multiplex constraints, particularly poor fluorescence performance of QSY-quenched probes compared with MGB probes. These issues hindered initial multiplex development, prompting evaluation of alternative probe chemistry such as Universal Nucleic Acid Detection (Rainbow) probes. Overall, findings highlight that assay transfer from qPCR to ddPCR is not straightforward and requires substantial optimisation and redesign of key probe components. Work is ongoing to refine assay performance and enable reliable multiplex ddPCR detection of myocarditis-related salmon viruses.

Industry relevance: This research is relevant to aquaculture industry by improving early, accurate and quantifiable detection of key myocarditis-related viruses in farmed Atlantic salmon, enabling faster intervention potentially reducing stock losses. Developing robust multiplex ddPCR assays enhances routine health monitoring and strengthens disease management.

Post-meeting PDF permission: No