Tuesday September 4th – Langeve / Cartier
Aquatic Epidemiology I
<u>Moderator</u> – **Ian Gardner** (Atlantic Veterinary College / UPEI)

3:15 PM		<u>Laurin</u> - Monitoring Data From Farmed Salmon *Salmo salar* and *Oncorhynchus* spp. In British Columbia, Canada, From 2011–2013
3:30 PM		<u>Marty</u> - Trends in Disease Prevalence Among Regulatory Audit Samples of Farmed Atlantic Salmon in British Columbia, Canada: 1990–2017
3:45 PM		**<u>Burnett</u> - Drivers of Spatio-Temporal Variability in Sea Lice Connectivity Among Salmon Farms in the Broughton Archipelago, British Columbia**
4:00 PM	**Aquatic Epidemiology I**	<u>McEwan</u> - Agent-Based Modelling as a Tool for Exploring Integrated Pest Management in Aquaculture
4:15 PM		**<u>Jia</u> - Literature Review of Historical Information on Pathogen Occurrence Among Wild Salmonids in British Columbia, Canada**
4:30 pm		<u>Ferguson</u> - An Epidemiological Model of Virus Transmission in Salmonid Fishes of the Columbia River Basin
4:45 PM		<u>Thakur</u> - Infectious Agent Detections in Archived Sockeye Salmon (*Oncorhynchus nerka*) Samples From British Columbia (1985–1994)
5:00 PM		<u>Sigurðardóttir</u> - A Survey of Three Viruses in Wild and Cultured Salmon in Iceland

ISAAC
CHARLOTTETOWN
PRINCE EDWARD ISLAND
2018

8th **International Symposium on Aquatic Animal Health**

September 2-6, 2018 - Charlottetown, Prince Edward Island, Canada

AFS

Monitoring Data from Farmed Salmon (*Salmo Salar* and *Oncorhynchus* Spp.) in British Columbia, Canada, from 2011-2013

Emilie L. Laurin[1*], Diana Jaramillo[1], Raphaël Vanderstichel[1], Hugh Ferguson[2], Karia H. Kaukinen[3], Angela. D. Schulze[3], Ian R. Keith[4], Ian A. Gardner[1], and Kristina M. Miller[3,5]

[1]   University of Prince Edward Island, 550 University Avenue, Charlottetown, Prince Edward Island, C1A 4P3, Canada; elaurin@upei.ca, dianajmt@gmail.com, rvanderstich@upei.ca, iagardner@upei.ca
[2]   Marine Medicine Programme, Pathobiology, School of Veterinary Medicine, St George's University, Grenada, West Indies, hf.fishpathology@gmail.com
[3]   Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo, British Columbia, V9K 6N7, Canada; Karia.Kaukinen@dfo-mpo.gc.ca, Angela.Schulze@dfo-mpo.gc.ca, Kristi.Saunders@dfo-mpo.gc.ca
[4]   Aquaculture Management Division, Aquaculture Environmental Operations – Fish Health, Fisheries and Oceans Canada, Courtenay, British Columbia, V9N 2M2, Canada, Ian.Keith@dfo-mpo.gc.ca
[5]   Forest and Conservation Sciences, University of British Columbia, Vancouver, British Columbia, V6T 1Z4, Canada

The purpose of this study was to describe spatial and temporal patterns of endemic and new infectious agents and histopathologically-identified lesions in dead-and-dying farmed non-native Atlantic (AS) and native Pacific (PS) salmon in British Columbia, Canada, between 2011 and 2013. Novel high-throughput molecular testing and blinded histopathological examination of tissues were used to evaluate these patterns in fish-level analyses. Twenty-five of 45 infectious agents were detected, and 87% of 897 total fish tested had mixed detections, with up to nine agents in a single fish, and a higher agent diversity in PS than AS. Most frequently detected agents were the parasite *Desmozoon lepeophtherii* (*D.lep*) in farmed AS (88%), and the bacterium *Candidatus Branchiomonas cysticola* (*Ca.B.cys*) in farmed PS (89%). Overall, 92% of AS and 88% of PS had some histopathological change, mostly of mild to moderate severity, with renal interstitial hyperplasia as the most frequent change (AS: 33%; PS: 48%). Spatial patterns were statistically significant for five agents in PS *versus* AS in southwest Vancouver Island, Sunshine Coast, and Discovery Islands. Statistically significant temporal patterns were detected for three agents each in AS and PS, with only *D.lep* common for both. Importantly, infectious salmon anemia virus, salmonid herpesvirus, salmon alphavirus, and infectious pancreatic necrosis virus were not detected. The majority of agents detected on BC salmon farms were known to be endemic, but new findings include the marine detections of some infectious agents reported to only cause freshwater or hatchery-based diseases (*Flavobacterium psychrophilum* and *Ichthyophthirius multifiliis*). The results of this descriptive study provide the proportion of positive test results in sampled dead-and-dying farmed AS and PS, and temporal-spatial information on both agent and lesion detection, targeting areas of interest and concern to researchers, regulators, and aquaculture industry veterinarians for future population-based analyses.

Conference Session Designation:　　　　　　　(Aquatic Epidemiology)
Presentation Format:　　　　　　　　　　　(Oral)

8ᵗʰ International Symposium on Aquatic Animal Health

September 2-6, 2018 - Charlottetown, Prince Edward Island, Canada

Trends in Disease Prevalence Among Regulatory Audit Samples of Farmed Atlantic Salmon in British Columbia, Canada: 1990 – 2017

Gary D. Marty[1], Ian Keith[2], Julie Bidulka[1], and Heindrich N. Snyman[1]

[1] Animal Health Centre, BC Ministry of Agriculture, 1767 Angus Campbell Rd., Abbotsford, BC, V3G 2M3, Canada Gary.Marty@gov.bc.ca
[2] Aquaculture Management Division, Fisheries and Oceans Canada, #103 – 2435 Mansfield Drive, Courtenay, BC, V9N 2M2, Canada Ian.Keith@dfo-mpo.gc.ca

Since 1990, government regulators have systematically assessed disease among Atlantic salmon (*Salmon salar*) farmed in marine net pens in British Columbia (BC), Canada. The first diagnostic assessment by BC included a total of 215 Atlantic salmon sampled from 1990 – 1992. The second assessment initiated by BC in the early 2000s continues today as the BC Fish Health Auditing and Surveillance Program administered by Fisheries and Oceans Canada (DFO).

Program staff sample moribund and recently dead Atlantic salmon cultured in marine net pens. Audited farms are selected to be representative of the number of farms in each region of the province. Annual sample size from 2006 – 2009 and 2014 – 2017—the years with the most complete data—ranges from 470 – 784 fish. Since 2006, diagnostic analysis to determine cause of death includes gross and microscopic lesions (up to 9 organs for histopathology), aerobic bacterial culture of kidney, and pooled PCR tests for *Piscirickettsia salmonis*, endemic viruses IHNV and VHSV, and exotic viruses IPNV and ISAV. Since 2014, exotic virus testing includes SAV, and fish with idiopathic cardiomyopathy are tested for PMCV. Trends based on sample prevalence of fish with a lesion/pathogen diagnosed as cause of death:

1. *Renibacterium salmoninarum* declined from 45% (1990 – 1992) to 6.8 – 9.4% (2006 – 2009), and further to 1.4 – 3.4% from 2014 to 2017;
2. *Piscirickettsia salmonis* affected 1 – 2% of samples each year since 2006 except for a 2-year outbreak peaking at 13% in 2015 and decreasing to 7.4% in 2016;
3. Idiopathic cardiomyopathy ranged from 1 – 3% through all years studied, 1990 – 2017.

For VHSV, the proportion of PCR+ sample pools declined from 3.1 – 9.7% (2006 – 2009) to 0.6 – 2.5% (2014 – 2017). During the reported years, *Paramoeba perurans* was first diagnosed by histopathology in 2014, and infection prevalence ranged from 0.3 – 2.2% through 2017. Severe cases of idiopathic meningoencephalitis affected 0.3 – 1.1% of sampled fish from 2007 – 2009 and 2014 – 2017. All samples were PCR-negative for IHNV, IPNV, ISAV, SAV, and PMCV.

Each year (2006 – 2009 and 2014 – 2017), 6.1 – 19% of Audit Program Atlantic salmon were diagnosed with an infectious disease that (i) could potentially affect wild Pacific salmon and (ii) was not primarily from an environmental source. The other 81 – 94% of the sampled fish had no evidence of these diseases. Epidemiologic principles inform us that diseases that do not spread widely among concentrated farm fish are less likely to spread among dispersed wild fish.

Conference Session Designation: (Aquatic Epidemiology)
Presentation Format: (Oral)

ISAAH
CHARLOTTETOWN
PRINCE EDWARD ISLAND
2018

8ᵗʰ International Symposium on Aquatic Animal Health
September 2-6, 2018 - Charlottetown, Prince Edward Island, Canada

Drivers of Spatio -Temporal Variability in Sea Lice Connectivity Among Salmon Farms in the Broughton Archipelago, British Columbia

Danielle L. Burnett[1], *, Ramón Filgueira[2], Erin E. Rees3, Raphael Vanderstichel[1], Jon Grant[4], and Crawford W. Revie[1]

[1]   Department of Health Management, Atlantic Veterinary College, University of Prince Edward Island, 550 University Ave, Charlottetown, PE, C1A 4P3, Canada
       dlburnett@upei.ca
[2]   Marine Affairs Program, Dalhousie University, Life Sciences Centre, Room 807, 1355 Oxford Street, PO Box 15000, Halifax NS, B3H 4R2, Canada
[3]   Land and Sea Systems Analysis, 14 rue Long Granby, QC, J2G 6S8, Canada
[4]   Department of Oceanography, Dalhousie University, LSC, Room 3631, 1355 Oxford St, PO Box 15000, Halifax, NS, B3H 4R2, Canada

Connectivity of aquaculture sites from the perspective of disease transmission is determined by a combination of hydrodynamic circulation and the biology of the organisms involved. For example, viral disease connectivity will likely be driven almost entirely by the underlying circulation. However, living infectious agents (such as sea lice copepods) have maturation, mortality, limited energy reserves, and behaviours (such as swimming avoidance or seeking behaviours) that can impact connectivity of farms. Here we analyze drivers of the temporal variability of an infectious agent network of farms that was determined from a coupled biological-physical particle-tracking model. The infectious agent whose biology we modelled was the sea louse. The simulation mimicked conditions from March- July, 2009 (150 days in total), in the Broughton Archipelago, British Columbia, Canada. Temporal analyses indicated large changes in the strength of connectivity of infectious agent networks, with large peaks in connectivity lasting for around 5 days at three specific points in the simulation. The peaks are largely driven by the biology of the organism, rather than the underlying circulation model, highlighting the importance of including a biological model in particle tracking simulations used to determine connectivity. The main drivers of the strength of connectivity include the temperature and salinity the particles were exposed to, which was driven in large part by the freshet run-off from the many rivers surrounding the BA. Additionally, several sub-networks of farm-to-farm connectivity emerged, each with distinctive space-time connectivity characteristics. Our results suggest that typical measures of connectivity, such as seaway distance, may not accurately capture the reality of high temporal variability and non-intuitive spatial relationships when the infectious agent has complex biology, such as is the case for sea lice.

Conference Session Designation: (Aquatic Epidemiology)
Presentation Format: (Oral)
Student Presentation: (Yes)

Agent-Based Modelling as a Tool for Exploring Integrated Pest Management in Aquaculture

Gregor F McEwan*, Crawford W Revie

Department of Health Management, Atlantic Veterinary College, University of Prince Edward Island, Charlottetown, PE, Canada gmcewan@upei.ca crevie@upei.ca

In aquaculture, there is an increasing move towards Integrated Pest Management (IPM) strategies. Previously, there was a heavy reliance on chemical treatments, whereas now physical, biological, and management controls are also being used. There are several motivating factors, such as increasing resistance to the chemical treatments, and public perception of the industry. The problem now is that farmers are faced with many options regarding treatments – chemical, physical, biological, management – and their combinations, with little guidance on how to choose the best strategy in any given situation. Real-world testing is not feasible as each treatment choice typically involves a large commitment of time and money. Testing more than a very few combinations would be a daunting and expensive task.

Our solution is to use computer simulation modelling. Modelling allows relatively cheap and quick exploration of a variety of treatment strategies. It also allows detailed tracking of information that is not easily obtained in the real world, such as genetic resistance. In particular, we use agent-based models (ABM). ABMs model each individual (agent) with simple parameters and behaviour. Complex patterns emerge from populations of agents interacting with each other. The advantages of ABMs in this context are extensibility – individual agents are extensible to capture new behaviour, and new types of agents are easily added – and agent sensing / memory can be used to make individual contextual changes.

In this presentation we describe our use of an ABM to explore IPM in the context of controlling sea lice on Atlantic salmon farms. We have used the ABM to explore the evolution of chemical resistance in the presence of wild salmon populations, using different strategies for using chemical treatments, and the efficacy of cleaner fish in different environments. These projects all relied on the unique strengths of ABMs in terms of extensibility and individual context.

Conference Session Designation: (Aquatic Epidemiology)
Presentation Format: (Oral)

Literature Review of Historical Information on Pathogen Occurrence Among Wild Salmonids in British Columbia, Canada

Beibei Jia *, Marina Delphino, Babafela Awosile, Ian A. Gardner

Department of Health Management, Atlantic Veterinary College, University of Prince Edward Island, Charlottetown C1A4P3, Prince Edward Island, Canada jbeibei@upei.ca

Maintaining healthy populations of wild salmonids in British Columbia is a high priority for numerous stakeholders including Fisheries and Oceans, Canada, the Pacific Salmon Foundation, First Nations, and NGOs. Farming of salmon in the same waters is a controversial topic, and strengthened control of infectious diseases is needed to minimize spread of important infectious agents from farmed to wild salmonids and wild to farmed salmon. The dynamics of wild salmon populations and complex interconnectivity of potential hazards have been regarded as challenging due to knowledge gaps and uncertainty of existing information. However, as stated in a recently published the Scottish historical review, the pathogens were detected in wild marine fish caught remotely from aquaculture sites, and hence limited evidence for clinical disease in wild fish due to the pathogens. During a recent workshop held in June 2018, various stakeholders agreed that wild salmonid dynamics in the region is a complicated issue with concurrent biological, environmental, social, and cultural ramifications. There is a need to reach mutual-understanding on host-pathogen-environmental interactions among the wild fish population and to shape the roles from diverse factors within the ecosystem. In this context, historical information on the spatiotemporal occurrence of diseases in wild finfish is necessary to inform discussions about their risk at a population level. Here we conducted a literature review of published journal and grey literatures for pathogens likely to occur in the wild finfish population in British Columbia. The objective of the literature review is to establish a transparent reporting process for historical information and also bias reduction through interrogating the databases that have reported the health events of wild fish in selected study areas. We started with a primary screening and identified literatures relevant to the infection of the 9 pathogens among the 5 species of Pacific salmon in freshwater and ocean environment in the province. Next, we appraised the quality and validity of the studies or documented information based on research designs, their implementation, statistical methods and their appropriateness of answering research questions. We then compiled the baseline occurrence of the 9 pathogens among salmonids with the application of multivariate information visualization through data mining techniques. In the last step, we synthesized snapshots of information on aspects other than health status alone, including spatial-temporal dynamics of stock assessment of wild fish, human activities impacting on both freshwater and seawater habitats, coastal environmental conditions, and meteorological indices. Thus we summarized what has been already known and what is still unknown about the challenging topic. This literature review will demonstrate a transparent way of contrasting the potential divergence of literature resources and provide new insights for the future research methods to provide an improved understanding the complexity of the marine ecosystem and interactions that occur within.

Conference Session Designation: (Aquatic Epidemiology)
Presentation Format: (Oral)
Student Presentation: (Yes)

8th **International Symposium on Aquatic Animal Health**

September 2-6, 2018 - Charlottetown, Prince Edward Island, Canada

An Epidemiological Model of Virus Transmission in Salmonid Fishes of the Columbia River Basin

Paige F.B. Ferguson[1,2], Rachel Breyta[2,3*], Ilana Brito[4], Gael Kurath[5], Shannon L. LaDeau[2]

[1] Department of Biological Sciences, University of Alabama, Box 870344, Tuscaloosa, AL 35487, United States, pfferguson@ua.edu
[2] Cary Institute of Ecosystem Studies, 2801 Sharon Turnpike, Millbrook, NY 12545, United States, breytar@ caryinstitute.org, ladeaus@caryinstitute.org
[3] Department of Microbiology, Nash Hall 226, Oregon State University, Corvallis, OR 97331, United States
[4] Meinig School of Biomedical Engineering, Cornell University, 289 Kimball Hall, Ithaca, NY 14853, United States, ibrito@cornell.edu
[5] U.S. Geological Survey Western Fisheries Research Center, 6505 NE 65th Street, Seattle, WA 98115, United States, gkurath@usgs.gov

We have developed a dynamic epidemiological model informed by records of viral presence and genotypes to evaluate potential transmission routes maintaining a viral pathogen in economically and culturally important anadromous fish populations. In the Columbia River Basin, infectious hematopoietic necrosis virus (IHNV) causes severe disease, predominantly in juvenile steelhead trout (*Oncorhynchus mykiss*) and less frequently in Chinook salmon (*O. tshawytscha*). Mortality events following IHNV infection can be devastating for individual hatchery programs. Despite extensive surveillance efforts, there are questions about how viral transmission is maintained. Modeling this system offers important insights into disease transmission in natural aquatic systems, as well as about the data requirements for generating accurate estimates. We simulated six scenarios in which testing rates and the relative importance of different transmission routes varied. The simulations demonstrated that the model accurately identified routes of transmission and inferred infection probabilities accurately when there was testing of all cohort-sites. When testing records were incomplete, the model accurately inferred which transmission routes exposed particular cohort-sites but generated biased infection probabilities given exposure. After validating the model and generating guidelines for result interpretation, we applied the model to data from 14 annual cohorts (2000–2013) at 24 focal sites in a sub-region of the Columbia River Basin, the lower Columbia River (LCR). We demonstrate that exposure to IHNV via the return migration of adult fish is an important route for maintaining IHNV in the LCR sub-region, and the probability of infection following this exposure was relatively high at 0.16. Although only 1% of cohort-sites experienced self-exposure by infected juvenile fish, this transmission route had the greatest probability of infection (0.22). Increased use of secure water supplies and continued use of biosecurity protocols may reduce IHNV transmission from adult fish and juvenile fish within the site, respectively, to juvenile salmonids at hatcheries. Models and conclusions from this study are potentially relevant to understanding the relative importance of transmission routes for other important aquatic pathogens in salmonids, including the agents of bacterial kidney disease and coldwater disease, and the approach may be useful for other pathogens and hosts in other regions.

Conference Session Designation: (Aquatic Epidemiology)
Presentation Format: (Oral)

ISAAH
CHARLOTTETOWN
PRINCE EDWARD ISLAND
2018

8th International Symposium on Aquatic Animal Health
September 2-6, 2018 - Charlottetown, Prince Edward Island, Canada

Infectious agent detections in archived Sockeye salmon (*Oncorhynchus nerka*) samples from British Columbia (1985-1994)

Krishna K. Thakur[1*], Raphaël Vanderstichel[1], Karia H. Kaukinen[2], Omid Nekouei[1], Emilie Laurin[1], Kristina M. Miller[2]

[1] Department of Health Management, University of Prince Edward Island, 550 University Avenue, Charlottetown, PE, Canada   kthakur@upei.ca
[2] Pacific Biological Station, Fisheries and Oceans Canada, 3190 Hammond Bay Rd, Nanaimo, BC, Canada

Commercial Atlantic salmon aquaculture expanded into British Columbia (BC) Canada between 1989-1993, concurrent with initial declines in productivity and abundance of Sockeye salmon stocks in southern BC. In response to concerns that novel infectious agents were introduced through movement of eggs during the development of Atlantic salmon aquaculture, we undertook a study to estimate the prevalence of infectious agents in archived historical return-migrating Sockeye salmon, spanning the period before and during aquaculture expansion in BC (mid-1980s to 1990s). Of 45 infectious agents assessed with molecular assays across 652 samples, 23 (7 bacterial, 2 viral and 12 parasitic) were detected in liver tissue across six regions in BC. Prevalence ranged from 0.5 to 83.3% and varied significantly by region and year. Agent diversity ranged from 0 to 12 per fish, median 4, with lowest diversity observed in fish from the Transboundary and Central Coast. Agents known to be endemic and associated with mortality in Sockeye salmon in BC, such as *Flavobacterium psychrophilum*, Infectious hematopoetic necrosis virus, *Ceratonova shasta,* and *P. minibicornis*, were commonly observed. Others, such as *Kudoa thyrsites* and *Piscirikettsia salmonis,* which have impacted BC salmon aquaculture, were also detected in the mid 1980s, suggesting they were likely present historically. Surprisingly, infectious agents described only recently in BC salmon, *Ca. Branchiomonas cysticola, Parvicapsula pseudobranchicola,* and *Paranucleospora theridion,* and common in salmon aquaculture in BC and Norway, were also detected, indicating their potential presence prior to the expansion of the aquaculture industry. Only two agents currently common in BC salmon aquaculture, gill chlamydia and Piscine orthoreovirus, detected in recently sampled liver tissue, were not detected in historic Sockeye. In general, our data suggest that agent distributions have not substantively changed since the expansion of the salmon aquaculture industry.

Conference Session Designation: (Aquatic Epidemiology)
Presentation Format: (Oral)

A Survey Of Three Viruses In Wild And Cultured Salmon In Iceland

Harpa Mjöll Gunnarsdóttir, Heiða Sigurðardóttir, Birkir Þór Bragason and Sigríður Guðmundsdótti

Institute for Experimental Pathology, University of Iceland, Keldur, Iceland   heidasig@hi.is

With increasing culture in net pens around Iceland, the need for information on the status regarding pathogens that are common in aquaculture around the North-Atlantic Ocean is obvious. The aim of the survey was to screen groups of wild and cultured Atlantic salmon for three viruses. These are infectious salmon anemia virus (ISAV), piscine myocarditis virus (PMCV) and piscine reovirus (PRV).

The survey groups included juveniles and adult fish and were divided into three categories: salmon from wild origin, offspring of an old stock of sea-ranching brood fish and cultured salmon. Tissue samples from individual fish were placed in RLT-buffer. RNA was isolated and used for RT-qPCR virus assays. PRV positive samples were sequenced.

All samples tested were negative for PMCV and ISAV. PRV was detected in all groups except one. In the wild fish category, PRV frequency ranged between 0-100%, while in the sea-ranching and cultured category it was 95-100%. The distribution of cycle threshold values varied in the groups, representing variable levels of virus in the samples. The lowest levels of virus were observed in the wild fish.

The results show that PRV is widespread in Atlantic salmon in Iceland. Similar observations have been reported in surveys elsewhere. Sequences obtained were identical within each group of salmon but there were differences between the salmon groups. The sequences showed similarity to PRV isolates from Norway and Canada and were classified as genotype 1a.

Conference Session Designation: (Aquatic epidemiology Session)
Presentation Format: (Oral)